
Supplementary information

Connecting chemical and protein sequence space to predict biocatalytic reactions

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Connecting chemical and protein sequence space in a predictive model for biocatalysis

Alexandra E. Paton,¹ Daniil A. Boiko,² Jonathan C. Perkins,^{1,3} Nicholas I. Cemalovic,^{1,3} Thiago Reschützegger,⁴ Gabe Gomes,^{2,5,6,7*} Alison R. H. Narayan^{1,3*}

¹Life Sciences Institute, University of Michigan, Ann Arbor, Michigan 48109, USA; ²Department of Chemical Engineering, Carnegie Mellon University, Pittsburgh, Pennsylvania 15213, USA; ³Department of Chemistry, University of Michigan, Ann Arbor, Michigan 48109, USA; ⁴Department of Chemical Engineering, Federal University of Santa Maria, Santa Maria, RS, Brazil; ⁵Department of Chemistry, ⁶Machine Learning Department, ⁷Wilton E. Scott Institute for Energy Innovation, Carnegie Mellon University, Pittsburgh, Pennsylvania 15213, USA.

Supplemental Information

* corresponding authors: gabegomes@cmu.edu, arhardin@umich.edu

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1. Description of additional documents

CATNIP – user interface is available at <http://catnip.cheme.cmu.edu>. tutorial is available in Supplemental Tutorial S1.

Code – All code is available at <https://github.com/gomesgroup/catnip>

Baseline Linear and Gradient Boosted Model Data – The model and metrics are available at <https://huggingface.co/gomesgroup/catnip>

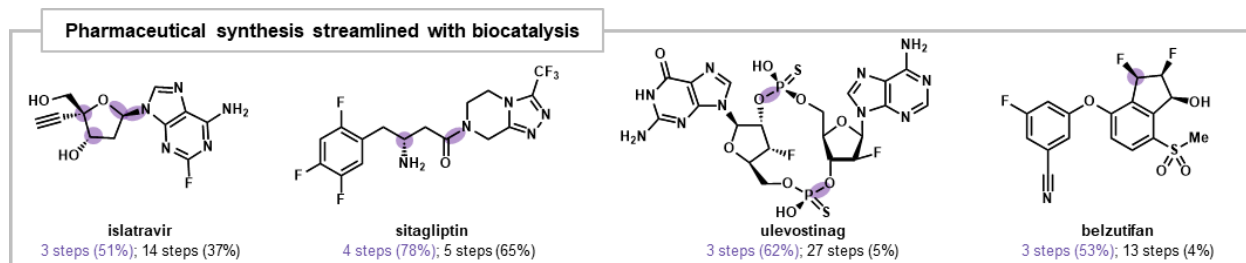
Enzyme Table – all enzymes included in the aKGLib1 library including amino acid and DNA sequences (csv, available on at catnip.cheme.cmu.edu).

Substrate Table – all substrates included in this study with MORFEUS features and PCA coordinates (csv, available on at catnip.cheme.cmu.edu).

Reaction Table – summary of all reactions used in the model building (csv, available on at catnip.cheme.cmu.edu).

Alignment Score Table – all connected nodes in the sequence similarity network with extracted alignment scores normalized with by calculations in Supplemental Section 15 (csv, available on at catnip.cheme.cmu.edu).

2. Supplemental schemes



Supplemental Scheme S1. Pharmaceuticals whose syntheses have been drastically improved with the use of biocatalysts. Bonds accessed through biocatalytic means are highlighted in purple. Step count and overall yield of synthesis are shown in purple (biocatalytic route) and black (highest yield and shortest step count chemical synthesis prior to biocatalytic route report). For example, Merck process chemists have developed biocatalytic-enabled routes to the blockbuster drug sitagliptin¹ as well as new-to-market and investigational drugs including islatravir², ulevostinag^{3,4} and belzutifan^{5,6}. Novel enzyme-mediated routes towards these products have decreased step counts by 33% and more than doubled overall yield, on average, compared to the highest performing chemical syntheses.⁷⁻¹⁰

3. General information

All reagents were used as received unless otherwise noted. All compounds purified by column chromatography were sufficiently pure for use in further experiments unless otherwise indicated. OpenTrons-2 was used to assist in high-throughput protein production and reaction profiling. ^1H and ^{13}C NMR spectra were obtained in CDCl_3 at rt (25 °C), unless otherwise noted, on Varian 600 MHz spectrometers. Chemical shifts of ^1H and ^{13}C NMR spectra were recorded in parts per million (ppm) on the δ scale. High resolution electrospray mass spectra were obtained on an Agilent 1290 Series Infinity II HPLC with a Dual ESI probe and a single quadrupole mass spectrometer.

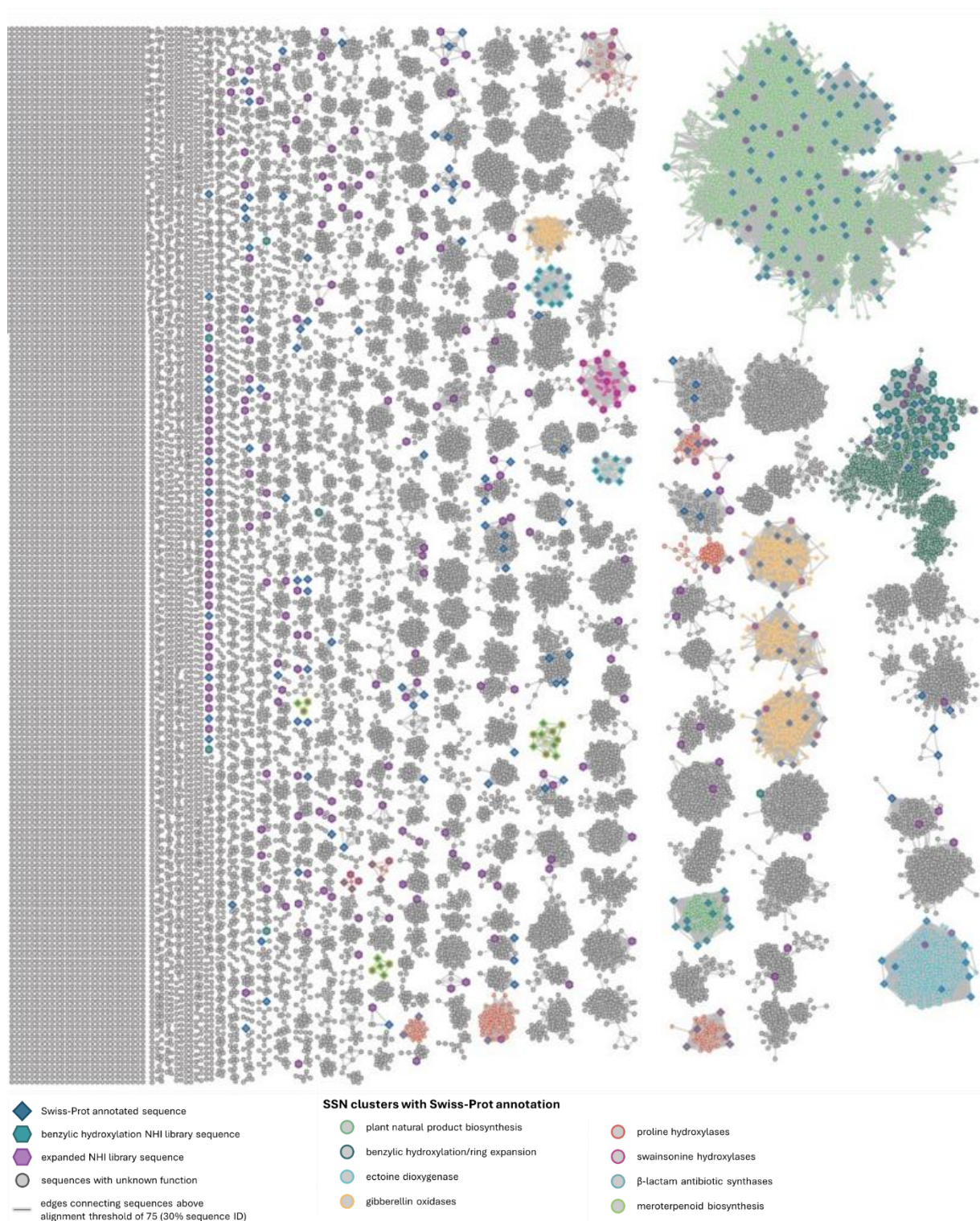
4. Sequence similarity network generation and enzyme selection

The sequence similarity network of proteins was generated through the Enzyme Function Initiative – Enzyme Similarity Tool (EFI-EST)¹¹ (<https://efi.igb.illinois.edu/efi-est/>) using InterPro families identified as being α -KG-dependent (IPR008775, IPR005123, IPR027443, IPR026992, IPR044861). This generated an enzyme dataset consisting of 265,632 sequences. To tackle this massive amount of sequence data, limitations were placed on the sequences during selection EFI-EST to generate a more manageable protein sequence space. First, the UniRef90 filter is applied to the bioinformatics, removing redundant orthologues in the library, by treating sequences that share >90% sequence identity as a single sequence in the SSN. Then, EFI-EST funnels the large sequence set to a more manageable dataset by applying an *e*-value = 5, effectively choosing only 1 of every 5 sequences. Because the selection is completely random it does not affect the distribution of sequences within the overall SSN, but the EFI-EST database always includes any sequences with SwissProt annotations as these are considered more reliable and typically comprise <1% of the total sequences. After these limitations, the generated SSN was comprised of a total of 27,865 unique sequences with a convergence ratio of 0.072. The convergence ratio is a representation of sequence similarity, whereas a convergence ratio closer to 1 implies greater similarity.

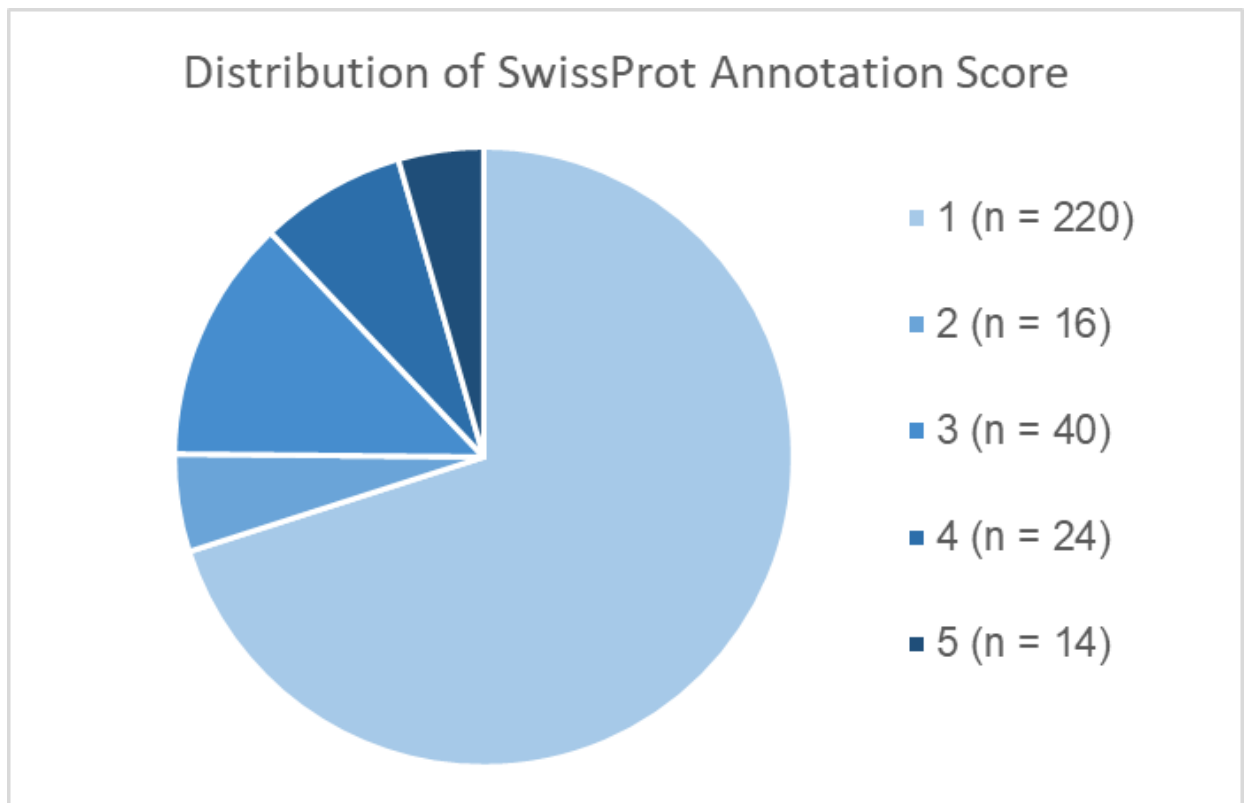
With these enzymes in hands, we set the alignment score threshold to 75 (minimum sequence identity ~30%) resulting in a significant number of clusters. Of the 27,865 sequences in the SSN, only 470 had full SwissProt annotations which we highlighted and used as a guide for annotating the possible substrates and functions of the various clusters (Supplemental Fig. S1). We started by removing any clusters with sequences known to contain NHI enzymes from primary metabolism such as the DNA dealkylase AlkB or those that hydroxylate lysine and proline residues of procollagen during collagen biosynthesis leaving 27,005 sequences in the SSN. The largest cluster was comprised of NHI dioxygenases from plant biosynthetic pathways including those catalyzing flavonoid synthesis and hydroxylation, coumarin synthesis, and codeine demethylation. The second largest subnetwork included enzymes already available in-house such as CitB, ClaD, TropC, and XenC. Many smaller clusters with characterized enzymes were also annotated including several proline hydroxylase clusters, gibberellin oxidase clusters, β -

lactam antibiotic synthase (IPNS or DAOCS) clusters, a fungal meroterpenoid biosynthesis cluster, and a swainsonine hydroxylase cluster.

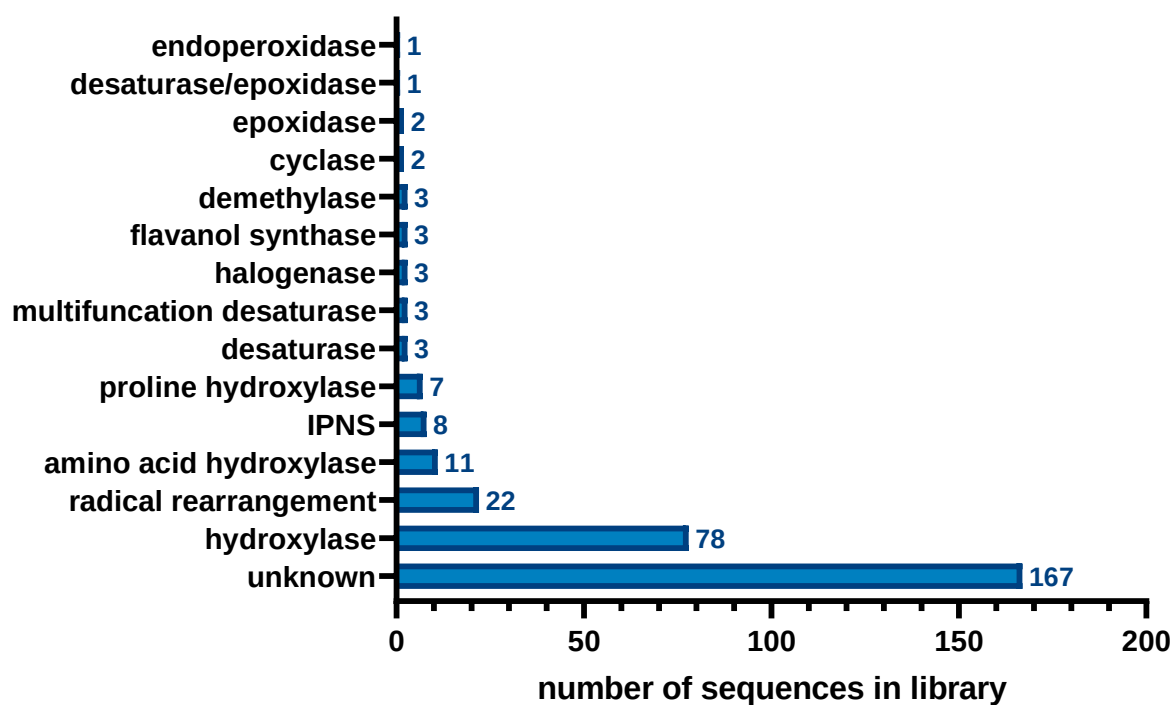
From the family-wide SSN, we started by selecting 94 sequences from the enzymes with known function seeking a broad range of substrates and catalyzed chemical transformations such as oxidation, C–C bond formation, desaturation, and halogenation reactions. The remaining 214 sequences were selected by sampling from clusters without annotated function (two to three sequences per cluster chosen) as well as a number of singleton sequences (~10% of total sequences chosen). We then had the sequences synthesized and cloned into a pET-28b- (+) expression plasmid through a collaboration with the Joint Genome Institute (JGI). We received plasmids containing the DNA and glycerol stocks of *E. coli* cells transformed with plasmids for heterologous expression. 6 enzymes identified through an ancestral reconstruction campaign were combined with this library to generate a 314 enzyme library, referred to as aKGLib1.



Supplemental Figure S1. SSN of ~27,000 α -KG-dependent NHI dioxygenase sequences generated using the EFI-EST protein family option and the following InterPro families as inputs: IPR008775, IPR005123, IPR027443, IPR026992, IPR044861.



Supplemental Figure S2. Distribution of SwissProt Annotation Score with number of samples.



Supplemental Figure S3. Graph of characterized or annotated function via UniProt database for sequences within aKGLib1.

All enzymes were subjected to enzyme classification prediction using Yu et al.'s contrastive learning model.¹² One enzyme was invalid based on the presence of an 'X' in the sequence.

Supplemental Table S1. The output of all of the CLEAN predictions for each enzyme sequence within AKGLib1.

Identifier	Predicted EC Number	Confidence Level
NHI_1 (CitB)	EC:1.21.3.1	Low
NHI_2 (ClaD)	EC:1.21.3.1	Low
NHI_3 (TropC)	EC:1.14.20.1	Low
NHI_4 (VioC)	EC:1.14.11.41	High
NHI_5 (SxtS)	EC:1.14.11.57	Low
NHI_6	EC:1.21.3.1	Low
NHI_7	EC:1.21.3.1	Low
NHI_8	EC:1.21.3.1	Low
NHI_9	EC:5.1.3.42	Low
NHI_10	EC:1.13.12.19	Low
NHI_11	EC:5.1.3.42	Low
NHI_12	EC:1.21.3.1	Low
NHI_13	EC:1.21.3.1	Low
NHI_14	EC:1.14.20.1	Low
NHI_15	EC:1.21.3.1	Low
NHI_16	EC:1.21.3.1	Low
NHI_17	EC:1.21.3.1	Low
NHI_18	EC:1.21.3.1	Low
NHI_19	EC:1.13.12.19	Low
NHI_20	EC:5.1.3.42	Low
NHI_21	EC:1.13.12.19	Low
NHI_22	EC:1.21.3.1	Low
NHI_23	EC:1.13.12.19	Low
NHI_24	EC:2.8.2.36	Low
NHI_25	EC:2.8.2.36	Low
NHI_26	EC:1.21.3.1	Low
NHI_27	EC:1.21.3.1	Low
NHI_28	EC:5.1.3.42	Low
NHI_29	EC:1.21.3.1	Low
NHI_30	EC:5.1.3.42	Low
NHI_31	EC:1.21.3.1	Low

NHI_32	EC:1.14.20.1	Low
NHI_33	EC:1.21.3.1	Low
NHI_34	EC:1.13.12.19	Low
NHI_35	EC:1.14.20.1	Low
NHI_36	EC:1.14.11.9	Low
NHI_37	EC:5.1.3.42	Low
NHI_38	EC:1.21.3.1	Low
NHI_39	EC:1.21.3.1	Low
NHI_40	EC:1.21.3.1	Low
NHI_41	EC:1.13.12.19	Low
NHI_42	EC:1.14.11.9	Low
NHI_43	EC:1.14.11.9	Low
NHI_44	EC:1.21.3.1	Low
NHI_45	EC:1.21.3.1	Medium
NHI_46	EC:3.4.13.9	Low
NHI_47	EC:1.21.3.1	Low
NHI_48	EC:5.3.1.9	Low
NHI_49 (AndA)	EC:1.14.11.18	Low
NHI_50 (AndF)	EC:1.14.11.38	Low
NHI_51 (CnsJ)	EC:1.14.11.18	Low
NHI_52 (SptA)	EC:1.14.11.38	Low
NHI_53 (SptF)	EC:1.14.11.38	Low
NHI_54 (Phex30848 2-ODD)	EC:1.14.20.8	High
NHI_55 (PpzD)	EC:1.13.12.19	Low
NHI_56 (PpzC)	EC:1.21.3.1	Medium
NHI_57 (PrhA)	EC:1.14.11.38	Low
NHI_58 (AneA)	EC:1.14.11.18	Low
NHI_59 (HimG)	EC:1.14.11.18	Low
NHI_60 (CdmA)	EC:1.14.11.38	Low
NHI_61 (CdmD)	EC:1.14.11.38	Medium
NHI_62 (BuaE)	EC:1.14.20.1	Low
NHI_63 (EasH)	EC:1.14.11.38	Low
NHI_64 (FLS)	EC:1.14.20.6	High
NHI_65 (F3H)	EC:1.14.11.9	High
NHI_66 (NCS1)	EC:4.2.1.78	High
NHI_67 (LDO1)	EC:1.14.20.4	High
NHI_68 (LDO2)	EC:1.14.20.4	High
NHI_69 (HxnY)	EC:1.21.3.1	Low
NHI_70 (T6ODM)	EC:1.14.11.31	High
NHI_71 (CODM)	EC:1.14.11.32	High
NHI_72 (PntH)	EC:1.14.11.35	High
NHI_73 (prolyl-4-hydroxylase 13)	EC:1.14.11.2	High
NHI_74 (FLS4)	EC:1.14.20.6	High

NHI_75 (FLS6)	EC:1.14.20.6	High
NHI_76 (F6'H1)	EC:1.14.11.61	High
NHI_77 (F6'H2)	EC:1.14.11.62	High
NHI_78 (HtyE)	EC:2.8.2.36	Low
NHI_79 (AniF)	EC:1.14.20.1	Low
NHI_80 (GA20ox1-A-D)	EC:1.14.11.13	High
NHI_81 (D4H)	EC:1.14.11.20	High
NHI_82 (PcbC P.chrys.)	EC:1.21.3.1	High
NHI_83 (PcbC A.lactam.)	EC:1.21.3.1	High
NHI_84 (PcbC L.lactam.)	EC:1.21.3.1	High
NHI_85 (IpnA)	EC:1.21.3.1	High
NHI_86 (CefEF A.chrys.)	EC:1.14.20.1	High
NHI_87 (CefE S.clav.)	EC:1.14.20.1	High
NHI_88 (CefE A.lactam.)	EC:1.14.20.1	High
NHI_89 (H6H)	EC:1.14.11.11	High
NHI_90 (CefF S.clav.)	EC:1.14.11.26	High
NHI_91 (Trt7)	EC:1.14.11.38	Low
NHI_92 (VldW)	EC:1.14.11.52	High
NHI_93 (EctD)	EC:1.14.11.55	High
NHI_94 (EctD homolog)	EC:1.14.11.55	High
NHI_95 (FtmOx1)	EC:1.14.11.38	High
NHI_96 (AusE)	EC:1.14.11.38	Low
NHI_97 (AsqJ)	EC:3.6.1.73	Low
NHI_98 (LoI O 1/2)	EC:1.21.3.1	Low
NHI_99 (LoI E 1/2)	EC:1.14.11.75	Low
NHI_100 (KanJ)	EC:1.14.11.37	High
NHI_101 (Downy Mildew Resistance)	EC:1.14.11.62	Low
NHI_102 (scopoletin-8-hydroxylase)	EC:1.14.11.60	High
NHI_103 (GloF - GLOXY2)	EC:1.14.20.1	Low
NHI_104 (GloC - GLOXY4)	EC:1.13.12.19	Low
NHI_105 (GloM - GLOXY1)	EC:1.14.20.4	Low
NHI_106 (CloE - GLOXY 3)	EC:1.13.12.19	Low
NHI_107 (Diox4)	EC:1.14.11.62	High
NHI_108 (Fum3p)	EC:1.14.11.38	Low
NHI_109 (PODA)	EC:1.14.11.31	High
NHI_110 (BX6)	EC:1.14.11.59	High
NHI_111 (BX13)	EC:1.14.11.59	High
NHI_112 (HPPD)	EC:1.13.11.27	High
NHI_113 (KthP)	EC:1.14.20.15	Medium
NHI_114 (WelO5)	EC:1.14.11.74	Medium
NHI_115 (AmbO5)	EC:1.14.11.74	Low

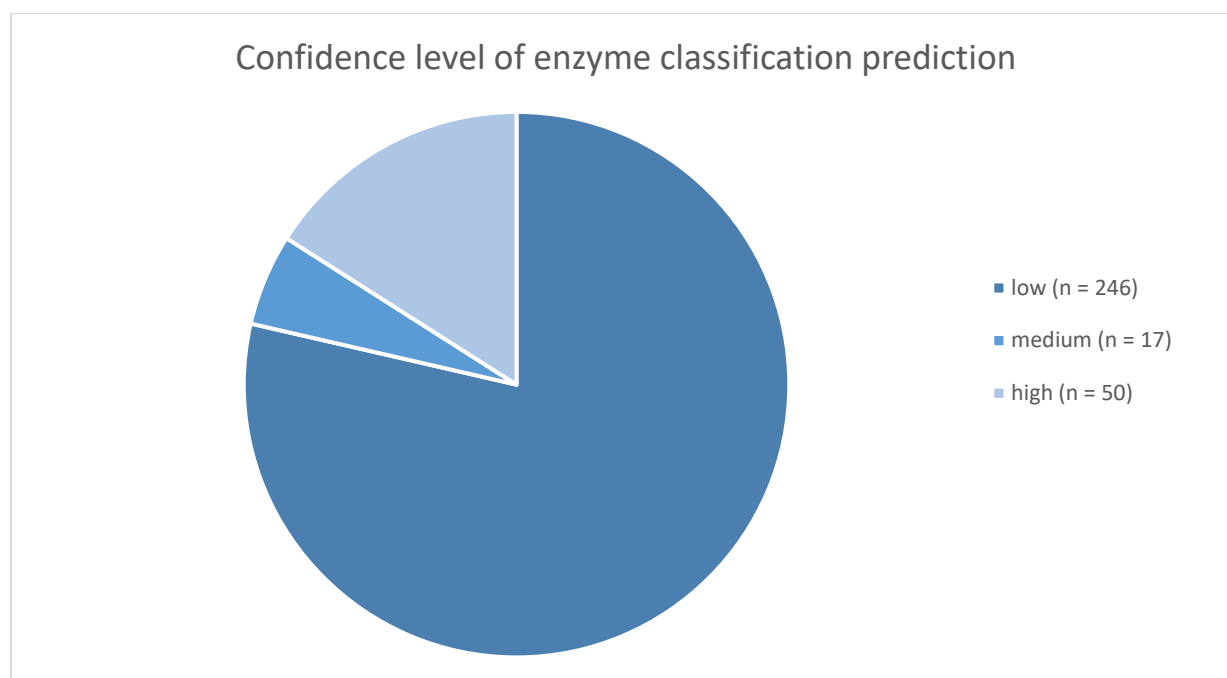
NHI_116 (DAO)	EC:1.14.11.13	High
NHI_117 (M2H)	EC:1.14.11.9	Medium
NHI_118 (EcdG)	EC:1.14.11.76	Low
NHI_119 (AniG)	EC:1.14.11.76	Low
NHI_120 (PhqC)	EC:1.14.20.1	Low
NHI_121 (ImqE)	EC:1.13.12.19	Low
NHI_122 (UcsF)	EC:5.1.3.42	Low
NHI_123	EC:1.14.17.4	Low
NHI_124 (ANS)	EC:1.14.11.62	Medium
NHI_125 (VrtI)	EC:1.14.20.4	Low
NHI_126 (GA2ox3)	EC:1.14.11.13	High
NHI_127 (GA20ox5)	EC:1.14.11.15	Medium
NHI_128 (GA2ox1)	EC:1.14.11.13	High
NHI_129 (GA2ox1-2)	EC:1.14.11.13	High
NHI_130 (GA3ox2)	EC:1.14.11.15	High
NHI_131 (GA3ox1)	EC:1.14.11.15	High
NHI_132 (OsGA3ox1)	EC:1.14.11.15	High
NHI_133 (Kendrick)	EC:1.14.11.2	Low
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NHI_135 (Jonny)	EC:1.14.11.29	Low
NHI_136 (Jose)	EC:1.14.11.2	Medium
NHI_137 (Lauren)	EC:1.14.11.29	Low
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NHI_139 (Anthony)	EC:3.8.1.5	Low
NHI_140 (Sarah A)	EC:1.14.11.2	Low
NHI_141 (Dan)	EC:1.14.11.56	Low
NHI_142 (Chad)	EC:1.14.11.38	Low
NHI_143 (Jessica)	EC:1.14.11.13	Low
NHI_144 (Chris)	EC:1.14.20.15	Low
NHI_145 (Di)	EC:1.14.11.2	Low
NHI_146 (Max)	EC:1.14.11.55	Medium
NHI_147 (Ye)	EC:1.13.12.19	Low
NHI_148 (Sarah C)	EC:1.14.11.33	Medium
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NHI_158	EC:1.14.11.2	Low

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NHI_160	EC:1.14.11.38	Low
NHI_161	EC:1.14.11.45	Low
NHI_162	EC:1.14.11.35	Low
NHI_163	EC:2.4.2.31	Low
NHI_164	EC:2.7.1.90	Low
NHI_165	EC:1.14.11.45	Low
NHI_166	EC:1.1.1.256	Low
NHI_167	EC:1.14.11.2	Low
NHI_168	EC:1.14.11.29	Low
NHI_169	EC:1.14.11.2	Low
NHI_170	EC:1.14.11.56	Low
NHI_171	EC:1.14.11.74	Low
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NHI_177	EC:1.14.11.74	High
NHI_178	EC:4.2.2.7	Low
NHI_179	EC:1.1.1.261	Low
NHI_180	EC:1.14.11.41	Low
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NHI_187	EC:1.3.1.120	Low
NHI_188	EC:1.13.12.19	Low
NHI_189	EC:1.14.11.56	Low
NHI_190	EC:1.14.11.28	Medium
NHI_191	EC:1.14.11.74	Low
NHI_192	EC:1.14.11.2	Low
NHI_193	EC:1.14.11.57	Low
NHI_194	EC:1.14.11.55	Low
NHI_195	EC:1.13.12.19	Low
NHI_196	EC:1.14.11.56	Low
NHI_197	EC:1.14.11.35	High
NHI_198	EC:1.14.11.56	Low
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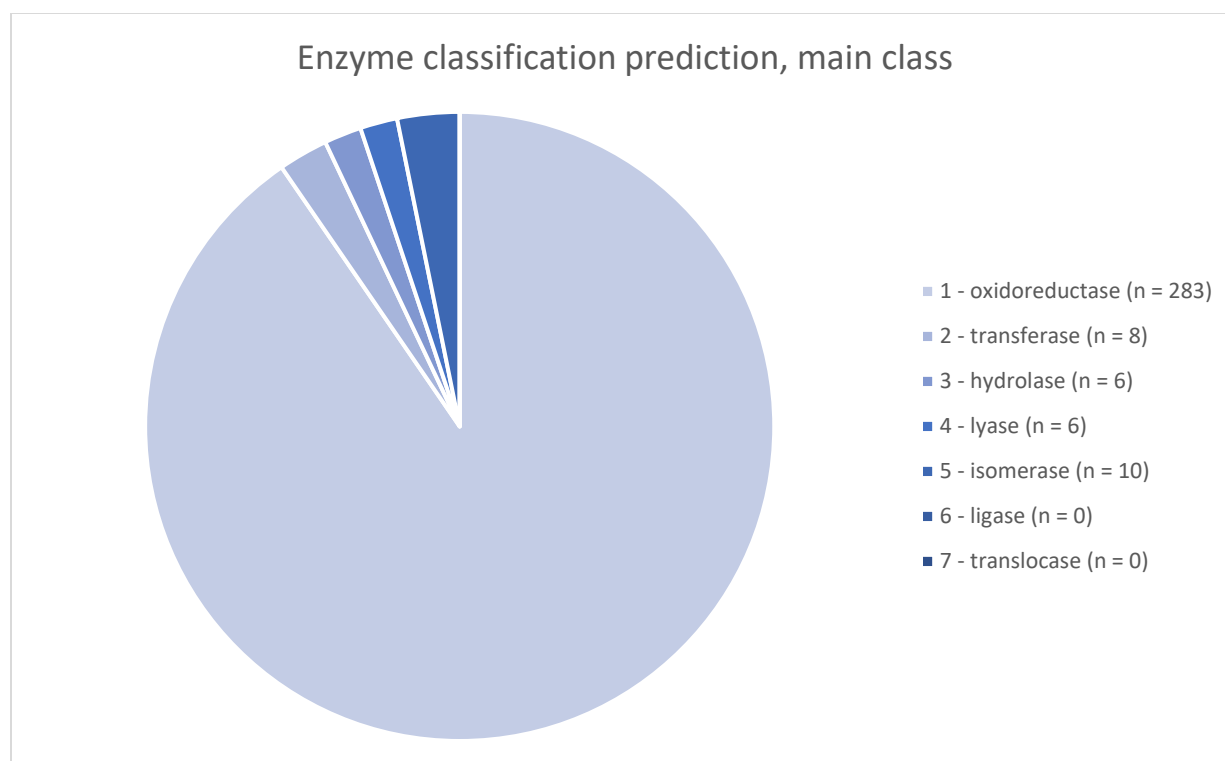
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NHI_206	EC:1.14.11.74	Low
NHI_207	EC:1.14.11.37	Low
NHI_208	EC:1.14.11.18	Low
NHI_209	EC:1.14.14.3	Low
NHI_210	EC:3.4.22.58	Low
NHI_211	EC:1.14.11.51	Low
NHI_212	EC:1.14.11.56	Low
NHI_213	EC:1.14.11.13	Low
NHI_214	EC:1.14.11.74	Low
NHI_215	EC:1.14.11.6	Low
NHI_216	EC:1.14.11.2	Low
NHI_217	EC:1.14.11.2	Low
NHI_218	EC:1.14.11.37	Low
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NHI_220	EC:1.14.11.13	Low
NHI_221	EC:1.14.11.35	Low
NHI_222	EC:1.14.11.2	Low
NHI_223	EC:2.1.1.157	Low
NHI_224	EC:1.14.11.37	Low
NHI_225	EC:1.14.11.56	Low
NHI_226	EC:4.2.1.148	Low
NHI_227	EC:1.14.11.75	Low
NHI_228	EC:1.3.1.49	Low
NHI_229	EC:1.14.11.55	Low
NHI_230	EC:1.1.1.256	Low
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NHI_233	invalid	
NHI_234	EC:1.14.11.2	Low
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NHI_236	EC:1.3.1.32	Low
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NHI_238	EC:1.14.20.1	Low
NHI_239	EC:2.7.1.67	Low
NHI_240	EC:1.14.11.18	Low
NHI_241	EC:1.14.11.45	Low
NHI_242	EC:1.14.11.2	Low
NHI_243	EC:1.14.11.29	Low
NHI_244	EC:1.14.11.2	Low

NHI_245	EC:1.14.11.13	Low
NHI_246	EC:1.14.20.15	Low
NHI_247	EC:1.14.11.2	Medium
NHI_248	EC:1.14.11.46	Medium
NHI_249	EC:1.14.11.35	Low
NHI_250	EC:1.14.11.29	Low
NHI_251	EC:1.13.12.19	Low
NHI_252	EC:3.5.1.13	Low
NHI_253	EC:1.1.1.340	Low
NHI_254	EC:1.14.11.6	Low
NHI_255	EC:1.14.11.38	Low
NHI_256	EC:1.14.11.56	Low
NHI_257	EC:1.14.11.37	Low
NHI_258	EC:1.14.11.18	Low
NHI_259	EC:1.14.17.4	Low
NHI_260	EC:5.3.99.3	Low
NHI_261	EC:1.13.11.19	Low
NHI_262	EC:1.14.11.37	Low
NHI_263	EC:1.14.11.57	Low
NHI_264	EC:1.14.11.13	Low
NHI_265	EC:1.14.11.4	Low
NHI_266	EC:1.14.11.7	Low
NHI_267	EC:1.14.11.35	Medium
NHI_268	EC:1.14.11.37	Low
NHI_269	EC:1.14.11.2	Low
NHI_270	EC:1.14.20.1	Low
NHI_271	EC:1.14.11.29	Low
NHI_272	EC:1.14.11.13	Low
NHI_273	EC:1.14.11.2	Low
NHI_274	EC:1.14.11.37	Low
NHI_275	EC:3.4.22.58	Low
NHI_276	EC:1.14.11.29	Low
NHI_277	EC:1.14.11.56	Low
NHI_278	EC:1.14.11.41	Low
NHI_279	EC:1.13.12.19	Low
NHI_280	EC:1.14.11.56	Low
NHI_281	EC:1.14.11.18	Low
NHI_282	EC:1.14.11.46	High
NHI_283	EC:1.14.11.37	Low
NHI_284	EC:1.14.11.37	Low
NHI_285	EC:1.14.11.18	Low
NHI_286	EC:1.14.11.18	Low
NHI_287	EC:1.14.11.75	Low

NHI_288	EC:1.14.11.56	High
NHI_289	EC:1.14.11.56	High
NHI_290	EC:4.1.1.46	Low
NHI_291	EC:1.14.11.75	Low
NHI_292	EC:1.14.11.55	Low
NHI_293	EC:1.14.11.13	Medium
NHI_294	EC:1.21.3.1	Low
NHI_295	EC:1.14.11.20	High
NHI_296	EC:1.21.3.1	Low
NHI_297	EC:1.15.1.1	Low
NHI_298 (XenC)	EC:1.14.11.9	Low
NHI_299 (SwnH2 X.hyp)	EC:1.14.11.18	Low
NHI_300 (SwnH2 T.ben)	EC:1.14.11.38	Low
NHI_301 (SwnH2 A.oxy)	EC:1.14.11.18	Low
NHI_302 (SwnH2 M.rob)	EC:1.14.11.18	Low
NHI_303 (SwnH1 E.spin)	EC:1.14.11.38	Low
NHI_304 (SwnH2 R.nec)	EC:1.14.11.38	Low
NHI_305 (SwnH1 X.hyp)	EC:1.14.11.38	Low
NHI_306 (SwnH1 A.oxy)	EC:1.14.11.38	Low
NHI_307 (SwnH1 M.rob)	EC:1.14.11.38	Low
NHI_308 (SwnH1 T.ben)	EC:1.14.11.38	Low
NHI_309	EC:2.8.2.36	Low
NHI_310	EC:1.21.3.1	Low
NHI_311	EC:1.21.3.1	Low
NHI_312	EC:1.21.3.1	Low
NHI_313	EC:1.21.3.1	Low
NHI_314	EC:1.21.3.1	Low



Supplemental Figure S4. The confidence level of enzyme classification predictions generated using a contrastive learning model.¹² One sequence (NHI_233) was invalid for interpretation due to the presence of an 'X' residue in the UniProt sequence.



Supplemental Figure S5. The distribution of main classes predicted using the contrastive learning enzyme classification prediction tool.¹²

5. Plasmids

The genes encoding each NHI enzyme were codon-optimized for overexpression in *E. coli* and synthesized by Twist Biosciences. The synthesized sequences were each cloned by Twist biosciences into a pET-28(a)+ or pET-29(b)+ vector containing the T7 expression system, kanamycin resistance, and 6xHis-tag. No further modifications to these plasmid constructs were necessary.

6. Enzyme sequences and DNA codons

Codon-optimized NHI 1 (CitB) sequence:

```
ATGCCTATTAGCACTAAGTCGAGTTTCTACCTTCCCGCCGTTGATATCAGTCCATATT
TACAAGACCCCAACTCTGACGCAGCAAGAAAGGTTATAGACGACGTGCGGGCCGC
CTGCACTAGCACGGGTTTCTTCCAATTACTTGGACATGGGATTTTCGCCTGCACTTCA
ACAGTCGGTATTCGCGGCAGCTGCCAAGTTCTTTGCCTTGCCGTCAGATGTTAAGT
CACGTTGCCGCAACGTAGGTTTCCGCGGTTACGACCCAATGGCAAGCCAGTCTTAC
GAGTTAGGAGTGCTGCCCCGATCTGAAAGAGGGGTTTCATCGCCGGCAAAGACATCC
CTCTTGACGATCCGCGGGTTCGCATCTCAGCGGTTCTTCATGGGTCAGAACGCTTG
GCCGCCTTCCGAGCTGCTCCCCGAGGCGAACTTTCGCCGACCTATTGAGGAGTAT
TACCAGGCCATGCTCAAACGTGTTGGGTAGTCCTGGACTTAGTAGCAGCAACTTTA
CCTTACGGTCCGCATGTTTTCGACGAGTTCAAAGAGAACGACCCTGCTTGCCCCTT
ACGGCTTCTGCACTACCCACCTGCTCCAGCGCCTGATGTGGCTAAGGGGCGTCAA
CTCGGGTCTCAGCCCATACAGACTTTGGCGCTATTACACTTTTGCTTCAGGACGA
CCATAGCGGACTTGAGGTGCAAGACTGCGAAACCGGTGAATGGATCGGCGTGCCA
CCTAACAAGGATGCGTACGTGGTGAATTTAGGCGACATGATGTCGCGTATCACCAG
AGGCCATTATAAGTCTTCCATTCATCGTGTGATCAACCAAACTTGACAGACCGTTAT
AGCGTCGTGTTCTTCTTCGATGGGAATCTTGACTACCGGCTTCGACCCTTGATAG
AGTTGGTCAAACTGGGACGAAGAGGACACACTTACTGTGGAAGAACACATGCTC
GAACGTACAACCACGACATATAACCTGAAGGTGAAGTAG
```

NHI 1 (CitB) protein sequence:

```
MPISTKSSFYLPVAVDISPYLQDPNSDAARKVIDDVRAACTSTGFFQLLGHGISPALQQSV
FAAAAKFFALPSDVKSRCRNVGFRGYDPMASQSYELGVLPDLKEGFIAGKDIPLDDPR
VASQRFFMGQNAWPPSELLPEANFRRIEYQAMLKLCWVVLDLVAATLPYGPHVFD
EFKENDPACPLRLLHYPPAPAPDVAKGRQLGSSAHTDFGAILLLQDDHSGLEVQDCE
TGEWIGVPPNKDAYVVNLGDMMSRITRGHYKSSIHRVINQNLDRYSVFFFDGNLDY
RLRPLDRVGQNWDEEDTLTVEEHMLERTTTTTYNLKVK
```

Codon-optimized NHI 2 (ClaD) sequence:

```
ATGGGCAGCAGCCATCATCATCATCACAGCAGCGGCCTGGTGCCGCGCGGCA
GCCATATGATGCCGGTGCTGTGCAATCCGAGCTTTTATCTGCCACTGGTGGATATCA
CCCCGTTCTTGAGAAACCCGCATGGCGCAGCGGCGCAGGATGTCATCGAAAGCG
TGCGTACCGCCTGCAAAAGCACCGGTTTTTTTCAGATCAAAGGTCATCAGGTGCCG
CTGCGTTTGCAAAAATCGGTGTTTCGAAGCCAGCGCGCGTTTCTTTGCGCTGCCTCT
CAAAAACAAACTCGAACTCGACAGCCGCAAAACCGTTGGCTTCCGCGGTTACGATG
TCATGGAAACGCAAAGCTACGAACCTGGAATTTGGCGCGGTGCAGGAAGCGGATGC
GTTGCGCGATATCAAAGAAGGCTTTTTTATTGCCACCGACCTGCCGCCGGATCATC
CGCATGTCGCCAACGGTCGTTTTTTGCAGGGCCCCGAACGTCTGGCCGAAACCAGA
ACAGCTGGCGCCGGAAGATTTCCAGAGCGTACTGGAAGAATATTACACCGAAATGC
AGCGTCTGTCTCATGTGGTGTGTCGCTGCTGGCAGCAACGCTGCCGTATGGTCC
GCACGTTTTTCGACGAGCTGGAAACCTGCGATCCGATGTCGTTGCTGCGCCTGCTG
```

CATTATCCGCGCGGCTTGGAAAAACAGGATGGCAAAAAACTGCAACTGGGTGCCG
GGGAACATACCGATTTTGGTACCTTTACCCTGTTACTGCAGGACGAGCATCCTGGC
CTGGAAGTGCAAGACAGTGTCAACCGGCGAATGGCACGGCGTGCCACCGCAGGAG
GATGTTTATATCGTCAACGTTGCCGATATTCTGTCCACCATGACCGAGGGCGATTAC
AAGTCTTCTGTGCATCGCGTGTGGAACATCAAGAGCAACGATCGCTACAGCGTCGT
GTTTTTCTACGACGGCAACCTGGATTACAAAGTCAAACCGTTACGCAGCAGCGGTC
AGGACGAAAACGAAGAAATCGATGCACCGACCATCGAAGAGCACGTCCGTTTCGCG
TCTCACTGCCAGTTATGCCATTTAA

NHI 2 (ClaD) protein sequence:

MPVLSNPSFYLPVLDITPFLENPHGAAQDVIESVRTACKSTGFFQIKGHQVPLRLQKS
VFEASARFFALPLKNKLELDSRKTVGFRGYDVMETQSYELEFGAVQEADALRDIKEGFF
IATDLPPDHPHVANGRFLQGPNVWPKPEQLAPEDFQSVLEEYYTEMQRLSHVVLSELLA
ATLPYGPHVFDELETCDPMSLLRLLHYPRGLEKQDGKKLQLGAGEHTDFGTFTLLLQD
EHPGLEVQDSVTGEWHGVPPQEDVYIVNVADILSTMTEGDYKSSVHRVWNIKSNDRY
SVVFFYDGNLDYKVKPLRSSGQDENEEIDAPTIEEHVRSRLTASYAI

Codon-optimized NHI 3 (TropC) sequence:

ATGTCCATTGGTGACGAAGTCATACCGACGGTTGATATAAGTGCGTGGCTCTCGTC
CACCGCGAGCCCGGAGTCAAAGAATAAGTTGTGCGAGGAAGTTCGTTCCGGCGTGT
AATAAATATGGATTCTTCAATCTTGTAGGTCACGGTATCCCGGCTGAGGCCCGCGAG
AAAATTTTCGGGTGCACTAAGAAATTCTTCGACCTGCCCCCTGGAAGAAAAGATGAA
GATCTCCGTTGACAAGTCACTTGGAAGTCTTCCGCGGGTATGAGCCTTCCCTGA
TCCAAACTCACCAAGACGGTTTGTACCAGACACGAAGGAGTGCTTCATTACTGGG
GCAGAAATTCCGGCTGACCACCCTGATGCTGGTAAATTCTCAACTGGGCCCAATCT
GTGGCCAGAGGGCCTGTCAGACAAGGAATTCCGTCAACCCGTGATGGAGTATAGA
GCGCTGATGCTGGACCTCGTGTCAACCATTGTGCGCATCTTAGGTCAGGGCATTCA
TAAGGCTTTCCGGCCATCCTAGTGATGTACTTAATGACATCCTCATTAACTAGCATC
CCCATGCGACTGCTTCACTATGCTCCTCAAGAGAACCCGGATCCACGACAATTTGG
AGTTGGCGACCACACTGATTTTGGCTGTGTCTCTATACTGCTGCAGCAAAAGGGTA
CGAAAGGCCTGGAAGTGTGGTACCCACCCAAAGAGACGTGGATAACAGTACCTGT
CATCGAAGACGCCTTCGTTATTAACATGGGCGATACTATGCATCGTTGGACCGGCG
GTTACTACAGAAGTGCCCGCCACCGTGTATACATAACGGGTGAGCGTCGGTACAGC
GTTGCATTCTTCTTGAACGGTAATCTGAATCTGAAGATAAAGCCTTTGGATGGAAGT
GGCGGAGAAGCTTCAGTAGGAGAACACATCAATAGTAGACTCGCACATACTTTGGG
AGACAATGCTAAATACCTGCGTTGA

NHI 3 (TropC) protein sequence:

MSIGDEVIPTVDISAWLSSTASPESKNKVVEEVRSA CNKYGFFNLVGHGIPAEAREKIFG
CTKKFFDLPLEEKMKISVDKSLGKSFRGYEPSLIQTHQDGLLPDTKECFITGAEIPADHP
DAGKFSTGPNLWPEGLSDKEFRQPVMEYRALMLDLVSTIVRILGQGIHKAFGHPSDVL
NDILINPSIPMROLLHYAPQENPDPRQFGVGDHTDFGCVSILLQQKGTKGLEVWYPPKET

WIPVPVIEDAFVINMGDTMHRWTGGYYRSARHRVYITGERRYSSVAFFLNGNLNLKIKPL
DGSGGEASVGEHINSRLAHTLGDNAKYLR

Codon-optimized NHI 4 (VioC) sequence:

ATGACTGAATCTCCTACAACGCATCATGGAGCGGCACCGCCTGACTCTGTAGCTAC
TCCAGTGCGCCCGTGGAGTGAGTTCCGTCTGACCCCTGCAGAAGCAGCAGCTGCT
GCTGCGCTGGCCGCACGTTGCGCACAAAGATACGATGAGACTGACGGACCCGAGT
TCTTGCTGGACGCTCCGGTAATCGCACATGAGTTGCCTCGGCGACTCAGAACGTTCC
ATGGCGCGGGCCCGGCTTGACGCATGGCCGCACGCATTAGTTGTTCTGTTGGGAACC
CAGTGGATGACGCCGCGTTGGGGTCTACACCTGTTCACTGGCGCACAGCCAGAAC
GCCTGGATCCCGGGCCCCTGTCTTTCTTACTGATGCTGTATGCCGGCTTATTGGGAG
ACGTTTTTCGGCTGGGCAACGCAGCAGGACGGTCGGGTCGTTACAGATGTGCTTCC
CATTAAAGGGCGGGGAGCATAACCCTTGTGAGTTCTGCTTCGAGACAAGAGTTGGGAT
GGCACACAGAGGATGCGTTCAGCCCTTATCGAGCGGATTACGTGGGCCTGCTGTC
TCTTCGTAATCCCGACGGCGTGCGGACCACTTTAGCAGGGGTCCCGTTAGACGAC
TTAGATGAGCGGACTCTGGACGTTCTGTTTCAAGAGCGGTTCCCTCATTAGACCCGA
CGACAGCCACCTTCAGGTAAATAACTCAACGGCCCAACAAGGGAGAGTGGAGTTC
GAAGGTATCGCTCAAGCGGCGGATCGGCCTGAGCCAGTGGCAATCTTGACCGGTC
ATAGAGCAGCTCCGCACCTTCGAGTTGACGGTGACTTTTCTGCCCCCGCCGAGGG
CGACGAGGAAGCTGCCGCTGCGTTGGGAACACTGCGCAAGCTTATCGATGCATCC
CTCTACGAATTAGTATTAGATCAAGGAGATGTCGCTTTCATCGATAATCGACGTGCTG
TACACGGGAGACGTGCGTTCCAACCGCGATATGACGGCCGTGACCGGTGGCTGAA
ACGTATTAATATTACTCGTGACCTGCACCGCTCCCGGAAGGCATGGGCAGGCGACT
CGCGAGTGCTTGGCCAGCGT

NHI 4 (VioC) protein sequence:

MTESPTTHHGAAPPDSVATPVRPWSEFRLTPAEAAAAAALARCAQRYDETGDGPEFLL
DAPVIAHELPRRLRTFMARARLDAWPHALVVRGNPVDDAALGSTPVHWRTARTPGSR
PLSFLMLYAGLLGDVFGWATQQDGRVVTDVLPKGGEHTLVSSSSRQELGWHTEDAF
SPYRADYVGLLSLRNPDGVATTLAGVPLDDLDERTLDFQERFLIRPDDSHLQVNNST
AQQGRVEFEGIAQAADRPEPVAILTGHRAAPHLRVDGDFSAPAEGDEEAAAALGTLRK
LIDASLYELVLDQGDVAFIDNRRRAVHGRRAFQPRYDGRDRWLKRINITRDLHRSRKAWA
GDSRVLGQR

Codon-optimized NHI 5 (SxtS) sequence:

ATGGTCGCGGCTGTTCTCACCTGTTATGGCGGGATGATCCATTGAACCCTTTAGA
CTGCGAGGGAATTAAGGAAATGTTGACAGTCGAACAGAAACAAGCCTACGTGAACG
ATGGGTATTTACGGTTGAGGAGACGGTACCGAAGGCGCTTATAGAGGAGATTTCGG
CATGAGGTAGAATTAATTACGGAGCAAAAGCGCGGTGGTGTGCTTGCGGGCGACTA
CGAGTGGTGGTCAGACCACACGATTCCCGACCCGATCCGCTATCAGAAAATCATAC
AACGCCTTCTGGAGCTCCCAACCGTTATGGAGCCAGTCCAAGCCCTGATCGGTTCA
GATATATTCCTCTTGATCACTGACCTCGCGATTATTCGCGCAGGGACCGGTTACATT
GCTTGGCACCAAGATCACGGCTACTTGGTCGAGGTCCTTATAGCCCCCGAGTCAAA

GAGCACAAATGTGCTGAACGACGACGCCTTCCGGTTGGTGTACCCGTTGTACAAC
AAACGACCGTCTTCATAACCATCTACCTGCAGGACACTGATAACACTATGGGAGCTA
TGCGGGTGATTCCGTCAAGTCACCAAGTGGGAACATTATTGGACCCTTCGTCTGCG
AACTCTTTAGATGCCGAAATTTGCCTTCCTTTGCCTGGTGGCGCGGCGATGTTCTAC
ACACCAACTGTGTGGCACACGGCCGCCGCCAACACCAGCATCACCGATTACCGTAT
GTTAACTCTTATCTTTACGAAGAACAACATCAAGCCGTTACTGGTGGATGCTCTTAA
GGGCGTATC

NHI 5 (SxtS) protein sequence:

MVA AVL TLLWRDDPLNPLDCEGIKEMLTVEQKQAYVNDGYFTVEETVPKALIEEIRHEVE
LITEQKRGGVLAGDYEWWS DHTIPDPIRYQKIIQRLLLELPTVMEPVQALIGSDIFLLITDL
AIRAGTGYIAWHQDHGYLVEVLIAPESKSTNVLNDDAFRLVLPVVQQTTFIT IYLQD TD
NTMGAMRVIPSSHQWEHSLDPSSANS LDAEICLPLPGGAAMFYTPTVWHTAAANTSIT
DYRMLTLIFTKNNIKPLLVDALKGRI

Codon-optimized NHI 6 sequence:

ATGCCAGTGCCGACCAAGTCATCTTTCTACCTTCCCGCTGTAGATATCAGCCCTTAC
TTGCAAGACCCGAAC TCGGACGGTGCGCGGAAGGTTATAAACGACGTGCGCGCCG
CATGTACCTCAACGGGATTCTTTCAATTACTTGGCCATGGAATATCTCCTGAGTTGCA
ACGGTCCGGTGTTTCGCAGCCGCGGCCAAAATTCTTTGCATTACCTACGGATGTAAAATC
ATCCTGCCGAAACGT CGGCTTCCGTGGCTACGACCCCATGGCTTCCAGTCTTACG
AACCGGGCGTTCTGCCCGACCTCAAGGAATCTTTCATTTCCGGGTACGGACATTCCT
CTTGACGACCCCCGCGTTATGAGTCGGCGTTTCTTCATGGGTCAAATGCCTGGCC
ACCCGGCGAACTCCTGCCAGAGACGGACTTTCGTGCCCCCGTCGAAGAATACTAC
CAAGCCATGATGAAGCTTTGCTGGGCTGTATTGGACTTAGTTGCGGCCACCTTGCC
TTACGGGCCGCATGTCTTCGATGAGTTCAAGGAGAATGACCCCGCGTGTCCTTTAC
GCTTGTTACACTACCCACCGACCCCCGCCCCCGACGTGGTCAAGGGTCGTCAGCT
GGGGTCTTCAGCTCACACTGACTTTGGCGCAATAACTCTCTTACTGCAGGATGACC
ACCCTGGGT TAGAGGTGCAAGATCGCGAAACCGGAGATTGGATTGGCGTGCCCCC
AAAGTCAGATGCGTACGTTGTTAATTTGGGCGATATGATGAGCAGAATCACTAGAGG
CCACTACAAGTCGTCAATACATCGTGTGATTAACAAGAACCTGACAGACCGTTATTC
TG TAGTATTCTTCTTTGACGGAAATCTCGATTATAAGTTACGCCCACTGGACCGTGTA
GAGCAAGATCAGGACGAGGAGAACGTGCTGACCGTAGAAGAGCACATGTTAGAGC
GGACGACAACAACCTATAACACCAAAGCTAAATGA

NHI 6 protein sequence:

MPVPTKSSFYLPV DISPYLQDPNSDGARKVINDVRAACTSTGFFQLLGHGISPELQRS
VF AAAAKFFALPTDVKSSCRNVGFRGYDPMASQSYEPGVLPDLKESFISGTDIPLDDPR
VMSRRFFMGQNAWPPGELLPETDFRRPVEEYYQAMMKLCWAVLDLVAATLPYGP HVF
DEFKENDPACPLRLLHYPPTPAPDVVKGRQLGSSAHTDFGAILLLLQDDHPGLEVQDR
ETGDWIGVPPKSDAYVVNLGDMMSRITRGHYKSSIHRVINKNLTD RYSVVFFFDGNLDY
KLRPLDRVEQDQDEENVLTVEEHMLERTTTTTYNTKAK

Codon-optimized NHI 7 sequence:

ATGCCTTCCTCAACAAAGTCAAGCTTCTACCTGCCAAGTGTTAACATAACACCGTAT
CTGCAAGACCCTGATAGCAGTGAGGCCCAAAGGTGATAGATGACATCCGTACCGC
GTGCCGGTCAACAGGTTTCTTTCAACTGCTTGGCCACGGGATCCCGCGTACCCTG
CAGCAATCCGTGTTTCGACGCGGGGAAACGTTTCTTTGCACTCCCGACCGATGTGA
AGCTCGGTATGGATTGTCGTGGAATGTAGGCTTCCGGGGCTACGACGCGATGGC
TAGCCAGTCTTACGAGTCTGGGGTACTCCCCGACTTAAAGGAAGGCTTTATGATGG
GCACTGACATGAGCGAAAACGACTTCCGAGTGATCAATAGAAGATTCTTTATGGGG
CCCAACGTTTGGCCCCCAGAGAGCTTACTGAAGAAGGAAGACTTCCGTCAACCGC
TGGAACGTACTTCGAAGCGATGATGAAGTTATGTTGGACCGTTATGGACTTAGTTG
CTGCCACCCTGCCGTACGGGCCCAATATATTCGATGAGTGGAAGGCGAACGACCCA
GCATGTCCATTCCGGTTATTACATTACCCACCTACCCCCGAGCCTGTTGAGGGACAA
AAGCGTCAACTTGGGTCAAGCGCACACACAGATTTCCGGCGCCATCACATTATTGCT
GCAGGACGAGCATGCAGGATTAGAGATCCAAGACCGTGAAACCGGAGAGTGGATT
CCGGTCCCGCCGAAGGAAGATGCGTACGTAATTAATATGGGAGACATGATTTACG
CATAACAGATGGCCACTACAAATCGTCAATCCATAGAGTCATAAACCGGAACTCGAA
CGACCGGTACTCCATTGTGTTCTTCTTCGATGGCAATATCGATTACAAGCTGCGACG
GCTTGACTCGAAGGTCCAGTCAGAGGACGAGGCACTGACTGTTGAGGAGCACATG
GAAGAACGTCGTAATACGACGTACGGCCTCAAGAAGAAGTAA

NHI 7 protein sequence:

MPSSTKSSFYLPSVNITPYLQDPDSSEAQKVIDDIRTACRSTGFFQLLGHGIPRTLQQSV
FDAGKRFFALPTDVKLGMDCRRNVGFRGYDAMASQSYESGVLPDLKEGFMMGTDMS
ENDFRVINRRFFMGPNVWPPESELLKKEDFRQPLETYFEAMMKLCWTVMDLVAATLPY
GPNIFDEWKANDPACPFRLHYPPTPEPVEGQKRQLGSSAHTDFGAILLLQDEHAGL
EIQDRETGEWIPVPKEDAYVINMGDMISRITDGHYKSSIHRVINRNSNDYRSIVFFFDG
NIDYKLRLRLDSKVQSEDEALTVEEHMEERRNTTYGLKKK

Codon-optimized NHI 8 sequence:

ATGCCTTCCTCTACTAAGAACTCATCATTTTATCTCCCATTAGTGAACATAACACCATA
TCTCCAGGACCCGAGCAGTATAGCTGGCCAACAAGTACTTGACGACGTTTCGACGG
GCGTGCACTTCAACAGGTTTCTTCCAGTTAGTTGGTCATGGCGTCCCTGCTACCTTA
CAGAAGAATTTGTACAACGCCGCGGCAAAGTTCTTCGCGCTGCCTATGGACGTCAA
GCTTCCTTTGGACGTACGAAAGAACATCGGGTTCGTTGGGTATGACGTGATGAGCA
GTCAATCATATGAGAAAGACGTTTTGCCGGACCTTAAAGAAGGTTACATTGTTGGTA
CGGATATCCCACTGGACGATCCCCGAGTAATGAAACGTCGCTTCTTCATGGGACGA
AACATATGGCCGCCAACCGAGTTCTTGCCTTACGAGGACTTCCAAAAGGTTGTTGA
GGAGTACAACGACGCAATGTTGCGTCTTTCGTGGGTTGTGGTCTGACTTAATAGCAG
CTACCCTGCCGTACGGTCCGCACGTCTTCGATGAATTAAGGAAAACGATCCGGCA
TGTCCACTTCGCTTGCTCCATTATCCGCCCACACCAAAGCAAGTTGGGAATGAGCG
CCGCCAATTCGGCTCATCAGCACACACTGACTTTGGGTTTCATAACACTCTTGTTGCA
AGACGAGAATCCCGGTCTTGAAGTACAAGACCGGGAGACTGGTGAGTGATTGGG

GTACCGCCTAACGAGGAAGCTTATGTGGTAAATATGGGAGATATGATATCTAGAGTG
ACTGGCAACCTCTATAAGTCATCACTTCACCGCGTACTTAACAAGGCTCCAACCGAT
CGGTATTCAAGTCGTGTTCTTCGTGGATGGTAATTTAGACTACAAGCTTCGTGCTTG
GATAAAATTGGTCAACCTGGCGAGGACGAAGAGGCCTTAACAGTGGAAGAGCACAT
GGAAGAGCGCCGCCGAACACTACATATGGACTTCGTAAGAAGTAA

NHI 8 protein sequence:

MPSSTKNSSFYLPLVNITPYLQDPSSIAGQQVLDDVRRACTSTGFFQLVGHGVPATLQK
NLYNAAAKFFALPMDVKLPLDVRKNIGFRGYDVMSSQSSEKDVLPDLKEGYIVGTDIPL
DDPRVMKRRFFMGRNIWPPTEFLPYEDFQKVVEEYNDAMLRLSWVVDLIAATLPYGP
HVFDELKENDPACPLRLLHYPPTPKQVGNERRQFGSSAHTDFGFITLLLQDENPGLEV
QDRETGEWIGVPPNEEAYVVMGMISRVGTGNLYKSSLHRVLNKAPTDRYSVFFVD
GNLDYKLRRLDKIGQPGEDEEALTVEEHMEERRRTTYGLRKK

Codon-optimized NHI 9 sequence:

ATGGCGAGTCCAATCCCGTTTAGCGTGCCTACCATTGACTTCACAGCATACTTAGT
GACCCGACGTCAGCAGAGTCTTCGAAGATTGTATCAGATATTAAACAGCTTGTACC
ACCACAGGCTTCTTTCAGCTGATAGGTCATGGTATCCCGGCGAGCTTACAGGAAGA
CGTGTTCAAGGGTTCCAAAGCTCTTTTCAAGCTGCCTATGGAAGAGAAGGTCAAGC
TTGACCGCGGTAAATCAGTAGGTGCTAGCAACCGAGGGTATGAGCTCATTGGCGGT
CAAGGACTGCAAGAGGGAACCTTACCGGATCTTAAAGAGGGATTCTACGTCGGACA
GGACATTCCTGCGACAGACCCACGTGTACAAAACAACGCGTTCCTGATGGGACCA
AACTTATGGCCAAGCAGTGATTTAGTGTCTGAGGCGGTCTTTAAGAAGCCAATGGA
AAAGTACTTTAGTAAGATGTTACCTTAACGTTGAAGGTCATGGATGCGATAGCCGC
TGGGATGCCATATGGATCGTCTGTTTTCGACGAGTTCACGAGTAACGACGCCGTTT
CCTCGATCCGCCTGCTGCACTACCCGCCAGACAAGAGCAATAACGAGCTGCAGCT
CGGGGCAGGCGCTCACACGGACTTTGGGGCAATTACTCTGCTGTTGCAAGACCAA
ATCGGCGGACTTCAGGTTTGGGATTATGGTAACAAGGAGTGGAAGGACGTAACCTC
GGTAAAGGATGCGTACGTCGTTAACGTTGGCGACATGCTGCAAATGTGGACTTCGG
GTGTGTATAAAAGTTCACTGCACCGAGTTCTCAATCGCTCCGGGAAAGACCGTTAC
TCGGTTCGGTCTTCTTCGACGGAAACGTCGATTGCGTACTGACACCCCTGGGTGG
CGGGGAAGAGGGTAAGAAGTACCCTACCGTCGAAGAGCATATGAAGGAGCGTTTT
GGGCAAACCTATGGTCGTGGTAAGAAGAGAGAAGACGGCGGCGAGAACGTTAAGT
TCTGA

NHI 9 protein sequence:

MASPIFVSPTIDFTAYLSDP TSAESSKIVSDIKTACTTTGFFQLIGHGIPASLQEDVFKGS
KALFKLPMEEEKVKLDRGKSVGASNRGYELIGGQGLQEGTLPDLKEGFYVGQDIPATDP
RVQNN AFLMGP NLWPSSDLVSEAVFKKPMKEYFSKMFTLT LKVM DAIAAGMPY GSSVF
DEFTSND AVSSIRLLHYPPDKSNNELQLGAGAHTDFGAITLLLQDQIGGLQVWDYGNK
EWKDVTPVKDAYVVNVGDM LQMWTSGVYKSSLHRVLNRSGKDRYSVPFFFDGNVDC
VLTPLGGGEEGKKYPTVEEHMKERFGQTYGRGKKREDGGENVKF

Codon-optimized NHI 10 sequence:

ATGAAAACTATGTTTCGTGAGCTATCGGCTTAATATTTGTGTTCCCTACAGTAGACATATC
ACCATATTTAGCAGATCCAAAGTCGGATGCTGCCCAAAGGTAATCGAGGACGTTTC
GTGAGGCCTGCATATCAACCGGCTTCTTTTCAGATAACAGGGCACGGAATTTCTAAGA
GTCTTCAACAAAACATATTTGACGCGGCTCATTCTTTGCCTTGCCGCTTGAGG
AGAAGAAGAACTGAACGCTGCAAATTTTCATCGGACATCGTGGCTACGACGTGCTG
GCTAGTCAGAGTTACGAGGAAGGTGTATTACCGGACCTGAAGGAAGGTTATTACGT
TGGGTCGGATGTTTTACCTAGTGACCCACTTTATGGACGCTTCTTCATGGGGCAAAA
CGTATGGCCAAGTACCGAACTTTTATCTATCATTCAAGAGCCTTGTGAGCG
CTACCACGAATCCGTACAACATCTCGCTTTCAAGGTCCTGCAATTGGTAGGAGATAC
GATGATACCTCACGGTCATTCAACCGTTGGAATGACCGAGAACATGCCGACAGTCT
TACATAACCTCATCCGCCTGGATAAAATACCAGCTTGCCCATTAAGACTTCTTCACTA
CCCCTCAGCAACAAGAAACGGTGGGTCTGTACAGGTAAACCTCAATACGGTGCG
TCGGCGCATACGGACTTCGGAGTTATCACTCTTCTGCTGCAAGACGACAACCCTGG
GCTGGAAGTGCTGGTTGAGAAGGATGGTAAGCAAGTTTGGTGGCCGATTGACCCC
AATCCATCTGCATATGTTGTAAATATCGGTGATATGATCAGTATGGTGACCAATGGCAT
CTATAAGTCCAGTATGCACCGCGTTGTGTGCAAACGGCCTGAGCGTGAGCGTTACA
GCATAGTGTTCTTCTTAGATGGATGCTTGAATGCTAATTTAGAGCCGGTCGAGGGTT
TCGGCCATCCGGAAGAAGGCGTCGGGTTTTCTCACAAGACCGTGGAGCAACACAT
GACCGAAAGACTGAGCATGTCTTATGCGAAAGAGGGTAAGGACCCTCGTCATAACG
AAGACACATTCTCTGCCTGA

NHI 10 protein sequence:

MKTMFVSYRLNICVPTVDISPYLADPKSDAAQKVIEDVREACISTGFFQITGHGISKSLQ
QNIFDAAHSFFALPLEEKKKLNAANFIGHRGYDVLASQSYEEGVLPDLKEGYVVGSDVL
PSDPLYGRFFMGQNVWPSTELLSIIQFQEPCEHYHESVQHLAFKVLQLVGD TMIPHGH
STVGMTENMPTVLHNLIRLDKIPACPLRLLHYP SATRNNGSVTGKPQYGASAHTDFGVI
TLLLQDDNPGLEVLVEKD GKQVWWPIDPNPSAYV VNIGDMISMVTNGIYKSSMHRVVC
KRPERERYSIVFFLDGCLNANLEPVEGF GHPEEGVGFSHKTVEQHMTERLSMSYAKE
GKDPRHNEDTFSA

Codon-optimized NHI 11 sequence:

ATGGCCATAGCCAGTTCATTTTCCGTGCCGACGATTGACATTTCTCCATATCTGAGT
GACGCGACCTCAGAGGCGGGCTTAAAGGTCATCGAGGACGTTAAGGCTGCCTGTA
CGGGCACGGGATTCTTCCAATTGATCGGACACGGCATCTCTCCGGAACCTCAAGAG
AAAGTCTTCAAAGGCGCAGAGCAGCTCTTTGCGCTTCCCATGGAAGAGAAGGTAAA
ACTTGATAAGTCACAATCGGTAGGTGCTAGTAATCGTGGGTACGAACTGATCGGTGG
CCAGGGGTTACAAGAGGGGACTCTGCCCGACTTAAAGGAAGGTTTCTACGTTGGT
CAGGACATTCCGGCTAGTGATCCGCGCGTACAGAAGAAGGCATTCTTAATGGGTCC
GAATCTTTGGCCCCCGAGCGACCTGGTCCCTGAGGACGTTTTTCAAGGAACCCATG
ACCAGCTATTATGCGCAAATCTTCGCTCTCTCGTTGAAAGTATTAGAAGTTATTGCGG
CCGGCATGGAGTATCCCGGTGTGAAAACAGTCTTTGAGGAGTTCACTGCCAACGA

CGCCGTCGCTTCTATTCTGCTTACTTCACTACCCGCCTGACAAGGGTAACGATGCAC
GACAATTGGGAGCTGGGGCACATACCGATTTCCGGTGCTATCACCTTATTACTGCAAG
ACGACATAGGTGGGCTGCAAGTGTGGGACTACGTCGGTAAGGAATGGCGGGACGT
TAAGCCTGTAAAGAAGCGTACGTAGTCAATGTGGGTGACATGTTACAAATGTGGAC
CTCTGGCGTCTACAAAAGCTCGCTGCACCGAGTTGTAAACCGTTCGGGGCGTGAT
CGGTATAGCGTTCCTTTCTTCTTCGACGGTAATGTCGACTTCGAGCTGCGTCCACTT
GACGGGCGTGAGCGCGAAGGTGGTGTTCCTTACGGTTGAAGCCCATGAAGGAG
CGCTTCGCGTCGACGTATGGCCGCGGCGCTCAAAGGTGCGCCGGTCTCTGA

NHI 11 protein sequence:

MAIASSFSVPTIDISPYLSDATSEAGLKVIEDVKAACGTGFFQLIGHGISPELQEKVFKG
AEQLFALPMEEEKVKLDKSQSVGASNRGYELIGGQGLQEGTLPDLKEGFYVGQDIPASD
PRVQKKAFLMGPNLWPPSDLVPEDVFKEPMTSYYAQIFALSLKVLEVIAAGMEYPGVKT
VFEEFTANDAVASIRLLHYPPDKGNDARQLGAGAHTDFGAILLLLQDDIGGLQVWDYVG
KEWRDVKPVKEAYVVNVGDMLQMWTSGVYKSSLHRVVNRSGRDRYSVPFFFDGNV
DFELRPLDGREREGGVLTV EAHMKERFASTYGRGAQKVAGL

Codon-optimized NHI 12 sequence:

ATGCCAGCGGCCAGCGCTACGACTAGCAGCTTCTATTTACCGGATATCAACATAGCC
CCATGGCTTGAGGATCCTGGTAGTCCATCAGGCCAACACGTCGTTAATGAGGTACG
TAGAGCATGTACATCGACAGGGTTCTTCCAATTAACAGGTCACGGTTTCCCGCCTG
CGGTAATTAAAGACATATTCGCCGCAGCAGCTAAGTTCTTCGCGTTGCCGAAGGAG
ATTAAGCAAGACCTGAACTTCACGAAGAACGCCGGTTTCAGAGGCTACGAGCTCGT
AGGAGCCCAAGTGTACGAGACGGATGTGCTCCCCGACCTCAAGGAAGGCTTTCTC
GCGGGCATTGACCTTCCTCGAGACGATGTCCGTGTTCAAATAAACGGTTCTTCGC
AGGACAAAACGTTTGGCCTAGCCCCGACGTTCTGCCATATTCGGAATTCGCACCC
CTGTCGAGACGTACTACAAGTCTATAATGCAACTGTGTTGGACCGTTATGGACCTGA
TAGCCTCGACGCTTCCTTACGGTCCTAATGTGTTGACGAATGGAAAGCTCACGAG
CCTGCGTGTCTCTGCGTCTCTTGCACTATCCGCCAACCCCGAAGCACGTCGCGG
GAAAGACTCGCCAACTGGGAAGCAGTGCACACACTGACTTCGGCGGGCGTTACACT
TCTGCTGCAGGACAGTCATGACGGTCTGGAAATACTTGATAGAGAGACTAGATCCT
GGGTACCGGTACCACCAAAGCCGGGTGCTTTCGTCATCAATGTTGCCGATATGATG
ACAATGATTACCGGCGGCGAGTACAAGAGCAGCATGCATCGAGTGATTAACCAAAA
CGAGACCGACCGTTACTCCGTTGTATTCTTCATGGATGGCAACGTCGATTACAAGTT
AAGACGTTTAGACAAAATAGGGCAACCGGTTGGCGAGGACGAAGAGCTCATTACAG
TCGAAGAGTACATGCTTGGTAAGCGCAATACTACGTACGTTAAGTGA

NHI 12 protein sequence:

MPAASATTSSFYLPDINIAPWLEDPGSPSGQHVVNEVRRACTSTGFFQLTGHGFPPAVI
KDIFAAAKFFALPKEIKQDLNFTKNAGFRGYELVGAQVYETDVLPLDKEGFLAGIDLPR
DDVRVQNKRRFFAGQNVWPSDVLPHYSEFRTPVETYYKSIMQLCWTVMDLIASTLPYGP
NVFDEWKAHEPACPLRLLHYPPTPKHVAGKTRQLGSSAHTDFGGVTLLLQDSDHGLEI

LDRETRSWVPVPPKPGAFVINVADMMTMITGGEYKSSMHRVINQNETDRYSVFFMD
GNVDYKLRRLDKIGQPVGEDEELITVEEYMLGKRNTTYVK

Codon-optimized NHI 13 sequence:

ATGACCAAAGGCAGCAGCCCAAATGTGCCAACGGTGGACATCTCACCATATCTGGA
AGATCCAAAAAGCAAAGCCGCCCGTAAAGTGATCGATGATGTTTCGCGAAGCGTGCA
CGTCAACCGGCTTTTTCCAAATCACGGGTCACGGCATTAGCAAAGAGCAACAAAAA
TCGGTGTTTGATGCGGCGCACGCCTTCTTCGCGTTACCATTAGAAGAAAAAAAAA
ACTGAATGCCGCGCACTTTATCGGCCATCGTGGGTATGATGTTTTAGCGTCGCAATC
ATACGAGGAAGGTGTATTACCGGATTTAAAGAGGGTTATTATGTAGGCTCGGATATT
CTGCCGAGCGATCCACTGTATGGCCGTTTCTTTATGGGTAGCAACGTGTGGCCGCC
GGCGACCTTACTGAGCGCCTCACAGTTTCAGGAACCGTGCGAACGCTATCATAAAA
ACGTGCAGCAACTGGCGTTTAAAGTGCTGCAATTAATTGGTGATACGATGATCCCAT
GTGAGCGTAGCACGATCTCGATGACGGGTGGCGTACCGACGGTTCTGCACGATTTA
ATTCGCTTAGATGAAACGCCGGCGTGCCCGCTGCGTCTGTTACACTATCCGTCAGC
GGCGCGTCACGGTGATGTTGCCGGTAAACCGCAATATGGTGCGAGCGCGCACACG
GATTTTCGGCGTAATCACGTTACTGCTGCAAGATGATAACCCAGGCCTGGAAGTTCT
GGTTGAGAAAGATGGGAAACAGGTTTGGCTGCCAATTAACCCGAACCCAGATGCCT
ATGTGGTGAATATCGGGGATATGGCGTCGATGGTGACGAATGGGGTATATAAATCGA
GCATCCACCGTGTGGTGTGCAAACGCCCGGAACGCGAGCGTTATAGCATCGTATTT
TTCCTGGATGGCTGTTTAGATGCGTGTCTGCGTCCGATCGAGGAGTTCGGGCATCC
GGAGGGTGGGATCGCGGATAGCCACAAAACCGTTGAGCAGCACATGATCGAACGT
TTATCAATGAGCTATGCGAAAGAGGGCAAAGATCCACGTCATAACGAGGATACGTTT
TCGGTG

NHI 13 protein sequence:

MTKGSSPNVPTVDISPYLEDPKSKAARKVIDDVREACTSTGFFQITGHGISKEQQKSVF
DAAHAFFALPLEEKKKLNAAHFIGHRGYDVLASQSYEEGVLPDLKEGYVVGSDILPSDP
LYGRFFMGSNVWPPATLLSASQFQEPCCERYHKNVQQLAFKVLQLIGDTMIPCERSTIS
MTGGVPTVLHDLIRLDETPACPLRLLHYP SAARHGDVAGKPQYGASAHTDFGVITLLLQ
DDNPGLEVLVEKD GKQVWLPINPNPDAYV VNI GDMASMTNGVYKSSIHRV VCKRPER
ERYSIVFFLDGCLDACLRPIEEFGHPEGGIADSHKTVEQHMIERLSMSYAKEGKDPRHN
EDTFSV

Codon-optimized NHI 14 sequence:

ATGAAAACGATGTTTCGTTTCGTATCGTCTGAACATTTGTGAGTTATATTTTGTGATTCT
GCAACAACCAACGCACAAAGTTAAAGATCGCTCACCAACGATCCATCCGTCGCGCG
ATATAGCCTGCATCGTATCACAATTTATTCTGAATAGCGATAAAATGACGAAAGGTAG
CTTCTCAGGTGTGCCAACGGTGGACATCTCGCCATATCTGGCGGATCCAAAAAGCG
ATGCCAGCCGCAAAGTGATCGAAGATGTTCTGTGAAGCGTGATCTCAACGGGGTTT
TTCCAGATTACGGGTCATGGCATTAGCAAATCGCTGCAACAAAACATTTTTGATGCG
GCGCATAGCTTCTTCGCCTTACCATTAGAAGAGAAAAAAACTGAATGCCGCGAAT
TTTATCGGTCATCGTGGGTATGATGTTTTAGCCAGCCAAAGCTATGAAGAAGGCGTA

TTACCAGATTTAAAAGAGGGTTATTATGTAGGCAGCAACGTGCTGCCAAGCGATCCA
TTATATGGTCGTTTTTTTTATGGGCCAGAACGTGTGGCCATCAACGGAATTACTGAGC
ACGATCCGCTTTCAAGAACCATGCGAGCGCTATCACGAAAGCGTGCAGCACCTGG
CCTTTAAAGTGCTGCAATTAGTAGGTGATACGATGATCCACACGGGCATAGCACGG
TGGGTATGACGGAATCGATGCCAACGGTGCTGCACAATTTAATTCGTTTAGATAAAAT
CCCGGCGTGTCGCTGCGTCTGCTGCACTATCCAAGCGCCACGCGTAACGGTGGG
TCGGTTACGGGCAAACCGCAATATGGTGCGTCAGCGCACACGGATTTTCGGTGTAAT
TACGTTACTGCTGCAAGATGATAATCCAGGCCTGGAAGTGCTGGTGGAAAAAGATG
GTAAACAAGTTTGGTGGCCAATCGATCCGAATCCAAGCGCCTATGTTGTGAATATCG
GTGATATGATCAGCATGGTGACGAACGGCATCTATAAAAGCAGCATGCATCGTGTGG
TATGCAAACGTCCAGAACGCGAGCGCTATAGCATCGTATTTTTCTGGATGGCTGTT
TAAACGCGAATCTGGAGCCAGTAGAGGGTTTCGGGCACCCAGAAGAAGGCGTGGG
TTTTTCGCACAAAACCGTAGAACAACACATGACGGAACGTTTATCAATGAGCTATGC
GAAAGAGGGCAAAGATCCACGTCATAACGAGGATACGTTTTTCGGCG

NHI 14 protein sequence:

MKTMFVSYRLNICELYFVILQQPTHKVKDRSPTIHPSRDIACIVSQFILNSDKMTKGSFS
GVPTVDISPYLADPKSDASRKVIEDVREACISTGFFQITGHGISKSLQQNIFDAAHSFFAL
PLEEKKKLNAANFIGHRGYDVLASQSYEEGVLPDLKEGYVVGSNVLPSPPLYGRFFMG
QNVWPSTELLSTIRFQEPCEYHESVQHLAFKVLQLVGDTMIPHGHSTVGMTESMPTV
LHNLIRLDKIPACPLRLLHYPSTRNGGSVTGKPQYGASAHTDFGVITLLQLDDNPGLEV
LVEKDQKQVWWPIDPNPSAYVVNIGDMISMVNTNGIYKSSMHRVVCKRPERERYISIVFFL
DGCLNANLEPVEGFHPEEGVGFSHKTVEQHMTERLSMSYAKEGKDPRHNEDTFSA

Codon-optimized NHI 15 sequence:

ATGAGCTCAACGACGGATCGGAGCCACATCAGAAAAAATTTTATATTCCACAGGTT
AATATTGAACCATTCCTGAAAGATCCAGATAGCGCCACGAGCAAAACGATTATTGAA
GAAGTGCGTGCCGCCTGCCGTTCAACCGGTTTTTTTTGAAATCACGGGCCACGGCA
TCCCAAAAAGCCTTCAGAAAGAAGTTTTTCGGTGCCGCGTCGCAGTTTTTTAACTG
AGCTTCGATGAAAAAAAACGTTTAGATGCGTCAAAACAGATTGGTTATCGTGGTTAT
GATATGCTTGCGTCACAGGCCTATGGCAAAGATCTGCTTCCGGATTTAAAGAAGGT
TTTTATATTGGCATAGATATACCAAAAACGGATCCTCGTGCGGGTCGTTTTTTTACGG
GCCCAAATGTGTGGCCAGATGAAAGCCTGCTGCCAGCCAGCCAGTTTAAAGATCCA
TGCACCATGTATTTTTTTCAGCCATGCTTCAGCTGAGCTTCCGTATAATGGCCCTGCTG
GCGCGTACGCTGCCATACGGTCCACATATTTTCGATGAATTTATCGCCAACGATCCA
GCCGCCCCACTTCGTCTGTTACACTATCCGCCACCACCAATGGCCTCAGTTGGCCC
AGAACAGCAGAAAAAACAGTTCGGCGCCTCGGCGCATACCGATTTTCGGTGCCATAA
CCATATTACTTCAGGATGAAAATCCGGGTCTGGAAGTTCTGGATCAGGATGCCGATA
GCTGGGTTCCAATCGATCCGAATCCAGGTGCCTATGTTGTGAATGTTGGTGATATGC
TGTCGTTATGGACGTCGGGTGAATATAAATCGAGCGTTCATCGCGTTATCAGCAAAA
ATCCGACGGATCGGTATAGCGTTGTTTTTTTCTTAGATGGGAATTTAGATTGTTCATT
AACCCATTAGATGGCTCGGAAAACCGGGGTCCGAAAACGGTTGAAGAACACATGAC
CCGGCGGTTAACGGCCTCGTATGGGGTTGAAAAAGAAAAAGAT

NHI 15 protein sequence:

MSSTTDRSPHQKKFYIPQVNI EPFLKDPDSATSKTIIEEVRAACRSTGFFEITGHGIPKSL
QKEVFGAASQFFKLSFDEKKRLDASKQIGYRGYDMLASQAYGKD LLPDLKEGFYIGIDI
PKTDPRAGRFFTGP NVWPDESLLPASQFKDPCTMYFSAMLQLSFRIMALLARTLPYGP
HIFDEFIANDPAAPLRLLHYPPPPMASVGPEQQKKQFGASAHTDFGAITILLQDENPGLE
VLDQDADSWVPIDPNPGAYVVNVGDMLSLWTSGEYKSSVHRVISKNPTDRYSVVFLLD
GNLDCSLNPLDGS ENRGPKTVEEHMTRRLTASYGVEKEKD

Codon-optimized NHI 16 sequence:

ATGGGAAGCGTGGCTCCTCCTCTGGTTCCAACGATTGATATTGCGGCGT TTTCTGGC
GGATTCAACCTCAGAAGAGGCGGAAGATATAGTAGATGCGGTTTCGTCAGGCGTGCA
CGAAAACCGGCTTTTTTTCAGATTACCGGTCATGGATTTCCAGAAGCGGTT CAGGAT
GCGATGTTCCAGGCGAGCAAAAAATTTTTTCGCGCTGCCAATGGAAGAAAAAGTGAA
ACTGGATGCTAAAACGACGATTGGCTATCGGGGCTATGATGTGCTGGCGTCACAGG
TGTATGATACCTCAGGAGAAGTATTACCTGACCTGAAAGAAGGCTTTTATGTAGGCC
ATGATCTGCCGCTGTCAGATCCAGTGGTAGTAGCGCGCCGCTTTTTTATGGGCCCA
AACGTGTGGCCACCAGTGAGCTCACTGGCGGCTGCGGAATTT CAGCATCCAGTGG
AGGCGTATCATGGCGCGGTGAACAGCCTGGCGCTGAAAATGCTGGATCTGGTGGC
GCGCACCTGCCATACGATACGAAACAAATTTTCGCGGAATTTGCGACCGGCTATG
TTATTGCGCCGCTGCGTCTGCTGCATTATCCGCCGGCGGATACCGATGCTGCGACC
CAGACCCGTCCGCGCACCGGGGCGGGCGCGCATACGGATATGGGCGCGATTACC
CTGCTGCTGCAAAACGATCAGCCAGGGCTGGAAGTTCTGCATCCAGGCACCGGCG
AATTTGTGGCGGTGGATCCAACCCAGGCGCGTTTCGTGGTGAACGTGGGCGATAT
GCTTAGCGCGTGGACGGGCGGGCTGTATAAAAGCAGCGTTCATCGCGTGATTAACC
GTAACCCAGTGGATCGCTATTCAGCTGCGTTCTTTTTTGATGGCTCACTGGATTGCC
CGCTGGACCCGCTGGATGGGAGCGGCACCGGACCAAAAGGGGA ACTGACCGTGG
AAAAACACGTTATAAATCGTATTATGCAGAGCTAT

NHI 16 protein sequence:

MGSVAPPLVPTIDIAAFLADSTSEEAE DIVDAVRQACTKTGFFQITGHGFPEAVQDAMF
QASKKFFALPME EKVKLDAKTTIGYRGYDVLASQVYDTSGEVLPDLKEGFYVG HDLPL
SDPVVVARRFFMGP NVWPPVSSLAAAEFQHPVEAYHGAVNSLALKMLDLVARTLPYDT
KQIFAEFATGYVIAPLRLLHYPPADTDAATQTRPRTGAGAHTDMGAITLLLQNDQPGLEV
LHPGTGEFVAVDPTPGAFVVNVGDMLSAWTGGLYKSSVHRVINRNPVD RYSAAFFFD
GSLDCPLDPLDGS GTGPKGELTVEKHVINRIMQSY

Codon-optimized NHI 17 sequence:

ATGCCATCAGCGATTGAACAACCAGGATTT CATATACCAACGGTCGATATAGCGAGC
TATCTTGCTGATCCGAGCAGCGCTGATGCTCAACAGGTGGTAGACGCTGTACGGCT
GGCTTGACAACGAGCGGCTTTTTTCAACTGGTGGGCCACGGC ATACCTATAACAC
TGCGGGCTACGATGTTTGCGGGCTCAAAGCTCTGTTTGAGTTACCGTTTGACCAG
AAAAAAGCGCTGAAACGGGCTGGAAATCGGGGCTATGAGGTGATGGGCTCACAGG

CGCTGCAAGATGGCACCCCTGCCAGATATGAAGGAAGGCTATTATATTGGCGAGGAA
ATACCATTTGAAGAAGGCCAAAGCGTACCGCCCGTTTATGGAACCAAACATTTGGCCA
TCAGAAGAACAGATTCCACATAGCATTTTTTCGGCTGCCAATGAACGAATATTATAAAC
GGGTGTCAGCGCTGGGCGTGGTGGTGGTATTTTGGCGGCGGCGCTTCCTTAT
GGCCCAAACGTGTTTGATAAATTAACAAGAACCCTTCAGCGGCGAGCATACGCCT
GCTTCATTATCCGCCTCAGCGGACGACGGATGAAAAGCAGCTGGGCGCGGGGGC
GCATACGGACTTTGGCGTGCTGACCCTGCTGCTGACCGATGGCCATCCAGGCCTG
CAAGTCCTGAACGCTGCGACCGACACCTGGGTGCCTGTACCACCGGATGCGGAC
GCGTATGTGGTGAATGTAGGAGATATGTTACAGCAGATAACGGACGGATATTTTAAAA
GCAACACGCATCGGGTGGTGAACCTAGGAGACGACGACCGGTATAGCGTACCGTAT
TTTTTCGATGGGTGTCTGGAAGTGTGCGTTAGAACGGTTAGATGGAAAGCACGAAGA
GAAAGTATTAACGGTCGAGGAACACATGAACGAACGGTTCGCTACCACCTACGGAC
GGGGCCAGCAAAAAACCGCT

NHI 17 protein sequence:

MPSAIEQPGFHIPTVDIASYLADPSSADAQQVVDVRLACTTSGFFQLVGHGIPITLRAT
MFAGSKALFELPFDQKKALKRAGNRGYEVMGSQALQDGTLPDMKEGYIIGEEIPFEE
GKAYRPFMEPNIWPSSEEQIPHSIFRLPMNEYKRVSA LGVVMDIFAAALPYGPNVFDK
LKQEPSAASIRLLHYPPQRTTDEKQLGAGAHTDFGVLTLLTDGHPGLQVLNAATDTWV
PVPPDADAYVVNVGDMLQQITDGYFKSNTHRVVNLGDDDRYSVPYFFDGLDCRLER
LDGKHEEKVLTVEEHMNERFATTYGRGQQKTA

Codon-optimized NHI 18 sequence:

ATGGCGAGCTCAGCGACGAGCAGCCCATATATTCCGGTTGTTGATATTACCCCATTT
TTAGAGAATCCACAGGGGACGGCCGCGCAACAGGTTGTGGATAACGTTCCGGCGTG
CCTGCATGTCAACGGGGTTTTTTCTGATGAAAGGCCACGGCATCAGCCCAAACTG
CAAACTCAGTGTTTCAGGCGTCAGCCAAATTTTTTTCGTTACCGCACGAGGCCAA
ACTGAGCTTAGATGCGCGGAAAAATGTGGGCTTTCGTGGCTATGATGTTATGGAGT
CACAATCATACGAGCTGGAAACCCGTAGCGGCCCAACAAGATGGGTCAGAAGTAATG
CGCGATACGAAAGAAGGCTTTTTTGGCAGCACCGATGTGCCACTGGATCACCCACG
CGTTGCCGCCGGCCGTTTCCTGGTTGGTCCAAATGTTTGGCCGGATGCCGATGTG
CTGAGCCACGAAGATTTCCGTGCCCCACTGGAAGAATATTTAGGGGAGATGAAACG
TCTGAGCCACGTTGTGCTGAATCTGATTGCCGCGACGCTGCCATACGGGCCGCAC
GTATTCGATGAACTGGAAGCCGATGATCCAATGTGCCTGCTGCGTCTGCTGCACTAT
CCGCCGACCCACACAGCGTAGATGGCATGAAATTAGGCGCCGGCGCCACACGG
ATTTCCGGTGCCATTACCCTGCTGTTACAGGATGAGCATCCAGGCCTGGAGGTGCTG
GATGAGAAAACCGGCGAGTGGCAGGGCGTTCCGCCACAAAAAGATGTGTATATCGT
TAACATGGCCGATATTATGAGCATTCTGACCAAAGGTGCCTATAAAAGCAGCGTTCAT
CGGGTTTGAACAAAAATACGGAAGATCGCTATAGCGTGGTTTTTTTCTTTGATGGC
AACCTGGATCTGAACTGAAACCGCTGGATGGGACGGAACAACGCCAGGATAATAA
CCAGGAGATTCTGACGCTGGAGGAGCATGTGCGCGGCCGTATGACCGGTAGCTAT
AGCATCCCAAAAAAT

NHI 18 protein sequence:

MASSATSSPYIPVVDITPFLNPQGTAQQVVDNVRRACMSTGFFLMKGHGISPQLQN
SVFQASAKFFALPHEAKLSLDARKNVGFRGYDVMESQSYELETRSGPQDGSEVMRDT
KEGFFASTDVPLDHPRVAAGRFLVGPVWPADVLSHEDFRAPLEEYLGEMKRLSHV
VLNLIATLPYGPHVFDELEADDPMCLLRLLHYPPTPHSV DGMKLGAGAHTDFGAILLL
LQDEHPGLEVLDEKTGEWQGVPPQKDVYIVNMADIMSILTKGAYKSSVHRVWNKNT
DRYSVVFFFDGNLDLKLKPLDGTQRQDNNQEILTLEEHVRGRMTGSYSIPKN

Codon-optimized NHI 19 sequence:

ATGGCGAAAGGTAACCTCTCGGGGGTGCCAACCGTGATATAAGCCCATATCTGAC
GGATCCAAAAAGCGATGCCGCCCGTCGTGTGATCGAAGATGTCCGTGAAGCGTGC
GTGTCAACGGGGTTTTTCCAGATTACGGGTCATGGCATTAGCGAATCGCTGCAACA
AAAAATTTTTGATGCGGCGCATGCCTTCTTCGCGCTGCCATTAGAAGAGAAAAAAA
ACTGAATGCCGCGAACTTTATCGGTCATCGTGGGTATGATGTCTTAGCCAGCCAAAG
CTATGAAGAAGGTGTATTACCAGATTTAAAAGAGGGTTATTATGTAGGCAGCGATGTG
CTGCCAAGCGATCCATTATATGGTCGTTTTTTTTATGGGCCAGAACGTGTGGCCATCA
ACGGGTTTACTGAGCCCAATCCAGTTTCAAGAACCATGCGAGCGTTATCACGAGAG
CGTGCGAGCACCTGGCCTTTAAAGTGCTGCAATTAATCGGTGATACGATGATCCACACA
CGGGCATAGCACGGTGGGTATGACGGAAAATATGCCAACGGTGCTGCACAATTTAA
TTCGTTTAGATAAAATTCCGGCGTGTCGGCTGCGCCTGCTGCACTATCCAAGCGCC
ACGCGCAACGGTGGTTCGGTCGCCGGCAAACCACAATATGGTGCGTCAGCGCACA
CGGATTTTCGGTGTAATTACGCTGCTGCTGCAAGATGATAATCCAGGCCTGGAAGTG
CTGGTGGA AAAAGATGGTAAACAAGTCTGGTGGCCAATCGATCCGAATCCAAGCGC
CTATGTCGTGAATATCGGTGATATGATCAGCATGGTGACGAACAGCATCTATAAAAGC
AGCATGCATCGCGTGGTATGCAAACGTCCAGAACGTGAACGTTATAGCGTGGTATTT
TTTCTGGATGGCTGTTTAAACGCGAATTTAGAGCCAATCGAGGGCTTTGGTCACCC
AGAGGAAGGGTTCGGGTTTTTCACACAAAACCGTAGAACACACATGACGGAACGTT
TATCAATGAGCTATGCGAAAGAGGGTAAAGATCCACGTCATAACGAGGATACGTTTT
CGGCG

NHI 19 protein sequence:

MAKGNFSGVPTVDISPYLTDPKSDAARRVIEDVREACVSTGFFQITGHGISESLQQKIFD
AAHAFFALPLEEKKKLNAANFIGHRGYDVLASQSYEEGVLPDLKEGYVVGSDVLPSPD
LYGRFFMGQNVWPSTGLLSPIQFQEP CERYHESVQHLAFKVLQLIGDTMIPHGHSTVG
MTENMPTVLHNLIRLDKIPACPLRLLHYP SATRNNGGSVAGKPQYGASAHTDFGVITLLL
QDDNPGLEVLVEKD GKQVWWPIDPNPSAYV VNI GDMISMV TNSIYKSSMHRV VCKRP
ERERYSVVFFLDGCLNANLEPIEGFGHP EEGFGF SHKTVEQHMTERLSMSYAKEGKD
PRHNEDTFS A

Codon-optimized NHI 20 sequence:

ATGGCGTCGCCAGCCAGCACGCCAGCCAGTAGCTCGTCACTGGTGCCAACTATCG
ATATTAGCCCATTCTTATTAAACCCAACGAGCGATGCAGCAAACGACGTATGCCAGG

CGATCCGGGCGGCCTGTCTGCATACGGGCTTTTTTTCAGGTGATCGGCCACGCCGT
GAGCACCAGCACGCTGACTGGTGGCTTTGAAGCATCACGGCGTTTTTTTACTTTAC
CACTGGAACAAAAACAGAAATTAGACATTACCAAACAACTGGGTTTTTCGGGGCTATG
ACGGCCTTGGCACTCAGTCATACAGCGGTGACACGCTTCCAGACCTGAAAGAATC
GTTCTTTCTGGGCCGTGATATACCACCAAGCCACCCAGACTATGGTCGCATACTGAC
GGGCCCCAACATTTGGCCTAGCTTCGCGGTGCTGCCGGCAACGACGTTTAAAGAA
CCAGTGGAAGCACTTTATTCAAGCACTGATGCAACTGGCATGCAAAATTCTGGAAATT
CTGGCCCCGCACCCTTCCACACGGTGCAGGCCGAAGGCATTTTTTGATCGGTTCGTGC
GCGACCCGGCCGCCCAATGCGGCTGCTTCATTACCCACCAATGGATGTGATTGAT
GAACGCCAGCTGGGTGCCTCAGCGCATACCGATTTTGGCGCAATTACTCTGCTTCT
GCAAGACCAGGTCCCGGGTTTACAGGTGCACGATTACAGACACCGGTGCCTGGCTG
GATGTGCCACCATGTCAGGACTCGATTGTGGTGAATGTCGGTGACATGATCACTCG
GTGGACTGCGGGCGAATACAAATCGAGCGTGCACCGTGTCTTAACCGGTCAGGT
ACCCACCGGTATTCAATCGCGTTCTTCTTTGACGGCAATGTGGATTGTCTGTTAGAC
CCGTTAGACGGTACCACTGCCCCGGGTGGTTCAATCACTGTGGAAAAACACATGAT
CGAATGTATACGTTTCATCATACGCGTCGAAA

NHI 20 protein sequence:

MASPASTPASSSSLVPTIDISPFLNPTSDAANDVCQAIRAACLHTGFFQVIGHAVSTSTL
TGGFEASRRFFTLPLEQKQKLDITKQLGFRGYDGLGTQSYSGDTLPDLKESFFLGRDIP
PSHPDYGRILTGPNIWPSFAVLPAITTFKEPVEALYSALMQLACKILEILARTLPHGAGEGI
FDRFVRDPAAPMRLLYPPMDVIDERQLGASAHTDFGAILLLLQDQVPLQVHDSDTG
AWLDVPPCQDSIVVNVGDMITRWAGEYKSSVHRVINRSGTHRYSIAFFFDGNVDCLL
DPLDGTTAPGGSITVEKHMIECIRSSYASK

Codon-optimized NHI 21 sequence:

ATGGTTAAAGGTAACCTTCTGTGGTGTGCCAACGGTGGACATCTCACCATATCTGGAA
GATCCAGGGAGCAACGCCGCCCGCAAAGTGATCGAAGATGTTTCGCGAAGCGTGCA
TCTCAACCGGCTTTTTTCAAATCACGGGTCATGGCATTCCAAAAAATCTGCAACAGA
ATGTGTTTGATGCGGGCGCATGCCTTTTTTCGCCTTACCATTAGAAGAGAAAAAAAAC
TGAACGCCGCGAACTTTATCGGTCATCGCGGGTATGATGTTTTAGCCAGCCAAAGC
TATGAGGAAGGTGTATTACCAGATTTAAAAGAGGGTTATTATGTAGGCAGCGATGTG
CTGCCATCAGATCCATTATATGGCCGTTTTTTTTATGGGCCGTAACGTGTGGCCATCA
ACGAAATTTTTAAGCACGGCGCAATTTCAAGAACCATGCGAGCGTTATCACGAATCG
GTGCAGCAACTGGCCTTTAAAGTGTTACAATTAGTGGGTGATACGATGATCCACGC
GGTCATAGCAGCATCGGTATGACGGATAATATGCCAACGGTGTGTCATGATTTAATT
CGTTTAGATAACATCCCGGCGTGCCCGCTGCGCCTGCTGCACTATCCATCGGCCGT
GCGTAACCGCGGGGATGTTGCCGGTAAACCGCAATATGGTGCGTCAGCGCATACG
GATTTTGGTGTAAATTACGTTACTGCTGCAAGATGATAATCCAGGGCTGGAAGTTCTG
GTAGAAATCGATGGTAAACAAGTTTGGTGGCCAGTGGATCCGAATCCAGGCGCCTA
TGTGGTGAATATCGGGGATATGACGAGCATGGTGACGAATGGCACGTATAAAAGCA
GCATGCATCGTGTGGTTTGCAAACAACCAGAACGCGAGCGTTATAGCATCGTATTTT
TTCTGGATGGTTGTTTAAATGCGAAATTTAAACCAATCGAGGGCTTCGGGCATCCGG

AAGAAGATATTGAAACGTGCGACAAAACCGTAGAGCAACACATGACGGAACGTTTAT
CAATGAGCTATGCGAAAGAGGGTAAAGATCCGCGTCACAACGAGGATGCCTTTAAC
GCG

NHI 21 protein sequence:

MVKGNFCGVPTVDISPYLEDPGSNAARKVIEDVREACISTGFFQITGHGIPKNLQQNVF
DAAHAFFALPLEEKKKLNAANFIGHRGYDVLASQSYEEGVLPDLKEGYVVGSDVLP
PLYGRFFMGRNVWPSTKFLSTAQFQEP CERYHESVQQLAFKVLQLVGDTMIPRGHSSI
GMTDNMPTVLHDLIRLDNIPACPLRLLHYPSAVRNRGDVAGKPQYGASAHTDFGVITLL
LQDDNPGLEVLVEIDGKQVWWPVDPNPGAYVVNIGDMTSMVTNGTYKSSMHRVVCK
QPERERYSIVFFLDGCLNAKLKPIEGFGHPEEDIETSHKTVEQHMTERLSMSYAKEGKD
PRHNEDAFNA

Codon-optimized NHI 22 sequence:

ATGCATAGCAGCTTTTATCTGCCACTGGTGGACATTACGCCATTTCTGGATGATCCA
AGCAGCCCAGCGGCCAGCAGGTGATTGATGACGTGCGTCGGGCCTGCCGTTTCG
ACCGGCTTTTTTCAGATGAAAGGTCATGGCGTTCCACTGAAACTGCAAAAAAGCATT
CTGGCCGCCGCCGCCAAATTTTTTCCCCTGCCGACCGAAACGAAACTGGCGCTGG
ATGCGCGCAAAAATGTGGGGTTTCGCGGGTATGATGTAATGGAAACGCAGAGCTAT
GAACTGGAAATTGGCGTACCACAGGGGCCAGGAAGCCCAGGTGGTGC GCGATATTA
AAGAAGGCTTTTTTATTAGCAGCGATCTGCCATTAGATCATCCGCGTGTTTCGCGACG
GCCGTTTTTTACAGGGGGCCAAACGTGTGGCCGGATAAAGAAGTTCTGGCCCCGCA
GGATTTTCGTGTCGTTCTGGAAGAATATCTGAGCGAAATGCAGCGTCTGTCACAGG
TTGTTCTGTCACTGGTTGCCGCGACGCTGCCGTATGGCCCCGCGTGTTTTTCGATGAA
CTGGACTCAGATGATCCAATGTGTCTGCTGCGTCTGCTGCATTACCCGCCGGATGG
GGAACAGGCCCGGCGTGAACGGGGGCAGCTGGGGAGCGGTGAACATACGGACTT
TGGTACCCTGACCCTGCTGCTGCAAGACGAACATGCGGGGGCTGGAAGTTCAGGAC
CATGAAACCGGCCGAATGGCATGGTGTTCACCGCAGGAAGATGTTTATATCGTGAA
CATGGCGGATCTGATGGAAATTATGACCAGCGGGGAATACCGGTCGTCGTGGCATC
GTGTCCTGAATCGTAACCCGGAAGACCGCTATTTCGGTTGTCTTTTTCTATGACGGCA
ACCTGGACTACAAATTACAGCCGCTGGACCCGGCGAAAAAAGTCGAAGAAGAAAAT
GTTCCAACGATCGAAGAGCATGTGCGTCTGCGCCTTACCAGTAGCTATAGCATCGC
GCAGAAA

NHI 22 protein sequence:

MHSSFYLPVLDITPFLDDPSSPAAQQVIDDVRRACRSTGFFQMKGHGVPLKLQKSILAA
AAKFFALPTETKLALDARKNVGFRGYDVMETQSYELEIGVPQGGQEAQVVRDIKEGFFIS
SDLPLDHPRVRDGRFLQGPNVWPDKEVLAPQDFRVVLEEYLSEMQRLSQVVL SLVAA
TLPYGPRVFDELDSDDP MCLLRLLHYPPDGEQARRERGQLGSGEHTDFGTLTLLQD
EHAGLEVQDHETGEWHGVPPQEDVYIVNMADLMEIMTSGEYRSSWHRVLNRNPEDR
YSVVFFYDGNLDYKLQPLDPAKKVEEENVPTIEEHVRLRLTSSYSIAQK

Codon-optimized NHI 23 sequence:

ATGACGAAAGGTAGCTTCTCAGGTGTGCCAACGGTGGACATCTCGCCATATCTGGC
GGATCCAAAAAGCGATGCCGCCAGAAAGTGATCGAAGATGTTTCGTGAAGCGTGC
ATCTCAACGGGGTTTTTCCAGATTACGGGTCATGGCATTAGCAAATCGCTGCAACAA
AACATTTTTGATGCGGCGCATAGCTTCTTCGCGTTACCATTAGAAGAGAAAAAAA
CTGAATGCGGCGAACTTTATCGGTCATCGTGGGTATGATGTTTTAGCCAGCCAAAGC
TATGAAGAAGGCGTATTACCAGATTTAAAAGAGGGTTATTATGTAGGCAGCGATGTG
CTGCCAAGCGATCCATTATATGGTCGTTTTTTCATGGGCCAGAACGTGTGGCCATCA
ACGGAATTACTGAGCATTATCCAGTTTCAAGAACCATGCGAGCGCTATCACGAAAGC
GTGCAGCACCTGGCCTTTAAAGTGCTGCAATTAGTAGGTGATACGATGATCCCACAC
GGGCATAGCACGGTGGGTATGACGGAAAATATGCCAACGGTGCTGCACAATTTAATT
CGTTTAGATAAAATCCCGGCGTGTCGCTGCGCCTGCTGCACTATCCAAGCGCCAC
GCGCAACGGTGGGTGCGTTACGGGCAAACCACAATATGGTTCGTCAGCGCACACG
GATTTTCGGTGTAATTACGCTGCTGCTGCAAGATGATAATCCAGGCCTGGAAGTGCT
GGTGGAAAAAGATGGTAAACAAGTTTGGTGGCCAATCGATCCGAATCCAAGCGCCT
ATGTTGTGAATATCGGTGATATGATCAGCATGGTGACGAACGGCATCTATAAAAGCA
GCATGCATCGCGTGGTATGCAAACGTCCAGAACGTGAGCGTTATAGCATCGTATTTT
TTCTGGATGGCTGTTTAAATGCGAATCTGGAGCCAGTAGAGGGTTTCGGGCACCCA
GAAGGCGTGGGTTTTTCGCACAAAACCGTAGAACACACATGACGGAACGTTTATC
AATGAGCTATGCGAAAGAGGGTAAAGATCCACGTCATAACGAGGATACGTTTTTCGG
CG

NHI 23 protein sequence:

MTKGSFSGVPTVDISPYLADPKSDAAQKVIEDVREACISTGFFQITGHGISKSLQQNIFD
AAHSFFALPLEEKKKLNAANFIGHRGYDVLASQSYEEGVLPDLKEGYVVGSDVLPSPD
LYGRFFMGQNVWPSTELLSIIQFQEP CERYHESVQHLAFKVLQLVGDTMIPHGHSTVG
MTENMPTVLHNLIRLDKIPACPLRLLHYP SATRNNGSVTGKPQYGASAHTDFGVITLLL
QDDNPGLEVLVEKD GKQVWWPIDPNPSAYV VNI GDMISMVTNGIYKSSMHRV VCKRP
ERERYSIVFFLDGCLNANLEPVEGF GHPEGVGF SHKTVEQHMTERLSMSYAKEGKDP
RHNE DT FSA

Codon-optimized NHI 24 sequence:

ATGAGCCCAAACGTGATTGTGGATGAAAACATTACCAGCAAACACCACGGTGGA
TAGCTTTCATATTCCAACGGTTGATATTT CAGCGTTTCTGGCGGATCCGGATT CACCA
GAAGCGCAGAGCATTATTCCAATTGTT CGGAGCGCGTGCCGCTCAACCGGTTTTTT
TCAGATTACCGGTCATGGCATCAGCAAAGATCTGCAACAGGCGGTTTTT GCGGGCG
CGAAACAGTTTTTTTAGCCTGCCATTTGAAACGAAAAAAGCGCTGGATGCGCATTTAA
ATCAGGGCCTGCGGGGTTATGATGTATTAAGCTCACAGAGCTATGAAGATGGGATTC
TGCCGGATCTGAAAGAAGGCTTTTTTACCGGTGTTGATCTGCCGGCGGATGATCCT
CGTGTT CAGGCGCGCAAATTTCTGATGGGTAGCAATGTGTGGCCAGATGCGAGCCT
GCTGCCAGAAGATGAATTT CGCAAACCAATTAAAGAATATCATGATGTTCTGATGAAA
CTGAGCATTA AACTGCTGAAACTGATCGAACGCACCCTGCCATACGGTCCGGGTAT
TTTTGATGAATTTATTGGCAACGATCCAATTATGCCGATGCGCATGCTGCATTATCCG
CCGGCGCGCCCAGAACATGAACGGAACGGTAAAACCCAGTATGGTGCGAGCGCG

CATACCGATTTTGGCGCGATCACGCTGCTGCTGCAAGAAAAAATCCAGGGCTGGA
AGTTTTTGAATCACGTACCGATGAATGGAAACCAATCCCGCCGAATCCGGATGTTTA
TGTTGTGAATATCGGCGATATGCTGTCGTTTTGGACCAAAAACGAATATAAAAGCTC
GGTTCATCGCGTTATTAATCGCGAACCAGGCGATCGGTATTGATTGTTTTTTTTGTT
GATGGGAATGGGGATGCGAAACTGTCACCGCTGGATGGGTCAGAAGAAGATAATCC
GCTGACGGTGGAACAGCATCTGATCCGTCGGCTGGCGGAAAGCTATGGCAAAAAA

NHI 24 protein sequence:

MSPNVIVDENITSKTTTVDSFHIPTVDISAFLADPDSPEAQSIPIVRSACRSTGFFQITGH
GISKDLQQAVFAGAKQFFSLPFETKKALDAHLNQGLRGYDVLSSQSYEDGILPDLKEGF
FTGVDLPADDPVQARKFLMGSNVWPDASLLPEDEFKPKIKEYHDVLMKLSIKLLKLIE
RTLPGPGIFDEFIGNDPIMPMLHYPPARPEHERNGKTQYGASAHTDFGAILLLLQE
KNPGLEVFDSTDEWKPIPPNPDVYVNVNIGDMLSFWTKNEYKSSVHRVINREPGDRYS
IVFFVDGNGDAKLSPLDGSEEDNPLTVEQHLIRRLAESYGKK

Codon-optimized NHI 25 sequence:

ATGCCGCCCTTACAGTACACCTGGAAAATTCTCCGCGGCGCGGCCCTTCAGAACG
CTTTGTCACCGTCTAGTACGACCAGCCAGCTGCGTGTGACGCGGCCGATTGCTGC
ATTTAACCCTTTTAGCCTAGCCACGTACGCACCTTCAAAGCACCTGCTCGCCGTC
GTCAATCATTGCGGGCAACGGAAACGACATCTACCGCGACCCCGTCATCGAGTGTG
CCGCCGACCCTGCCCACGCCGCGCGCTGCGACCACCACCCACCTAGCTTCACC
ATTCCGACTGTAGACATCGCCCCCTATTTGAGCAATCCAAGCTCGCCGGCAGCTCA
GCGCGTAATTGAGCAGATTAACCAAGCATGCCGTAGCACGGGCTTCTTCCAAATAG
TTAATCATGGTGTCCCTGCGGCCCTGCAATCAGAGGTGTTTAGAGCTGCCGAACGC
TTCTTTTCGCTTACCGCTGGAAGAAAAGAAGAACTGGATGCGAAAACCACCGTGGG
TCATCGTGGCTACGATGTGCTGGAATCCCAGAGCTATGAAGAAGGTGTGTTGCCTG
ACTTAAAAGAAGGCTTTTATGTGGGTAACGACATTCCAGCGAGCGACAGCCGTGCC
CAAGCGCGCCGCTTCTTTATGGGCCCGAATGTGTGGCCGTCGTCACTGCAACCTC
ATGAACTGCAACAACCGGCAGAAGCGTATTTTCGCAGCAGTGTATACCCTGTCATTAC
GCATACTTGACATGATTGCGGCATCACTCCCGTACGATGTCTCGCCTATGTTTCGCAC
GTTTCACCCAGCCAGCTGACCTGGTTGCCGCGCCACTACGTCTGCTTCACTATCCG
CCTGCCCGACGCTCTAAACAGAGGCAGCTGGGGGGCGTCTGCGCATACTGATTTTG
GCGCTATCACCTGTCTGCTACAGGATGGTAATCCGGGCCTGCAAGTGCTTGATCAG
CATAGCGAAAGCTGGGTGGACGTGCCCTCGACGCGTAATACGTATGTCGTGAATGT
TGGTGACATGCTTGAGAAATGGACGGGTGGCTACTACCGCAGTAGCGTTTCATCGTG
TGCTGAATCCGCAGCCAAAAGATCGCTATTGATCGTTTTCTTCTTTGATGGTAACTT
GGACTGTCCCTTAGTTCCGCTCAATCCGAATGATGCCGCGAAATCGTCAGCCCTGC
CGGGTGGCGAGGGCGGTAAAGAAGATGGTGTGCTGACTGTGAGAAACACATGAT
TAACCGCATGACAACTAGCTATGGTAAGGGCTCGAAGAAGTAA

NHI 25 protein sequence:

MPPLQYTWKILRGAALQNALSPSSTTSQLRVTRPIAAFNPFLATSRTFKAPARRRQSF
AATETTSTATPSSSVPTLPTPRAATTTTPSFTIPTVDIAPYLSNPSSPAAQRVIEQINQA

CRSTGFFQIVNHGVPAALQSEVFRAAERFFRLPLEEKKKLDKTTVGHRGYDVLESQS
YEEGVLPDLKEGFYVGNIPASDSRAQARRFFMGPVWPSSLQPHLQQPAEAYFAA
VYTLSLRILDMIAASLPYDVSPMFARFTQPADLVAAPLRLLHYPPARRSKQRQLGASAHT
DFGAILLLLQDGNPGLQVLDQHSESWVDVPSTRNTYVVNVGDMLEKWTGGYYRSSV
HRVLNPQPKDRYSVVFVFDGNLDCPLVPLNPNDAAKSSALPGGEGGKEDGVLTVEKH
MINRMTTSYGKGSKK

Codon-optimized NHI 26 sequence:

ATGCCTAGCGCGATCGAACAACCACAGTTTCACATTCCGACGGTGGACATCGGTCC
ATATTTGGCTGACCCGTCTAGTGCGGAAGCACATCATGTTGTCGATGCGGTTCGCC
TGGCGTGTACGACTTCGGGCTTCTTCCAATTAACGGGTCATGGCATTGAGCCGGAG
ATTCGCGATGCAATGTTTAGCGGTTTCGAAAGCCTTATTTCGATCTGCCGTTTCGATCAG
AAGAAAGCGCTGCGGCGCGGGAAGAACC GCGGTTATGAAGTCATTGGCTCGCAG
GCCTTACAAGATGGGACCTTGCCTGATCTGAAAGAAGGGTATTATATCGGTGAAGAT
ACCACAGATTTTGAAGAGGGGAAAACCTACCGCCCGTTTATGGATCCTAACGTTTG
GCCGTCAGAGGATCAGGTCCCGAGTAGTGTGTTTCGGAAACCGATGAATCAATATT
ATGAACGTGTAGCTGCGCTCAGCAAAACCGTAATGGACATTATTGCGGCAGCGCTC
CCGTATGGGCCCACGGTGTTTGATCAATACAAGCTGGAACCAATTGCCGCGAGCAT
CCGCCTGCTGCATTATCCGCCGCAGCGAACCAACGACGGTAAACAGCTGGGTGCC
GGCGCGCATACCGACTTCGGCTGGATCACTCTGCTGCTCACCGACGGACATCCAG
GCCTGGAAGTGTTAAATCAGAGCACCGGCGAATGGGTACAAGTCCCGCCGAACAA
GGATGCCTACATTGTGAATGTCGGCGATATGCTGCAACAGATTACCGGGGGCTATTT
TAAATCGAACTTTTCATCGTGTTTTGAACTTAGGTGAATCAGATCGTTATAGCGTTCCG
TACTTCTTTGATGGTTGCCTCGACGCGAAACTCGCGCGCCTTGACGGTCGCGACG
AAGGTAAAGTACTGACAGTGGAAGAACACATGCTGGAGCGTTTTGCGACGACTTAT
GGTCGCGGCCAGGCCAAAAGATTAA

NHI 26 protein sequence:

MPSAIEQPQFHIPTVDIGPYLADPSSAEAHHVVDVRLACTTSGFFQLTGHGIEPEIRDA
MFSGSKALFDLPFDQKKALRRGKNRGYEVIGSQALQDGTLPDLKEGYIIGEDTTDFEE
GKTYRPFMDPNVWPSEDQVPSSVFRKPMNQYYERVAALSKTVMIDIILPYGPTVFD
QYKLEPIAASIRLLHYPPQRTNDGKQLGAGAHTDFGWITLLLTDGHPGLEVLNQSTGE
WVQVPPNKDAYIVNVGDMQLQKITGGYFKNFHRVLNLGESDRYSVPYFFDGCLDAKL
ARLDGRDEGKVLVVEEHMLERFATTYGRGQAKD

Codon-optimized NHI 27 sequence:

ATGAGTCCAAGCAAGACCCCGAGCTTTACCATTCCGACGGTAGACATTAGCAGCTAT
GTCGCCGACCCGACCTCGCCCGCTGCGAAATCCGTTATTGAGGATGTTAGAAACG
CATGCATCACTAGCGGTTTCTTTACGCTGGTGGGTCATGGAGTTCCACGCGAACTG
CAAGAAGCCGTGCTGAACGGCGCTAAAGCATTCTTTAATTTACCGCAAGACGAAAA
GCTGAAGTATGAGAAAAGCACAGTCGGCAAAGGGAATCGTGGCTACGAGATCATG
GGGAAACAGATCTTACAGAAAGGAGCGCTGCCAGATCTAAAAGAAGGTTTCTATGT
GGGCGAAGATTTTGAGCCAAGCCCGGATCCCAACCATAAGTATAGCTGGTTCAATC

CGCCCAATGTGTGGCCACGTCGTTGGCTGACAGCGAAATCGTATTTTCGCAAACCT
ATCAACGAATACTATTCCCACATGTTCCCATTAAGCACGACGATTCTGGACATTATGG
CCGCAGGTATGCCGTATGGTCCTTCCGTTTTTCGATGAGTTCAAAAGCGATCCAGTG
GTAGCAGTGATGCGCCTGTTACATTATCCACCGCAGCCTGAATCTTCTGACGCCTTG
CAGTTCGGTGTGCGGCACATACCGATTTTGGCTCTATCACACTGCTCCTACAGGAT
ATGGCTGGCGGTTTAGAAGTGTTGAACCACGACACGAACGAATGGGTCCCTGTTAC
CCCTAATCCGGACGCGTATGTAGTGAACCTCGGTGACATGATGCAGCGTTGGACGC
GCGGTGCTTACCGCTCTAACTTGCATCGTGTAAGAATATGGGTGGGGGGGATCGC
TACAGCGTACCGTTCTTCTTCGATGGCAACATGAAAACAAAGCTCGCCCCGTTCTGA
CGGCGGAGAAACCGATGAGGAAGTAATTACCGCCGAAGATCACATGATGGAACGAT
TTAGAACCACCGCAGGCTTTTAA

NHI 27 protein sequence:

MSPSKTPSFTIPTVDISSYVADPTSPAASKSVIEDVRNACITSGFFQLVGHGVPRELQEAV
LNGAKAFFNLQPDEKLKYEKSTVGKGNRGYEIMGKQILQKGALPDLKEGFYVGEDFEP
SPDPNHKYSWFNPPNVWPTSLADSEIVFRKPINEYYSHMFPLSTTILDIMAAGMPYGPS
VFDEFKSDPVVAVMRLHYPPQPESSDALQFGVGAHTDFGSITLLLQDMAGGLEVLNH
DTNEWVPVTPNPDAYVVNLGDMMQRWTRGAYRSNLHRVKNMGGGDRYSVPFFFDG
NMKTKLAPFDGGETDEEVITAEDHMMERFRTTAGF

Codon-optimized NHI 28 sequence:

ATGCCTAGCTTCACGGAAAATTCGGGCTCGACCAGCTTTCAGATTCCGACAATTGAT
ATTTCCCCGTTTATTACCAGCCCAGCATCTCTTAAAGCGGGCAAAGTAATTCAAGCC
ATCCAACCTGGCATGTCGCTCCACGGGCTTCTTTCAGATTACAGGTCACGGCGTGCC
GGAATCGGTGCAGGAACAAGCTCTGGATGCCTCGAAACGCTTCTTCAGCATGCCG
CTTGAGGACAAAGAACTTTGAACATTAACTTAATCCGGGCTTTTCGCGGCTACGAT
CCGTTGTGCACGCAGACTTATGGGCCGGATGCCCTGCCCGATCTGAAAGAAAGCT
TCTTCGTTGGCCACGACATCCCGCTCGACGATGTGCGGGTGAAAGCCCGCAGGCT
CCTGACCGGCCCAATGTCTGGCCGAGCGGGCTGCCAGCGTCCAGCTTCAAAGAT
TCCATCGAAACGTATTATAATGCGCTTCATGATTTGACGCTACGTATTTTAGAAATGAT
TGCCCTTGGTCTGCCGTATGGGGCCGACGTATTTAGTAATTTTATCTCAAACAGCCC
GGCGGCTCCTATGCGTCTGTTGCACTACCCACCGCAGGAAATCGACGATGACAAAC
GTCAGCTGGGTGCATCCGCTCACACTGACTTCGGCGCAATTACTCTCTTGCTCCAG
GATAAGAACGAAGGACTCCAAGTGCATGATGTTCAAACGGATTCTTGATGACTGTA
CCGCCGCGCAAGGATGCGTTTGTCTTAATGTAGGGGACATGTTAGAAAAGTGGAC
GGCGGGCGATCTTAAAGTTCTCTTCATCGCGTCCTCAACCAGGGGGGGCGCGAC
CGCTACTCGATCGCCTTCTTCTTCGATGGGAACCTGGACTGCACACTCAGCCCGCT
GGATGGGACGCGCGTCGAAGGCGAACCGCTGACTGTTGAGAAACACATGATTCAA
TGTCTATCTGCTAGCTATAAGGAAACGGTCGAGTAA

NHI 28 protein sequence:

MPSFTENSGSTSFIPTIDISPFITSPASLKAGKVIQAIQLACRSTGFFQITGHGVPESVQ
EQALDASKRFFSMPLEDKETLNIKLNPGRGYDPLCTQTYGPDALPDLKESFFVGHDP

LDDVRVKARRLLTGPNVWPSGLPASSFKDSIETYYNALHDLTLRILEMIALGLPYGADV
SNFISNSPAAPMRLHYPPQEIDDDKRQLGASAHTDFGAILLLLQDKNEGLQVHDVQTD
SWMTVPPRKDAFVVNVGDMLEKWTAGDLKSSLHRVLNQGGDRYSIAFFFDGNLDCT
LSPLDGTRVEGEPLTVEKHMIQCLSASYKETVE

Codon-optimized NHI 29 sequence:

ATGGCAAGCAGCGGCTTTTACATACCATCTGTTGATATTGCGCCTTTCATTACGATC
CTTCCAGTGACGCCGCGAAAGACGTGATCGAAAAGGTCAAGAAAGCGTGCGTCAG
CACCGGCTTCTTTTCAGATTTTCGGTCATGGAGTGCCGAAGCAGGTACAGAAATCCG
CATTTGATGCATCCGCGGCGTTCTTTAGCCTGCCGGTCGATACGAAGATGGCGCTG
AAGGCAGGCCCTAGCACTGGCTTTAAGGGTTATGAACAGCTGGAGAGCCAAATCTTA
CAGCTATGATGTTAAAGGAGATATTAAAGAAGGGTTCACCATTTCCACCGATTATCCT
GACGGACATCCACTCCGCACCCCTCTGAATGGCCGCCCTCGTTTTCTGACAGCTC
CGAATATTTGGCCCAACACCGAAATGATGGGCGATGCAGAGTGTTCCATGCTTCT
TTGGAAGCCTACCAAGAAGCAATGGTTACCCTGCGAGCGCATGTTTTATCTCTTATT
GCCGCGACCTTACCGTACGGCCCGCATGTCTTTGATGAAATGAATCAGGAGCCGGC
ATGCCCGCTGCGTTATCTCCACTACCCGCCGATGTCTGAAGGGACCGATATTGTGA
AACAGCAGGGAGCTTCCGCACACACTGATTTTAGCGCGGTCACTCTGCTGCTCCA
GGGTCAACAGGACGGCCTTGAGGTGCTGGATTACGACACGGGTGAATGGCATTG
GTACCGCCGAACCCGGATGCCTACGTAATTAATCTTGGCGATATGATGGCGAAATTA
CTGCGCGGACAGTATAAAAGTAGCAAACACCGCGTCATTAATCGCGCGAAAGTGGA
TCGTTACTCAATTGTTTATTTCTGGGACGGCAACCGCGATTTTGAAGTGAACCGCT
GGATGGCGCAGAAATGGATCAAAAGCACATGACGTGTGAAGAATACATGTTTCGATA
GATTGAAATTCAGCTTTGGGCGTCACGAAACCAAACCAAGTGCAGGCGCAGTAT
TAA

NHI 29 protein sequence:

MASSGFYIPSVDIAPFIHDPSSDAAKDVIEKVKKACVSTGFFQIFGHGVPKQVQKSAFD
ASAAFFSLPVDTKMALKAGPSTGFKGYEQLESQSYSYDVKGDIKEGFTISTDYPDGHP
LRTPLNGRPRFLTAPNIWPTTEMMGDAEWFHASLEAYQEAMVTLRAHVLSLIAATLPYG
PHVFDEMNPQEPACPLRYLHYPPMSEGTDIVKQQGASAHTDFSAVTLLLQGGQDGLV
LDYDTGEWHLVPPNPDAYVINLGDMMAKLLRGQYKSSKHRVINRAKVDYRYSIVYFWDG
NRDFELKPLDGAEMDQKHMTCEEYMFDRCLKFSFGRHETKPEVQAQY

Codon-optimized NHI 30 sequence:

ATGGCGAATTTTCATATCCCGACCATAGACATTAGCCCATATCTCCAGGATGCCACGT
CAGATGCGGCAGACCAGGTGGTGCGTGATGTGGGTAAAGCGTGTGCCACCGTGG
GGTTCTTTAGCTTGGTTGGTCATGGCATCCCCGAAACATCCAAGACAACGTGTTC
GAAGCGGCGAAGAAGTTGTTTAACCTACCCGCCGAGGAGAAGCGTGCGCTGAGAC
ATCCACTGATGAAGAATCGTGGATATGAGCTAATTGGGAGCCAGGCACTCCAGGATA
ACACGCTGCCCAGATCTGAAAGAAGGGTTTTACATTGGCAAGCATATCCCAGCGGAA
TCGGAACGGTCGCGCGCCCATCCCGAACTGCTGGGAGAGAATATCTTTCCGGCCT
CACTTCACGATACCGTGTTTAAGAAGCCCACCGAAGCCTATTATACCGCGGTCTTGG

AGCTGTCCTTAAAAGTCTTAGAAATTCTGGCAAAGGGCCTTCCTTATGGTGATGACA
TTTTCAAGGAATTTGTCTCTAACGATCCAGTTTGTATCATGCGCCTCTTGCATTACCC
GCCACAGGCATCACAGGACGAACGTCAGCTCGGCGCGGGCGCACATAACCGATTTT
GGTGCAATCACTCTGCTGTTACAGGACACTTCCGGCGGTCTGGAAGTCCTGGATCA
TAATACAGGAACGTGGCACGCGGTAGCTCCTAACCCAGACGCGTACGTGGTGAATA
TAGGTGATATGCTGGCCCTGTGGACTAAAGGAATTTACAAAAGCGCCGTTCATAGAG
TTATTAATAAGTCCGGTGGAGATAGATATTCCGTGCCGTTCTTCTTCGATGGCAACG
CGGAAGTAAAGCTTAAGCCCTTTGATGGCAGCGAACCAGTCGGCGGGCAAAATTATC
ACCGTTGAAGATCACATGTTAGAACGTCTTGGCACTTCGTATGCACGTGTGCAACAA
GGTGCTGGCCAAGCGGTCAGCGCCAGTGCGTAA

NHI 30 protein sequence:

MANFHIPTIDISPYLQDATSDAADQVVRDVGKACATVGFFSLVGHGIPRNIQDNVFEAAK
KLFNLPAAEEKRALRHPLMKNRGYELIGSQALQDNTLPDLKEGFYIGKHIPAESERSRAH
PELLGENIFPASLHDTVFKKPT EAYYTAVLELSLVLEILAKGLPYGDDIFKEFVSNDPVC
MRLHYPPQASQDERQLGAGAHTDFGAILLLLQDTS GGLEVL DHNTGTWHAVAPNPD
AYV VNI GDM LALWTKGIYKSAVHRVINKSGGDRYSVPFFFDGNAEVKLKPF DGSEPVG
GKIITVEDHMLERLGT SYARVEQGAGQAVSASA

Codon-optimized NHI 31 sequence:

ATGGCCGTCCTCCGCTGATGCATCAGACAATGCACAGCCAGGTGCATGAAGCCAGCG
ATGCATCACACGAAATCCCGACCATTGACATCTCCGGCTTTTCGTTCCAGCCCGGAA
ACTGCGCAGGAACGTATCGAGACTCAACATGTGGTTGACCGGGTGCGTAGTGCGT
GCCTGACGACCGGGTTCTTCTGTCTCACGGGCCATGGCATTCCGCGCGAATTGCA
GGAGCGTGTTCTTGATGGTGCAGAGAAATTCTTCGACATGCCGCTTGAAGAAAAGC
TGAAACTTGTTACCCGACTCAGAAGAACCGCGGTTATGAGGTGCTTGGTGGCCAA
ACTCTGCAACGTGGTGCAAAACCGGATCTGAAAGAAGGCTTTTACATCGGCAAACA
CCTGGATGGTAACGACCCCCGAGTGCGGCGGCCACCCGCGCCTGATGGGCCCAAA
TATTTTCCCGAGCGGCAGTCTTGAGGATCATGAATTTAAGAACCCACTGGAAACCTA
TTATGAAGCTATCTTAGCGTTGTCTCTGACGGTTTTCAAATACTGGCGAAAGGCCT
GCCATACGGGGATGATGTGTTTGACCGATTTCGTGAGCGATGATCCGGTCTGCATTC
TCAGACTGCTGCATTATCCGCCGCAGACCAGTAAAGATCCTCGCCAGCTGGGCGC
CGGCGCGCATACAGATTTTGCGCGGTTACCTTGCTATACCAAACGGCACCAGGTT
TACAGGTGAAGTCTCCGAGTGGCTCAGGCTCAAGCGGTGCCGATCGTTGGATTCC
GGTGCCGCCAAACCGTGACGCGTACGTTGTCAATATAGGCGACATGCTGCACGCG
TGGACAGAAGGACTCTATAAATCCTCGATGCACCGCGTGCTAAATCTGGGTGGCAG
TCACCGTTATAGCATTCTTTCTTCTTCGATGGTAACGCAGACTGTCCGCTGACTCC
GTTCCGAAAATCAGACGACGTTGGCGCTGAGACTGCCAGCGAGCATTTACTGCGT
CGCCTCGACGAAACGTATGCAATGGCAGCCAAAATCTAA

NHI 31 protein sequence:

MAVPLMHQTMHSQVHEASDASHEIPTIDISGFRSSPETAQERIEQHVVD R VRSACLTT
GFFCLTGHGIPRELQERVLDGA EKFFDMPLEEKLVHPTQKNRGYEV LGGQTLQRGA

KPDLKEGFYIGKHLDGNDPRVRRHPRLMGPNIFFSGSLEDHEFKNPLETYYEAILALSL
TVFKILAKGLPYGDDVFDRFVSDDPVCILRLLHYPPQTSKDPRQLGAGAHTDFGAVTLL
YQTAPGLQVKSPSGSGSSGADRWIPVPPNRDAYVVNIGDMLHAWTEGLYKSSMHRVL
NLGGSHRYSIPFFFDGNADCPLTPFGKSDDVGAETASEHLLRRLDETYAMAAKI

Codon-optimized NHI 32 (XenC homolog 1) sequence:

ATGATTCCCACGGTGGATATTTCCGCCTTCAACGACGATAGTGCTACCGCGGATAGC
AAGAACGAAGTGGTGCAGGCTGTGGCGCACACCTGCTCTACGTATGGGTTCTTCTA
TCTGGTGGGCCATGGTATTCCGGAAGCGGATCGTCAGCAGATTTTGGATTGTGCCC
GCTTATTTTCATCCCTGCCCATGGATGAGAAAATGATCATCTCGGTGAGCAAGCGCA
TGGGGCAGTCGTTTCGTGGTTATGAACCCCCAGCCCTGCAATTGCACCAGGAAGG
TCTACTTCCTGATACGAAAGAGGCTTTTCATTTTCGGTCGCGAGGTTAGCGCGGACC
ATCCGGATGCCGGCCGTTTCAGCACCGGCCCGAACCAGTGGCCGCCGTCCTACTGC
CGGATTTCGACGTTTTGTATCCCACTGCTGGAATACCAGCGTAAAATGGTGCAGCTG
GTGAAAACCATTCTGAAGATTCTGGCCTCGGGCCTGCCGGAAGAATGGAATTGTCC
ATGCGATGTGTTTGATGCCGCTACCGTTCGAACCAAGCATCCCTATGCGCTTACTCCA
TTATGCGCCTCAGTCAGTTAAGAGCGAAAACCAATTTGGCGTTGGCGATCACACCG
ATTTTGGCAACGTGTCCATTCTTCTCCAGGAAGAAGGCACGGAAGGCTTAGAAGTG
TGGTATCCGTTGACAGAGGATTGGATCCCAGTGCCCGTTATTCCGGGTTCTTACGT
AATCAATATCGCGGACATGATGCAAAAGTGGACGGCGGGCTTCTACCGTAGCGCTC
GTCACCGAGTTGTAAACCATAATAAACGTCCGAGATATAGTGCAGCGTTCTTTCCCA
ACGGCAATATTGACCTGAAGTACCGTGCGCTGGATGGAAGTGGTGTGAGAGAAAC
GATTGGCAAACACATACGCCAGCGCCTGTTTGAGACAATAGGTGGCGAGGCGGGT
AAGAAGCTGGAGAACGACGCCGTCAAACGCTAA

NHI 32 (XenC homolog 1) protein sequence:

MIPTVDISAFNDDSATADSKNEVVQAVAHTCSTYGFFYLVGHGIPEADRQQILDCARLFS
SLPMDEKMIISVSKRMGQSFRGYEPPALQLHQEGLLPDTKEAFIFGREVSADHPDAGR
FSTGPNQWPPSLPDSTFCIPLLEYQRKMVQLVKILKILASGLPEEWNCPCDVFDAATV
EPSIPMRLHYAPQSVKSENQFGVGDHTDFGNVSILLQEEGTEGLEVWYPLTEDWIPV
PVIPGSYVINIADMMQKWTAGFYRSARHRVNHNRPRYSAAFFPNGNIDLKYRALDG
SGVEKTIGKHIRQLFETIGGEAGKKLENDVAVKR

Codon-optimized NHI 33 (XenC homolog 2) sequence:

ATGAAAGAACAGGTGACCCCGGGCATTACCAATCCTTGGCCAGTCTGTACTTCTT
CAGCATTACGAGCATCCCCATTGTTGACATATCGCCGTTTCTCGATGAAGAAGTGTC
GCAGGAAATGATGAACCAGGTGGTGGAAAGCCATGCGTGAGGCTTGTAACACGTGT
GGGTTCTTCTATTTACTGGGCCATGGCATATTCGAGGAAGATTGTAAGAGTGCCATG
GGCAAATCCTTTTCGCGGCTACGAACCGCCTGCGCTGCAAATGCATCAGGAAGGGC
TCCTGCCTGATACCAAAGAAGGTTTTATCCTGGGTTGCGAAATTCGGGCAGATGCG
CCCGAAGCGGGCACGTTCCATACTGGCCCGAATCAATGGCCGGAGAGCATTCTAT
GATGGAATACCATAGCAAAATGATAGAAATGGTGAAGGTTGTGGTCAAATCTGGC
GCTGGGTCTGCCTGATCAGTGGAAGTCTCGCCGGATGTATTCGATGAGATGACGC

ATAATCCGTCCGCGCCTCTGCGTTTGCTGCACTATGCCAGCCAACCGCTAAAATGC
GAAAATCAGTATGGTGTAGGCGATCATAACGATTTTGGGAATGTGAGTGTTCTGCTC
CAGGAAGAAGGACGTGATGGTCTGGAAGCGTTTTACCCGCCGACGCATGTGTGGG
TACAGTCCCTGCGTTGGAACACTCCTATGTTATTAACATCGGCAACATGATGCAGA
AATGGACCGGTGGATATTATAAAAGTGCCCGTCACCGAGTCATCAATCACAAGACTA
AAAGCCAATATATCACTCCGTTTTCTATGAACGGTAACTTAGGCTTAAAATGTCGCGC
ACTGGACGGATCCGGCACGGAGACTGTGATTGGTGATCATATTCGGCAGCGCTTG
GTTGAAACCATCGGTGGTGAAGCTGGGAAGAACTGGGTTACTAA

NHI 33 (XenC homolog 2) protein sequence:

MKEQVTPGIYQSLASLYFFSITSIPIVDISPFLDEEVSQEMMNQVVEAMREACTTCGFFY
LLGHGIFEEDCKSAMGKSFRGYEPPALQMHQEGLLPDTKEGFILGCEIPADAPEAGTFH
TGPNQWPESIPMMEYHSKMIEMVKVVVKILALGLPDQWNCSPDVFDEMTHNPSAPLR
LLHYASQPLKCENQYGVGDHTDFGNVSVLLQEEGRDGLAFYPPTHVWVPVPALEHS
YVINIGNMMQKWTTGGYYKSARHRVINHKTKSQYITPFSMNGNLGLKCRALDGSGETV
IGDHIRQRLVETIGGEAGKKLGY

Codon-optimized NHI 34 (XenC homolog 3) sequence:

ATGGGCTCTATCGAAGCCATTCCTACGGTGGACATCTCTGCGTGGATCGATACATCC
TCTACTGAAGAAGAACGCCAGCGTGCCGTGGATGAAATGCGAAATGCTTGCACCC
GCTACGGCTTCTTTAATTTAATTGCCACGGCGTCAGTCCCCAGGCGCAATCACAA
GCGTTAAATTGTGCTAAGTTATTCTTTACCTTGTCCGAACAGGAAAAGATGAAGGTC
TGATTAGTAAATCGGTTGGCCGTAGCTTTCGTGGGTACGAGCCCCCTGGCATTCAA
GTACATCAAGAAGGCTTACTGCCGGATACTAAAGAGTGTTTCATTATCGGACACGAG
GTGCCAGAGCATGATCCGGAATGCGGCACATTTTCGACTGGGCCGAATTTATGGCC
CAAATCTCTGCCCCGAAGATGAATTTAGGATCCCTATCATGGAATATCAGGCCCCGCAT
GGTAGCCCTGGTGAAAGTGCTTTTGAAGATCCTGGCCCCGCGGGCTGCCGAAGGAA
TGGAAGTGTCTCCAGATGTACTGGATCCGCTCGGCGAGAATAACCCGAGCATTCC
GATGCGTTTGTTCATTACGGCCCCGCAACCAATTCGTGATGACCGCCAGTTTGGCG
TTGGCGATCACACAGATTTTGGATGTGTGACCATCTTGTTACAAGACATGGGTACTG
AAGGCCTGGAAGTGTGGTATCCCCAACGGAAACCTGGATCCCGGTTCCCCCACA
AGAAAATGCGTATGTAATTAATGTGCGCGATATGTTGCAGAAGTTTACGGGGGGTTA
CTACCGTAGCGCCCGGCATCGTGTGGTGACATTCACGGCCAATCATCGCTACAGTG
TCCCCTTCTTCTTGAACGGACAACCTCAAATCAAATGTAAAACGCTGGATGGAAGC
GGCACCGAAACCATTTAGGCGAACACATCCGTGGGCGCTTGTTGGAGACAATGG
GAAAGGCGGGGGGAAAAGTTAAAGTAA

NHI 34 (XenC homolog 3) protein sequence:

MGSIEAIPTVDISAWIDTSSTEEERQRAVDEMNRNACTRYGFFNLIAHGVSPQAQSQALN
CAKLFFTLSEQEKMKVCISKSVGRSFRGYEPPGIQVHQEGLLPDTKECFIIGHEVPEHD
PECGTFSTGPNLWPKSLPEDEFRIPIMEYQARMVALVKVLLKILARGLPKEWNCSPDVL
DPLGENNPSIPMRLHYGPQPIRDDRQFGVGDHTDFGCVTILLQDMGTEGLEWYPP

TETWIPVPPQENAYVINVRDMLQKFTGGYYRSARHRVVTFTANHRYSVPFFLNGQLKL
KCKTLDGSGTETIVGEHIRGRLLLETMGKAGEKLK

Codon-optimized NHI 35 (XenC homolog 4) sequence:

ATGGCTGAGGTGCCTCAGCAGATCCCGACGATTGACATCAGCGCGTGGGTGAATC
CGGCGTCGTCCGCCGCAGATAAACAGCGGGTCGTTGATGAAGTCCACCATGCCGC
GACGACTTACGGGTTCTTCCAGTGTGCCGGGCACGGCATTACACCCGAAACCCGT
GAACAGATTTTCAACCTGAGCAAGCGGTTCTTCTCACTTCCAATGAAGAGCGGAT
GGAAATCTCCGTGAAGAAGAGCTTGGGCCAGTCTTTCCGCGGCTACGAGCCGCCC
TTTCTCCAGAACCACCATAAACATTTGCTCCCGGATACCAAGGAAACCTTTGTGGTG
GGCGCGGAAATCCCGGCGGACCACCCGGACGCTGGCACCTTTCTGAATGGTCCA
AATTTGTGGCCTACGAGCATTCTGAGGACGAGTTTCGTAAACCGATTATTTTCATATC
AGAGCCAAATGGTTGCGTTAGGAAATACGTTGTTAAAGATTCTGGGGCACGGCTTG
CCGAAGAGTTGGAATTGCAGCCCTGATGTTTTCGATTCATTAGCCGAAAACCCGGC
CATTCCGATGCGCATGCTGCATTATGCGGCCACGCCGTACATGACGAGAAACAAT
TCGGTGTCCGTGCTCATAAGATTTTGGCAGCGTTACCATACTACTGCAACAGCTG
GGCACCAAAGGTCTGGAAGTGTGGTATCCACCAACGGAAACGTGGATTCCGGTTC
CGCCAAAAGAAAATACCTTCGTGATTAATATCGGTGATTTTGTA

GACCGGTATACGAACGGTTATTACCGGTCTGCGCGCCATCGCGTAATTACCACCGAT
AAGGAACGGTATTCGGTGGCGTTCTTCTTTAATGGGAACATGAAGCTTAAAGCCCC
AGTTTTGGACGGCTCAGGAGATGAAGTGAAGTTAGGTGATCATATACGCCAGCGTG
CGATTGCCACTTATGGTGCAGCTCCTACTCTGATCGAGAGCAAAGTGTA

NHI 35 (XenC homolog 4) protein sequence:

MAEVPQQIPTIDISAWVNPASSAADKQRVVDEVHHAATTYGFFQCAGHGITPETREQIF
NLSKRFFSLPMEERMEISVKKSLGQSFRGYEPPFLQNHKKHLLPDTKETFVVGAEIPAD
HPDAGTFLNGPNLWPTSIPEDFRKPIISYQSQMVALGNTLLKILGHGLPKSWNCSPDV
FDSLAEENPAIPMRMLHYAAQPVHDEKQFGVGAHTDFGSVTILLQQLGKGLVWYPPT
ETWIPVPPKENTFVINIGDFVDYRNGYYRSARHRVITTDKERYSVAFFFNNGNMKLKAP
VLDGSGDEVNLGDHIRQRAIATYGAAPTILIESKV

Codon-optimized NHI 36 (XenC homolog 5) sequence:

ATGGGATCGCTCACGGAAACCGCCACAATCCCCACGGTGGACATCTCAGCATTTCT
TGACCCGAATGCTTCTGACCAGGCGCGTCAGGATATTGTTAAAGCTATGTCACATGC
TTGTCATGTCTATGGCTTCTTTAATCTGGCAGGTCATGGCATTCCGCAAGAGACACT
GAGAACAGCGCTGGAGCTTAACAAAATGTTCTTCACGTTACCGGAAGAAAGCAAGA
AGGAAGTGCTTATCTCTAAGTCAGTGGGTCAAAGTTTCCGTGGATATGAACCCCCG
GGGATCCAAACCCATCACCGGGGCCTTCTGCCGGATATTAAGGAAACCTTTATGGT
GGGCCGCGAAGTACCGCTCGATGACCCTGATTGCGGCACATTCTCACGTGATCCG
AATCTCTGGCCGACCAGCTTACCGAAAGAAAAGTTCCAGGATCGTATCATGGCCTA
CCAGGGCAGCATGCTTCAACTGGTGAAATCCATCCTGGCAATTCTGGCCCAGGGTC
TGCCGAAAGAATGGGAATGTTCTCCGACCGTGTTTCGATTCACTGCTGGAAAAGCCC

TCTATCCCGATGCGTTTTCTGCATTATGCACCAGTGCCGTCACAGCTGGAAGATGCA
CGTCAGTTTGAGGTGGCGGACCACACCGACTTTGGCTGTGTTTCTATTCTGCTTCA
GGAACCCGGAACCAGTGGGCTGGAAGTGTATTATCCCCCGTCTGACAGTTGGATTC
CGGTACCCGTGGTTAATGATGGCTTTGTTATCAACATGGGCGATATGATGCAGCGTT
ATACAGGCGGTTACTATCGCTCGGCGCGTCATCGCGTTCTGACCAATAGGGAGAAA
CATCGCCACAGCGTAACTTTCTTCCTTAATGGGAACCTGAGTCTTAAAGCGAAAGCT
CTGGATGGGTCCGATACCGAAACTGTCGTTGGTGACTGGATCCGCGGGGCGCCTGT
TGGAACAATGGGCCAGACCGGTAAATTGTTGCAGCGTGAATCCAGCAAAACCCAA
TAA

NHI 36 (XenC homolog 5) protein sequence:

MGSLTETATIPTVDISAFLDPNASDQARQDIVKAMSHACHVYGFFNLAGHGIPQETLRTA
LELNKMFFTLPEESKKEVLISKSVGQSFRGYEPPGIQTHHRGLLPDIKETFMVGREVPL
DDPDCGTFSRDPNLWPTSLPKEKFQDRIMAYQGSMLQLVKSILAILAQGLPKEWECSP
TVFDSLLEKPSIPMRFLHYAPVPSQLEDARQFEVADHTDFGCVSILLQEPGTSGLEVYY
PPSDSWIPVPVVNDGFVINMGDMMQRYTGGYYRSARHRVLTNREKHRHSVTFFLNGN
LSLKAKALDGSDTETVVGDWIRGRLLTGMGTGKLLQRESSKTQ

Codon-optimized NHI 37 (XenC homolog 6) sequence:

ATGACCGTGCAGCACCAGATTCCGACCATCGATATTAGCGCGTTCCTCGATCAGAC
CGCCAGTGAAAAGGCGCGGGGAAGCAGTGGTGGCAGAGGTTTCGCGATGCGTGTAT
GACGTATGGCTTCTTCCAGCTGATTGGCCATGGCATTCTCTGGCTATCCAGGAAC
ATGTCCTTCGCTGTGCCAAGGTATTCTTCGACCAGCCCCTAGAGAAGAAACAGGCA
CTGGGCATGGATAAAGCCATGGGTCAGAGTAATCGTGGCTACGAACGGATCGGGG
GCCAAGCGCTCCAGGCAGATATGCTGCCTGACCTAAAAGAAGGTTTCTATATTGGC
CGCGAAGTGCCGGCCGACGATCCTAGAGCTGGCCAGTTTCACCAAGGTCCAAATC
TATGGCCCGAAATTCCGGAAGAAGAGTTCCGCGTACCTCTGTGCGGAATACTATCGTA
TGATGATTCAATTGGATTATCAGCTGCTGAATATCATCGCATTAGGCCTGCCGTTTTTC
CAACGACATCTTTGAAGAATTTAAGAAGGAACCGGCCGCGAGTCTGCGCTTGTTGC
ATTACCCCCCTCAGATCAGTATCGATGAGCGCCAGTTTGGTGCGGGGGGCCACAC
GGATTTTGGTTGTATGACCCTGCTGTTACAGCAGCCGGGTCAGGAAGGCCTGCAA
GTTTTCTATCCGCCGACCAAAGAGTGGATTCTGTTCAGCTGCGGCTAACACCTT
TGTCGTCAACATCGGTGACTTGTTACAGCTGTGGACGAAAGGTCAGTATCGTAGCG
CGCTCCACCGAGTGTTAAACGCTACTAACGAGGATCGCTACTCTGTGCCGTTCTTC
TACAACGGTAACCTCGCATGTAACTGGCCCCGCTGGACGGGTCCAGTGATGTGAA
TACGCTAACAGTGGAAGAACACGTCAAACGGAAATTTCAAACATCTTATGCGGTGTA
A

NHI 37 (XenC homolog 6) protein sequence:

MTVQHQIPTIDISAFLDQTASEKAREAVVAEVRDACMTYGFFQLIGHGIPLAIQEHVLR
AKVFFDQPLEKKQALGMDKAMGQSNRGYERIGGQALQADMLPDLKEGFYIGREVPAD
DPRAGQFHQGNLWPEIPEEEFRVPLSEYYRMMIQLDYQLLNIALGLPFSNDIFEEFKK
EPAASLRLLHYPPQISIDERQFGAGAHTDFGCMTLLLQQPGQEGLQVFYPPTKEWIPV

PAAANTFVVNIGDLLQLWTKGQYRSALHRVLNATNEDRYSVPFFYNGNLACKLAPLDG
SSDVNTLTVEEHVKRKFQTSYAV

Codon-optimized NHI 38 (XenC homolog 7) sequence:

ATGAGCAGCGAGAAATCGGAAGGTGGGATTCCAACTGTGGATATTGGCGCCATCCT
TAGCCCGGCCGCGAATGAAGCCGATCGTCGCCAGGTTGTGGAAGCCGTACGTTAT
GCCAGCACTACCTTCGGGTTCTTCAACTTGGTTGGCCACGGCATTCTCGCGCTCA
GTTGCGCCAGATTTTCGAATCTTCTAACTGTTCTTCGCACTGCCGGAAGAGAAAC
GTCGTGATGTGCATGTTGGTCAGGCATTAGGTCGCAGTTTCCGTGGTTGGGAACCG
CCGCTGATCCAACAGCATCAAGAAGGAGTGCTGCCGGATACTAAAGAAACCTTTAT
CATCGGGCGAGAGGTCCCGGCTGACGATCCGGAAGCGGGGCACCTTTCTAACGGG
TCCGAATCTGTGGCCAGACCTGCCTACTGAAGATTTCCAAGAAGTCATTCTGGCCT
ACCAAGCGCGCATGATTGAGCTGGCTCGTGTGCTAGTGCGTATTTTAGTACAGGGC
CTGCCTGAAGCGTGGGGATGTCCACCGGATGTTCTGGATGGTCTGACCGTCGATC
CGGCCATCCCGATGCGCATGCTGCACTATGGCCCCGTCAAAGAAAAGGATCCACG
TCAATTTGGTGTTGCTGCCCATAACCGACTTTAGTGCTATTACCATTCTTTTGCAACAG
CCGGGAAGTGAAGGTCTGCAAGTTTGGTATCCGCCGACAGACGAGTGGATTCCGG
TCCCTGTATCTGAAGATGGTTTTGTGATTAACATTGGAGACTTAATGCAGCAATATAC
CGCGGGCTATTATCGATCTGCACGCCACCGCGTGATTACCTTCTCAGAAGAAGATAA
ACACCGGTATAGCGTAGCTTTCTTCCTGGATGGTAATCTGCAATTCAAGACCAAAGC
GCTGGATGGCTCTGGTACCGAGATCGTCGTTGGAGAGTACGTATATTCATGCCTCAA
TCGTACCCTGGGAGCGCGTGGCCCCGTCCCTGTAA

NHI 38 (XenC homolog 7) protein sequence:

MSSEKSEGGIPTVDIGAILSPAANEADRRQVVEAVRYASTTFGFFNLVGHGIPRAQLRQI
FESSKLFFALPEEKRRDVHVGQALGRSFRGWEPPLIQHQEGVLPDTKETFIIGREVP
DDPEAGTFLTGPNLWPDLPTEDFQEVILAYQARMIELARVVVRILVQGLPEAWGCPPDV
LDGLTVDPAIPMRMLHYGPVKEKDPRQFGVAAHTDFSAITILLQQPGETGLQVWYPPT
DEWIPVPVSEDGFVINIGDLMQQYTAGYYRSARHRVITFSEEDKHRYSVAFFLDGNLQF
KTKALDGSgteIVVGEYVYSCLNRTLgARGPSL

Codon-optimized NHI 39 (XenC homolog 8) sequence:

ATGACAAGTCCGGTGGGAAGCCATTCCGACTGTGGATATTTGCGCGTTCGTAGCCAA
CGCACCTGCCAAAGCGCTACTGGACGTGGTAAAAGCGATGCGTCACGCCTGTACG
ACCTATGGCTTCTTTTATTTGGTCGGTCATGGGATTTGCTTGAAGAACAAAACGGC
GCGTTAGATTGCGCCAACTATTCTTCACGCTGAGTCAAGAACAGAAAATGGATGTC
TGGCTGAAGAAATCTTTAGGTAAATCGCACCGAGGGTATGAACCACCTGGCATCCA
AACCCACCAGAAGGGTCTGTTACCGGATACAAAAGAAGCATTTATCTTTGGTGCTGA
AATCCCCGAGGATGATCCCGAAGCAGGTACCTTTAGCACCGGCCCGAACCTGTGG
CCAAAAGCGCTGAAGCCGCATGAGTTTCGCAACCCGATCATGGAATACCAGGGCAA
AATGCTGGAAGTGGTGAAAATCCTACTTAAATCTTGGCACTAGGCCTGCCGGAAG
AATGGGAATGCGCCCCAGACGTGTTTGATGAGCTTGCGATAAATCCATCTATGCCGA
TGCGCCTGCTACACTATGCCCCAAACCCGACGCATAACAATACTCAGTTCGGGGTG

GGGGATCATACCGACTTTGGGTGTATCACTGTGCTGTTACAAGAGCCAAACCGTGA
GGGGCTCCAGGTCTGGTATCCGCCGACTGAGACTTGGATTCCGGTACCGGTAAAG
GAAGGATCATACGTTATAAACATCGGTGACATGATCCAGAAATACACCGGTGGCTAC
TACCGTTCGGCGCGCCACCGTGTGGTCAATGGCGGTAAAGAGCACCGGTACTCTG
CTCCATTCTTCTTAAATGGTCAGTTAAACTTAAAGTTACCGCCCTTGACGGCAGCG
GCGTGGAGACAGTTGTGCGGCGAACATATCCGTCAACGTTTGATCGATACGATGGGA
GAATCCGGTAACGTGTTAAAATAA

NHI 39 (XenC homolog 8) protein sequence:

MTSPVEAIPTVDISPFVANAPAKALLDVVKAMRHACTTYGFFYLVGHGISLEEQNGALD
CAKLFFTLSEQKMDVWLKKSGLKSHRGYEPPGIQTHQKGLLPDTKEAFIFGAEIPED
DPEAGTFSTGPNLWPKALKPHEFRNPIMEYQGKMLELVKILLKILALGLPEEWECAPDV
FDELAINPSMPMRLLHYAPNPHTNNTQFGVGDHTDFGCITVLLQEPNREGLQVWYPPT
ETWIPVPVKEGSYVINIGDMIQKYTGYYRSARHRVVGKKEHRYSAFFFLNGQLKLK
VTALDGSQVETTVVGEHIRQRLIDTMGESGNVLK

Codon-optimized NHI 40 (XenC homolog 9) sequence:

ATGGGTAGCATAAATGAAACCCAGACCACCTCAATTCCCACCGTTGACATCGGCCC
ATTTCTGGATGGACAGGCCGCTCAGGAAGCTAAGGACGCAGTCGTGGCCGCGATG
CGCCATGCCTGCTCTACCTTCGGTTTCTTCTATCTGGTGGGACACGGCATCCCAGA
AGAAGATCGCTTGCAGATTCTGAAATGCACGAAACGCTACTTTGATCTGCCGATGG
AAGAAAAGATGGAAACATGGATTGGCAAAGCGATAGGCCGATCATTCCGCGGCTAT
GAGCCGCCAGCGCTGCAAGTGCACCAGGAAGGCCTGCTGCCTGATACAAAGGAA
GGTTTCATCCTGGGTGCGGAGACTCCCGCGGACGCCCCCGAGGCAGGTACATTCC
ATACGGGGCCCTAATCAGTGGCCCAAACCTGCCGGACGAGGAATTTGCGGTGCC
AATCATGAGATACCACGCGAAGATGATTGAGATGGTGAAAGTGATTCTCAAATCTTA
GCTCTTGGACTGCCGGCAGAATGGAATTGTCCATCTGATGTCTTTGACGAATTGAC
GATAAACCCATCGGCTCCCTTACGTTTACTCTACTATGCCCCCAGCCGGTCAAGCA
CGAAAATCAGTTTGGCGTCGGTGCTCATACCGACTTTGGAAATGTTTCTGTGCTGCT
ACAAGAAGAAGATTCCGAAGGCCTAGAAGTGTTTTATCCCCCCTCAGACGTGGG
TGCCGGTCCCAGCCAAACCTCATAGTTATGTTATTAATATGGGCGATATGATGCAGAA
ATGGACCGCGGGCTATTACCGTTCCGCTCTGCATCGTGTAGTTAATTCAAATACGAA
GCCTCGTTATTCGGCCCCGTTCTTCATGAATGGGAACCTGGATGTGAAGTGTTACG
CGTTGGACGGTTCTGGGGAAGTGACTACGATTGGCGAGCATATTCGCAAACGTTTA
ATGGAAACGATCGGGGGCGAAGAAGGTAAGAAGCTGGGCCTGTAA

NHI 40 (XenC homolog 9) protein sequence:

MGSINETQTTSIPTVDIGPFLDGQAAQEAKDAVVAAMRHACSTFGFFYLVGHGIPEEDR
LQILKCTKRYFDLPMEETWIGKAIGRSFRGYEPPALQVHQEGLLPDTKEGFILGRE
TPADAPEAGTFHTGPNQWPKTLPDEEFRVPIMRYHAKMIEMVKVILKILALGLPAEWNC
PSDVDELINPSAPLRLLYAPQPVKHENQFGVGAHTDFGNVSVLLQEEDSEGLEVFY
PPTQTWVPVPAKPHSYVINMGDMMQKWTAGYYRSALHRVNSNTKPRYSAPFFMNG
NLDVKCYALDGSGEVTTIGEHIRKRLMETIGGEEGKKLGL

Codon-optimized NHI 41 (XenC homolog 10) sequence:

ATGGGGAGCGTTGAAACCATTCCAACCGTTAATATCTCCGCCTGGCTCGATCCGTC
AAGTACCGAGGAAGAAAGGCAGAACGTGGTCTGAAGAGATGCGTCATGCTTGTAACC
ACTTACGGTTTCTTATCCCTGGTTGGTCATGGCGTTTCGCCTGAGGAGCAGAAACA
AGCAATGGACTGCGCCAACTCTTCTTCACATTGTCTGAGGAAGAAAAGATGGATG
TGTGGATCGGTAAATGTAAAGGTCGTTCTTTTCGTGGTTACGAACCGCCTGGTATTC
AAGTACATCAGGAAGGTCTGCTTCCTGATACCAAGAATGTTTTATTATTGGCCATGA
AGTTCCAGAGGATCACCTGACTCTGGCACCTTTAGTACTGGTCCGAACTTGTGGC
CGAAATCGCTTCCAGAAAATCAGTTCCGCATTCCGATTATGCAATACCAGGCGCGTA
TGGTGCAACTTGTTAAAGTTCTTCTCAAATCTTGGCTCGTGGCCTGCCGTCCGGAAT
GGAATTGCCCCCGGATGCGCTGGACGCCTTAGCTGAAAATGAACCCTCTATCCCA
ATGCGCTTGCTCCATTATGCGCCGCAGCCGGTCCGCGATGAGCGGCAGTTCGGCG
TTGGCGATCATACCGACTTCGGTTGTATTACCATTCTGCTCCAGGAAATGGGTACTG
AGGGCTTGGAAGTGTGGTATCCACCCACGGAAACATGGATTCCGGTGCCGCCTCA
GGAGAACGCGTATGTAATTAACATAGGAGATATGATTGAGAAATTTACCGGGGGGTAT
TATCGCTCTGCGCGTCATCGTGTGATTACTTTTACGGAGAAACATCGGTATTCCGTT
CCATTCTTTCTCAATGGCCAACTGAAATTGAAATGTACGGCCCTGGACGGTAGTGG
CGTCGAAACCATAGTCGGCGATCATATCCGAGGTGCCTCATCGAAACCATGGGCA
AAACCGGCGAGAAATTGAAGTAA

NHI 41 (XenC homolog 10) protein sequence:

MGSVETIPTVNISAWLDPSSSTEERQNVVEEMRHACTTYGFLSLVGHGVSPEEQKQA
MDCAKLFFTLSEEEKMDVWIGKCKGRSFRGYEPPGIQVHQEGLLPDTKECFIIGHEVP
EDHPDSGTFSTGPNLWPKSLPENQFRIPIMQYQARMVQLVKVLLKILARGLPSEWNCP
PDALDALAENEPSIPMRLHYAPQVRDERQFGVGDHTDFGCITILLQEMGTEGLEVW
YPPTETWIPVPPQENAYVINIGDMIQKFTGGYYRSARHRVITFTEKHRYSPVFFLNGQL
KLKCTALDGSVETIVGDHIRGRLIETMGKTGEKLG

Codon-optimized NHI 42 (XenC homolog 11) sequence:

ATGGGGCTCGATTGGGACTGCACCTGAAGCGATTCCAACCTGTTGATATTTGCGCGTT
CATTAGCAATGCATCAGAGAAAACCTTACGTGAAGTGGTGGGAAGCAGTGCGGCACG
CGTGCACCACTTACGGCTTCTTCTATCTGGCGGGCCATGGTGTAAAGCCTTGAGGAC
CAGAACAAAGCACTTGAGTGCGCAAAATTATTCTTTACTCTGCCGATGGAAGATCGT
ATGGAAGCGTTTATTATTGGTGCCGAAGTGCCTGCCGACGATCCAGAAGCGGGTAC
TTTTAGCACGGGTCCGAACCTGTGGCCGAAATCTCTGCCAAAAGAGGATTTCCAAA
TCCCCATCATGGAATATCAGCGCAAGATGGTTCAGTTGGTGAAAGTCTTGTTACAGA
TTTTAGCTCTGGGGCTGCCTAAAGAATGGGGATGCCTGCCGTGAGTGTGTTGACGAA
CTGGCCGTTAATCCGAGCATCCCCATGCGTCTGCTGCACAGCGCGCCACAAACGG
TCCGTGATGAACGTCAGTTCGGCGTCGGCGACCATAACCGACTTTGGTTGTATTGCA
ATCCTGCTGCAAGAACCGGCGCGCGAAGGATTACAGGTGTGGTACCCGCCGACGG
AAACCTGGATCCCGGTACCGGTAAAAGAAGGTTCCCTATGTGGTGAACATTGGCGAT
ATGATGCAGAAATACACAGCGGGCTACTACCGCAGTGCCAGGCATCGGGTGGTTAA

CTCTGCGAAGGAACACAGATACAGTGTGCCGTTCTTTCTCAATGGCCAGTTAAAGC
TGAATGTTAAAGCACTGGATGGATCGGGGGTGGAGACAGTTGTCGGCGAACACAT
CCGTCAGCGTTTAGTTGAACCCATGGGAGAAAGCGGTAAAGTTCTGGGTAA

NHI 42 (XenC homolog 11) protein sequence:

MGSIGTAPEAIPTVDISPFISNASEKTLREVVEAVRHACTTYGFFYLAGHGVSLDQNK
LECAKLFFTLPMEDRMEAFIIGA EVPADDPEAGTFSTGPNLWPKSLPKEDFQIPIMEYQ
RKMVQLVKVLLQILALGLPKEWGCLPSVFDELAVNPSIPMRLLSAPQTVRDERQFGV
GDHTDFGCIALLQEPAREGLQVWYPPTETWIPVPVKEGSYVNVNIGDMMQKYTAGYYR
SARHRVVNSAKEHRYSVFFLNGLKLNKALDGSVETVVGHEIRQLVEPMGESG
KVLG

Codon-optimized NHI 43 (XenC homolog 12) sequence:

ATGGGATCGAACTATGGTACCGGCGCGACCGCGATTCCGACCGTTGACATCTCGG
CTTTCCTGAGTCCTACGGCCAGCGACGCGACACGTCAGGCCGTGATCGAAGGAGT
ATCAAAAGCCTGCCACACCTATGGATTCTTTAACCTGGTTGGCCACGGCATCCCCC
AGGATGTGATGCGACGAGCGTTTGAATGTAACAAAATGTTCTTCGAACTGCCCAT
GACAAGAAGATGGAAGTCCGTATAAGTAAAAGCGTGGGTCGCAGCTTTCGCGGCTA
TGAGCCCGCCGGGCATCCAGACGCACCATGAAGGGCTTCTGCCGGACACCAAAGA
GACTTTCATGGTTGGTCGTGAAGTGCCCGAAGATGATCCTGATTGTGGGAGCTTCT
CTACAGGACCCAACCTGTGGCCTTCGTCCCTTTCGAAAGAGAAATTCAGGACCTT
ATCATGGATTATCAGGGGCGAATGCTTGCGCTGGTGAAGAACATCTTAGACATCCTG
GTACTGGGTCTGCCGAAAGCGTGGAAGTGCCCAACCAATGTGTTTCGATAGCCTGCT
GGATAAACCGTCAATCCCGATGCGTTTTCTGCACTATGCTCCGGTGCAAGCTATGGA
TCCACGTCAGTTCGGGGTTGCCGACCATAACGATTTTGGCTGCGTGTCAATCCTGC
TTCAAGAGCTGGGCACGGAAGGTCTGGAAGTTTTCTACCCGCCGAGTGAGACTTG
GGTACCGGTCCCAGTGGTGAGCGATGGCTTCGTAGTAAACATGGGGGACATGATG
CAGAAATACACCGGGGGCTACTACCGGAGCGCGCGCCATCGCGTGCTGACGAACA
AGGACAAACATCGTCATAGTATTGCCTTCTTCCTGAACGGCAACTTGAACTTAACG
CCAAAGCCCTGGATGGTTCGGGCGCCGAAACCGTCGTTGGCGAGCACATCCGTCA
ACGCCTTATCGAAACGATGGGCGACATGGGGAAATTATTGAAACGAGAGGTGGCGG
CAGCTCAAACCTAA

NHI 43 (XenC homolog 12) protein sequence:

MGSNYGTGATAIPTVDISAFLSPTASDATRQAVIEGVSKACHTYGFFNLVGHGIPQDVM
RRAFECKMFFELPHDKKMEVRISKSVGRSFRGYEPPGIQTHHEGLLPDTKETFMVG
REVPEDDPDCGSFSTGPNLWPSSLSKEKFQDLIMDYQGRMLALVKNILDILVLGLPKAW
KCPPNVFDSLDDKPSIPMRFLHYAPVQAMDPRQFGVADHTDFGCVSILLQELGTEGLE
VFYPPSETWVPVPVSDGFVVMGDMMQKYTGGYYRSARHRVLTNKDKHRHSIAFFL
NGNLKLNALDGS GAETVVGHEIRQLIETMGDMGKLLKREVAAAQN

Codon-optimized NHI 44 sequence:

ATGACGACGATCAACATGCTCAAAACGGCCACCAACACTCTGGTTCCTCACTCTGGA
TCTGGCAAATGCAGAAGCGACCGGCGAGGGCCTGGCGGCGCTGGACGAAGCATG
TCGTAATCATGGATTCTTTCTGTTACAGAACCATGGCCTGGACCGCGAAATCGAGGC
CATGTGGCAAGCGTCCGAAGATTTCTTCAAACAACCCCAGGCCTCAAAGCGCGCG
ATTAACGAACCGAAAGCTCACCCTAGGATATTTTCGATCAGGAAATGACTAAACGT
CAGCGAGACTTGAAGGAAGTTTTTCGATTTTCATGCGCCCCACGGCTACCGGGCGTAA
TCTGAACCAATGGCCCGACGATGAAGCCTTTAAACAGACCCTGAGCGACTTCTTCG
AAGCAGCCTCTTCCGTCGCCCCACCGTACACTGACCCTGGTGTACCAAGCGCTGGC
CGCGGCTCCGAGCGACGCCCTGCCTATGGGCGACCCAGCGACGTCCACCGTGCG
CCTCAACTTTTACCCTACAGAAGATCCACTGCCTGCGAACGAACGGGGCACAAGCAG
GCGTCCTGGGTAAATATGGCATTACATCATACCGATCCTGGAATCCTGACCCTGC
TGTTGCAGGACCTGACGGGCGGGCTCCAGACCCTGACCCAAGACCAACATTGGAT
CGACGTGCCGCCGCGAGGCGGGGACCATTGTTGTGAATCTGGGCGATGCTATGCAA
GTCTGGTCTAATGACGCGTATCGCGCTGCGATCCATCGCGTCACCCCTCGCGACC
GCAGTGACGATATAGTACGCCCTACTTCTATAACCCGAAGTCCGATGCGGTGTTGG
CGCCCATCACACACCTTACTCAAGACCCGCCACACTTCCGCCCCGTTTACCTGGCGT
GAGTATATCAAAGGTCGCGTAGACGACAACCTTTACAGATTTAGGCGTGGATGACATT
CAGATCGATCGATTCCGTATTGCGGTATAA

NHI 44 protein sequence:

MTTINMLKTATNTLVPTLDLANAEATGEGLAALDEACRNHGFFLLQNHGLDREIEAMWQ
ASEDFFKQPQASKRAIKRTESSPLGYFDQEMTKRQRDLKEVFDFMRPTATGRNLNQW
PDDEAFKQTLSDFFEAASSVAHRTLTLVYQALAAAPSDALPMGDPATSTVRLNFYPTED
PLPANERAQAGVLGNMALHHHTDPGILTLLLQDLTGGLQTLTQDQHWIDVPPQAGTIVV
NLGDAMQVWSNDAYRAAIHRVTPRDRSARYSTPYFYNPKSDAVLAPITHLTQDPPHFR
PFTWREYIKGRVDDNFTDLGVDDIQIDRFRIAV

Codon-optimized NHI 45 sequence:

ATGACACTTCCGCAGTCGCGTCGCTTAGACTTTTCCGAAATCCCGATTGTTGATGTG
GGCCCGCTTATCGCTGGCGACCAACGACCCAACTTTGATTAAACGGCCTGCATCAGG
CTTGTACGGATGTCGGCTTCCTATATGTGCGCAACCACGGTGTTAGCATGGCACTG
GTTGAAGCGCTGAAAGAAAGTGCGGTACATTCTTCGCCGACCGATGGCAGAGA
AAATGAAAATAGTGATTGATCCGCGTATCCAAGGCTATTTACCGCTCGGGTATCGCA
GCTATGAAGGCGAGGCTCGCGCTGGCACTTCGCAACAGGAAGGCTTTTGGATCGG
TCATGATCGTCCGTTGAGCAACGATGCGTTGCTGGATGGTCCGAACCAATGGCCG
GATGGCCAGCCGGACTTAAACAAGCGATGCTTCGCTACTTCGACGCACTGGAAG
GTCTAGCAGGCGTTCTGCTGCGCGGTTTTGCCTTAGCTTTGGGCTTGGACGAGCAT
CGATTGCAACCTTCTTCAAGAAACCTCTGTCCCGCCTAAAAGTCAATCATTACCCG
CCGCAGGATACGCCGACTGCCGACAACGATATTGGCGTTGTGCCCCACAGCGACT
CTGGGGGGCTTTACCATCCTGTGGCAGGACAACCTGCGGCGGGTGTAGAGATACAGAA
CAAGAACGGCGAATGGGTAGGCGCTCCGCCACTGGAAGAGACTTTTGTCAATCAAC
CTTGGCAACATCATGCAAATTTGGAGCAACGGCCGCTTTTCGAGTACACCGCATCG
CGTGATTAACCGCTCCAACCATGATCGTTACAGCATTCCACTGTTTCGTGAATCCGTC

TGCCGATGTTTCCATTAAACCTTTAATCGACTTCGACTGCAACCATAGCACCACCTTT
AACTACGGTACCTACCAGCGAGATCTGTGGCGTCAGACGTTTCCTGTGCGCGAAAT
CCCAGTCTAA

NHI 45 protein sequence:

MTLPQSRRLDFSEIPIVDVGPLIAGDHDPTLINGLHQACTDVGFLYVRNHGVSMALVEA
LKESAVTFFAAPMAEKMKIVIDPRIQGYLPLGYRSYEGEARAGTSQQEGFWIGHDRPLS
NDALLDGNQWPDGQPDLDKQAMLRYPDAVEGLAGVLLRGFALALGLDEHRFATFFKK
PLSRLKVNHYPPQDTPTADNDIGVPHSDSGGFTILWQDNCGGLEIQNKNGEWWGAP
PLEETFVINLGNIMQIWSNGRFSSTPHRVINRSNHDRYSIPLFVNPSADVSIKPLIDFDCN
HSTTFNYGTYQRDLWRQTFPVAEIPV

Codon-optimized NHI 46 sequence:

ATGGATGTTCTGAATAGCATTAGTCTGGAGCGCCTGGAAAGCACTCAAGCCGACTAT
GAAATTAGCTGCCTACGGAAATGTTGCGTTAACGATGGGTTCTTTTACCTGGCGGAC
CATGGGATTCAACCGAGCCTGATTGCAGACGCCCTGGATACCGCCCCGCCAGTTCTT
CGCCCTGCCTCTCAGTACCAAGAACCAGTTTTTGCCAGGACCGCCAGGTTGTCATC
CCGAAAACGTGCCGTGGCTATGTGGATACCTTCGGCGAGACATTGCACCCGCCGA
CCGGGCCCGGATCGTAAACAGCATTTTGACATGGGGCGCGAGGCCCCAGCGTGCG
ATTTGCCGTTCACTGGTCCGAATCTGCTCCCTTCCGAGGGCCAAGCGCCTGGATTC
GCGAAATCAATGCTCGCCTTGACGCAAGAGGTGTTAGATCGTGTGGTGCCCGCACT
GCTGCGAGGCCTGGCACTTAGTTTTGGGTTTGGATCGCGATTTCTTCCAGGCTTTCT
TTAGCAACCCGGTTCTCATAACAGCGTGCCTTATATTACCCCCCTCGGGCAGCGGT
GCGGGCAAGCACACAGATAATGGTATGTTTACATTACTGTTTCAGGATCCGCGGGAT
GCCTGCGCACTGAGCGCATTACGCCAAGGTCGTTGGATTGATGTGCCGTGCCGAG
CTAATGAAGTTGTCGTGAACCTGGGGGATATGCTGATGAAATGGTCAAACGGTCTAT
TTACGTCCACTCCTCATCAAGTAATTCACCGTGCCTCTTCGGCGCGAGTCAGTCTG
CCATTCTTCGTGTATCCGGATATTGATGCCGTGTTACGCCGCTCGGGAGCGATCA
GACTGTTGCGTGCCGCCAAGTCATGTTGGATAACTTTAACAGCATTTGGGTGTCTG
GCCAGGGTGCAGGGCGCGCGCGCGAATTTGCCTAA

NHI 46 protein sequence:

MDVLNSISLERLESTQADYEISCLRKCCVNDGFFYLADHGIQPSLIADALDTARQFFALP
LSTKNQFCQDRQVVIPKTCRGYVDTFGETLHPPTGPDRKQHFDMGREAPACDLPFTG
PNLLPSEGQAPGFAKSMALQQEVLDRVVPALLRGLALSLGLDRDFFQAFFSNPVLIQR
ALYYPSPSGAGKHTDNGMFTLLFQDPRDACALSAFSQGRWIDVPCRANVVNLGD
MLMKWSNGLFTSTPHQVIHRASSARVSLPFFVYPDIDAVFTPLGSDQTVACRQVMLDN
FNSIWVSGQGAGRAREFA

Codon-optimized NHI 47 sequence:

ATGAGTAATATTTTGCGCCGCCGAGAAGTGCATAGCGTGGTGGTGGGCGGGCAAC
GCTCACAGGCCATTACTAATGAAGTACCTATTATCGATGTGGGACGGTTCTTCGCCG
GCGTCCCGGGTGCCCTGGATGAGGTTGCGCAACAGATTCATAAAGCGTGCACCGA

AATCGGTTTCTTCTATATTGTAAACCATGGCGTATCACAGCCGGTAATCCGCCGTGTT
TTCGAAGCAATGGAAAATTTCTTTACTCTTCCGGCGAGCGAAAAGTTTAAAGTGCGT
ATGAACGAACATCAGGCCGGTTGGCAAGCGCCGAACGTCGCGATTACGGCGATA
GCTTTGACAAAGTGGTCAAACCCCAAGGCCACTGAAGCGTTCAAATTCGGCCCCGGA
ACTGGACCCGGCGGATCCCGACTTCCAGGGATCTAAAAGATTTTCGCGGACATAACC
AGTGGCCCGGAAGGTCTGAGCGTAGAGGATAAACAGGCATTCTGACCTATCACGC
CCAATTTAATGAGCTGGCTAAGCGTCTGCTGGCAGCGGTGGCTGTTGCCCTGGGC
AGCGTGCCCAATTTCTTCGATGACGCATTCCGCCGAACGGATTCTGTATGCGCTG
CGCGTACTATCCGGTCGTTAAACCCCAAGAAAATCAGTTCGGATTACCTGGACACAC
GGATCTGTCAATTCCTGACTCTTATTCCGCCGGCGACAGCGCCGGGCTTACAGATCC
TGACCGCCGCAGGCACCTGGATCGACCAGCCGATAGTAGAAGGTGGCATTCTGGT
GAACACCGGTGACGCTCTGCGCACCTGGTCCAACGATCAATTTATTGCGACCCCTC
ATCGTGTACTGGCTAGCACCAAGGAAGAACGCTACTCCGCAATCTTCTTTCTGTATC
CCGATCTGGATGTGACTATTTTCATGCGTACCGACGTGCTGGAGCGCCGATTATCCC
AAGAAATATACTGATCAGAAGTTCTCTGATTTCTATGCCGGGTATGCCGCGCGAAAC
TTCGGGTACGCGGAAAAGAAGGCTTAA

NHI 47 protein sequence:

MSNILRRREVHSHVVVGQRSQAITNEVPIIDVGRFFAGVPGALDEVAQQIHKACTEIGFF
YIVNHGVSQPVIRRVFEAMENFFTLPASEKFKVIRMNEHQAGWQAPNVAIHGDSFDKVV
KPQATEAFKFGPELDPADPDFQGSKRFRGHNQWPEGLSVEDKQAFITYHAQFNELAK
RLLAAVAVALGSPNFFDDAFRRDTSVMRCAYYPVVKPQENQFGLPGHTDLSFLTIPP
ATAPGLQILTAAGTWIDQPIVEGGILVNTGDALRTWSNDQFIATPHRVLASTKEERYSAIF
FLYPDLDVTISCVPTCWSADYPKKYTDQKFSDFYAGYAARNFGYAEKKA

Codon-optimized NHI 48 sequence:

ATGCCACATACCCTTGACATCACTGCGCTGCCGACCTTGGATCTGTGCGAGTTCGA
AGGGACAGCACAAACAGCGTTATGAGTTCCTGGAAGATTTGCGTCACGCCGCACGC
GACGTGGGATTCTTCTACCTGACGGGCCATGGCATTGATAGTGATCTGCTGAAGCA
GGTGCAAACGCATGCCCGCCAGTTCTTTGCGCTGCCGGATTCCGAGAAAGCGGCG
GTAGGTATGATAAACAGTCCTCATTTCCTGGCTACAACCGTGACGCCTCGGAAATT
ACTCGTGGTCAGCCGGAAGTTGCGCGAACAGTTCGACTTGGGTGCGGAACGTGAA
GCCCTGCCACTCACAGCAGACTCACCGTTTTGGGCACGCTTGACAGGGCCCTAACC
AGTGGCCCGGCGGCCCTGCCGGAACCTCAAACCGCTGCTGCTGGAATGGCAAGAGG
CAATGACACGCATGAGCTTACGCTTGCTTCGGGCTTTTGACAGGCACTGAGCTTG
CGTGACAGATGCATTTGACCAACTATATGGAGATAAGCCAAATGAACATATTAAATTAAT
GCGTTATCCGGGTCAATCGTCGGAATCCTCGCACCAAGGCGTGGGAGCGCACAAAG
GATAGCGGCTTTCTGAGCTTCTTGCTTCAGGATCAGCAGGCTGGTCTGCAAGTGGA
GATAGAAGAAGGACGCTGGATAGACGCTCTGCCGCGCGAGAATACGCTGGTTGTG
AACATAGGTGAATTATTGGAGCTAGCGTCGAATGGGTATCTGCGTGCCACAGTGCAT
CGCGTAGTTAGCCCGCCAGAGGGCACCGAACGCCTGTCCGTAGCTTTCTTCCTGG
GGGCGCAGTTAGATGCAGCCGTACCACTGTATCCACTGCCTACAGCCCTGCTGCGT
GAAGCTCGCGGTCCCGCTAGTGACCCCTTGAACCCTCTTTTCCGTGATGTGGGTT

GGAAGTACTTGAAAGGGCGGTTACGTAGCCATCCGGATGTAGCCCAACGCTTTTAT
GCAGACGCGCTGCTGCCGCCGCCACCGGTACGTAAAAGCGCATAA

NHI 48 protein sequence:

MPHTLDITALPTLDLSQFEGTAQQRYEFLEDLRHAARDVGGFFYLTGHGIDSDLLKQVQT
HARQFFALPDSEKAAVGMINSPPHFRGYNRAASEITRGQPDRLREQFDLGAEREALPLTA
DSPFWARLQGPNQWPAALPELKPLLEWQEAMTRMSLRLLRAFAQALSLRADAFDQL
YGDKNPNEHIKLMRYPGQSSESSHQGVGAHKDSGFLSFLQDQQAGLQVEIEEGRWID
ALPRENTLVVNIGELLELASNGYL RATVHRVSPPEGTERLSVAFFLGAQLDAVPLYPL
PTALLREARGPASDPLNPLFRDVGWNYLKGRLRSHPDVAQRFYADALLPPPPVRKSA

Codon-optimized NHI 49 (AndA) sequence:

ATGACTATCGAATCAAAAACTACCCCCCATTCGACGCGTCAATGCCTCGCAGGG
TTCCGATGCCGCCTATCAGATTCTTCAGGAAGACGGCTGTGTAATTGTAGAGCAGG
TGATTTGTCCTAATATTATTGCGAAAATTCAGACGACGTTAACCGCGTGATGGACAA
AGCCACCATTGGCGCTAAAAAGGGTGAACAGACCCATATCATCAATATGCATAATCG
TACCATTACATGGGCGACTTAGTACTGACTAGTAAACATACCGTGATGAGCTTTTG
AATCTGCCGTTTGCCCATGAAGTGTTAGAAAAAGTGTTTAAAAAGGACAGTGGCGAT
TACTGGCTGAACATGGGCAACATTCTCAACATGCTCCCGGGAGCGGAGGCGCAAC
GTCCTCACAGAGATGACTACCTGTACCCGGTAAGTCAACATATGGACCCCGCCACT
TCACCTGATCTGATGATTAACATTACCTTTCCATTAAACGAGTTTCGCCACGATAATG
GCGGAACTCTTCTGTTGCCTAAATCGCATAACCGGACCGAATGCCGATTTTTACGCCA
ATGCAGAAGATCTGCCGGCCGCGGAGATGCAGGTCGGCGATGCTCTGATTTTCAC
CGGGAAATGCGTCGACTTTTCATGAGGCCCTGGGGCTGAAATCTAAACAGCGCATG
GTGGGGGGGGCCAACCGTTCGGATAAGCCTCGCATAGGGCTGGCTCTGGCAGCGC
AGCCGGGTTATCTCACTCCGCGTGAGTCAAACGTAAATGTGCCACGGGACATCGTT
GAAACCATGACACCGCTGGCGCAACGTATGATTGGCTGGGGGACCGTTTCGGACAA
AAGATACTTATGGCCTTAATATGTTACAGGACAAGTAA

NHI 49 (AndA) protein sequence:

MTIESKNYPPIRRVNASQGSDAAYQILQEDGCVIVEQVICPNIIAKISDDVNRVMDKATIG
AKKGEQTHIINMHNRTIHMGDLVLTSKTYRDELLNLPFAHEVLEKVFKKDSGDYWLNMG
NILNMLPGAEAQRPHRDDYLPVVSQHMDPATSPDLMINITFPLNEFRHDNGGTLLLPKS
HTGPNADFYANAEDLPAAEMQVGDALIFTGKCVDFHEALGLKSKTAHGGGANRSDKP
RIGLALAAQPGYLTpresNVNPRDIVETMTPLAQRMIGWGTVRTKDTYGLNMLQDK

Codon-optimized NHI 50 (AndF) sequence:

ATGACTGTGCCTCAACTGCACTATGTGCCTTATGATACGCCGGTCAAGACGTGAT
GAGAATTCTGGAAGAGTGTGGTACCCTAGTAATTCGTAACCTTTCTAGATCAAAAAAC
CGTTCAAAACGTGCAGAACGAGGTGGATGATTACGTTAGAAACTGGAATCCAGGAC
CAAAGTATAATCATGATATCAAAACCGTAGGCAGCAAAACCAAACAGCCGTGCAACC
TTAGTCTCATGAGTAAACGTACAGATGCGAAGTTTTAAACCATCCGTGGATGCACG
CAATTTGCGAACGTATGTTTGGGCCCACGTATGGTGATTATTGGTTTAAATGGCGGCT

CTATTTTACACTTGGAGCCTGGCGAACATACCCAGCCAATTCATCAGGACCATGTGT
TTTATCACATTAGCAAATGGCGTCGACCTACTGACCCAGACCTAACAATTAATTTTGC
CATGGCGTTGACCGAATTTACGGTTGAAAACGGTGGTACCCGTGTGTGTCCGGGTT
CGCATCTGTGGGAAAACGGCCATGCTCCGCCGGCAGAAGAAGACATGGTCCCGG
CGCTGATGCAGCCAGGTGATGCTCTGATTTTACCGGGATCAATGTGGCACTCAGCC
GGGGCCAATCGCAGTAGTGAGTATCGGCGCGGATTTGCGGCCTCGTTTCACCCCT
GTCATTTTACCCCCATTGAGTCACATCATCATCTGCCCCGTGAGATGGTTGAGGAAA
TGTCGCCGTTAGTTCAGAAGATGTTGGGTTTCCGTACGCTTAATCTTCATAATAATGT
AAAGGTCTGGAAAGCGGGAGAGGGGAAACCTCGAGGATGCTACTGGTCTTAAGTCA
ATTGCAGTATGA

NHI 50 (AndF) protein sequence:

MTVPQLHYVPYDTPVEDVMRILEECGLVIRNFLDQKTVQNVQNEVDDYVRNWNPGP
KYNHDIKTVGSKTKQPSNLSLSKTYRCEVLNHPWMHAICERMFGPTYGDYWFNGG
SILHLEPGEHTQPIHQDHVYHISKWRRPTDPDLTINFAMALTEFTVENGGTRVCPGSH
LWENGHAPPAEEDMVPALMQPGDALILPGSMWHSAGANRSSEYRRGFAASFHPCHF
TPIESHHLPREMVEEMSPLVQKMLGFRTLNLHNNVKVWKAGEGNLEDATGLKSIAV

Codon-optimized NHI 51 (CnsJ) sequence:

ATGACGGTTGATACTGCACCACAGAGCCATTATCAGGAAACAAAGGTATCCGAAATA
CCGATAGTAATTCTGAAAAGCTCTGCAACCGACGATGTTGCGGCGCACGAGGCCAT
TGAAGCTTTAAAGGTTGCAGGTGTTTGCATTGTGAGAAATCTGCTTGATCGAAGCAC
TGTTGATAAAGTTAGACAGGAATTACAACCATATGATAAACAGGCGGACTCATTGAA
GGGTTTCTCTAAAAATTATTGCCAAGTTGCTGGTCTGCTGAGTAAAAGTCCGACTTAC
GCCATTCTATAGTTGGCAATAAACTTTTCACTGCGGTCCGGAATTATTTTCTGACTA
GTACGTACGAGTGTTGGGCCGAAAAAGGTACGTGGATGTCAGTTAAATCACCACCA
CAGTTGGATTCAACACTGGCACTGTATGTTAACCCTGGCTCAGGCGATCAGGGACT
ACATCGGGACGACGCGACTCAGCAAAATTGGAACCTCTGGCGCAAGTGAGTACAGC
CTGGGACGTGATTCAGGATGTGCGATGATGGTTGCTCTGACTGAATGTGCCCGAGA
AGATGGTACAACCCGCTTCATCCCAGGTTCTCACCTTTGGGACTACCAGTACGATCA
TCCATCAAACGATGATCCTCGTATTAGGTATGCGGAAATGCGGCCCGGCGATGCATA
CCTTATGCTGTCATCCGTGATCCATGCGGGCAGCGTGAATTACTCAACGGACCGCC
GGCGCGTTCTAGCAGCCGTGTTTCGCTGCTCGATCCCATTTAAGACAGGTAGAAAAT
CAATATCTGACCTATGATATTGAAACCGTACGTACGTTTCCGACGTGGTTACAAAGAT
TCATGGGGTACAGTTTAAGCAAGTTATTTCAAGGTTGGGTAGATAAGAAAGATCCCC
TTCTGGTCGTAGACCCGAACGCCCAACCAGAAGGTGAGGATGATGGAGGCATGAA
GCCAAATGAGGGCGAGCATGTAGTCGAAGCACAAATTTAA

NHI 51 (CnsJ) protein sequence:

MTVDTAPQSHYQETKVSEIPIVILKSSATDDVAAHEAIEALKVAGVCIVRNLLDRSTVDKV
RQELQPYDKQADSFEGFPKNYCQVAGLLSKSPTYAHSIVGNKLFTAVRNYFLTSTYEC
WAEKGTWMSVKSPPLDSTLALYVNP GSGDQGLHRDDATQQNWN SGA SEYSLGRD
SGCMMVALTECAREDTTRFIPGSHLWDYQYDHPSNDDPRIRYAEMRPGDAYLMLS

SVIHAGSVNYSTDRRRVLAAVFAARSHLRQVENQYLTYDIETVRTFPTWLQRFMGYSL
SKLFQGWVDKKDPLLVDPAQPEGEDDGGMKPNEGEHVVEAQI

Codon-optimized NHI 52 (SptA) sequence:

ATGACGATAGAGTCCAAAACTATCCGCCAATTCGTAGGGTTAACGCATCACAAGGA
TCAGATGCGGCTTATCAGATTCTTCAGGAAGATGGGTGCGTCATCGTCGAACAGGT
TATCTGTCCTAACATCATTGCGAAAATTAGTGATGACGTGAATAGAGTTATGGATAAA
GCTACAATAGGCGCAAAAAAAGGTGAACAGACACATATTATTAACATGCATAATCGTA
CCATTCATATGGGCGATTTAGTACTGACATCTAAGTCTTATAGGGACGAACTTCTCAA
CCTTCCATTTGCGCATGAAGTCTTAGAGAAGGTGTTCAAAAAAGATTCTGGGGATTA
CTGGCTAAACATGGGCAACATATTGAATATGCTTCCGGGGGCAGAGGCACAACGCC
CTCATCGGGACGACTATCTGTACCCGGTAAGTCAACATATGGATCCGGCGACTAGTC
CGGATTTAATGATCAACATTACATTTCCGCTTAATGAATTCCGCCATGATAATGGAGG
TACTCTGCTTTTGCCCAAAGCCACACTGGTCCAAATGCTGATTTCTATGCAAATGC
CGAAGACCTGCCGGCTGCTGAAATGCAGGTAGGCGATGCACTCATTTTTACCGGTA
AATGTGTGCATGGGGGAGGTGCCAATCGTTCGGATAAACCTCGAATAGGATTGGCT
CTGGCAGCACAGCCCGGCTACCTTACTCCAAGAGAATCTAACGTCAACGTTCCCCG
CGATATAGTGGAACAATGACCCCGCTGGCTCAAAGAATGATCGGCTGGGGGACC
GTCCGTACAAAGGATACGTATGGTTTAAACATGCTGCAGGATAAGGACTTTCATGAA
GCGCTAGGTCTTAAATCAAAAACGGCGTGA

NHI 52 (SptA) protein sequence:

MTIESKNYPPIRRVNASQGSDAAYQILQEDGCVIVEQVICPNIIAKISDDVNRVMDKATIG
AKKGEQTHIINMHNRTIHMGLVLTSKSYRDELLNLPFAHEVLEKVFKKDSGDYWLNM
GNILNMLPGAEAQRPHRDDYLYPVSQHMDPATSPDLMINITFPLNEFRHDNGGTL LLPK
SHTGPNADFYANAEDLPAAEMQVGDALIFTGKCVHGGGANRSDKPRIGLALAAQPGYL
TPRESNVNVPRDIVETMTPLAQRMIGWGTVRTKDTYGLNMLQDKDFHEALGLKSKTA

Codon-optimized NHI 53 (SptF) sequence:

ATGACAGTACCGCAGCTGCATTATGTCCCATATGACACCCCTGTCTGAAGATGTAATG
CGGATTCTTAAGGAAAGCGGCACCCTGGTCATTTCGTAAATTCCTAGATCAGAATACG
GTCCAGAAAGTACAAGACGAGGTTGACGATTACGTACGAAATTGGAACCCGGGACC
GAAATACAATCATGACATTAAGAATGTTGGTTCGAAGACCAAACAGCCCAGTAATCTA
AGCTTAATGAGCAAAACGTATCGCTGTGAGGTTCTTAATCACCCGTGGATGCATGCG
ATTTGTGAGCGGATGTTTGGTCCTACCTATGGCGACTATTGGTTTAACGGGGGTTCA
ATACTGCATCTTGAGCCTGGTGAAAATACTCAACCTATCCATCAGGATCATGTGTTCT
ATCAGATTTCAAATGGCGCCGGCCGACGGATCCGGACCTTACGATTAATTTTACGA
TGGCCTTAAGTGAATTCACAGTTGAAAATGGCGGTACTAGAGTTTGCCCCGGCTCG
CATTTATGGGAAAACGGACATGCAAGCCCGGCGGAGGAAGATATGGTGCCAGTGTT
GATGCAGCCTGGAGACGCGCTTATTCTCCCCGGCTCAATGTGGCATAGCGCCGGC
GCCAATCGCACCTCGGAGTATCGCAGAGGATTTGCGACTAGTTTTTCATCCCTGCCA
TTTTACACCTATTGAATCCCACCATCATCTGCCCGGGAGATGGTCTGAAGAAATGAC
CCCGTTGGTACAGAAAATGTTAGGTTTTTCGGACGCTGAACTTACATAATAACGTGAA

AGTATGGAAGGCGGGCGAGGGTAATCTGGAGGATGCGACCGGTTTAAAGTCAGTAGCAGCTTAA

NHI 53 (SptF) protein sequence:

MTVPQLHYVPYDTPVEDVMRILKESGTLVIRNFLDQNTVQKVQDEVDDYVRNWNPGPKYNHDIKNVGSKTQPSNLSLSKTYRCEVLNHPWMHAICERMFGPTYGDYWFNGGSILHLEPGENTQPIHQDHVIFYQISKWRRPTDPDLTINFTMALTEFTVENGGTRVCPGSHLWENGHASPAEEDMVPVLMQPGDALILPGSMWHSAGANRTSEYRRGFATSFHPCHFTPIESHHLPREMVEEMTPLVQKMLGFRTLNLHNNVKVWKAGEGNLEDATGLKSVA

Codon-optimized NHI 54 (2-ODD) sequence:

ATGGGAAGTACAGCGCCTCTTCGCCTACCGGTGATCGACCTCTCTATGAAAAATTTA
AAGCCAGGTACAACGAGTTGGAATAGCGTCCGGACTCAGGTTCGTGAGGCGTTAG
AAGAATACGGTTGCTTTGAAGCGGTTATAGACGCCGTCTCCCCCGAGCTGCAGAAA
GCTGTTTGCAACAAAGGACACGAGCTTCTGAATCTTCGGTTAGAGACGAAAATGCT
TAATGGAAATAAGCCTGAGTACGACGGTTTTACCTCAATTCGAATCTGAATGAAGG
GATGGGAGTTGGTCGTATAACTGACTTAGAAAAAGTTGAACGCTTTACCAACCTAAT
GTGGCCCGAGGGCAACAAAGATTTTTGTGAAACAGTTTATAGCTACGGTAAAAGAAT
GGCAGAAGTGGATCATATCCTGAAAATGATGGTTTTTGAGTCGTTTGGTATGGAAAA
ACATTTTGATAGCTTCTGCGAAAGTACCAATTATCTTCTTCACTTTATGCGTTATCAGC
AGCCCGGTAAAGATGGGAGGTCGCCCGCTCTGTCATTACATAAAGATAAGTCCATAT
TGACGATTGTAAACCAAAATGATGTGAAGGGTCTCGAATTCGAGACTAAAGACGGC
GAATGGATCTTACCGACGGCGGATAATCACATAGTGCTGTTGGGCGACTGTTTTATG
GCCTGGAGTAATGGCCGTTTACATTCCCCCTGCATAGGGTTACGCTGGTTGCGAA
CCAGGCACGTCTTTCCACATCCTCGTTCAGTTTTCTTAAAGATATCATAGAAACCCC
TGCTGAGTTGGTAGACGAAGAACATCCACTGTTGTTTAAACCCTTTCGAAATCACAGA
GCTGTTGGCATATTGCTTTACGAAAGAGGGCGCAAAAGCTGTTTGCATCTGAAAC
AATACAAAGCATATACTGGTGCCTAA

NHI 54 (2-ODD) protein sequence:

MGSTAPLRLPVIDLSMKNLKP GTTSWNSVRTQVREALEEYGCFEAVIDAVSPELQKAVC
NKGHELLNLPLETKMLNGNKPEYDGFTSIPNLNEGMGVGRITDLEKVERFTNLMWPEG
NKDFCETVYSYGKRMAEVDHILKMMVFESFGMEKHFDSESTNYLLHFMRYQQPGK
DGRSPALSLHKDKSILTVNQNDVKGLEFETKDGEWILPTADNHIVLLGDCFMAWSNGR
LHSPLHRVTLVANQARLSTSSFSFPKDIIETPAELVDEEHPLLFPFEITELLAYCFTKEG
AKAVCDLKQYKAYTGA

Codon-optimized NHI 55 (Ppzd) sequence:

ATGGCGCGAACCCTGAACGCCGGGTTCTGACATTAGATTTGCTCAGTTTTGTCAT
GGGGAGCCTTCTTCTAGCCATGGCTTTTGCAGGGAAGTGGTCTGACTGTCTTCGTAG
TTTGGGGTTTGTAAAAATTCGTAACCACGGAATTAGTGGCGAAGAGATAGAAAAAGT
ATTTGTCATGAACAAATTGTTCTTTAGTCTGCCTCAGGCGGCAAAAGCCAAGGCCG
CACACCCACCCGAAGCTAATCCACATCGTGGTTATTCCTACGTGGGTCAGGAAAAG

CTGAGCCGTGTCAAAGACTACGAAAAAGGTAAACGCAGCATTGTTGATGTTTATGAT
ATTAAGGAGAGCTATGATCAGGGCCCCGCCGTTGATAAACTATATCCGAACCGTTGG
CCAGATAAACAGGACATTCCGGGTTTTTCGCGTAGTTATGGAAAAATTTTATGAGCGC
TGTCACCAAGTTTCATCAGGACGTTCTGCGTGCAATAGCAACTGGATTTGACCTGTCT
CCGTCTTTTTTTGACCGACCTCTGTTGCGAAAACACGTCTGAACTGAGATTAAATCAC
TATCCAGGCGTGCATCCTTCGTCCTTACGTAAAGGCGCAAAACGCATCTCAGAACAT
ACTGACTTTGGGACGGTTACCCTGCTGTTTCAAGATAGTGTAGGGGGTCTGGAAAT
CGAAGATCAAAATTCTCCGGGGACTTATTTCCCTGTAAGTTCTGAGCGCAAAAGTGA
TATGATTGTGAATGTGGGCGATTGCATCCAACGATGGACCAACGACAAAATTCTGTC
AACGAGTCATCGGGTAGTGTTGCCGGAAGACAGGGATGCTCTCATAAAAGATCGTT
ACTCAGTCGCATACTTCGGCAAACCCAGTCGTTCTCAGTTGGTGAGCCCCCTAAGA
GAATTCGTGAAAGAGGGCGAGAAGCCCAAATATAGTGCCATCTCCGCTTGGCAGTA
TAATCAGGAAAAACTCGTTCTTACTTACGGTGGAGATGAGGAGATTTTGGTTCCCAA
GCCTAGCTCAAGTGTATGCACCGGAGTGGGGCAGTTGCAATAA

NHI 55 (PpzD) protein sequence:

MARTPERRVRTLDFAQFCHGEPSSSHGFCRELVDCLRSLGFVKIRNHGISGEEIEKVFV
MNKLFFSLPQAAKAKAAHPPEANPHRGYSYVGQEKLSRVKDYEEKGRSIVDVYDIKES
YDQGPVAVDKLYPNRWPDKQDIPGFRVVMKFYERCHQVHQDVLRAIATGFDLSPSFLT
DLCCENTSELRLNHYPGVHPSSLRKGAKRISEHTDFGTVTLLFQDSVGGLEIEDQNSP
GTYFPVSSERKSDMIVNVGDCIQRWTNDKILSTSHRVVLPEDRDALIKDRYSVAYFGKP
SRSQLVSPLREFVKEGEKPKYSAISAWQYNQEKLVLTYGGDEEILVPKPSSSVCTGVG
QLQ

Codon-optimized NHI 56 (PpzC) sequence:

ATGGCAACTGATACCGCCGTCACCGGCGCGCCTGAGACCACGGAGTTACGTCTGG
CGTCTGGGAATGGGCCAGTTACCCGTACGGTATTGCGTACACCTGTTTCGAGATGCA
TTACCATCCGAAGTGCCATTGATCGATATTAGTCTATTTTCTCAACCTGTGTGGCAG
ATCGCAAGGCCGTAGCACGTAAGATACATGATGCCGCGACCAATATCGGCTTCTTTT
ATATTCAGAATCATCGCGTTCCGAGCCAGGATATTGATCTGGCGTATTCAGCTAGCC
AGGATTTTTTTTCGCCAGGAGATGGAAGTGAAAGTGGAAGCGGACGCTAAAGATGGT
CCGTTTGATTACAGGCTACCGGGGTCCAGGCACGCAAAGAGTTAACCTACGGAAG
GTGCAGATCTGAGAGAGACTTATTCGATACTGTATGACCCAATGCTTGACCCAACCG
TGCCGGATCCGGCAAATATACCAGAACCGGCCTCTCGCTTCCTTCATCTCGGGCGG
GCCCCATTTGAATCCACAGCAACTTTGCCTCACTTTAAGGATGCATTTGTCAGGTAC
TTTCAGGCGTGCCCTCGTTCTGGCCCGTGCCCTGACTCGGGCGTTCCGCCCTGAGCT
TGGATCTGCCGGAATCTGCCTTTGATGGAAAAGTCCAGTACCCGGATGCAAGCCTT
GAAATTAATTTCTACCCACCCATCTCGACCGGACATGCCGTCTCGGCCCCCGGGGA
TGCAGATACTCGGGTTTCAATTGGCAGCCATACGGACTTTTTACTGTTACGATACT
CTGGCAAGATTCAAATGGCGGTCTGCAGGTGTTAAATCGTGAGGGCCAGTGGATAC
GCGCTATACCTGTTGAGGGCACTTTTGTGGTTAACATTGGGGATTACCTGCAAAGAG
TGACAAACGATAAATACGTTTCCACTGTCCACAGAGCACAGAATTTAGTGGCCGC
GAACGTGTCTCGATGCCCTTTTTTTGGGGCTTTGGAATGCATGAGTCGTGTCAGGT

ACTGCGCAATTGCTGTGGGGAAGATGAGAAATCAAATATGATGAGGTTAAATGCGT
GGATTGGGTAAGCCGTCGTCTCGGCAATTTATTTGACCTGAGTGACAAAGGTTGA

NHI 56 (PpzC) protein sequence:

MATDTAVTGAPETTELRSLASGNPVTTRTVLRTPVRDALPSEVPLIDISPIFSTCVADRKA
VARKIHDAATNIGFFYIQNHRVPSQDIDLAYSASQDFFRQEMEVKVEADAKDGPFD SGY
RPGGTQRVNPTEGADLRETYSILYDPM LDPVPDPANIP EPASRFLHLGRAPFESTATL
PHFKDAFVRYFQACLV LARALTRAFALSLDLPESA FDKVQYPDASLEINFYPPISTGHA
VSAPGDADTRVSIGSHTDFLLFTILWQDSNGGLQVLNREGQWIRAI PVEGTFV VNIGDY
LQRV TNDKYVSTVHRAQNFSGRERVSM PFFWGF GMHESCQVLRNCCGEDEKSKYD
EVKCVDWVSRRLGNLFDLSDKG

Codon-optimized NHI 57 (PrhA) sequence:

ATGGCGCCGATGATTCCCCCCCCGCCTGCAGAGGTTTCCGGCCACTGCCAGCGCG
GATGAAATATTTGCCGCCTTTCAGGAAGATGGTTGCGTGGTAATCGAAGGATTTATC
AGCCCAGAACAGGTGGCACGCTTTTCGCAAGAAGTGGATCCCGCGATGGAGAAAA
TTCCGGTTGAAGTTACAAACAATGGAAATAGCAATGATCGTACTAAACGCTTTAGTAA
ATGCGTTATTGCCTCTCCAACATTCAGGAATGAAATCATAGAATCTGATCTTATGCAC
GAACTGTGTGATCGCGTGTTTTCGAAGCCGGGAGAAGGCATGGGATACCATTTTAA
TGATAATATGGTTATTGAGGTACAGCCGGGCGCACCCGCTCAGCGTTTTGCACCGAG
ACCAGGAATTGTACCCCTGGTGGAATTCGATGGGTCCGGCAGGCCCGGAATGTGT
TATTAATTTTTTTTTGCGCGGTAACGCCGTTTACCGAAGAGAATGGTGCTACACGTCT
GGTACCGGGTAGTCATCTGTGGCCAGAATTTACTCAAATCAACGAACGTGATTGCC
CTCAATTTGGTAAGATTGAAACTGTTCCAGCAATTATGCAGCCTGGAGATTGTTATCT
GATGAGCGGTAAAGTGATCCATGGCGCCGGACATAATGCGACCACTACTGACCGGC
GTCGGGCGCTAGCTCTGGCGATCATACGTCGCGAGTTAAGGCCGATGCAGGCTTTT
TCTCTGAGTGTGCCTATGAACTGGCACGCGAAATGTCCGAACGGTCCCAGACCAT
GTTTGGTTTTTCGTTTCATCCGTTTCAGCATTGCGACGTGGACATGGTTCAATTTTTGGGG
CAACGACGGTAAAGATATTGCACATCATCTCGGTCTCGAAGCTCCGTCAGTGCACG
TCTAG

NHI 57 (PrhA) protein sequence:

MAPMIPRLQRF PATASADEIFAAFQEDGCVVIEGFISPEQVARFSQE VDPAMEKIPVEV
TNNGNSNDR TKRFSKCVIASPTFRNEIIESDLMHELCDRVFSKPGEGMGYHFNDNMVI
EVQPGAPAQRLHRDQELYPWWNSMGPAGPECVINFFCAVTPFTEENGATRLVPGSHL
WPEFTQINERDCPQFGKIETVPAIMQPGDCYLMMSGKVIHGAGHNATTTDRRRALALAI
RREL RPMQAFSLSVPMKLAREMSERSQTMFGFRSSVQHCDVDMVHFWGNDGKDIAH
HLGLEAPSVHV

Codon-optimized NHI 58 (AneA) sequence:

ATGACCCGGTCAAGTCCGAAATCAATACTGCGTCTGTAGCAGCACATGAAGGTGC
ACCTAAAATTCTGCAGGTGTTGAAAGAGGATGGCGCGGTAATTATCCGTGGCTTTCT
TAATCAAACCTCTTTCAGAAATTGAATAAAGAGATGGAGGATGAACTGGCAAAGCG

CCCGCTGATTTGTGAACATAATGGCGAATGGGTAAAGTGGTCTGGCCGGCTCTCAGA
CTCGCCGTCTTAATCAACTGCCGGCATTTCACCAACTTTTAGACAGGAGATTTTGA
ACCATCCCTTATTCCATGAAATCTGTGAACCGCTGTTTGGTACTCATGGATGCGACT
ACTGGATGAACACGGCGACGGTTCGTCCAGATTGGTCCGGGCAACGCAGCACAGTC
ATTACATCGGGATCAGGAACTCTATCCCGTATTCAATCCGATCGGCAAAGATGCGCC
AGAGGCATTAGTTAACTTCTTTTGTGCGCTTAGTACCTTCACAGATGAAAACGGAGC
GACCCGGGTGATTCTGGCTCTCACCAATGGGATGATTTACAACGGATGTGACAC
GTTGTGTCCCTCAGACAATTCCGGCCGAAATGGAGGCGGGGGACTGCTTACTGTT
CTCTGGTAAAACCGTCCATGGAGGCGGCGCCAACAGATCAAAAGATAATGTTTCGGA
GAGGTATGGCCCTTGGAGTGCAGGCTACTTACCTTACCGCCGAGGAGAATTATCAG
CATATTCCTCGGGAGATTGTTGAAAGTATGACGCCTTTGGCACAGAAAATGATCCAT
TGGCGATCTTCATATTGCCCAGGTGGAGCCGGGCTCTGGCAGATTAACGGTACAGA
GCTGGCTAATGAAATCGGCCTGAAAGCAAATCAACCGAAAAAGACGATCTAA

NHI 58 (AneA) protein sequence:

MTRSSPKSILRRVAAHEGAPKILQVLKEDGAVIIRGFLNQNLFFQKLNKEMEDELAKRPLI
CEHNGEWVSLAGSQTRRLNQLPAFSPTFRQEILNHPLFHEICEPLFGTHGCDYWMN
TATVVQIGPGNAAQSLHRDQELYPVFNPIGKDAPEALVNFFCALSTFTDENGATRVIPG
SHQWDDFTTDVTRCVPQTIPAEMEAGDCLLFSGKTVHGGGANRSKDNVRRGMALGV
QATYLTAENYQHIPREIVESMTPLAQKMIHWRSSYCPGGAGLWQINGTELANEIGLKA
NQPKKTI

Codon-optimized NHI 59 (HimG) sequence:

ATGGCACCCAGCACTGACGCAGAGCCTGAATGGTGCAACTCCTCAGGTTAAAGCGG
CGCTGCATCATCTTGATGCTAACACGGTATCTATAGACGACATCATTATTATTTGAA
GCATCACGGCGGAGTAGTGGTTCAAATCTGATCAGTGAAGAGATCCTTCAAGAGG
TTGGCGCTGACATCAAACCGTATTTTGTGCGCTTGTGGAACCTGGATTTTCTCTT
CCAAAACCCGAATAGTCACACGACTGCCCAATAAATCAATTGCCTTTGTGCAAAAGA
TCTTTGGGAATCAAGTCTTTCAGGACATATGTGATCATTTTTTGACATCACATCACAG
GGGTTGGTATGGCAACGAACAGTATACATACTCCCCACATCCGGTGTTTAATAGCGC
CCTGGCATTCTCTACACTTCTGGTAATGAGACACAGTCATTACACAGAGAATGCAT
GGGCCAACACAATAAATTACCAGCTATTGCCCTGAGGATTATCCGATCGGACGCGA
CACTGTGCTGGGCATGTTTGTAGCCGACACACGGACCACAAGAGAAAACGGAGCC
ACGAGGTTTATACCTGGCTCCCATCTGCAGAGCACATTAGATCCACCTGATGAAAGC
CAGACCGTGCCTGTAGAAATGAACAGAGGCGATGTTTTCTAATGCTGGGTTCTTG
CTATCACGGCGCTTCTGCCAACGTCTCCAGGCCGAAGAACGTATCCTTTACTCCA
CCTTTATGACCCAGTCAACAAGAAGGCAGCTGACGACTTGCCTCTTTCTGGTGCAG
GAGGAAAATATTTATCTGTGAGTCCCGTAGATCGCGTTAGAGTTTTAGCCCGCGT
ATGCAGAAACGTCTGGGTTTTTCAGCCTCAGACCCGCTTTTCGGCTGGGTTGACGT
CAAGGATCCGCGTAAAGTATTTAATCTCCCTGGTTTGTCTGAAGGTCAGCACATCGA
CGTTTGA

NHI 59 (HimG) protein sequence:

MAPALTQSLNGATPQVKAALHHL DANTVSI DDIIHYLKHHGGVVVQNLISEEILQE VGADI
KPYFDALVEPGFFSSKTRIVTRL PNKSIAFVEKIFGNQVFQDICDHFLTSHHRGWY GNE
QYTYSHPHPVFN SALAFSTLPGNETQSLHRECMGQH NKLP AIAPEDYPIGRD TVLGMFV
ADTRTTRENGATRFIPGSHLQSTLDPPDESQTVPVEMNRGDVFLMLGSCYHGASANV
SQAERILYSTFMTQSTRRQLTTCLFLVQEENIYLSVPVDRVRVFS PRMQKRLGFSASD
PLFGWVDVKDPRKVFNLPLGLSEGQHIDV

Codon-optimized NHI 60 (CdmA) sequence:

ATGACTAAACTGCCCAGCGATGCGTCTGCGATCAAAAGAGTAGAAGCTAATACCTCC
CCGGAGCAGGTTATCGAATTATTGAAACAGGACGGCGTTGTAGTGCTCAAAGACTT
CTTAGATCAGGCCACCGTACAGTCCTTTTCGCGAGGAAATTAACCGGCAATTGACG
ATTTTGAAGGGGGGCCGAATTTCAATCCTGATGGAGTTAAAGTCGATATAGGCAGAG
GCACAAAGCATGTTGCTAATTTAACGGCCATTTCTAAACTTATAGGCACGACATCCT
TAATAACAAGTGGATGCACTCAATCCTGGAGCCTTTATTCCGTCCGCATTTTCGGCGA
TTACTGGATGAATCGCGGTAGCGTCTTACACATCGAACCGGGCGAACCTGCGCAGA
ATCTGCATCGTGACGATATCCTGTACAGGGTGACGAAACTCCGGCAGCCAGGCGA
CCCGGATCTGATGATTAACATCCTGATTGCTGTACAGAGTTTCGTGATGATAATGG
CGCAACACGTTTTCTGCGCGGATCGCATGTGTGGGATGACACGCGGGGCGTTCCA
ACACCTGATCAGGCCTCTAGTGCTGCCTTAAGACCGGGCGATGCCCTATTGTTTGT
CGGAAGTCTTTGGCATGGCGCTGGCTCTAATCAGAGTGATGCGTTTTCGCCAGGGT
CTGCTTCTTTGTATACATCCCTGCCACTTCACTCCGATGGAATCGCATCTCCATGTTT
CGCGCACCATCGTTGAAAGTATGACCCCTCAAGCGCAGAAAATGATTGGCTGGCGT
TCAGGTATAACGCAGCACGATGTTCCAATTTGGCTGGCGGGTGATCATAAAATGGAA
GAAACTATGGGCCTTAGATCCCAGGAGGTTTCAGTAA

NHI 60 (CdmA) protein sequence:

MTKLPSDASAIKRVEANTSPEQVIELLKQDGVVVLKDFLDQATVQSFREEIKPAIDDFEG
GPNFNPDGVKVDIGRGTKHVANLTAISKTYRHDILNNKWMHSILEPLFRPHFGDYWMN
RGSVLHIEPGEPANLHRDDILYRVTKLRQPGDPDLMINILIAVTEFRDDNGATRFVPGS
HVWDDTRGVPTPDQASSAALRPGDALLFVGSLWHGAGSNQSDAFRQGLLLCIHPCHF
TPMESH LHVPRTIVESMTPQAQKMIGWRSGITQHDP IWL AGDHKMEETMGLRSQEV
Q

Codon-optimized NHI 61 (CdmD) sequence:

ATGACCGTCACAATTAATAAGTCCTCTGTGCCACACAAGGTAGATTTTCGCGACCCCG
TTGTCAGATGTTATCTGT CATATTAAGAAGACGGCGCGGTTATTGTACGAGGTTTCA
TGGATGTGGAAACAATTCAGAACTGCAAGAGGAAGTTGATACTGCAGTCGAAAAA
GGATCCTTTGGACCGCGGTATCAAGAATATAATGAGGAGGCTGGGGAGATTCCGAA
ACATGAAATTTATAACGCGGAGAAAGGTAAGAAAACCAAACACATGAAGAATCTGGC
ACTTACTTCCGAAACGTTTCGTAAATGATGTGCTGAATCACAATGGATGCATGCCGT
CTGTGAGCAGATTTACGGTGAAGAGTTTGGAGACTACTGGATGAATTGTGCCCATAT
TCTGCACTTAGAACCGGGTGAAAAAGCCCAATTTTTTCATCGCGACACCGGGGTCT
ATCGCGTTTCTGATTTTCGCGCTCGACTCAACGATCCGGAGTTTATGATAAATTTCTT

GGTGAGTTTAAACAGAGTTTAGAGAGGATAATGGAGCAACGCAACTCATTCTGGTA
GCCATAAATGGGATGCGGCGCATCCGCCTACATTTTATGGTAGCGATGAAGCAGTTC
CTGCGATTCTCGAGCCCGGAGATGCGGTGGTGTATCTGGGGTCTCTCTTTCATGGA
GCGGGTGAGAACCGCAGCCTGGATTATAGACGCGGGATGATTGTAAGTATGCATCC
GGCTCATTTCACACCAATGGAATCCCATTTCCTTACCCAAAGAGATTGTTGAATC
AATGACGCCGCTGGCACAGCAAATGGTTGGATGGCGTACCATGAATAATCAGAATAA
AATTCCGATATGGCAGGCGGGAGACGATAAGATCGAGGATGTGCTCCGTCTGCAGC
ATAAAGAAGTTTATTAA

NHI 61 (CdmD) protein sequence:

MTVTINKSSVPHKVDFATPLSDVICHIKEDGAVIVRGFMDVETIQKLQEEVDTAVEKGSF
GPRYQEYNEEAGEIPKHEIYKRGEKKTGHMKNLALTSETFRNDVLNHHKWMHAVCEQI
YGEEFGDYWMNCAHILHLEPGEKAQFFHRDVGVRVSDFRRLNDPEFMINFLVSLTE
FREDNGATQLIPGSHKWDAHPPTFYGSDEAVPAILEPGDAVVYLGSLFHGAGENRSL
DYRRGMIVSMHPAHFTPMESHFHLPEIVESMTPLAQQMVGWRTMNNQNKIPIWQAG
DDKIEDVLRLQHKEVY

Codon-optimized NHI 62 (BuaE) sequence:

ATGGAGGTGGAACGTCTGGATTATACCGACTTCTTGAATGAGGCACCCGGGCGTCA
AGAGGCCTTCGTCCAACATCTTTATGCGGCATTATCCAGAGTTGGATTGCAAAGAT
TACGAATCACCCCTATTCCAGAGTCTGTTATACTTCAGTTGTTTCGCATGGACGAAGGG
GTTCTTCACTCTACCCTTAGAACATAAGCGTAAGGCCGCACATCCCCGCAACCGA
ACCCGCATCGCGGATGGTCTTGCATTGGTCAGGAAAAATTAAGCGTTATAGCGCAG
GGTAAAGCCGTCCTGGATCTGAAAGAATCATTCGACATGGGCCAGGCGATGATGA
ATTGTATCCGAATATCTGGACCGACGAGGGGGACCTGCCAGGCTTTCGTGCTTTTAT
GGAAGATTTTTACGGCCGTTGTCAGTCTTTGCACCTACAACCTTCTTTCTGCGATCGC
TCGTTCAATGCAGTTCCAGACTCGTATTTTGCGCCGCTGTGCAGCCAAAACCTCGT
CCGAACCTTAGATTAAATCACTATCCAGCGGTGAGTCGGCACGACCTGACGACCGGA
ACTATGCGCATTAGTAGTCACACCGATTTTGGCACTATTACCCTTCTGTTCCAAGATA
GTGTGGGCGGCTTAGAAGTTGAAGATCAAACCTCGTCCGGGGCCATTACATGCCGGTC
GCCGCAGATGATTGTACAGATATTATAGTCAATGTAGGCGATTGTCTGCAACGTTGG
ACGAACGATAGGTTACGCTCCGCGAATCATCGAGTTAACTCCCGAGAGGACTGAC
CCACGGGATGGTTGACGACCGTTATTCTATCGCCTATTTTGGAAAGCCGTCGCGTG
ATGTTAGTGTGCGTACCCTGTCCGCGCTGCTGCGTGCGAATGAGGAAGCTAAATAC
CGTGAAGAAATGACCGCGTGGCAGTACAATCAGTCGCGCCTATTACAAACCTACTA
G

NHI 62 (BuaE) protein sequence:

MEVERLDYTDLNEAPGRQEAFVQHLYAALSRVGFAKITNHPIPESVILQLFAWTKGFFT
LPLEHKRKAHPPQPNPHRGWSCIGQEKL SVIAQGKAVLDL KESFDMGPGDDELYPNI
WTDEGDLPGFRAFMEDFYGRCSLHLQLLSAIARSMQLPDSYFAPLCSQNSSELRLN
HYPAVSRHDLTTGTMRISHTDFGTITLLFQDSVGGLEVEDQTRPGHYMPVAADDCTDI

IVNVGDCLQRWTNDRRLRSANHRVTLPRGLTHGMVDDRYSIAYFGKPSRDVSVRTLAL
LRANEEAKYREEMTAWQYNQSRLLQTY

Codon-optimized NHI 63 (EasH) sequence:

ATGACATCTCAGCACCAGGAGCACACCGGAACAAAACGGTTTTCCATTTCAGAGTGA
CCCCGTGGAGATTCACCGGGCAATCGTGGAGGACGGAGTAGCAATTATTGAAGGG
TTTCTGACCCCGGAACAGGTTCAAAAGTTGAACAAGGATGTTGATGCTCCCCTCAA
GGCGGACCGTGAGCAACTGAAATTCAAAGCGGATAAGAAAGATGATCCACACTTCT
GGCTCGCTGATTTTCATCCCTGACCATGTGCGAAGGGTTCATAATCTGGTTGACTTCT
CCCACTGCTTCCGTCATGAAATCTTGAACCACGAACTACTTCATAAAATATGCCGTCT
GACCTTCGAGGAGTCTGGAGACTACTGGCTTGGGTACGGTGCAAGTATTGAAAATG
GCCCCGGGGACACGGAACAGAAAGTGGCATAGAGACCAGCCACGTTATCCGCTCGT
GAAAGAAGGACCGGACGCACCGGAAGGTATGTTGAATTTTTTACCGCTCTGACAG
ATTTTGATGCGGAGACAGGAAAAACACAGTATATACTGGGTAGCAATAAACGTGTGG
AGCTTGGCGAACCGGATGCCGACCATCCGATTGAATATGTAGGTCTTAAACCGGGC
GATACTACCATAGTTAGTGGTAAATAACACATCGCGGTAGTGACAACCGATCTGAC
AAGATGCGGCGTGCCATGCCTATTATGATAATCCCTTCTATTCTGACTCCATTTGACG
CCACCTGCCACCTTTCCCGAGAGCTGGTGGAACGATGACTCCGCTAGCACAAAA
GATGATATGTAGACGGTCAGTTATGATTCCGGCGCCTGGGACGGTAGAAGTGAAAA
CAGGAATATGGTGCGTGAATATGAGAGAGGCTGGCGAACAGATCGGGCTGAAATCC
AACCAGCGTGCAAAAGAAGATGCCGAAGCTACGGATGCAGTTTAA

NHI 63 (EasH) protein sequence:

MTSQHQEHTGTKRFSIQSDPVEIHRAIVEDGVAIEGFLTPEQVQKLNKDVDAPLKADRE
QLKFKADKKDDPHFWLADFIPDHVARVHNLVDFSHCFRHEILNHELLHKICRLTFEESG
DYWLGYGAVIENGPGTTEQKWHRDQPRYPLVKEGPDAPPEGMLNFFTALTDFDAETGK
TQYILGSNKRVELGEPDADHPYVGLKPGDTTIVSGKITHRGSDNRSDKMRRAMPIMII
PSILTPFDATCHLSRELVETMTPLAQKMICRRSVMIPAPGTVEVKTGIWCVNMREAGEQI
GLKSNQRAKEDAEATDAV

Codon-optimized NHI 64 (FLS) sequence:

ATGGAAGTGGAGCGCGTTCAAGCGATTGCTAGCTTAAGCCATTCCAATGGTACCATT
CCGGCAGAATTTATTCGGCCGGAGAAAGAACAGCCGGCTTCCACCACGTATCACG
GTCCAGCCCCAGAGATCCCTACCATTGATCTTGATGATCCGGTACAAGATCGACTG
GTCCGCAGCATTGCGGAAGCGTCTCGGGAGTGGGGCATCTTTCAGGTTACCAATC
ATGGAATTCCGTCAGACCTGATATGCAAACCTACAGGCAGTGGGTAAAGAATTTTTTG
AACTGCCACAGGAGGAAAAAGAGGTGTATCCCGTCCTGCTGACGCAAAAGACGT
GCAGGGGTATGGCACCAAGCTTCAAAAAGAAGTAGAAGGTAAAAAATCATGGGTGCG
ATCATCTTTTCCATCGAGTGTGGCCGCGTCGAGTATTAACCTACCGTTTCTGGCCTA
AAAATCCTCCTTCCATCGTGCTGTGAATGAGGAATATGCGAAATATATGCGCGAAGT
TGTCGATAAGTTATTTACTTACTTATCATTAGGCCTAGGAGTAGAGGGCGGCGTACTT
AAAGAAGCCGCTGGGGGTGATGATATCGAGTATATGTTAAAAATCAACTATTATCCTC
CGTGCCCGAGACCAGATCTTGCGCTGGGCGTTGTGGCTCACACCGATCTCTCAGC

GTTGACCGTCTTGGTGCCCAACGAGGTCCCGGGCTTGCAGGTCTTCAAGGATGAT
AGGTGGATAGACGCTAAATATATTCCCAACGCACTTGTGATCCACATTGGGGATCAA
ATTGAAATCCTAAGTAATGGAAAATATAAAGCTGTTTTACATCGCACAACTGTAAACAA
GGATAAACGAGAATGAGTTGGCCGGTTTTTCTTGAACCGCCGGCAGACACAGTAG
TTGGACCTCTCCCGCAACTGGTTGATGACGAGAACCCGCCGAAATATAAAGCGAAG
AAATTCAAAGATTATTCGTATTGTAAATTAAATAAACTGCCCCAATGA

NHI 64 (FLS) protein sequence:

MEVERVQAIASLSHNGTIPAEFIRPEKEQPASTTYHGAPEIPTIDLDDPVQDRLVRSIA
EASREWGIFQVTNHGIPSDLICKLQAVGKEFFELPQEEKEVYSRPADAKDVQGYGTKL
QKEVEGKKSVDHLFHRVWPPSSINRFWPKNPPSYRAVNEEYAKYMREVVDKLFY
LSLGLGVEGGVLKEAAGGDDIEYMLKINYPPCPRPDALGVVAHTDLSALTVLVPNEV
PGLQVFKDDRWDIAKYIPNALVIHIGDQIEILSNGKYKAVLHRTTVNKDKTRMSWPVFLE
PPADTVVGPLPQLVDDENPPKYKAKKFKDYSYCKLNKLPQ

Codon-optimized NHI 65 (F3H) sequence:

ATGGCCCCCGGGGCGACAGCTACACCATTCCTTCCGACCGTCTCTAACGAGACAA
CTTTGCGTGAAAGTTTCGTGCGGGACGAAGATGAACGCCCGAAAGTGGCGTATAAC
GTATTTTCCTCTGAAATACCCGTAATATCTCTGGAGGGTATAGACGAAATTGAAGGAC
GCCGTGTGGAGATTTGTAAAAAAATTGTGGCAGCTTGTGAAGATTGGGGAGTGTTT
CAGGTCGTTGATCACGGAGTTGACGCCGGTGTTATCGCAGATATGACGAGACTGGC
TCGTGAATTCTTTAGCCTTCCGCCGGAAGATAAACTGCGCTTTGATATGTCTGGGGG
TAAAAAAGGTGGGTTCATAGTTTCATCACATCTTCAGGGCGAGGCCGTGCAGGATT
GGCGAGAAATAGTTACCTATTTTAGTTATCCTATTAGAGCCCGAGACTATTCTCGTTG
GCCTGATAAACCGGAGGATTGGCGGTCCGTCAACGAAAAGTATTCCGAAACTCTGA
TGGAGTTGGCCTGCAAACTTCTCGGGGTTTTGTCCGAAGCAATGGGCCTGGATACC
GAGGCCATAACAAAGGCGTGTATTGATATGGACCAAAAAGTGGTTGTCAATTTCTAT
CCAAAATGCCCTCAGCCGGATCTTACCTTGGGCCTAAAACGACACACGGATCCCGG
AACTATAACTCTGTTATTGCAAGACCAGGTCTGGAGGTCTGCAAGCCACTAAGGATG
GAGGGAAGACATGGATAACTGTTCAACCGGTGGAGGGTGCCTTCGTAGTTAATCTG
GGTGACCACGGCCACTTTTTGTCAAACGGCCGGTTTAAAAACGCAGATCACCAGG
CAGTGGTGAATTCTAATACTAGTCGTCTCTCAATAGCGACTTTCCAGAACCCTGCAC
CTGATGCAATCGTATATCCGTTGGCAATTCGCGAAGGGGAAAAACCAGTGCTGGAC
GAACCGATTACCTTTGCGGAGATGTACCGGCGGAAAATGTCACGTGATCTGGAAC
AGCCAAGATCAAAAAACTTGCCAAAGTAGAAAATCAGGAAGTTCTTGAGAAGACTAA
AGTTGAAGCAGTCGCGCAGCCCAAGGGTCTGGGAGAGATCCTGGCGTAA

NHI 65 (F3H) protein sequence:

MAPGATATPFLPTVSNETTLRESFVRDEDERPKVAYNVFSSEIPVISLEGIDEIEGRRVEI
CKKIVAACEDWGVFQVVDHGVDAAGVIADMTRLAREFFSLPPEDKLRFDMSGGKKGGFI
VSSHLQGEAVQDWREIVTYFSYPIRARDYSRWPDKPEDWRSVTEKYSETLMELACKLL
GVLSEAMGLDTEAITKACIDMDQKVVVNFYPKCPQPDLTGLKRHTDPGTITLLLQDQV
GGLQATKDGGKWTWTVQPVGAFFVNLGDHGHFLSNGRFRKNADHQAVVNSNTSRLSI

ATFQNPAPDAIVYPLAIREGEKPVLDPEITFAEMYRRKMSRDLELAKIKKLAKVENQEVL
EKTKEVAQAQPKGLGEILA

Codon-optimized NHI 66 (NCS1) sequence:

ATGAGTAAGAACCTGACCGGCGTTGGCGGTTCTCTCCCAGTTGAAAACGTCCAGG
TTCTGGCGGGCAAAGAACTGAAGAATCTGCCGAACCGCTATGTCCGCCCCGAGCT
TGAGCACGATGACGTGGTCCCGATTGACAACTCTCTGGAAATTCCGGTTATTGACC
TGAGTAGACTCTTGGATCAACAGTATGCCTGTGATGAACTTGCAAATTCATAGCG
CATGCCTGGATTGGGGGTTTTTCCAACCTGATTAACCATGGAGTCCGAGAAGAAGTA
ATTGAAAAAATGAAAGTGGATACTGAAGATTTCTTCCGACTTCCGTTTAAAGAAAAAA
ATGCATATCGTCAGTTACCCAACGGTATGGAGGGGTATGGCCAAGCCTTTGTGACAT
CGGAGGAACAGAAACTGGATTGGGCGGACATGCATTTTCTCATTACGAAGCCGGTT
CAGGAGCGAAACATGCGATTTTGGCCGACATCCCCGACTAGTTTTCTGTGAAACTAT
GGAAAAATATTCTATGGAACCTGCAAAGGTCGCAATGTGTTTGACCGGGATGATGGC
GAAAAATCTCGGGTTGGAGTCAGAAATCTTAACAAAACCTTTGCGCACTGTTTTTAA
TCGCGAGGATGAGCTACTCCCCAGCATGAGTTCATGCGGTGAAGGCTTAGGCCTG
TCGCCACACTCAGACGCCACCGGGTTAACGTTACTGATACAGGTAAATGAAGTGAA
TGGGCTCCACATCAAAAAAGATGAAAAGTGGGTTCCGATTAAGCCTATCCTAGGTGC
TTTCGTTGTTAATATTGGAGACGTTATTGAAATTATGTCTAATGGTATCTACAAATCAAT
AGAACATAGAGCTGTCATCAATACAGACAAAGAACGCCTGTCTATTGCGGCCTTTCA
TGACCCAGAATATGGCACGAAGATCGGACCGCTGCCCGACTTGTTAAAGAAAATG
GTGTCAAATATAAAACGATTGATTACGAGGATTATTTAATTCTGTTGAGTAACATTAAG
TTGGATGGTAAATCACTGCTGGACCAGATGAAACTGTAA

NHI 66 (NCS1) protein sequence:

MSKNLTGVGGSLPVENVQVLAKGKELKNLPNRYVRPELEHDDVVPIDNSLEIPVIDLSRL
LDQQYACDELAKFHSACLDWGFFQLINHGVRREEVIEKMKVDTEFFRLPFEKKNAYRQ
LPNGMEGYGQAFVTSEEQKLDWADMHFLITKPVQERNMRFWPTSPTSFRFRETMEKYS
MELQKVAMCLTGMMAKNLGLESEILTKPLRTVFNREDELLPSMSSCGEGLGLSPHSDA
TGLTLLIQVNEVNGLHIKKDEKWWPIKPILGAFVVNIGDVIEIMSNGIYKSIEHRAVINTDKE
RLSIAAFHDPEYGTKIGPLPDLVKENGVKYKTIDYEDYLIRSSNIKLDGKSLLDQMKL

Codon-optimized NHI 67 (LDO1) sequence:

ATGACGGATGTGGAACCTGCGCGTGGAAGCTTTATCTCTTTCCGGGGTAAGTGCTAT
CCCGCCTGAATATGTGAGGCCCGAAGAAGAGAGAGCGGACCTTGGGGATGCGCTG
GAGTTAGCGCGAGCAGCCAGCGACGACGACGCAACAGCGCGCATACTGTTGTG
GATATATCGGCCTTTGATAACGACGGTGATGGTCGCCACGCCTGTGTGCAAGCGGT
CCGTGCAGCAGCTGAAGAATGGGGAGTTATCCATATAGCTGGACATGGCTTACCGG
GAGATGTTCTTGGTAGGCTGCGTGCTGCGGGTGAAGCTTTCTTCGCTCTGCCTATT
GCTGAAAAAGAGGCATACGCGAATGACCCGGCTGCGGGCCGCTTGCAAGGTTATG
GCTCTAAGCTGGCCGCCAATGCATCAGGTAAACGGGAATGGGAGGATTATCTTTTT
CATTTGGTACATCCAGATCATTTGGCCGACCATTGCTTTGGCCGGCTAATCCGCCG
GAATATGTTCCAGTTTCCCGCGATTTTGGAGGACGAGTTCGAACCTTGGCGTCTAA

ATTACTGGCAATTCTCAGTTTAGGTCTGGGACTGCCGGAGGAGACTCTCGAGCGCA
GACTTCGTGGCCACGAATTGGCCGGCGTGGATGACGATCTTCTGCTTCAACTGAAA
ATTAATTATTATCCTCGGTGTCCACGACCTGATCTTGACAGTGGGCGTTGAAGCTCAC
ACTGATGTGTCTGCTCTTTCTTTTATTTTACATAATGGGGTTCCAGGACTGCAGGTG
CATCATGCAGGAAGCTGGGTGACTGCCCCGTCCAGAACCGGGCACCATCGTCGTAC
ATGTGGGCGACGCACTGGAAATTCTTACCAACGGACGTTATACAAGTGTACTGCAC
CGCGGCCTGGTGAGTAGAGATGCAGTACGATTAAGCTGGGTGGTATTCTGTGAACC
GCCGCCCGAATCAGTACTCCTGCAACCCGTCCAAGAGCTGCTGGCCGATGGAGCA
GGGAAACCGCTGTTTGCACCAAGAACGTTCAAACAACACGTCCAGCGTAAACTATT
TAAAAAGCTCAAGGATCAGCAGGATAATAATGCAGCAGCCGCTTCGAATGGCATGAT
TACCAAATAA

NHI 67 (LDO1) protein sequence:

MTDVELRVEALSLSGVSAIPPEYVRPEEERADLGDALELARAASDDDATARIPVVDISAF
DNDGDGRHACVEAVRAAAEEWGVIIAGHGLPGDVLGRLRAAGEAFFALPIAEKEYA
NDPAAGRLQGYGSKLAANASGKREWEDYLFHLVHPDHLADHSLWPANPPEYVPVSRD
FGGRVRTLASKLLAILSLGLGLPEETLERRLRGHELAVDDDLLLQKINYYP RCP RPD L
AVGVEAHTDVSALSFILHNGVPGLQVHHAGSWVTARPEPGTIVVHVGDALEILTNGRYT
SVLHRGLVSRDAVRLSWVVFCEPPPESVLLQPVQELLADGAGKPLFAPRTFKQHVQRK
LFFKKLDQQDNNAASNGMITK

Codon-optimized NHI 68 (LDO2) sequence:

ATGACAGACGTGGAGCTGAGAGTCGAAGCACTGTCATTGTCCGATGTGAGCGCAAT
CCCGCCCGAATACGTGCGTCTTGAGGAAGAACGCACCGACCTGGGCGATGCGTTG
GAGGTGGCTAGAGCAGCATCTGATGACGCAGATGCAGCTCGGATCCCGGTAGTGG
ACATTAGCGCATTTCGATGGTGATGGTCTGAAGGGCGTGCGTGGAGGCCGTGCGTGC
GGCCGCGGAAGAGTGGGGAGTAATGCATATAGCCGGACACGGCTTACCGGGTGAC
GTCCTAGACAGACTGCGCGCGGCGGGTGAAGCCTTTTTTCGCGTTGCCGATAGCTG
AGAAGGAAGCCTACGCCAATGACCCGGCCGCTGGGCGGCTTCAAGGGTATGGGTC
CAAGCTGGCGGCTAATGCATCAGGCAAACGGGAATGGGAAGATTATCTGTTCCATT
TAGTTCATCCGGATCACCTGGCCGATCATTCACTGTGGCCGGCAAATCCCCGGAA
TATGTTCTGTGTCTAGAGATTTTCGGTGGGCGGGTCCGAACACTGGCTAGCAAGCT
ACTAGCCATTCTCTCCCTAGGTCTGGGTTTACCGGAAGAAACCCTAGAAAGGCGCT
TACGCCGGCATGATCAACATGGTGTTGATGATGATTTACTTCTTCAGCTGAAAATAAA
CTATTATCCTCGTTGTCCAAGACCTGATCTGGCCGTGGGCGTAGAGGCCCATCTG
ATGTGTCTGCTTTAAGTTTCATCCTTCACAACGGTGTACCTGGACTGCAGGCACACC
ATGCTGGGACCTGGGTAAGTACCCGATCAGAGCAGGGCACGATAGTAGTTCATGTG
GGAGATGCCCTTGAGATTCTGACCAACGGAAGGTATACATCAGTGCTTCATAGGAG
CCTCGTTTCCCGGGATGCTGTGAGGGTTTCTTGGGTGGTGTCTGTGAGCCTCCA
CCAGAAAGCGTACTGCTGCAGCCTCTTCCGGAAGTGTAGCAAATGGTGCTGGGA
AGCCTCTGTTTTCGCCGAGAACCTTCAAACAACATGTTTCAGCGTAAGCTATTTAAAA
AACTGAAGGATCAGCAGGATAATAACGCGGCAGCTGCGTCGAACGGCATTATCCCC
AAATGA

NHI 68 (LDO2) protein sequence:

MTDVELRVEALSLSDVSAIPPEYVRLEEERTDLGDALEVARAASDDADAARIPVVDISAF
DGDGRRACVEAVRAAAEEWGVMIAGHGLPGDVLDRRAAGEAFFALPIAEKEAYAN
DPAAGRLQGYGSKLAANASGKREWEDYLFHLVHPDHLADHSLWPANPPEYVPVSRDF
GGRVRTLASKLLAILSLGLGLPEETLERRLRRHDQHGVDLDDLLQLKINYYPKPRPDL
AVGVEAHTDVSALSFILHNGVPGQLQAHAGTWVTARSEQGTIVVHVGDALILTNGRYT
SVLHRSLSVRDAVRVSWVVFCEPPPESVLLQPLPELLANGAGKPLFAPRTFKQHVQRK
LFFKKLDQDNNAAAASNGIIPK

Codon-optimized NHI 69 (HxnY) sequence:

ATGGCACCGACGGCCCCGCCGATCCTTGATTTTTCTCCGTTCTATGGAACGGACGG
TGCTGCTAAAGCTAAATTGGTGCAACAAGTCCGTGAGTCATGTGAATATAATGGCTT
TTTCCAGATTACAGGTCATAGAATTCCTCGCGAATTACAAGTGAGAGTAATGGATGC
GGCGAAGCGTTTTTTTTGCTCTGCCTTTGGAAGAAAAAATGGCCATTGACAAAAATCT
CAATAGTTTCAATCGAGGTTATGAACTGCTCCGTTACAGATGCTTGAGGTAGGAAC
CGCGCCTGAGTTGAAAGAAGGACTGTACATTGGAGAAGAGATAGGTGCCGATCATC
CGTATTATATCAACGGTCGCTTGAATAGCGGACCTAATCAGTGGCCAGCTACCGTGC
CTGATGCACAAGAATTCGCGCAACAAGTATGGAGTATTATCATGCAGTGTACGAAC
TCGCTAAGGATGTCCTTGCGGTTTTAGCCCTCACCTTAGACGTCGAAGAATCCTTTT
TTGATCCGTTGACAGAGGGCGGAGTAGCCACCATGCGGATGTTACATTATCCGAGC
CAACCGAAGGATGAAGATGAAAACTAAATCGCGGGATTGGCGCGCATACGGATTT
TGGATGTATCACGCTGCTGCTCCAAGATGAAGTTGATGGCTTACAGGTGCTTGATG
CGCCGTCCGGACAATGGCTGGATGTACAACCGGTACTTGGTGCTTATGTAGTGAAC
TTAGGTGATCTTATGATGCGGATGGCTAATGATCGGTACAAGTCTAACATCCATCGTG
TAATCAATAAATCGGGCAGAGAACGTTACTCTATTCCTTTTTTTTTTTCAGTGGCAACCC
GGATCATGTTTGCAAGTGTCTTCCCAATTGCTGTAAGGCAGGGGAACAGCCCAAAT
ATCCGCCGATTACAGTGGAAGATATGGTGCGTGGGGCGTATAAACAGAGCTATGGC
CGGGCCGAAGCGTACAAAAAAGAACTGGCGGAAAAGGCAAAGGCGCACAAAATCG
AAGCCGCGTCCGCCACGGCCATGGTCTCGTGA

NHI 69 (HxnY) protein sequence:

MAPTAPPILDFSPFYGTDGAAKAKLVQQVRESCEYNGFFQITGHRIPRELQVRVMDAA
KRFFALPLEEKMAIDKNLNSFNRYELLRSQMLEVGTAPELKEGLYIGEEIGADHPYYIN
GRLNSGPNQWPATVPDAQEFRETSMEYYHAVYELAKDVLAVLALTLDEESFFDPLTE
GGVATMRMLHYPSQPKDEDEKLNRGIGAHTDFGCITLLLQDEVLDGLQVLDAPSGQWL
DVQPVLGAYVVNLGDLMMRMANDRYKSNIHRVINKSGRERYSHIPFFFSGNPDHVCKCL
PNCKKAGEQPKYPITVEDMVRGAYKQSYGRAEAYKKELAEKAKAHKIEAASATAMVS

Codon-optimized NHI 70 (T6ODM) sequence:

ATGGAAAAAGCTAAACTGATGAACTCGGTAATGGAATGGAAATCCCGTCTGTTCAG
GAGCTGGCCAAATTAACACTCGCAGAAATTCCAAGCCGCTATGTTTGTGCTAACGAA
AATTTATTATTACCGATGGGTGCGAGCGTAATCAACGATCACGAGACCATTCCAGTG

ATTGATATTGAAAAC TTGTTAAGCCCGGAGCCGATCATTGGTAAACTAGAATTAGACC
GTTTACATTTTCGCTTGCAAAGAATGGGGTTTCTTTCAGGTAGTGAACCATGGGGTTG
ATGCCTCACTCGTGGATAGTGTGAAATCTGAGATCCAAGGTTTCTTTAACCTTTCTAT
GGATGAAAAAACGAAATATGAACAGGAAGATGGTGTATGTGGAAGGTTTTGGCCAGG
GCTTCATAGAGAGCGAAGATCAGACCCTTGACTGGGCGGATATTTTTATGATGTTTA
CCTTACCGTTACACTTACGGAAGCCTCATTTATTAGTAAACTGCCTGTTCCATTGCG
CGAAACTATTGAATCTTACAGCTCGGAGATGAAGAAGCTGTCTATGGTACTGTTCAA
CAAGATGGAAAAAGCGCTGCAAGTACAGGCTGCAGAGATCAAAGGCATGTCGGAA
GTTTTTATAGACGGCACGCAGGCGATGCGCATGAATTATTATCCACCTTGCCACAG
CCGAATCTGGCGATAGGGCTTACTAGCCACTCGGACTTTGGCGGCTTGACGATATT
GTTACAGATTAATGAAGTAGAAGGTTTACAGATTAAGCGCGAGGGTACATGGATTTC
AGTCAAACCCCTTCCGAACGCATTGTTGTTAATGTGGGCGATATACTGGAAATAAT
GACCAACGGCATCTACCATAGTGTGGATCATCGTGCTGTTGTAAACAGTACAAACGA
GCGTCTTAGCATCGCCACATTTTCATGACCCGTCTCTTGAAAGTGTTATCGGACCAAT
CAGTAGCTTAATCACGCCCCGAAACACCGGCGCTCTTTAAATCAGGTTCAACATATGG
GGATCTGGTGGAAGAGTGTA AACACGAAAGCTAGACGGTAAATCATTTCTCGACA
GTATGCGCATCTGA

NHI 70 (T6ODM) protein sequence:

MEKAKLMKLGNGMEIPSVQELAKLTAEIPSRVVCANENLLLPMGASVINDHETIPVIDIE
NLLSPEPIIGKLELDRLHFACKEWGFFQVNVHGVDA SLVDSVKSEIQGFFNLSMDEKTK
YEQEDGDVEGFGQGFI ESEDQTLDWADIFMMFTLPLHLRKPHLFSKLPVPLRETIESYS
SEMKKLSMVLFNKMEKALQVQAAEIKGMSEVFIDGTQAMRMNYYPPCPQPNLAIGLTS
HSDFGGLTILLQINEVEGLQIKREGTWISVKPLPNAFVVNVGDILEIMTNGIYHSVDHRAV
VNSTNERLSIATFHDP SLESVIGPISSLITPETPALFKSGSTYGDLVEECKTRKLDGKSFL
DSMRI

Codon-optimized NHI 71 (CODM) sequence:

ATGGAGACCCCGATTTTAATAAAACTAGGTAACGGCCTGTCCATCCCTAGCGTGCAA
GAGCTAGCAAAGCTAACTCTGGCTGAAATTCCGAGTCGTTATACCTGTACAGGTGAA
TCCCCGCTGAATAATATCGGTGCCTCAGTGACTGATGATGAAACTGTGCCGGTCATA
GACTTGCAAAACTTGTTAAGCCCAGAACCAAGTGTTGGCAAATTAGAATTAGATAAA
CTACATTCTGCATGCAAAGAGTGGGGGTTCTTTCAGCTGGTAAATCATGGAGTTGAC
GCCCTGCTAATGGATAACATTAAGTCCGAAATCAAAGGTTTCTTTAACCTTCCCATGA
ATGAAAAAACAAAATATGGTCAGCAGGATGGTGATTTTCGAGGGTTTTGGACAGCCTT
ATATCGAATCGGAAGACCAGCGACTCGATTGGACGGAGGTGTTCTCCATGCTTTCA
CTGCCTCTGCATCTGAGAAAACCTCACTTATTTCCGGAACCTCCGTTACCATTTTCGC
GAAACACTGGAGTCGTATTTGTCTAAGATGAAAAAACTGTCTACCGTCGTGTTTCGAG
ATGCTTGAAAAATCCCTGCAGTTAGTGGAGATCAAAGGTATGACTGATTTGTTTGAA
GATGGTCTGCAGACCATGCGTATGAATTATTATCCGCCGTGTCCTCGGCCGGAGTT
GGTACTTGGACTCACGTCGCACAGCGACTTTAGCGGTTTAACAATTCTTCTGCAGC
TCAACGAGGTAGAAGGTCTGCAGATTCGCAAAGAGGAGCGATGGATCTCCATCAAG
CCTCTGCCTGACGCTTTTATCGTTAACGTCGGGGACATCCTGGAAATCATGACCAAT

GGGATTTATCGCAGTGTGGAGCATCGTGCCGTTGTCAACAGCACGAAGGAACGTCT
GTCCATTGCCACTTTTACGACTCCAAACTGGAATCAGAAATTGGTCCGATTTCTAG
CCTGGTCACACCGGAAACTCCGGCGTTGTTTAAACGTGGTCGTTATGAGGACATTT
TGAAAGAAAATTTAAGTCGCAAGCTGGATGGGAAATCGTTTTTAGACTATATGCGCAT
GTGA

NHI 71 (CODM) protein sequence:

METPILIKLGNLSIPSVQELAKLTLAEIPSRYTCTGESPLNNIGASVTDDETVPVIDLQNL
LSPEPVVGKLELDKLHSACKEWGFFQLVNHGVDALLMDNIKSEIKGFFNLPMNEKTKY
GQQDGD FEGFGQPYIESEDQRLDWTEVFSMLSLPLHLRKPHLPPELPLPFRETLESYL
SKMKKLSTVVFEMLEKSLQLVEIKGMTDLFEDGLQTMRMNYYPPCPRPELVGLTSHS
DFSGLTILLQLNEVEGLQIRKEERWISIKPLPDAFIVNVGDILEIMTNGIYRSVEHRAVVNS
TKERLSIATFHDSKLESEIGPISSLVTPETPALFKRGRYEDILKENLSRKLDGKSFLDYMR
M

Codon-optimized NHI 72 (PntH) sequence:

ATGACAGACACTTTTTCTGACTACGCGGACTGTACACCGCTGCTGGATGACCGGGA
AGCGCTCGACCGCTTTTACGACGAGCACGGATACGTTTACCTCCGCGGTGTCCTC
GATAGGGAATTGGTTCGACGACTGCTGAGCAAATGCTCCAGGGACTGATCGCACT
GGGACATGCCGCACCCGGAACCACTTTAGATACATTGACCATAGAGTCCTATGAGG
CGGTTGACGAGGTGGCAATGCATGATCACGTCCGATACGATGATCTTTGGAATCATC
CGTCCACATTGAAAGTTTGGGAAAAAGTCTTTGGTGAACCGGTTTTTGTTCCTCAAAA
GCACGACGATTGCTATTACCCATCTGCACCCGATAGTGCTGAACCGAGCTTTTTGA
CGCCCCTGCATCAAGACGGGTCTATATTGGACCGAACAAGATTTCCGTACCGCG
TGGATCCCACTCCTCCCGACAACCTCGGGGCACGGGCGGCGTTGCGATCGCGGAC
GGGAGTCATAAGAAAGGCCCGCGTGAACACGTTCTAACCGAAAACCTTCGTGCTT
TGGTCATGCCGTTTCGCGGGATCCCGCCTGCAGAATTCGGAGCCGATGAAGAATTG
CTTTTCTCTCTATGGAACAGGGGATGTCCTGTTATTTTCATGCGTTCATGTGTCAC
AAAAGCCTGCCAAATGTAAGTGTTGATCCGGCAGGTATGCGTATGTCTATGGATACC
CGAATTCAGCCAGCCAGCTCGCATCGTGGCTTTAATGCCCTCACACCGTGGCCGG
AGTCTGCCAAGGACGCCTCAAAGGCATTATGTCTAAATAACGGGTACCCCAACC
ACAGCGGAGTAA

NHI 72 (PntH) protein sequence:

MTDTFSDYADCTPLDDREALDRFYDEHGYVYLRGVLDRELVRTTAEQMLQGLIALGH
AAPGTTLDLTIESYEAVDEVAMHDHVRYDDLWNHPSTLKVWEKVFGEPVFVFKSTTIR
YYPSAPDSAEPSTPLHQDGFYIGPNKDFRTAWIPLPTTRGTGGVAIADGSHKKGPR
EHLVTENFRRFGHAVRGIPPAEFGADEELLFSPMEPGDVLLFHAFMCHKSLPNVSVD
AGMRMSMDTRIQPASSHRGFNALTPWPESAKDASKGIMSKITGTPTTAE

Codon-optimized NHI 73 (prolyl-4-hydroxylase 13) sequence:

ATGCGGAGCTATGGTAAAGAAAAAAACTTGTATTTCCGTATGTTTTTATCGCATGCT
GTTTCTTTCTCGCTATTTTTGGTTTTTGCTTCTTTAACCTTTTTTCACAGGGGATCTCT

TTCTCGGAGATCCCCACTACACGTCGTTCCGGTCAACGACGAAACAGATAGTCTGGA
TCATGGGAGTTCCGGTGTCAAACATCCCGTTTTACGGTCTTAGTTGGAACCCCTCGGG
TCTTTTATTTACCCAACCTTCGCCACAAAACAACAGTGTGAAGCTGTTATTGATATGGC
TAAACCGAAACTGAAACCATCAACATTAGCACTGAGAAAGGGAGAAACCGCGGAAA
CTACCCAGAACTATAGGTCCCTTCACCAACATACGGACGAAGATGAATCTGGGGTTC
TGGCGGCCATTGAAGAAAAAATCGCGTTGGCGACAAGATTTCTAAAGATTACTATG
AGTCCTTTAACATTCTTCGGTATCAATTGGGACAAAAATACGATAGCCATTATGACGC
CTTTCATTGAGCTGAATATGGACCGCTGATTTCCCAGAGAGTTGTAACTTTTTTGTTA
TTCCTGTCTTCCGTGGAAGAAGGAGGTGAAACTATGTTCCCCTTTGAGAATGGGCG
TAATATGAATGGTCGTTACGATTATGAAAAATGTGTTGGACTGAAAGTCAAACCGCG
CCAGGGTGACGCCATATTTTTCTACAATCTGTTTCCAAACGGGACAATCGATCAGAC
GAGCCTTCATGGTAGTTGTCCCGTAATTAAAGGGGAGAAATGGGTGCTACTAAATG
GATAAGAGATCAGACCTACGATTAA

NHI 73 (prolyl-4-hydroxylase 13) protein sequence:

MRSYGKEKKLVFPYVFIACCFFLAIFGFCFFNLFSQGISFSEIPTTRRSVNDETDSLHDG
SSVSNIPFHGLSWNPRVFYLPNFATKQQCEAVIDMAKPKLKPSTLALRKGETAETTQNY
RSLHQHTDEDESGVLAAIEEKIALATRFPKDYYESFNILRYQLGQKYDSHYDAFHSAEY
GPLISQRVVTFLLFLSSVEEGGETMFPFENGRNMNGRYDYEKCVGLKVKPRQGDAIFF
YNLFPNGTIDQTSLHGSCPVIKGEKWVATKWIRDQTYD

Codon-optimized NHI 74 (FLS4) sequence:

ATGGAAGTAGAACGCGACCAGCACAAACCACCCCTATCATTGCAGAACAAATAAAATT
CCCAGTTCCCAAAACTTCCCAGTGGTGGATCTTAGCAATACTAATGGAGAACTGGTT
GCGCGGAAAGTTGCGAAGGCCTCTGAAGAGTGGGGCATTTTTTCAGGTCGTAAACC
ATGGCATAACCAACCGAATTAATTAGACGTCTGCATAAGGTGGATACTCAGTTTTTTGA
ACTCCCTGAGTCTAAAAAAGAAGCAGTTGCAAAACCGGCGAACTCCAAGGAAATCC
AGGGGTATGAAATGGATGATGTGCAAGGCCGCCGTAGCCATATCTTTCATAACTTATA
TCCTAGTAGTTTCACTTAAGTACGCCTTTTGGCCGAAGAACCCTCCAGAGTATCGCGA
AGTTACGGAAGAATTTGCTAAGCACGCTAAGCAACTGGCCGAGGAAATACTGGGCC
TGTTATCTGAAGGAGCAGGCTACCTCATGAAAATAAATTATTACCGCCCGTGTCCTG
AACCAGACTGGGTGATGGGTATTAAGGCCACACCGATTTTAATGGGCTCACTTTAC
TGATCCCGAACGAAATTTTTGGGCTGCAAGTTTTCAAGGAAGACCGATGGTTGGAT
GTGGATTATATTTATCCGGCAGTTATCATAATTATCGGAGACCAAATAATGAAAATGTC
CAATGGTCGCTATAACAACGTGCTGCATCGAGCACTAATGGATAAAAAGAAGACTAG
GATGTCATCAGTAGTACATATTAAACCCCGTATGACATGGTGGTTTCTCATTTTCCA
AATAGTCCGGCCGCTATCATATTACCAAGCTCGAGCCTGTAA

NHI 74 (FLS4) protein sequence:

MEVERDQHKPPLSLQNNKIPSSQNFPVVDLSNTNGELVARKVAKASEEWGIFQVVNHG
IPTELIRRLHKVDTQFFELPESKKEAVAKPANSKEIQGYEMDDVQGRRSIFHNLYPSSS
VNYAFWPKNPPEYREVTEEFAKHAKQLAEEILGLLSEGAGYLMKINYRCPPEPDWVM

GIKAHTDFNGLTLLIPNEIFGLQVFKEDRWLDVDYIYPAVIIIIGDQIMKMSNGRYNNVLHR
ALMDKKKTRMSSVVHIKPPYDMVVSHPNSPAAIILPSSSL

Codon-optimized NHI 75 (FLS6) sequence:

ATGAATGTGGAGCGCGATCAACATATATCTCCCCCATGCCTGTTGACTAAAAAGATC
CCTATCGTGGATTTGTCCGATCCATCGGATGAACTCGTAGCGCATGCGGTTGTGAA
AGCCTCCGAGGAATGGGGAATTTTTCAGTTAGTAAATCATGGGATTCCCGCAGAATT
GATGCGACGTCTGCAGGAAGTCGGTCGCCAGTTTTTTGAGCTGCCGGCTAGCGAA
AAAGAGTCCGTTACAAGGCCGGCTGACAGCCAGGACATAGAAGGTTTCTTTTCGAA
GGACCCGAAAAAGCTGAAAGCATGGGACGACCACCTGATTCACAATATTTGGCCCC
CGTCGTCGATTAACATCGCTATTGGCCAAATAATCCTAGCGACTATTCAGGTGACG
GATTCCGTGAAGTCACAAAAGAATACACCCGTAACGTCACCAACCTTACAGAGAAG
ATTGTAGGCGGGGATAAAGCCCAGTACGTGATGCGGATTAACATATCCACCTAGC
GATAGCGCGATCGGTGCGCCAGCCCATAACCGATTTTTGCGGATTGGCGTTATTAGT
CAGCAACGAAGTGCCAGGTTTGCAGGTCTTTAAAGATGACCATTGGTTCGATGTTG
AATATATTAATTCTGCCGTGATCGTACTGATTGGCGACCAGATCATGCGGATGTCGAA
TGGCAAGTATAAGAACGTGTTGCACAGAAGTATCATGGATGCCAAGAAGACGCGTAT
GAGCTGGCCGATCCTAGTCGAACCAAAGCGCGGTCTGGTGGTGGGGCCCCCTGCC
GGAACCTCACAGGTGACGAAAATCCGCCGAAATTCGAATCATTAAACGTTTCGAAGATTA
CGTTTATCGGAAGATCATTAAAGGTTTTACGGGATTAG

NHI 75 (FLS6) protein sequence:

MNVERDQHISPPCLLTKKIPIVDLSDPSDELVAHAVVKASEEWGIFQLVNHGIPAELMRR
LQEVGRQFFELPASEKESVTRPADSQDIEGFFSKDPKCLKAWDDHLIHNWPPSSINYR
YWPNNPSDYSYSGDGFREVTKEYTRNVNLTAKIVGGDKAQYVMRINYPPSDSAIGAPA
HTDFCGLALLVSNEVPGLQVFKDDHWFDVEYINSVIVLIGDQIMRMSNGKYKNVLHRS
IMDAKKTRMSWPILVEPKRGLVVGPLPELTGDENPPKFESLTFEDYVYRKIIKVLRD

Codon-optimized NHI 76 (F6'H1) sequence:

ATGCCTGCAGTGTTATCAAGTGTTCTTTCTAATATTACGGATTTTGTGGTTCACGAGG
GAAATGGAGTCAAGGGATTAGCAGATATGGGTCTGGAAGCCCTGCCAAAACAGTAC
GTTACGCCCCGAGGAAGAACGGATCACAAACATCTACGGTTATAGTGGATGATACGATA
CCGGTGATAGATCTGTCCGAGTGGGGGTCAGATCCAAAAGTGGGAGACATGATCT
GTGAAGCCGCGGAGAAGTGGGGTTTTTTCCAAATAGTGAACCATGGTGTTCCTCTT
GAAGTTCTGGAAGAAGTCAAGGCTGCAACCTACCGCTTCTTTGTTTACCTGCTGA
GGAAAAAATAAACACTGCAAGGATAATAGTCCTTCAAATAATGTGAGATACGGCAC
GTCTTTTACGCCTCATGCCGAAAAAGCACTAGAATGGAAAGATTTTCTGTCACTGTT
TTATGTATCTGACGAGGAAGCTGCAGCGCTGTGGCCTAGTGCATGTCGCGACGAG
GCCCTGACATTCATGCGGAATTGCGACGCGGTTATAAACGGCTGTATAAATCCCTT
ATGAAGGGGCTGAATGTTACTGAAATTGATGGGACGAAAGAGTCGTTACTGATGGG
CTCCAAACGTATCAATATGAATTATTATCCGAAATGTCCGAATCCGGAATTAACCGTG
GGTGTGTTGGTCGTCACAGTGATGTTTCGACACTGACGATCTTATTGCAAGATCAGATT
GGGGGTTTATATGTCCGTAAGTTGGACTCAGATACCTGGGTCCATGTTCTCCAATT

AATGGGGCTATCGTGATTAACGTCGGGGACGCCCTGCAGATACTGAGTAACGGTCCG
GTATAAATCTATTGAACATCGTGTTATTGCCAATGGTAGCAATAATCGAATTAGCGTAC
CCATATTTGTGAACCCGCGCCCAAATGATATTATTGGCCCTCTGCCTGAATTGCTCG
AATCTGGAGAAAAAGCGGTATATAAGAACGTTCTGTACAGTGATTATGTCAAACATTT
TTTTCGTAAAGCGCATGACGGTAAGGAAACCGTTGACTTTGCGAAAATCAATTAA

NHI 76 (F6'H1) protein sequence:

MPAVLSSVLSNITDFVVHEGNGVKGLADMGLEALPKQYVQPEERITTSTVIVDDTIPVI
DLSEWGSDPKVGDMICEAAEKWGFFQIVNHGVPLEEVKAATYRFFRLPAEEKKNKH
CKDNSPSNNVRYGTSFTPHA EKALEWKDFLSLFYVSDEEAAALWPSACRDEALTFMR
NCDAVIKRLKLSLMKGLNVTEIDGTKE SLLMGSKRINMNYYPKCPNPELTVGVGRHSDV
STLTILLQDQIGGLYVRKLDSDTWVHVPPINGAIVINVGDALQILSNGRYKSIEHRVIANG
SNNRISVPIFVNPRPNDIIGPLPELLESGEKAVYKNVLYSDYVKHFFRKAHDGKETVDFA
KIN

Codon-optimized NHI 77 (F6'H2) sequence:

ATGCCATCTACAACTTTAAGTACCGTTTTATCTGACATTAACGAATTTGTAGTTAAACA
GGGACACGGCGTAAAGGGGTTGTCTGGAGTTAGGGTTGCAGACGCTGCCAAACCAA
TATGTGCATCCGCCAGAAGAGAGACTGTCCTCGATGGATGTCGTTTCGGATGATAG
CATACTGTAAATTGATGTATCCAATTGGGAAGACCCAAAAGTAGCCAAGTTGATCTG
CGATGCCGCTGAAAAACGTGGCTTTTTTCAGATTGTAAATCACGGGATACCGTTGGA
AATGTTGGAGAAGGCTAAAGCCGCTACTTACCGCTTCTTTTCGCGAACCTGCAGAAG
AGAAGAAAAAATACTCCAAAGAGAATTGTCCTACCTCTCACGTTAGATACTCCACGA
GTTTCCTGCCTCAGATTGAAAAAGCGCTAGAATGGAAAGACCATCTGTCAATGTTCT
ATGTCAGTGACGAAGAAGCTGCACAATATTGGCCTCCGTCATGCCGCGATGATGCA
CTTGAATATCTGAAAAGTTGCGAAATGGTTTCGCGAAAGCTGCTGGAGGCATTAATG
CAGGGTCTGAATGTTAACGAGATCGACGACGCTAAAGAAAGCTTACTGATGGGTAG
TCGGCGCATCAATATCAATTATTATCCAAAATGCCCGAATCCGGACCTGACAGTGGG
CGTAGGTCGCCATAGTGATATATCCACATTAACACTGTTGCTTCAGGATGACATCGGT
GGGTTGTACGTTAGAAAAGTGGAGCACGAAGCGTGGAGCCATGTACCCCCAGTGA
AAGGTGCACTTGTGATTAAACATTGGAGATGCTTTACAGATTATGAGTAATGGCAGATA
TAAGAGCATCGAGCATAGAGTTCTGGCCAACGAGACAAATGATCGGATTTAGTTCC
GGTGTGTTGTTAACCCGAAACCTAACGACATAGTGGGACCGCTTCCGGAGGTGTTGG
CCTCGGGCGGAGAAGCCGGTATATAAACCGGTCCTCTATTTCGGATTATGCAAAACACT
TTTACCGCAAAGCTCATAATGGAAAGGATACCATTGCGTTTGCCAGAATTGAGTGA

NHI 77 (F6'H2) protein sequence:

MPSTTLSTVLSDINEFVVKQGHGVKGLSELGLQTLPNQYVHPPEERLSSMDVVSDDSI
PVIDVSNWEDPKVAKLICDAAEKRGFFQIVNHGIPLEMLEKAKAATYRFFREPAAEEKKKY
SKENCPTSHVRYSTSFLPQIEKALEWKDHL SMFYVSDEEAAQYWPPSCRDDALEYK
SCEMVSRKLLEALMQGLNVNEIDDAKESLLMGSRININYYPKCPNPD LTVGVGRHSDI
STLTLLLQDDIGGLYVRKLEHEAWSHVPPVKGALVINIGDALQIMSNGRYKSIEHRVLN

ETNDRISVPVFVNPKPNDIVGPLPEVLASGEKPVYKPVLYSDYAKHFYRKAHNGKDTIA
FARIE

Codon-optimized NHI 78 (HtyE) sequence:

ATGGCCATCACAACACTCGATTTTAATCAGTTCCGTAGTACATCGGCCGATGAGCGT
CAAATCTTTTTCGCTGATCTCTGCGAAACCCTTTCTGTTTATGGCTTCGCAAAAATAC
GTAATACGACGTTAAGTAATGAGTTGATCGATGAAATCTTTAAATACACCCGCTCATTT
TTTGCTCTTCCAAATGATATTAAAGCTAAAGCGAAACATCCAAATGCACCTAATCCGC
ACCGAGGCTGGTCAGCGATTGGCCAAGAACGAGTTTGGAAAATCAGTGGTTTCGA
GCAGAATAAGGAACGGACCGATTCTGTATAATGAATTTTCGCGAATCCTTTGACCAGGG
TGCAGCGGACGATCAATTGTTCCCTAACAGATGGGTGATGAAGATGATTTACCTGG
TTTTCAAGCTTTTCATGGAAGGATTCTATAAATCATGCGATGAACTGCATGCCCATTTAT
TACGTGCGATCTCGACGGGACTGAAATTACCAGATACACTGTTGCCCTCTAAACATC
GGCATAACACCTCCGAGCTGAGATTACTGCACTACCCGCCGATCCCTTGAGCGCA
CTGCGGAGCAATATGCGGATTGGCGAACATTCTGATTTTCGGCACTCTTACACTGCTT
CTGCAAGATAGTGTGGGTGGTTTACAGGTTGAAGATCAGAGAAATCCTCGCTCATTC
ATCCCTGTTGAGCCGGAAGACGGATATGAGGTTGTTATTAATATCGGCGACTGCCTG
CAGCGCTGGACCAACCGCCGCCTTTGTTCCGCCAATCACAGGGTGATGCTGCCTG
AAGGGAAAGATGTGGACAGCGAGGAGGTGTTGGATGATAGGTATAGCGTGGCATAT
TTCGGCAAACCGGACAGAGATGTGCTTGTGGATACCCTGCCAGAGTGTGTGGAAG
TGGGGGAACGCGTCGAGTATGGTGACCACCTCACTGCTCTCCAGTATAATCAAATTA
AGTTGACGCGCACTTATGGTTGA

NHI 78 (HtyE) protein sequence:

MAITTLDFNQFRSTSADERQIFCADLCETLSVYGFAKIRNTTLSNELIDEIFKYTRSFFAL
PNDIKAKAKHPNAPNPHRGWSAIGQERVWKISGFEQNKERTDSYNEFRESFDQGAAD
DQLFPNRWVDEDDLPGFQAFMEGFYKSCDELHAHLLRAISTGLKLPDILLPSKHRHNT
SELRLHYPPIPCSALRSNMRIGEHSDFGTLTLLQDSVGGGLQVEDQRNPRSFIPEPE
DGYEVVINIGDCLQRWTNRRLCSANHRVMLPEGKDVDSEEVLD DRYSVAYFGKPDRD
VLVDTLPECVEVGERVEYGDHLTALQYNQIKLTRTYG

Codon-optimized NHI 79 (AniF) sequence:

ATGGCCATTACTACGTTGGACTTCAACCAATTCCGCTCTACTTCCGCAGACGAGCGT
CAAAAATTTTTCGCGCGGATTTACGTGAGACGCTCTCAGTATACGGTTTCGCCAAAATT
CGGAATACTACCCTGTCTAACGAACTTATCGACGAGGTATTTAAATACACAAGATCCT
TTTTTGCACTCCCGGACGATATTAAAGCAAAGGCGAAACATCCTAAAGCACCGAACC
CCCACAGAGGTTGGAGTGCAGATTGGTCAGGAGAGAGTCTGGCGTATCTCGGGTTT
TGAGCAGAATAAGCAACGTACCGATTCTACAACGAATTTTCGCGAATCCTTTGATCA
GGGCGCAGCGGATGATCAGCTGTTCCCAAATAAATGGGTCGATGAAGATGATTTAC
CGGGGTTTTCGCGCTTTTCATGGAAGAGTTTATAAATCTTGCGATGAATTACACGCGC
ATCTGCTGCGCGCAATATCTACAGGACTGAACTGCCGGATACACTGCTGCCAAGC
AAGCATCGTCATAATACCTCGGAACTGCGTCTGGTTCATTATCCGCCGATTCCGTGT
AGCGCTCTTAGGAGCAATATGCGTATCGGTGAACATTCAGATTTTGGCACCCCTTACT

TTGCTTCTGCAAGACAGCGTTGGCGGCCTGCAGGTTGAGGATCAGCGGAATCCGG
GAAGCTTTATTCCCGTCGAGCCCGAGGATGGTTATGAAGTTGTTATCAATATCGGAG
ACTGCCTGCAGCGTTGGACCAATAGACGTCTTTGCTCCGCTAATCATCGCGTCAGG
TTACCTGAAGGAAAAGATGTGGAGTCCGATGAAATGTTGGACGATCGTTATAGCGTC
GCTTATTTCCGGAAACCGGATCGTGATGTTTTGGTCGATACGCTGCCGGAGTGCCT
GGGGGTAGGGGAAAAGGTTGAGTATGGCGACCATTGACCGCCTTGCAATACAATC
AGCTTAAGCTGACGCGTACATACGGTTGA

NHI 79 (AniF) protein sequence:

MAITTLDFNQFRSTSADERQKFCADLRETL SVYGF AKIRNTTLSNELIDEVFKYTRSFFA
LPDDIKAKAKHPKAPNPHRGWSAIGQERVWRISGF EQNKQR TDSYNEFRESFDQGAA
DDQLFPNKWVDEDDLPGFRAFMEEFYKSCDELHAHLLRAISTGLKL PDTLLPSKHRHN
TSELRLVHYPPIPCSALRSNMRIGEHSDFGTLTLLLQDSVGG LQVEDQRNPGSFIPVEP
EDGYEVVINIGDCLQRWTNRRLCSANHRVRLPEGKDVESEM LDDRYSVAYFGKPDR
DVLVDTLPECVGVGEKVEYGDHLTALQYNQLKLTRYG

Codon-optimized NHI 80 (GA20ox1) sequence:

ATGAGTATGGTTGTT CAGCAGGAGCAAGAAGTGGTTTTTGACGCCGCTGTGCTTTC
TGGCCAGACCGAAATACCTAGCCAGTTCATTTGGCCGGCGGAAGAAAGTCCAGGAT
CTGTTGCTGTGGAGGAAC TTGAGGTGGCATTGATTGATGTTGGTGCCGGCGCCGA
GCGGAGTAGCGTTGTGCGGCAAGTTGGTGAAGCATGTGAACGTCATGGTTTCTTTC
TTGTAGTGAACCATGGCATTGAAGCCGCGTTGCTTGAAGAGGCTCATCGTTGCATG
GACGCGTTCTTCACCCTCCCATTAGGGGAAAAACAGCGGGCGCAGCGTAGAGCCG
GTGAATCTTGTGGATATGCGAGCAGTTTCACAGGACGCTTTGCGTCAAAATTGCCG
TGGAAGAAACTCTTAGCTTTTCGCTATTCCTCTGCGGGGGATGAAGAAGGTGAAGA
GGGTGTGGGTGAGTACTTGGTTCGAAACTGGGCGCAGAACATGGGCGCCGGTTA
GGTGAAGTCTATTC CGTTATTGTCATGAGATGAGTAGACTGTCACTCGAACTGATG
GAAGTGCTGGGTGAAAGTCTCGGTATCGTGGGGGACCGACGGCACTATTTCCGTC
GTTTTTTTCAACGAAATGACTCTATTATGCGGCTTA ACTACTATCCAGCGTGCCAACG
CCCGCTGGATACACTGGGAACTGGCCCGCACTGTGATCCGACATCCCTCACGATTC
TGCATCAGGATCATGTAGGCGGGCTGGAGGTTTGGGCAGAAAGGTAGATGGCGCGC
AATTCGTCCGCGCCCTGGCGCACTTGTCTGTAATGTTGGAGATACGTTTATGGCTCT
TAGTAATGCGAGGTATCGCAGTTGTCTGCATCGTGCCGTAGTTAATAGCACAGCACC
GCGTCGTAGCCTGGCATT TTTTCTTTGCCCGGAGATGGATACCGTGGTGCGTCCCC
CAGAAGAACTCGTAGATGATCACCATCCCCGCGTGTATCCTGATTTACATGGAGAG
CACTCCTTGATTTCACTCAACGTCATTATCGTGCCGACATGCGAACCCCTGCAGGCAT
TTAGCGATTGGCTTAATCATCACCAGACATTTGCAGCCAACAATCTATAGTTAA

NHI 80 (GA20ox1) protein sequence:

MSMVVQQEQEVVFDAAVLSGQTEIPSQFIWPAEESPGSVAVEEELEVALIDVGAGAERS
SVVRQVGEACERHGFLLVNVNHGIEAALLEEAHRCMDAFFTLPLGEKQRAQRRAGESC
GYASSFTGRFASKLPWKETLSFRYSSAGDEEGEEGVGEYLVRKLGAEHGRRLGEVYS
RYCHEMSRSLSELMEVLGESLGIVGDRRH YFRFFQRNDSIMRLNYYPACQRPLDTLG

TGPHCDPTSLTILHQDHVGGLEVWAEGRWRAIRPRPGALVVNVGDTFMALSNARYRS
CLHRAVVNSTAPRRSLAFFLCPEMDTVVRPPEELVDDHHPRVYPDFTWRALLDFTQRH
YRADMRTLQAFSDWLNHHRHLQPTIYS

Codon-optimized NHI 81 (D4H) sequence:

ATGCCGAAGTCATGGCCAATCGTGATATCTTCTCACTCATTTTGCTTTCTTCCTAACT
CTGAACAGGAACGTAAAATGAAGGATCTGAATTTCCATGCTGCCACCCTTTCAGAAG
AGGAGAGCTTAAGGGAACGTGAAAGCGTTCGATGAAACCAAAGCCGGTGTGAAGGG
GATTGTTGATACTGGCATCACAAAAATTCCACGTATATTTATCGACCAGCCAAAAAAC
CTTGATAGAATTAGTGTGTGCCGTGGCAAATCTGACATCAAGATAACCAGTGATTAAC
TAAACGGACTTTTCATCGAACTCTGAGATTAGACGCGAGATCGTAGAAAAGATCGGTG
AGGCTTCTGAAAAATATGGTTTTTCCAGATTGTTAACCATGGTATACCTCAGGACGT
GATGGACAAGATGGTTGACGGCGTTCGTAAATTCCACGAACAAGATGATCAGATTAA
GCGTCAGTATTATTCCCGTGATCGCTTCAATAAAAATTTTCTCTACTCATCAAATTATG
TCCTCATCCCTGGGATTGCGTGTAAGTGGAGAGACACTATGGAATGCATTATGAATA
GCAATCAACCTGATCCGCAGGAGTTTCCAGATGTCTGTAGGGATATTCTTATGAAATA
TAGTAACACGTACGTAATCTGGGTCTGATCCTTTTCGAATTGTTGTCCGAAGCGCT
GGGCCTCAAGCCAAATCATCTCGAAGAAATGGATTGTGCCGAAGGTTTAATTCTTTT
GGGGCATTACTATCCGGCTTGTCTCAGCCTGAACTTACATTTGGTACCTCCAAGCA
CTCTGATAGCGGCTTTCTGACTATTCTAATGCAGGATCAGATTGGAGGCCTTCAGAT
CCTGCTTGAAAACCAATGGATAGACGTGCCGTTTATACCTGGCGCATTAGTCATCAA
TATTGCAGATCTGTTGCAGCTGATACCAATGATAAGTTTAAGTCAGTGGAGCATCG
GGTGTGGCTAACAAGGTCGGTCCTCGTATTTAGTAGCAGTCGCCTTCGGCATAA
AAACCCAGACACAGGAAGGTGTATCTCCACGCCTCTATGGTCCTATTAAAGAGTTAA
TTAGCGAAGAAAATCCACCTATCTACAAGGAGGTAACCGTCAAAGACTTCATTACTAT
ACGCTTTGCAAACGCTTCGATGATTCAAGCTCTCTTAGTCCGTTCCGTTTAAACAA
CTGA

NHI 81 (D4H) protein sequence:

MPKSWPIVISSHSFCFLPNSEQERKMKDLNFHAATLSEESLRELKAFDETKAGVKGIV
DTGITKIPRIFIDQPKNLDRISVCRGKSDIKIPVINLNLSSNSEIRREIVEKIGEASEKEYGF
FQIVNHGIPQDVMMDKMVDGVRKFHEQDDQIKRQYYSRDRFNKNFLYSSNYVLIPGIAC
NWRDTMECIMNSNQPDQPQEPDVCRDILMKYSNYVRNLGLILFELLSEALGLKPNHLE
EMDCAEGLILLGHYYPACPQPELTFGTSKHSDSGFLTILMQDQIGGLQILLENQWIDVPF
IPGALVINIADLLQLITNDKFKSVEHRVLANKVGPRISVAVAFGIKTQTQEGVSPRLYGPIK
ELISEENPPIYKEVTVKDFITIRFAKRFDSSSLSPFRLNN

Codon-optimized NHI 82 (PcbC *P. chrys.*) sequence:

ATGGCAAGCACCCCGAAGGCGAACGTCCCGAAAATTGATGTGTCACCGCTTTTTTGG
TGACAATATGGAAGAAAAAATGAAGGTCGCGCGTGCAATAGATGCAGCGAGTAGGG
ACACTGGATTCTTTTATGCCGTTAACCATGGGGTAGACGTAAAACGATTGTCTGAATAA
GACCAGAGAATTTCAATTTCTCCATTACTGATGAAGAAAAATGGGACCTGGCAATCCG
GGCCTATAATAAAGAGCATCAGGACCAGATACGTGCCGGGTATTATCTGTCTGATTCC

AGAGAAGAAGGCGGTGGAATCATTCTGTTATTTAAATCCTAATTTTAAGCCTGATCAT
CCTTTGATACAGAGCAAGACCCCAACCCACGAAGTAAATGTGTGGCCTGACGAAAA
GAAACATCCGGGGTTTCGTGAATTCGCGGAACAATACTACTGGGACGTTTTTCGGTC
TGAGCTCAGCTTTGTTGAGAGGATATGCGTTAGCACTTGGAAGGAAGAGGATTTTC
TTTAGTCGTCATTTCAAGAAAGAGGACGCGTTATCTTCTGTCGTCCTGATTAGATATC
CATACTCAATCCGATTCCCCCTGCCGCTATAAAAAACAGCTGAGGACGGTACCAAGT
TGTCCTTTGAATGGCATGAAGATGTGTCGTTGATCACTGTCCTATATCAGAGTGACG
TTGCAAATCTTCAGGTAGAGATGCCGCAGGGCTATTTAGATATCGAAGCAGACGATA
ATGCATATTTAGTTAACTGCGGCTCTTACATGGCGCACATTACCAATAATTATTATCCT
GCCCCAATTCATCGAGTGAAGTGGGTAAACGAAGAAAGACAGTCCCTTCCTTTCTTT
GTCAATCTAGGTTTTAATGATACGGTTCAGCCGTGGGACCCCTCCAAAGAAGATGG
GAAGACTGATCAGCGGCCGATCTCATATGGAGATTATTTACAGAATGGTCTGGTTAG
CCTCATAAATAAAAATGGCCAGACTTAA

NHI 82 (PcbC *P. chrys.*) protein sequence:

MASTPKANVPKIDVSPLFGDNMEEKMKVARIDAASRDTGFFYAVNHGVDVKRLSNKT
REFHFSITDEEKWDLAIRAYNKEHQDQIRAGYYLSIPEKKAVESFCYLNPNFKPDHPLIQ
SKTPTHEVNVWPDEKKHPGFREFAEQYYWDVFLSSALLRGYALALGKEEDFFSRHF
KKEDALSSVVLIRYPYLNPIPPAAIKTAEDGTKLSFEWHEDVSLITVLYQSDVANLQVEM
PQGYLDIEADDNAYLVNCGSYMAHITNNYYPAPIHRVKWVNEERQSLPFFVNLGFNDT
VQPWDPSKEDGKTDQRPISYGDYLNGLVSLINKNGQT

Codon-optimized NHI 83 (PcbC *A. lactam.*) sequence:

ATGAAGATGCCTTCAGCGGAAGTTCCGACAATAGACGTTAGCCCTCTGTTCCGAGA
TGATGCTCAAGAAAAAGTTCTGTGTTGGACAGGAGATTAATAAAGCCTGCCGCGGGT
CAGGTTTTTTTTTATGCAGCAAACCATGGTGTGATGTGCAACGACTGCAAGATGTAG
TCAACGAATTCATCGAACTATGTCACCGCAAGAAAAATATGATTTGGCTATACATGC
CTACAACAAAAATAACAGCCATGTACGCAACGGTTACTACATGGCCATTGAAGGTAA
AAAAGCGGTGCAATCCTTCTGCTACTTAAATCCATCCTTCAGTGAAGATCACCCCGA
GATTAAGGCCGGTACCCCGATGCATGAGGTTAACAGTTGGCCGGACGAAGAAAAG
CATCCTTCTTTTACAGGCCGTTTTGCGAGGAATACTACTGGACTATGCATCGCCTATCTA
AGGTATTGATGCGTGGCTTCGCACTTGCCTCGGTAAAGACGAAAGGTTCTTTGAG
CCCGAACTGAAAGAAGCTGATACATTGTCTTCAGTGTGCTCATTCCGGTATCCGTAC
CTGGAAGATTACCCTCCTGTAAAGACCGGCCCGGACGGTGAAAACTGTCATTTGA
GGATCATTTTGACGTATCTATGATTACGGTATTATACCAGACACAGGTTTACGAATTTAC
AAGTGGAACGGTTGATGGATGGCGGGATCTACCTACAAGCGATACCGATTTTTTAG
TGAATGCTGGCACTTATCTGGGTCATCTTACTAATGACTACTTTCCGAGTCCATTACA
TAGAGTCAAGTTTGTTAACGCAGAACGTCTCTCCCTGCCTTTTTTCTTTCATGCCGG
TCAGCATACTCTCATTGAACCATCTTCCCCGATGGCGCGCCGGAAGGCAAGCAGG
GAAACGAAGCTGTTTCGTTATGGTGATTATCTTAATCACGGATTGCATAGCCTGATCGT
GAAGAACGGTCAAACCTTAA

NHI 83 (PcbC *A. lactam.*) protein sequence:

MKMPSAEVPTIDVSPLFGDDAQEKVRVGQEINKACRGS GFFYAANHGV DVVQRLQDVV
NEFHRTMSPQEKYDLAIHAYNKNNSHVRNGYYMAIEGKKAVESFCYLNPSFSEDHPEI
KAGTPMHEVNSWPDEEKHPSFRPFCEEYYWTMHRLSKVLMRGFALALGKDERFFEP
ELKEADTLSSVSLIRYPYLEDYPPVKTGPDGEKLSFEDHFDVSMITVLYQTQVQNLQVE
TVDGWRDLPTS DTD FLVNAGTYLGHLTNDYFPSPLHRVKFVNAERLSLPFFFHAGQHT
LIEPFFPDGAPEGKQGNEAVRYGDYLNHGLHSLIVKNGQT

Codon-optimized NHI 84 (PcbC *L. lactam.*) sequence:

ATGAACCGTCATGCGGATGTCCCAGTGATTGACATCAGCGGTCTGTCGGGTAACGA
CATGGATGTAAAAAAGATATTGCAGCACGTATCGATCGCGCCTGCCGTGGTTCCG
GCTTTTTTTATGCCGCTAATCATGGTGTTCGATCTGGCGGCACTCCAAAAATTTACGA
CTGATTGGCATATGGCAATGTCCCCAGAGGAAAAATGGGAGTTGGCAATTCGCGCA
TATAATCCGGCCAATCCACGGAACCGGAATGGTTACTACATGGCTGTTGAAGGCAA
GAAAGCAAATGAGTCATTTTGT TACTTAAATCCATCCTTTGATGCCGATCACGCCACT
ATCAAGGCTGGCCTCCCCTCCCATGAGGTGAACATCTGGCCAGATGAGGCACGCC
ATCCAGGGATGAGGCGATTTTATGAGGCGTACTTTTCAGACGTATTTGACGTAGCAG
CTGTCATCCTACGGGGATTTGCGATCGCGCTGGGTGCGGAAGAATCATTCTTTGAA
AGACATTTTTCCATGGATGATACCCTGAGCGCGGTTTCACTTATTAGGTACCCGTTTC
TGGA AA ACTACCCGCCGCTGAAACTGGGTCCAGATGGAGAAAAATTAAGCTTTGAA
CATCATCAAGACGTATCGCTGATAACCGTATTATATCAAACCGCAATTCCAAATCTGC
AGGTGGAAACCGCTGAAGGTTATCTTGACATTCCCGTATCCGATGAACACTTTCTAG
TTAATTGCGGCACTTACATGGCACATATTACAAACGGGTATTATCCAGCTCCAGTCCA
TCGCGTGAAATACATTAAACGCAGAGCGGCTGTCCATTCCCTTTTTTGCAA ACTTAAG
TCATGCTAGCGCGATAGACCCATTTGCTCCACCGCCTTATGCTCCAGCTAGGGGAA
ATCCAACGGTGTCTTACGGTGATTACTTACAGCATGGTCTCCTTGACTTAATTCGCG
CTAACGGTCAGACATGA

NHI 84 (PcbC *L. lactam.*) protein sequence:

MNRHADVPVIDISGLSGNDMDVKKDIAARIDRACRGS GFFYAANHGV DLAALQKFTTD
WHMAMSPEEKWELAIRAYNPANPRNRNGYYMAVEGKKANESFCYLNPSFDADHATIK
AGLP SHEVNIWPDEARHPGMRRFYEAYFSDVFDVA AVILRGFAIALGREESFFERHFSM
DDTLSAVSLIRYPFLENYPPLKLGP DGEKLSFEHHQDVSLITVLYQTAIPNLQVETAEGYL
DIPVSDEHFLVNCGT YMAHITNGYY PAPVHRVKYINAERLSIPFFANLSHASAIDPFAPPP
YAPARGNPTVSYGDY LQHGLLDLIRANGQT

Codon-optimized NHI 85 (IpnA) sequence:

ATGGGGAGTGTTTCGAAGGCGAACGTGCCTAAAATTGACGTAAGTCCGCTGTTCCG
CGATGATCAAGCAGCAAAAATGCGAGTGGCTCAGCAGATCGATGCAGCGAGCCGT
GATACGGGCTTCTTTTACGCAGTGAATCATGGCATTAAACGTT CAGCGTCTGAGTCAG
AAAACGAAAGAGTTTCATATGTCCATAACGCCGGAGGAAAAGTGGGATCTGGCTATC
CGTG CATATAATAAGGAACATCAGGATCAGGTT CAGCCGGTTATTATTTGTCTATAC
CAGGTAAGAAAGCAGTGGAAGTTTTTGT TACCTGAACCCGAATTTTACACCGGAC
CATCCGAGAATTCAAGCTAAGACGCCGACTCATGAAGTCAATGTGTGGCCGGATGA

GACCAAACATCCTGGTTTTTCAGGACTTTGCCGAACAGTATTATTGGGACGTTTTTGG
CCTCTCGTCTGCACTGCTGAAAGGCTATGCACTCGCACTGGGCAAAGAGGAAAAC
TTCTTTGCGCGCCATTTCAAACCAGATGACACGCTGGCAAGCGTGGTTTTAATCCG
ATACCCATATCTGGACCCTTATCCTGAAGCAGCGATTAAACCGCAGCGGACGGTAC
CAAACCTTAGCTTTGAATGGCATGAAGATGTCTCACTGATAACTGTGCTTTATCAGAG
CAACGTCCAGAATTTACAGGTGGAAACAGCTGCCGGATATCAAGATATTGAGGCGG
ATGATACCGGGTACCTGATTAATTGTGGAAGTTACATGGCCACCTGACCAATAATTA
TTACAAAGCTCCCATACATAGAGTTAAATGGGTTAATGCAGAACGTCAGTCGTTACCA
TTTTTCGTTAATTTAGGCTATGACTCTGTCATTGATCCTTTTGATCCCCGTGAACCAA
ATGGGAAAAGCGATCGTGAACCTTTATCATATGGTGACTATCTCCAAAATGGGCTGG
TTAGCCTGATTAATAAGAACGGTCAGACATAA

NHI 85 (IpnA) protein sequence:

MGSVSKANVPKIDVSPLFGDDQAAKMRVAQQIDAASRDTGFFYAVNHGINVQRLSQKT
KEFHMSITPEEKWDLAIRAYNKEHQDQVRAGYYLSIPGKKAVESFCYLNPNFTPDHPRI
QAKTPTHEVNVWPDETKHPGFQDFAEQYYWDVFGFLSSALLKGYALALGKEENFFARH
FKPDDTLASVVLIRYPYLDPYPEAAIKTAADGTKLSFEWHEDVSLITVLYQSNVQNLQVE
TAAGYQDIEADDTGYLINCOSYMAHLTNYYKAPIHRVKWVNAERQSLPFFVNLYGYS
VIDPFDPREPNGKSDREPLSYGDYLNGLVSLINKNGQT

Codon-optimized NHI 86 (CefEF A. chrys.) sequence:

ATGACAAGCAAAGTGCCGGTGTTTAGACTGGATGATTTAAAAAGTGGTAAAGTCCTC
ACTGAACTTGCCGAAGCAGTCACCACCAAAGGCATCTTTTATCTTACCGAAAGCGG
ATTAGTCGACGACGACCATACCTCCGCTCGTGAAACATGTGTGGATTTTTTCAAAA
TGGTTCCGAGGAAGAAAAACGCGCAGTTACCCTGGCGGATCGAAATGCCAGAAGA
GGATTTTCAGCTTTAGAATGGGAGAGTACTGCCGTGGTTACAGAGACTGGTAAATAT
TCAGACTACTCGACCTGCTACTCAATGGGAATTGGTGGTAATTTGTTCCCGAATCGT
GGCTTTGAGGATGTGTGGCAGGACTATTTTGATCGTATGTACGGCGCAGCGAAAGA
TGTTGCCAGGGCAGTATTAATAAGTGTTGGCGCACCGCTTGCCGGTGAAGATATTG
ATGATTTTGTGCAATGTGACCCACTACTGCGCCTGCGGTACTTTCCGGAAGTTCCC
GAGGATCGTGTAGCGGAAGAAGAGCCGCTGCGTATGGGACCTCATTATGACCTTTC
TACGATAACCTTGGTCCATCAGACCGCATGTGCAAACGGTTTTGTAAAGCCTTCAGTG
CGAAGTCGATGGTGAGTTTGTGGATTTGCCAACGCTGCCAGGTGCTATGGTTCGTAT
TTTGTGGCGCCGTTGGCACCCCTCGCAACCGGTGGGAAAGTTAAAGCTCCTAAACAT
CGCGTTAAATCACCGGGCCGTGATCAGAGAGTTGGGTCCAGTAGAACGTGCGAGTG
TATTTTTTCTTCGTCTAAACCAGACTTCAGTTTTAATGTCCAACAGTCACGCGAGTG
GGGGTTTAACGTCCGCATTCCGTCCGAACGTACGACCTTTAGAGAATGGCTTGGCG
GCAATTATGTTAACATGCGGAGGGATAAGCCGGCGGCGGCGGAAGCTGCTGTCCC
CGCCGCGGCCCCAGTGAGTACCGCTGCTCCCATAGCCACTTAA

NHI 86 (CefEF A. chrys.) protein sequence:

MTSKVPVFRLLDLKSGKVLTEAEAVTTKGIFYLTESGLVDDDHSTARETCVDFFKNGS
EEEKRAVTLADRNRARGFSALEWESTAVVTETGKYSDYSTCYSMGIGGNLFPNRGFE

DVWQDYFDRMYGAAKDVARAVLNSVGAPLAGEDIDDFVECDPLLRLRYFPEVPEDRV
AEEEEPLRMGPHYDLSTITLVHQTACANGFVSLQCEVDGEFVDLPTLPGAMVVFCGAVG
TLATGGKVKAPKHRVKSPGRDQRVGSSRTSSVFFLRPKPDFSFNVQQSREWGFNVRI
PSERTTFREWLGGNYVNMRRDKPAAAEAAVPAAAPVSTAAPIAT

Codon-optimized NHI 87 (CefE *S. clav.*) sequence:

ATGGACACGACTGTTCCAACTTTTTCTTGGCCGAACCTCAACAGGGCCTGCATCA
GGACGAATTCCGTCGATGCCTTCGTGACAAAGGGCTGTTCTATTTGACCGATTGTG
GTCTGACGGACACCGAGCTGAAAAGTGCAAAAGATCTCGTAATTGACTTTTTTGA
CATGGAAGCGAGGCAGAAAAGCGCGCAGTGACGAGCCCGGTACCTACAATGCGTC
GGGGTTTCACAGGTCTTGAAAGCGAGTCTACTGCTCAGATCACCAACACAGGCTCA
TATTCAGATTACTCGATGTGCTACTCCATGGGTACTGCCGATAATCTTTTTCCATCTG
GAGATTTTGAGCGCATTGGAAGTCTGCTCAGTACACAGCGTCTCGCG
CCGTGGCAGGGAAGTTCTACGTGCGACAGGCACGGAGCCTGACGGCGGTGTAG
AAGCATTGTTGATTGTGAACCACTGCTCAGATTTCTGCTATTTTCTCAGGTCCCGG
AGCATCGGAGTGCCGAGGAGCAGCCGTTGCGCATGGCCCCCATTATGATCTGTC
AATGGTTACGCTTATTCAGCAGACACCGTGTGCTAACGGATTCTGATCTTTACAGGC
CGAGGTTGGTGGTGCCTTACCGACCTTCCCTACCGCCCCGATGCTGTCTTAGTCT
TCTGTGGGGCAATTGCAACACTTGTAAACCGTGGCCAGGTTAAAGCGCCGAGACAT
CACGTGCTGCGCCCCGTGCGGATCAAATCGCTGGAAGTAGTAGGACATCTAGCGT
CTTTTTTCTGCGTCCGAATGCCGATTTTACATTCTCAGTGCCACTCGCAAGGGAATG
TGGCTTTGATGTATCTCTGGACGGTGAACCGCAACATTTCAAGATTGGATTGGTGG
CAACTACGTGAACATCCGCCGAACGTCGAAAGCCTGA

NHI 87 (CefE *S. clav.*) protein sequence:

MDTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGS
EAEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGADNLFPSPGDFE
RIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEAFDCEPLLRFYFPQVPEHRSAE
EQPLRMAPHYDLSTMVTLIQQTTPCANGFVSLQAEVGGAFDLPYRPDAVLVFCGAIATLV
TGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGET
ATFQDWIGGNYVNIIRRTSKA

Codon-optimized NHI 88 (CefE *A. lactam.*) sequence:

ATGACGGATGCAACAGTTCCGACCTTCGATCTGGCAGAACTGCGTGAAGGTCTGC
ATCAGGAGGAGTTTCGGCATTGTCTGCGCGAGAAAGGAGTGTTTTACCTGAAAGGC
ACAGGTCTGCCGGCTGAAGCAGATCATGCCTCTGGTCGCGAAATTGCGGTAGATTT
TTTCGATCATGGCACGGAAGCCGAAAAAAGCTGTTATGACTCCAATCCCGACGA
TTCGTCTGGATATGCTGGTCTTGAAAGTGAATCGACAGCGCAGATCACAAACACC
GGCAAATATACGGATTACAGTATGAGTTATTCCATGGGGACGGCCGATAACCTGTTT
CCATCTGCCGAGTTTGAGAAAGCGTGGGAAGACTATTTTGC GCGCATGTATCGCGC
GTCTCAAGATGTAGCGCGTCAAGTTCTGACATCAGTTGGCGCCGAACCCGAAGTC
GGCATGGACGCGTTCCTGGATTGTGAACCGCTGCTCAGGTTACGTTATTTCCCTGA
AGTGCCGGAAGATCGCGTAGCGGAGGAACAGCCTCTTCGGATGGCCCCACATTAT

GACTTGTCCATCGTGACATTGATCCACCAGACACCCTGTGCTAATGGCTTCGTGAG
TCTTCAAGTTGAGGTGGATGGGAGCTACGTTGACATTCCGGCGCAACCAGGAGCC
GTCCTTGTATTTTTCGGCGCTGTAGCGACCCTTGTGGCCGATGGTGCATCAAGGC
GCCGAAACATCATGTCGCGGCACCGGGCGCTGACAAACGAGTGGGCAGCAGTCG
TACCAGTTCAGTTTTTTTCTGCGTCCGAATGGTGATTTTCGGTTCAGTGTGCCGCG
AGCACGAGAATGTGGCTTTGACGTTTCTATCCCGGCAGAGACGGCCACCTTTGATG
ATTGGATAGGTGGGAACATATAAATATCCGTAAAACCGCTGCCGCCCGTTAA

NHI 88 (CefE A. lactam.) protein sequence:

MTDATVPTFDLAELREGLHQEEFRHCLREKGVFYLKGTGLPAEADHASGREIAVDFFD
HGTEAEKKAVMTPIPTIRRGYAGLESESTAQITNTGKYTDYSMSYSMTADNLFPSAEF
EKAWEDYFARMYRASQDVARQVLTSGAEPEVGMDFLDCEPLLRLRYFPEVPEDRV
AEEQPLRMAPHYDLSIVTLIHQTPCANGFVSLQVEVDGSYVDIPAQPGAVLVFCGAVAT
LVADGAIKAPKHHVAAPGADKRVGSSRTSSVFFLRPNGDFRFSVPRARECGFDVSIPA
ETATFDDWIGGNYINIRKTAAAR

Codon-optimized NHI 89 (H6H) sequence:

ATGGCCACTTTTGTGAGCAATTGGAGCACGAAAAGTGTCTCTGAATCATTATTGCT
CCCTTGCAGAAACGCGCGGAGAAAGGATGTGCCGGTGGGAAATGATGTGCCTATAAT
AGATCTGCAGCAACATCATCACCTTCTCGTCCAACAGATAACCAAGGCCTGTGAGG
ATTTTGGGCTTTTTCAGGTTATCAATCACGGCTTCCCGGAGGAACTGATGCTGGAAA
CAATGGAGGTTTGCAGGAGTTTTTTCGATTACCGGCAGAAGAAAAAGAAAAGTTC
AAACCAAAAGGTGAAGCAGCTAAATTTGAGTTGCCGCTTGAGCAGAAAGCTAAACT
TTATGTAGAAGGTGAGCAGCTTAGTAACGAGGAGTTTTTGTACTGGAAAGATACCCT
GGCCCATGGTTGCCACCCCTTAGATCAAGATTTGGTTAATTCCTGGCCGGAGAAAC
CGGCAAAATACCGTGAGGTGGTCGCCAAATATAGCGTTGAAGTCCGTAAGCTGACG
ATGAGAATGCTAGACTATATTTGTGAAGGCTTAGGCTTAAATAGGGTATTTTGATAA
TGAAGTGTCTCAGATCCAGATGATGCTGACTAATTATTATCCGCCCTGTCCGGATCC
TTCGTCAACGCTGGGCAGCGGGGGACATTACGATGGGAACTTGATAACACTGCTG
CAACAAGACCTTCCAGGGCTGCAGCAACTGATTGTCAAAGACGCAACGTGGATCG
CTGTGCAACCTATTCCGACTGCATTTGTGGTAAACCTTGGACTGACATTAAAGTTAT
AACTAACGAAAAATTTGAAGGCTCTATCCATAGAGTTGTGACTGACCCGACTCGTGA
TCGGGTGAGCATTGCAACATTAATTGGGCCCGATTATAGTTGTACGATCGAGCCGGC
AAAAGAGCTGTTGAATCAGGACAATCCACCGTTATATAAGCCGTATTCCTATTCAGAA
TTTGCAGATATTTATTTAAGCGATAAAAGTGATTACGATTCAGGTGTCAAACCTTATAA
AATTAATGTATGA

NHI 89 (H6H) protein sequence:

MATFVSNWSTKSVSESFIAPLQKRAEKDVPVGNDVPIIDLQQHHHLLVQQITKACQDFG
LFQVINHGFPPEELMLETMEVCKEFFALPAEEKEKFKPKGEAAKFELPLEQKAKLYVEGE
QLSNEEFLYWKDTLAHGCHPLDQDLVNSWPEKPAKYREVVAKYSVEVRKLTMRMLDYI
CEGLGLKLGYFDNELSQIQMMLTNYYPPCPDPSSSTLGSGGHYDGNLITLLQQDLPLQL

QLIVKDATWIAVQPIPTAFVVNLGLTLKVITNEKFEGSIHRVVTDPTRDRVSIATLIGPDYS
CTIEPAKELLNQDNPPPLYKPYSYSEFADIYLSDKSDYDSGVKPYKINV

Codon-optimized NHI 90 (CefF *S. clav.*) sequence:

ATGGCAGACACACCGGTTCCGATTTTTAATCTCGCTGCACTCCGTGAGGGCGCTGA
TCAAGAAAAATTTCCGGAATGTGTGACAGGTATGGGCGTATTTTATCTGACAGGTTAT
GGTGCTGGCGATAAAGATCATAGACTGGCTACCGATACGGCGATGGATTTTTTTGCG
AATGGGACTGAGGCAGAAAAGGCGGCAGTGACGACGGATGTTCCAACCATGCGTA
GAGGTTATTCAGCTCTTGAAGCAGAATCCACCGCCCAGGTTACTCGCACAGGAAGC
TATACAGATTATTCTATGTCGTTTTCTATGGGAATTTCTGGGAACGTGTTTCCATCGC
CTGAATTCGAGAGAGTGTGGACTGAGTATTTGATAAGTTATACGCAGCGGCCCAA
GAAACCGCCCGTCTGGTATTAAGTGCCTCCGGCGGGTACGACGCTGAAATTGTGG
GATCTCTGGATGAATTGCTGGATGCCGATCCGGTCCTCCGGCTGCGCTATTTTCCG
GAAGTGCCCGAACATCGATCCGCGGAACATGAACCTAGACGCATGGCCCCACACT
ACGACCTGTCTATAATAACTTTTATTCATCAAACCCCGTGTGCGAATGGTTTTGTGAG
CCTGCAGGCAGAGATTGGAGGTGAAGTAGTGTCTTTACCTGTGGTTGAGGATGCTG
TTGTGGTTATGTGCGGAGCTATGGCACCGCTGGCCACCCAGGGTGCCCTGCCCGC
GCCCCGCCATCACGTCCGCTCTCCTGGTGCCGGTATGCGTGAAGGATCGGATCGT
ACAAGTTCGCTGTTTTTCCTTCGACCAACGACAGATTTTTCGTTCTCAGTAGCAAAA
GCCCGTTCCCTACGGTTTGGCTGTGGATCTTGATATGGAGACGGCGACTTTCGGGGA
CTGGATCGGAACGAAGTATGTCACAATGCACGCGAAGAATGAGCCACAGGCGGGT
TAA

NHI 90 (CefF *S. clav.*) protein sequence:

MADTPVPIFNLAALREGADQEKFRECVTGMGVFYLTGYGAGDKDHRLATDTAMDFFA
NGTEAEKAAVTDDVPTMRRGYSALAEASTAQVTRTGSYTDYSMSFSMGISGNVFPSP
EFERVWTEYFDKLYAAAQETARLVLTASGGYDAEIVGSLDELLDADPVLRLRYFPEVPE
HRSAEHEPRRMAPHYDLSIITFIHQTPCANGFVSLQAEIGGELVSLPVVEDAVVVMCGA
MAPLATQGALPAPRRHHVRSPGAGMREGSDRTSSVFFLRPTTDFSFSAKARSYGLAV
DLDMETATFGDWIGTNYVTMHAKNEPQAG

Codon-optimized NHI 91 (Trt7) sequence:

ATGACTGGTCAAGCGGAAGCAATACGGCGCGTTACCCGACCGTAAGCCCCAAAAC
AGGCGGCCAGATGCTTCAGGAAGACGGTGTAATCATCCTTAAATCATTCTGGCG
CCAGATGTTATGCAGCGCTTCCAGGCGGAGGTGGATGAAGATGTCGAAAAAACTTC
AACAGGTGCGCGTATGAAAGCGTATAAATTAGTTAATGATAAGACCAACATATGGCA
GATTTAATTGTTTCGTTCCGAAGTTTTTAGATCTGATATTCTGACACATCCCTTGACCA
TGCAATAGCGGATGAACTCTTCCGAGCAGACTACGGGGATCATTGGCTTAACGCTT
CGGCAGTGCTTCAGTTGATGCCAGGCGCGCCCGCGCAGCAGCTCCATAGAGACG
AAGAAATATTTGCCGCCTCCAAATTCGTTCTCCAACCGACCCTCAGTTAAGCCTGA
GTTGTCTGGTAGCACTTACTGAATTTACTGAAGAAAATGGTGCAACACGCCTGATTC
CCGGTTCCCATCTTTGGGATTCGGCCCATCCCGCACCTTCCCCGGACCAGACCGT
TCCGGCCATAATGCAGCCTGGCGAAGCAATTCTATTTCTCGGTTCTCTGTTTCACGG

AGGAGGCGAGAACCGGACTGAAAATGTGAGACGGGGACTTGGGATGTCATTAATT
CCTTGCCAGTTTACCCCCTATTCCTCTCATATGCATGTGCCCCGCACCATTATCGAAA
CCATGACACCGCTGGCTCAGAAATTGGTTGGCTGGCGGACCGTTGAATCACACCG
ACAGTATCCTTTTTTGGCAGGGAGGTGATCGCCGACTGGAGGATGTGCTTGGGTTAG
CCAGCCGCGAGGCCTAA

NHI 91 (Trt7) protein sequence:

MTGQAEAIRRVHPTVSPKQAAQMLQEDGVILKSFLAPDVMQRFQAEVDEDVEKTSTG
ARMKAYKLVNDKTKHMDLIVRSEVFRSDILTHPLYHAIADLFRADYGDHWLNASAVL
QLMPGAPAAQLHRDEEIFAASKFRSPTDQLSLSCLVALTEFTEENGATRLIPGSHLWD
SAHPAPSPDQTVPAIMQPGAILFLGSLFHGGGENRTENVRRGLGMSLIPCQFTPYSS
HMHVPRTIETMTPLAQKLVGWRTVESHRQYPFWQGGDRRLDVLGLASREA

Codon-optimized NHI 92 (VldW) sequence:

ATGACCGGTTTCAGTCCCCATAGTGGATCTTGAGGCATGGCGCGCGGCTGACGAAG
AAAACCGTGCATCCCTGGCAGAGATCATTGACGGAGCGTTGCACACAGTTGGAAC
ATTTCTGCTGGCAGGGCATGGTGTTCCTGCAGAACTCACCGCGCGCATGCGTACC
GCGGGTAGAAGTTTTTTTCGATCTGCCTTGGGAAAAAAGAACCACACGCGGTTCA
ACGACCACACGACAACGGATGGCGTGGCCTGGTTAAACACCGTACCGATACCATAG
AAGGTACCGGAGGAGCGCCCGACCTGCATGAAGCTTTTCACATGGGGCCTACACA
CCGCACGGGGCGACGATGCATTTGATGCGCTGTACTATCCGGCCAATAAGTGGCCG
GCCGAGCTGCCGGAAGTGAAGAGAACTGCCCTTGCATACACCGCACATATGACGC
GGGTAGCAGGTGCTGTAATGGAGATGCTAGCGGGCGTTCTTGGTCTGGAACCGGC
TTTTTTTACATCTCGCTGCGAGCATGCCACTTGGACCCAGTCAGTGAAGTGGTATCC
GTCCTTGGATACGGTGGGGCAGACCGCAGAAGGTCAGATGCGAGTAGGTCCCCAC
ACTGATTTTGAACAATTACGCTGTTGGATCGACAACAAGGAGTATCTGGCTTAGAA
GTGTGGTCAGAAGAGGACGGATGGTTTGCACCGCCATTTGTGGAAGGTACCTTACT
GGTTAACCTCGGCGATCTGATGCATCAGTGGACAGATGGCCGCTGGCGCAGTCTA
CGTCATCGGGTACTTGCACCGAGTGCCTCGGCGCCACAGGAAGAGCTGGTTAGCC
TGGTATACTTCTTCGATGCGGATCCGGAGGCTGAACTTGTTCCGCTTGCGGCTCCT
GTAGGGGGAGGGGCGGCATGCCTACCGTGAATGTTGGCGAAACCATTTCTGAAAA
AGAATATACAAATGTTGACTGATTTGAAAGGTCACGGGCTTTTCCAGGGTGAGCTTT
CGTTATCGCGTCCTGGAAGCGCTGATTCACCCGGTTCTTCACCTGCCGATGATCAT
CCTTCACGTCCTGGTCGTCACCCGGCTCAAGGGCCACAATAA

NHI 92 (VldW) protein sequence:

MTGSVPIVDLEAWRAADEENRASLAEIIDGALHTVGTFLLAGHGVPAELTARMRTAGRS
FFDLPWEKKEPHAVQRPHDNGWRGLVKHRTDTIEGTGGAPDLHEAFHMGPTHRTGD
DAFDALYYPANKWPAELPELRETALAYTAHMTRVAGAVMEMLAGVLGLEPAFFTSRCE
HATWTQSVNWYPSLDTVGGQTAEGQMRVGPHTDFGTITLLDRQQGVSGLEVWSEEDG
WFAPPFVEGTLLVNLGDLMHQWTDGRWRSRLRHRVLAPSASAPQEELVSLVYFFDADP
EAEVPLAAPVGGGAGMPTVNVGETILKKNIQMLTDLKGHGLFQGELSLSRPGSADSP
GSSPADDHPSRPGRHPAQGPQ

Codon-optimized NHI 93 (EctD) sequence:

ATGGAGGATCTGTATCCGAGTAGACAAAACAACCAGCCAAAAATACTTAAACGTAAA
GATCCAGTTATCTATACGGATCGGTCAAAAGATAACCAAGCGCCGATAACTAAAGAA
CAGTTGGACAGCTATGAGAAAAATGGTTTTCTCCAAATTAAAAATTTTTTTCTGAAG
ATGAAGTCATTGACATGCAAAAAGCAATATTCGAACTGCAGGATAGCATTAAAGACG
TTGCCTCGGATAAGGTCATTCTGAGCCCGAATCGAATGATATACGTAGTATTTTTCA
TGTGCATCAGGACGATAACTATTTTCAGGACGTAGCGAACGATAAGCGAATCTTAGA
TATAGTACGCCATCTGCTTGGGTGAGATGTATACGTGCATCAGTCTCGGATCAATTAT
AAACCAGGATTTAAAGGAAAAGAATTTGACTGGCATTCCGATTTTGAACTTGGCAT
GTAGAGGACGGTATGCCCAGGATGAGAGCGATTTCCGTCTCAATTGCTCTGAGTGA
TAACTACTCCTTTAACGGACCCTTAATGCTTATTCCTGGCAGTCATAACTATTTGTTT
CATGCGTGGGAGAGACTCCAGACAACAACCTATAAAGAATCCTTAAAAAAGCAGAAA
CTTGAGAGTCCAGATGAAGAGTCTTTGCGCGAGCTTACGCGAATCGGTGGAGGTAT
ATCAGTCCCGACGGGGCAAAGCTGGCAGTGTTACATTGTTTCGAGTGAACACCATGC
ATGGCAGTACGTCTAACATCACGCCGTATCCGCGCAACAATTTATTCATGGTATACAA
TTCCGTTAAAAACCGGCTGGTGAACCGTTCTCTGGCGGCGAGAAACGTCCGGAA
TATATCGCTGTACGCGAAAAACAACCAGTTTATTCCGCAGTGAATTAA

NHI 93 (EctD) protein sequence:

MEDLYPSRQNNQPKILKRKDPVIYTDRSKDNQAPITKEQLDSYEKNGFLQIKNFFSEDE
VIDMQKAIFELQDSIKDVASDKVIREPESNDIRSIFHVHQDDNYFQDVANDKRILDIVRHL
LGSDVYVHQSRINYKPGFKGKEFDWHSDFETWHVEDGMPRMRAISVSIALSDNYSFN
GPLMLIPGSHNYFVSCVGETPDNNYKESLKKQKLGVPDEESLRELTRIGGGISVPTGKA
GSVTLFESNTMHGSTSNITPYPRNNLFMVYNSVKNRLVEPFSGGEKRPEYIAVREKQP
VYSAVN

Codon-optimized NHI 94 (EctD homolog) sequence:

ATGGCAGAAAATAAGTTTTATTTGGATTCCTATCCTACGAGAACGTCATCTGAAAGCA
AGATCATACAACGCACGAATTCAGTGGTCTACTGTGACTCGTACGATGAACCTCAACA
AGGAGCAGGTGGACTTTTTTCGAGAAAAACGGTTATCTGATTTTTTGAGAATTTGTTCA
GCTCTGATGAAATTACTAACTTTTCGATGAGCTCACCTCACTTTCTCAGGACGAAAT
TAAAAAAGATCTGCCTCAATTCATATTAGAGGAAACCCAGCGGGATGTGAGGTCAAT
TTTTGAGATACATAAAATTAGCAAACCTCTATGGCAAACCTTTGCCGTGATAAAAGAATTT
TGAAAATTGCACAGCAACTGCTGGGGTCTAAGGTCTATATTCATCAAAGCCGTGTTA
ATTTAAAACCGGGTTTTGATGGTAAAGAATTTTACTGGCATTCTGACTTTGAAACGTG
GCATAGCGAAGACGGGATGCCCAACATGCGCGCAGTCTCATGCTCTATTTCACTGA
CGAAAAATTACGAATTTAATGGACCGCTGATGGTCATTCTGCGCAGTCATAAGGAAT
TTGTCTCCTGCAGTGGCAAACTCCGGATGAACACTATAAGCAAAGTTTAAAACGCC
AGGAGATCGGTACTCCGCAGAAAGAATTCCTGGAGCAGATGGTTGAGAAAAGCAAA
ATCGTTTCAGCAAAAGGAGATGCCGGTAGCGTGATATTTTTCGACTGTAATATCATGC
ACGGTTTCAACGGTAACATTACCCCTATCCTCGCTCGAACGCCTTCTTCGTGTACA
ATTCTATTCATAATACTTTGGTCGATCCTTTTTGCGGATTAAATCCGCGCCCTACGTAT

ATTGCCGAACGTGAATTCTTGCCGTTAGAACCGGTCGATAATTTCTTAGACTCAAAAT
AA

NHI 94 (EctD homolog) protein sequence:

MAENKFYLDSPTRTSSESIIQRTNSVVYCDSDYDELNKEQVDFFEKNGYLIFENLFSS
DEITKLFDELTSLSQDEIKKDLPPQFILEETQRDVRSIFEIHKISKLYGKLCRDKRILKIAQQL
LGSKVYIHQSRVNLKPGFDGKEFYWHSDFETWHSEDGMPNMRAVSCSISLTKNYEFN
GPLMVI PGSHKEFVSCSGKTPDEHYKQSLKRQEIGTPQKEFLEQMVEKSKIVSAKGDA
GSVIFDCNIMHGSNGNITPYPRSN AFFVYNSIHNTLVDPFCGLNPRPTYIAEREFLPLE
PVDNFLDSK

Codon-optimized NHI 95 (FtmOx1) sequence:

ATGACCGTTGACTCAAAACCGCAGTTGCAGCGTCTCGCTGCAGATGCCGACGTGG
ATCGTATGTGTCGTCTCCTCGAGGAAGATGGAGCGTTTATATTAAGGGCTGTTGC
CATTTGATGTTGTGGAGTCATTTAATCGTGAATTAGATGTGCAGATGGCCATCCAC
CCCCAAGGGTGAGCGGCTGCTAGCCGACAAGTACCCACCTCACTTCAAGTACGT
CCCCAATGTTGCAACTACTTGCCCGACATTTAGAAATACCGTTCTGATAAACCCCGT
GATTCACGCCATTTGTGAGGCGTATTTTCAGCGTACCGGTGACTATTGGTTAAGCGC
CGCTTTCCTCCGTGAAATAGAAAGTGGGATGCCCGCGCAGCCATTTTCATCGCGATG
ATGCAACCCACCCGCTGATGCACTACCAGCCTTTGGAGGCCCTCCTGTCAGCCTA
AGCGTCATTTTCCCGCTGACAGAGTTTACTGAGGAGAATGGTGCCACGGAAGTAAT
CTTAGGTTCTCACCGATGGACCGAAGTCGGCACCCCCGAACGCGATCAGGCTGTG
TTAGCGACCATGGATCCGGGTGATGTTTTGATCGTGCGCCAGCGGGTGGTGCATG
CGGGAGGAGGTAATCGAACGACAGCAGGTAAGCCACGGCGCGTCTGTTCTGGCCTA
CTTTAATTCTGTTCAACTTACTCCATTTCGAGACGTACCGGACCATGCCGCGTGAGAT
GGTTGAGTCCATGACCGTCCTGGGTGAGCGGATGTTAGGATGGCGAACAATGAAA
CCGAGTGACCCAAACATCGTTGGTATTAATCTTATTGATGATAAACGCCTGGAAAAC
GTTCTGCAGCTGAAAGCAGCGGATTCTCCAGCATAA

NHI 95 (FtmOx1) protein sequence:

MTVDSKPQLQRLAADADVDRMCRLLEEDGAFILKGLLPFDVVESFNRELDVQMAIPPP
KGERLLADKYPPHFKYVPNVATTCPTRNTVLINPVIHAICEAYFQRTGDYWL SAAFLRE
IESGMPAQPFHRDDATHPLMHYQPLEAPPVSLSVIFPLTEFTEENGATEVILGSHRWTE
VGTPERDQAVLATMDPGDVLIVRQRV VHAGGGNRTTAGKPRRVVLAYFNSVQLTPFET
YRTMPREMVESMTVLGQRMLGWRTMKPSDPNIVGINLIDDKRLENVLQLKAADSPA

Codon-optimized NHI 96 (AusE) sequence:

ATGGGCAGTGCGACCCCTAGCAGACTGCAAAAGTTTCCCGCGACCGCCCCCGCAG
ATGAAATTTATGCAGCCTTTAAAGAAGATGGGTGTGTAATTATTGAGGGTTTTGTCCC
GCCTGATCAGATGGCGAGATTCTCGCAGGAAATACAGCCTGCAATGGAGAAAATTC
AGGTACAGGTTACTAACGATGGGAACAGCAATGATCGCGTAAAACGTTTTTTCGAAAC
TAGTTACCACTAGTCCAACCTTTTCGCCATGAAATTCTGGAGAACGATCTTATGCACG
AACTGTTACAGCGTGTCTTTTCAAAACCGGGTGAGGGAATGGGTACCATTTTAATG

ACACCATGGTGATCGAGGTACAGCCGGGGGCACCCGCTCAGAGGCTGCACCGCG
ATCAAGAACTTTATCCGTGGTGAATTCCATGGGTCCAGATGCTCCTGAATGTTTAG
TGAATTTCTTTTGC GCGGTGACTCCGTTACGGTTGAAAATGGTGCGACGCGTTTG
GTTCCAGGATCTAACCGTTGGCCAGAACTTACCTTAATTAATGCTACAGATTGCCCC
CAGTATGGTAAAATCGACTCCGTGCCTGCCATCATGCAGCCTGGGGATTGCTATATG
ATGTCAGGCAAAGTTATTCATGGCGCTGGCCACAATGCAACACTTTCCGACCAACG
TAGGGCTCTAGCATTTAGTACGATCCGAAGAGAACTCAGACCCGTGCAAGCCTTTC
CATTGTGGATTCCGATGCAAATCGCCACCGAACTCTCACCGAGAACGCAGGCAATG
TTCGTTTTTCGTTCTTCAACACAGCACTGTGACGTTGACACGGTACACTTTTGGGG
TAACGATGGCAAAGACATAGGTGAACACCTCGGATTAATATCAAGCGCCTAA

NHI 96 (AusE) protein sequence:

MGSATPSRLQKFPATAPADEIYAAFKEGDCVIEGFVPPDQMARFSQEIQPAMEKIQVQV
TNDGNSNDRVKRFSKLVTTSPTRHEILENDLMHELLQRVFSKPGEGMGYHFNDTMVI
EVQPGAPAQRLHRDQELYPWWNSMGPDAPECLVNFFCAVTPFTVENGATRLVPGSN
RWPELT LINATDCPQY GKIDSVP AIMQPGDCYMMMSGKVIHGAGHNATLS DQRRALAFS
TIRREL RPVQAFPLWIPMQIATELSPRTQAMFGFRSSTQHCDVDTVHFWGNDGKDIGE
HLGLISSA

Codon-optimized NHI 97 (AsqJ) sequence:

ATGGGATATCCTAAAGCCTTTACGAGTTCGGATTCTGAGCCGGAGCCTGACTTGAG
CAGAGATCTTGGAACCCGGTTATGGGAAATCCGGGTGTTGTGAGCCGCTCCTCAT
CCACCGTGCGCGACGACAGCGTACGTAACAATCCAACGGGCCCGATGGTCGCTT
GGCGGGGGCTTTGGAATGCCCGTGCTCTGCTACGTTTCCCCGCGGAGGTGAATGGC
GTACGCTTAGATTTCAAAGTGTAAGTTCCCGCCGCCCTACATCACGGCTCAGCTTG
TTACCTTACTCTCTGTGTTCTATCTGCCCTTCATCTCAGGCAACAATGACTAGTAAGG
ATCATGTGAAGTCACAAATTCCGCGGCTCTCCGCAATCAATGACTTACATAAAATTTG
GCCTACTGTAGAAGAGCACGGTGCTGCCATTATAGAAAGTTTCCTGTCTTAGATAT
CGTACGTCGGCTGAATGAAGAGGTGGATCCGTTTGTGAAAATTGAGCCGATTCCGG
CAGCCAAAACGAAGGATCATCAAACCATGTACTGTCTACAACGACCAGGCTGGTG
AATGTGCTGGCACCCATTAGTAAAGCCTACCGCGAAGATGTTCTGAATTCAAAGTG
CTGCATCGCATTTGCTCAGATGCTTTCCATGTTTACGGGGATTATTGGGTTCTTATGG
GGGCTGTAATGGAATTAGCCCCATCAAACCCCGCTCAACCGTTACACAGGGATATG
CGGTTTAGTCACCCTATTGTAGAGTATCTTAAACCGGACGCGCCAGCAACCAGCATC
AATTTTTTAGTGGCTCTGAGCCCGTTTACCGCGGAAAACGGAGCGACCCATGTAAT
CCTGGGCTCTCATAAGTGGCAGAATCTTCAAATGTGAGCATGGACGCAACGGTCC
GGGCGCTGATGAATCCGGGGGACGCGCTGTTGATAACCGACTCGACCATTCAATTGT
GGCGGTGCCGAACTACTGGAACGGAGACACGGCGGCTGTTAACGATTACGATGG
GTATCTCGCAGCTGACCCCACTGGAATCGAACCTTGCCGTCCCCCGTCCGGTTATT
GAGTCCCTACCCCGCTAGCTCAACGCTTGCTGGGATGGGCCTCGCAGCGTAGTG
CTGCCCCCGTGATATAGGCCTGTTGACTATCCGCGGTAATAGTATTGAAAAACGA
TGAATCTCAAAGCAGAGCAGCCTTTGCATGATGATGAAGCCGAACCTCTGTGTCGT
GAAACGATTTGA

NHI 97 (AsqJ) protein sequence:

MGYPKAFSTSSDSEPEPDLSRDLGNPVMGNPGVVSRSSSTVAQHSVRNNPTGPDGRL
AGLWNARALLRFPAEVNGVRLDFKSVSSRRPTSRLSLLPYSLCSICPSSQATMTSKDH
VKSQIPRLSAINDLHKIWPTVEEHGAAIIESFLSLDIVRRLNEEVDPFVKIEPIPAAKTKDH
PNHVLSTTTTRLVNVLAPISKAYREDVLNSKVLHRICSDAFHVG DYWVLMGAVMELAPS
NPAQPLHRDMRFSHPIVEYLKPDAPATSINFLVALSPFTAENGATHVILGSHKWQNLSNV
SMDATVRALMNP GDALLITDSTIHCGGAETTGTETRLLTITMGISQLTPLESNLAVPRP
VIESLTPLAQ RLLGWASQRSAAPRDIGLLTIRGNSIEKTMNLKAEQPLHDDEAEPLCRET
I

Codon-optimized NHI 98 (LoLO) sequence:

ATGACAGTCACAAACAAACCAGTTGAACCTGCCAATGTCCCGGTTATGGATTTTGAA
GCAATTCATGCATCGGTGGGCAATGAGCGTAAGGAATATTTGCGTCAGCTTGACGA
AGCGTGGTCTCATCACGGCGCAGTCTATGTCATTAATCATTCTATAGGGACAGAGAC
CTTAGAAGAGGCCTTCGTGTGGTGCAAAAAATTTTTTACTTGCCTCTTGCCGTGAA
AAATAGCGTCCATATCCCTCCTGATGTATCCAAACATTTTCAGGGCTGGACTGGCAC
CGGTGAAGCGATTTCAAGTCAAGGCGTCTGGGATCCTGACGAAATTGAAAGACTGC
GTAAGGAAATGCCAACGGAAGTGAAGAAGCCATGGAATTGCAGGATCCATGCGGA
ACTTACCCCCCTGGCAATCCCGATCTGAATCTCGTGGAACAACATCTACCCGGCTA
CCTCGATTTTCTGAAAAAATGGTTCGCAGCTTGCTATAAACAGTCCCTGCAGAATAT
GCGTCTGGTTTGTGAAATCTTGGGGATGGAAGACCTTGATTACATTGGAAAAAATT
TGAACCACGGCATATGAGTACACACTCAACTTGAATTATTTTTTAGGCCAGCCGGT
ATCTCAGCTTGCCTCAGGATCTTCAATCGCTTAAATGCGCATAAGATTACTGCCA
GTTACAGATGCTATTTTCAAGACATGGTTGGCGGTTTAGAGCTTCACGACTATGAAGA
AGACATTTATCGTCCAGTGCCGCCGATCAAAGGCGCCATGATAGTGCAGGTGCGTG
ATCTGCTGGAGAAACAGACGAATGGACGGTGGAGAAAGTGCTTTGCACAGGGTCAC
CGCACCCCTCTCGTTACATGTATGGGGGAAGTCCAGGTGGAGATGATGAACTGGTGC
AGCGCTATAGTCTGGTGTTTTTTGGACACCTTAACCTGGATGAAATGATTAAACCACT
GCCGGGATGTGAGAAACCGGGGCAAATGGTCCACCCTGGAATGGAAAGATCTCATG
ACAGCCGGCCAGTGGTTAGCAAGGCGTGTAGCCCTGGAGTATGAGCGTAAAACCG
CAGCCACGGTAATGTGA

NHI 98 (LoLO) protein sequence:

MTVTNKPVEPANVPVMDFEAIHASVGNERKEYLRQLDEAWSHHGAVYVINHSIGTETL
EEAFVWCKKFFDLPLAVKNSVHIPPDVSKHFQGWGTGEAISSQGVWDPDEIERLRKE
MPTELKEAMELQDPCGYPPGNPDLNLVEQHLPGYLDFLKKWFAACYKQSLQNMRLV
CEILGMEDLDYIGKKFEPRHMSHTSTWNYFLGQPVSQLASGSSNRLNAHTDYCQFTM
LFQDMVGGLELHDYEEDIYRPVPIKGAMIVQVGDILLEKQTNGRWRWSALHRVTAPSR
MYGGSPGGDELVQRYSLVFFGHLNLDDEMIKPLPGCEKPGKWSTLEWKDLMTAGQW
LARRVALEYERKTAATVM

Codon-optimized NHI 99 (LoLE) sequence:

ATGACAGCCGCAAGTTCACCGCATCCGGGGGTATCCGCGGAAGACATTGAGTTTTTA
CCAGGCAAACGGGTATTTGCGTCTCCCGCAAGAAGCTCATGGACTGTTTGACGAC
CTGGCCAAGTTACAGGCATGGGTGCGCCGAGATTTTCGCAGTGGGGCCTTGAAACAG
GTAAGTGGCGTCATTATTATGAAACAACGAACGGCAAACATCTCCTGTGGGGTACG
GAGAAGCTGATGGAATATCATGCTCCGATGCGTGACCTCATTGCTGGAGAAGCGCC
CCTGACCTTGTTAAAAAGCCTAACGGGGCAAAGATATGGTAGTCTTTAAAGACGAAAT
AGGTTGGAAACTGCCGGGTGGTAAAGGTGCCGTCCCCCATTGATCGGCCTGCG
TACAGCATGTTTGCTCCTGAGTTTATCGAAATTATGATCGCTGTTGATGCGCACACC
GTCGAAAACGGGTGTCTCCAGTTTGTGCCAGGTAGTCACAAAGAGGCAGTTCCGA
TCAGCGCCGATGGGCGTATTGCCTCTGCATGGCTGGAAGGGAAGGAATTCATTCCG
ATGGTCCTGGATCCGGGAGATGTTCTGATCTTCAATGAATCTATGGCGCATCGTCTC
GATCCAAATAAACTGATCAGCGCCGGGCAGCTGTATTTGGTACGTACCATTTTGAT
CGATCACAGCCCGACTTACGAGATAAATTCTACGCTCATAGATTAATTCATTCTCCAC
CAGAGAACGCCTGGGTAGAAACAGTGGAAGCTCAGACTTGA

NHI 99 (LolE) protein sequence:

MTAASSPHPGVSAEDIEFYQANGYLRLPQEAHGLFDDLAKLQAWVAEISQWGLETGK
WRHYYETTINGKHLWGTEKLMEYHAPMRDLIAGEAPLTLKSLTGKDMVVKDEIGWK
LPGGKGAVPHLDRPAYSMFAPEFIEIMIAVDAHTVENGLQFVPGSHKEAVPISADGRIA
SAWLEGKEFIPMVLDPGDVLIFNESMAHRLDPNKTQRRRAAVFGTYHFDRSQPDLRDK
FYAHRLIHSPPENAWVETVEAQT

Codon-optimized NHI 100 (KanJ) sequence:

ATGGCTCTCGCCGCGCCCCCAGGCGAACTAACCCTGGCTCTGACACCGGATGATA
AGACTTTGGATCCGGCAAGCCTTGATAGAGCACTGGCCATTCTCGCCGAACACGG
GATTCTGGTCCTGACAGGTATGCTTCGTACGCGTCTTACGGACCAATTAAGAACCG
CTATGCTGGATGATTTGCCTGAAGTCCTGAGGCAACAAGATGTGCCTACCAATTTTG
TACCTGGGCATGTGCAGCAAGATCCGCCGGTACGCGAATCCTTGCTGTTTCCGGAT
GTACTCCTAAATCCGGTGGTATACCAGATCACGCATGCCGTCTGGGCGCAGATGC
GCGGAATGCGGTATATTCCGGAAATATGAATCTGCCTGGCTCTCACGAACAGCCTGT
TCACTTAGACGAACCGCATCTGTGGCCGGGCATCTCACATCCCCCGTACTGTCTTT
GTGTAGATGTTCCGCTTATTGACTTTACCCTGGAGAATGGCTCTACAGAATATTGGC
CGGGGTGCGATGTCCTGAACCCTGATGAATGTTATGACGAGCGTGGGTGCGTTCT
GCCGGCGGAGCTGGAACGCAGGCGCGCAGTTGCTCCACCGGTACGGTTTCCGAT
TCCGGTGGGCTCCGTTGTCATCCGCGATGGCCGCCTCTGGCATAGAGGGGTTCCT
AATCTGAGCGCGGCCCGCGGCCCTGCTCGCCATGACCCATTATACCGAGTGGT
TCGATATGCCGCCTATCCAACCTGCCGGATACGGTGAAATCCTGGGTAGACGGGTCC
GACAGACATACCCATGCCCATTTTCGTGGCGGGTGATGTGGATCATCTTACGGGTGA
CCATCCGTTTGCAGTTAGATAA

NHI 100 (KanJ) protein sequence:

MALAAPPGETLALTPDDKTLDPASLDRALAILAEHGILVLTGMLRTRLTDQLRTAMLDDL
PEVLRQQDVPTNFPVGHVQQDPPVRESLLFPDVLLNPVVYQITHAVLGADARNAVYSG

NMNLPGSHEQPVHLDEPHLWPGISHPPYCLCVDVPLIDFTLENGSTEYWPGSHVLNPD
ECYDERGCVLPAELERRRAVAPPVRFPIPVGSVIRDGRLWHRGVPNLSAAPRPLLAM
THYTEWFDMPPIQLPDTVKSVDGSDRHTAHFVAGDVDHLTGDHPFAVR

Codon-optimized NHI 101 (Downy Mildew Resistance) sequence:

ATGGCGGCCAAATTAATTTCAACCGGCTTCAGACATACAACGTTACCAGAGAATTAT
GTGCGTCCGATATCAGATAGACCACGCTTAAGCGAAGTCTCCCAACTGGAGGATTT
CCCCCTTATTGATCTCTCATCTACTGATCGCTCGTTTCTCATTACAGCAGATACATCAA
GCTTGTGCTAGGTTTGGATTCTTCCAGGTGATTAATCACGGAGTAAATAAACAGATC
ATCGATGAAATGGTATCTGTGGCAAGAGAATTTTTTCCATGAGCATGGAAGAAAAA
ATGAAACTGTATTCGGATGATCCCACTAAACTACACGGTTAAGTACGTCCTTCAATG
TTAAAAAGAAGAAGTTAATAACTGGCGCGATTACCTGCGATTGCATTGCTATCCAAT
ACACAAATATGTTAATGAGTGGCCATCCAATCCTCCGTCATTTAAAGAGATCGTTAGT
AAATATAGTCGGGAGGTCCGTGAGGTGGGTTTTAAATGAAGAACTGATCTCCGAA
TCTTTAGGTTTGGAGAAAGACTATATGAAAAGGTTCTTGGGGAACAGGGGCGAGCA
TATGGCGGTCAATTATTACCCACCTTGCCCCGAACCGGAATTGACTTATGGCCTGCC
GGCGCACACCGATCCCAACGCATTGACCATTCTGTTGCAGGATACTACCGTTTGC
GGTTACAGATCTTAATTGACGGTCAGTGGTTCGCAGTTAATCCCATCCCGACGCTT
TTGTTATTAATATTGGAGATCAGCTCCAAGCACTTAGCAACGGTGTATACAAGAGCGT
GTGGCATCGGGCAGTTACGAATACGGAGAATCCGAGACTTTTCAGTCGCTTCTTTTTT
ATGTCCAGCGGATTGTGCGGTGATGTCCCCGGCGAAGCCATTATGGGAAGCCGAG
GATGATGAGACGAAGCCGGTGTACAAAGATTTTACTTATGCGGAATATTATAAGAAGT
TCTGGTCCCGAAATCTGGACCAGGAGCATTGTCTTGAAAACTTTTTGAATAATTGA

NHI 101 (Downy Mildew Resistance) protein sequence:

MAAKLISTGFRHTTLPENYVRPISDRPRLSEVSQLEDFPLIDLSSTDRSFLIQQIHQACA
RFGFFQVINHGVDNKQIIDEMVSVAREFFSMSMECKMKLYSDDPTKTTRLSTSFNVKKEE
VNNWRDYLRLHCYPIHKYVNEWPSNPPSFKEIVSKYSREVREVGFKIEELISESLGLEK
DYMKKVLGEQGQHMAVNYYPPCPEPELTYGLPAHTDPNALTILLQDTTVCGLQILIDGQ
WFAVNPFPDAFVINIGDQLQALSNGVYKSVWHRAVTNTENPRLSVASFLCPADCAVMS
PAKPLWEAEDDETKPVYKDFTYAEYYKKFWSRNLDQEHCLNFLNN

Codon-optimized NHI 102 (scopoletin-8-hydroxylase) sequence:

ATGGGTATTAATTTTGAAGACCAGACTACATTATTTAACTTCGTGGTGCGGGAAGGC
AATGGTGTCAAGGGTATGATTGACAGCGGACTGTCTTCAGTCCCGCGGCCTTTTGT
TCAACCGTTATCGGAACGGATCCCAACCCAGAAAGCCTTGACATGTGAAGCCACCC
AGCCTATTGATTTGTCAAATCTTGACGGGCCTCAACACAAAGAAGTGGCAAAGCAG
ATCGTTGAAGCAGCTGAGACGCTCGGCTTCTTTCAGGTTGTTAACCACGGCGTGTC
AGTTGAGTTATTGGAATTCTGAAGTCATCTGCACATGAGTTCTTTGCACAAGCTCC
GGAGGAAAAATCTATGTACCTGAAAGAAGTTTCACCATCGAAGCTGGTTAAGTATGG
CACTAGCTTTGTCCCAGATAAAGAAAAAGCGATTGAATGGAAGGACTATGTTAGTAT
GTTGTATACCAATGATAGCGAAGCTTTACAGCATTGGCCGCAGCCATGTCGTGAAGT
CGCATTAGAGTTCCTGAACAGCTCGATGGAAATGGTCAAAAATGTGGTCAACATTCT

GATGGAAAATGTGGGTGTGACACTGGAGGAAGAAAAAATGAATGGTTTGATGGGAA
CGAAGATGGTTAACATGAATTACTATCCGACTTGCCCTTCTCCGGAACATACTGTGG
GAGTAGGAAGACACTCAGACATGGGGATGTTGACTGTCCTGTTGCAAGATGGGATC
GGGGGACTGTACGTGAAATTAGACAATGGGGAATGGGCAGAAATACCACCGGTACA
TGCGCTCTCGTTATTAATATTGGTGATACGCTACAGATTCTGTCAAATGGAAAGTAT
AAATCTGCAGAGCATCGTGTCAGAACCACAAACATCGGTTCCCGCGTTTCCGTTCC
GATTTTCACCGCACCTAATCCGAGCCAAAAGGTAGGTCCGTTGCCAGAAGTTGTTA
AACGTGATGGTGTTGCACGCTATAAAGAGTTTCTCTTCCAGGATTATATGAATAATTT
CTTCGGTCAGCCGCACGATGGTAAAAAGAGTCTGGACTTTGCACGTGCCGAATAA

NHI 102 (scopoletin-8-hydroxylase) protein sequence:

MGINFEDQTTLFNFVVREGNGVKGMIDSLSSVPRPFVQPLSERIPTQKALTCEATQPI
DLSNLDGPQHKEVAKQIVEAAETLGFFQVNVHGVSVELLELLKSSAHEFFAQAPEEKS
MYLKEVSPSKLVKYGTSFVPDKEKAIEWKDYVSMLYNDSEALQHWPPCREVALEFL
NSSMEMVKNVVNILMENVGVTL EEKMNGLMGTKMVNMNYYPTCPSPELTVGVGRH
SDMGMLTVLLQDGIGGLYVKLDNGEWAEIPPVH GALVINIGDTLQILSNGKYKSAEHRV
RTTNIGSRVSVPIFTAPNPSQKVGPLPEVVKRDGVARYKEFLFQDYMNNFFGQPHDGK
KSLDFARAE

Codon-optimized NHI 103 (GloF) sequence:

ATGGCTATTCAGACCCTTGATTATCGTGACTTCCAGTACGGGGGCCAGGAACAACAT
CGTACCTTTTGT CATAACCTGTGTGAAACGCTCAGCACGTGGGGATTTATCAAATC
CAAAACACCAGTATTCCTGACGCCGTTATAGACGAGTTATTTTCGTACAACAAAAAAT
TTTTTGCACTTCCCGAACATATTAAACAGAAGGCAAGGCATCCGGCAGCTCCAAATC
CGCACCGTGGTTGGAGTGCAGTCGGTCAAGAACAGTTGTGCGGTATCGCAGGTTT
TGAAAAAGACGAAGAAACAGATGGCTTCGTTCCGGAATATCGTGAATCTTTCGATCA
GGGTGCCGCGGACGATGAACTCTTCCAAATCGGTGGATTGATGAAGACGATTTAC
CGGGTTTTCGGAAATTTATGGAAACTATTACGAGATGTGTTATAACTTTCATACTCA
GCTGTTACGTGCAATCTCCACCGGTCTCTCGCTCCCTGAAGATCTCTTACTGAGTC
GCCATCAGACGGATACCTCAGAACTGCGCATGAATCACTATCCAGCCATCGCCTGT
GAAAACCTGAAATTCGGCATGCGTATCGGCGAACACTCTGATTTTGAACTCTTACG
TTATTACTCCAGGATTCCGACCGGGGGTTTACAGGTGGAAGACCAGAAGAAGCTTGG
AACTTTTATTCCCGTCGAGTCGGACAGTCGTTACGAGGTCATTGTAAACGTTGGCG
ACTGTCTTCAACGCTGGACGAATCGTCGTCTGCGTTCAGCCAATCATCGGGTACAT
CTTCCTGAAGGCAAAAACCTTCAAATCCGACGAAGTCCTTGCGGATCGCTATAGCGT
TGCTACTTTTGGTAAACCGGACCGTAATGTACTGGTCGACTCATTCCCCGAGTTTTG
CCGCGGTGGTGAAAGCAAATATAACGATCATATGAATGCACTTGAATATAATCAGACA
AAGCTGCTTCGTACTTACGCCTGA

NHI 103 (GloF) protein sequence:

MAIQTLDYRDFQYGGQEQHRTFCHNLCETLSTWGFIKIQNTSIPDAVIDELFSYNKKFFA
LPEHIKQKARHPAAPNPHRGWSAVGQEQLSRIAGFEKDEETDGFVPEYRESFDQGAA
DDELFPNRWIDEDDLPGFRKFMENYYEMCYNFHTQLLRAISTGLSLPEDLLLSRHQTD

TSELRMNHYPAIACENLKFGMRIGEHSDFGTLTLLQDSTGGLQVEDQKKLGTFIPVES
DSRYEVIVNVGDCLQRWTNRRLRSANHRVHLPEGKNFKSDEV LADRYSVAYFGKPDR
NVLVDSFPEFCRGGESKYNDHMHNALEYNQTKLLRTYA

Codon-optimized NHI 104 (GloC) sequence:

ATGAGAATCGAGACACTGGATTTCTCTAAGTTTCATGTGGGGACTGATGCTGAACG
GTATGAATTTTCTACCGCTCTTCTTACAGGATTTGCGAATGCCGGCTTCATCAAACCTT
ATTAATCATGGCTTCAGTCAGGAAGAAATTAGTCAACTGTTTGAAGAAAACCGACGC
TTTTTTGATCTCACCAGACAGTATTAAGGCACAAATAGCTAACGAAGATGGACCAAAG
CCGCAGCGGGGTTGGTCAGCCGTGGGCGCCGAAAAAACCGGACTCCTAAATACTG
GTGGCAAAACGAATTTAACCAAACCCGACATTGAGGCCCGCAGGACGCGAAGGA
ACACTTTGATATTGGACCATCTGAGGATACTGAATCCCAAATAAATGGCCAGATAAT
GAACTGATACCAGGATTTAGCCATGGTTAGAATCCTTTTACGAACGCTCACGCTAT
ATAAGCTTTGCCCTTATGGAGGCGCTCGAGATAGCAATGCATCTGCCGAAGGGTGC
TTTTATCCAGAAATGCCAGGGCCATGCCAGTGAACCTACGGCTGAATCATTACCCTAA
GATTACGGTAAAGACCTTGCAAGGCGGTAAAACCAAGTCGTATTTGGCCCCATACCG
ATTTTGGCGTAATTACGTTACTTGCACAGGACGATGTAGGCGGACTTGAGATCCAGG
ACAAAGACAATCCGACCAACTTCTTACCGGTCAGCCGGGAGGACGTCTCAGAGTTA
GTCGTTAACATAGGGGACACACTGGAACGGTGGACGAATGGCTTTCTGAAAGCCG
GCTTACATCAAGTGACTACCCCTAGGGAAATTGTCAACCAGAGCACAGAAACGGTT
CGGCCGCGGCGTAGCATTGCCTTCTTTCTGAAAGCGCATCGCCAAATGTCTGTGG
GACCGCTACCGCAGTTCGTTGCCGAAAAAACCCCGGCAAAATATGAGGATATCACC
GCCTTGGCATACCAACAACGCCGAACCTGCCATTGTTTATTAA

NHI 104 (GloC) protein sequence:

MRIETLDFSKFHVGTDAERYEFSTALLTG FANAGFIKLINHGFSQEEISQLFEENRRFFD
LTDSIKAQIANEDGPKPQRGWSAVGA EKTGLLNTGGKTNLT KPDI EAPQDAKEHFDIGP
SEDTEFPNKWPDNELIPGFQPWLESFYERSRYISFALMEALEIAMHLPKGAFIQKCCQH
ASELRLNHYPKITVKT LQGKTSRIWPHTDFGVITLLAQDDVGGLEIQDKDNPTNFLPV
SREDVSELVNVNIGDTLERWTNGFLKAGLHQVTPREIVNQSTETVRPRRSIAFFLKAHR
QMSVGPLPQFVAEKTPAKYEDITALAYQQRRTAIVY

Codon-optimized NHI 105 (GloM) sequence:

ATGTATAAAATTTCTTCGCCGGGTACTACGTGGAAATGATAAAGACGTTGAGGCG
CTGGCCGAGGCTGCTACTACGCAGGGGTTTCTTGAATTGGAACCTGGATTGTATGGA
AGCGAAAGCGCTGCAGAAAGATGTAAATTTCTTGAATCATTTGCCGAATCAATACTT
GATTCCCCCGAAGATGTAAAGCAGCGTATCATTTTACAAAACCGGTGCTTTTCGA
ACTACTGGTTTTAAACCGCTGGGGAGTGAGGAAGGTGCGAAAGCAGGAAATCCAG
ACGGCTTTGAATTCTTTTTCTGCCCAAAGGAGATATTACTTTCTGAATTTGAGA
ACAGCTGAATTGTCCGCCACTGGCGATGTCGAATATTGATACGTTAACAGACTGTTT
CAAACATTATGAAAGAACCGCCGAGATGCTTTTACAAAGGCTGACAGAAGGTTTAA
ACTGGGAAACGAGCTCCTGAATGCTCACAACACCAGCCTGCCCTGCGTAACCAATA
TGGGTCTGATCCGGTATCCACCCAGCCGAAAGAATCGGGGAATTTCCGGTCATATC

GCACACACCGATGTCGGGAGTCTGACCATTCTTGCAGCTACCCAGCGTGGTCTTCA
GACACTGGATAATATTACACAAAAATGGATCTGGGTCGATCCCAGTGATGAATGCCT
GTTCTGTCAGTTGGGAGATTCAATTGAAGTTTCTAAGCCGCGGTAAAATCCTGCCCT
CCTTGCACAGAGTTTTGCCGTCTGATGTTGCCCCCGAAGCAACCAAATATACAATCG
CCTATTTTCTTCGTCCGAACGAAGAAGCCGAGATCACAAGCGATGATGGGAAAGTG
TGGCTGTATAAAGATTACCAATTGCCGAAAATTTGATGCCTTCGCACGTCCGCTGGGT
TACCGTCCGGATGGTGAAGAATCACTTATCTCATTGCGCGACTATACGGGTGTCGAG
TAA

NHI 105 (GloM) protein sequence:

MYKISFAGLLRGNDKDVEALAEAATTQGFLELELDCMEAKALQKDVKFLESFAESILDS
PEDVKAAYHFHKTGRFRTTGFKPLGSEEGAKAGNPDGFEFFFLPQKEILLSEFREQLN
CPPLAMSNIDTLTDCFKHYERTAQMQLLQRLTEGLKLGNELLNAHNTSLPCVTNMGILRY
PPQPKESGNFGHIAHTDVGSLTILAATQRGLQTLDNITQKWIWVDPSECLFVQLGDSL
KFLSRGKILPSLHRVLPDVAPEATKYTIAYFLRPNEEAEITSDDGKVWLYKDYHCRKFD
AFARPLGYRPDGEESLISLRDYGVE

Codon-optimized NHI 106 (GloE) sequence:

ATGGATTATATTAACAGGCGGAAAGCACCCAATTGTCGTCTCTGTCACTGTCTAGG
CTGGAAGGTAATAACGCAGAGGAGTCCAAACGTCTGTTAGAAGCATGTGCGCAGGA
TGGCTTCTTCTACTTAGATCTGAGAGACCACAAACAGTTATTGGTGGATTATGAAGC
ACTCTTAGAGATAATCAAACAGTATTTTAATGAACCACTGGATCAAAAAATGAAAGAT
GATCGTAAAAGCGACACCATAGGTTACGAACCGGTCGCGACCAGCGCGGGCGTAC
TGGACGGCCTGCCGGACTATTACGAATCTTTTAAGGTGTCCTGGAACCAATTACGC
GATCATGTGCAGGAGCTTCCAACGGTAGTTGAGACAAACATTGAAGTGTTTCGATCG
GTTTGCCAAGTATGTCCATAGCATCTTACTGATGATCCTGAGTCGTCTATCACAGACA
ATGGGTAGAAATAACGACAACCGGTTTCGAAAGTTACCATCGTGATTCTATTGCTACA
CGCACCAACCTTACATTTCTGAAGTATCCCAAACAAGACACGACAGAGCACGGCGT
CGGGCATAACAAACACACCGATGTGGGAACCTCACATTCCTGCTTTCCGGTCAGC
GCGGGCTTCAGAGGCTGACGCCTGAGGGGTGGTGTACGTGGAGCCAAGATCTG
GCTTTGCTGTTGTAAATGTTGGAGATAGTTTACGGTTCCTGTCTGACTGCGTACTTA
GCTCAGTTATTCACCGCGTTTTTGCCGGTGGGCGCGCATCAGACCGAGGATCGTTAT
ACCCTGGCCTATTTTTTACGTCCTGAAGATGACGCCGTATTCAAGGACATTAACGGG
AATCTGGTTAGCGCGCGCAGCTGGCATGACCGGAAGTTCGATCATTTCCGCGCGA
GCCATAATCAGCAGAAAAATGATACAATCTTGATGGGCGGTATGGAAGAAAATCAAA
AGTTTTTACAGTATAAATTTACAGGCTTGA

NHI 106 (GloE) protein sequence:

MDYIKQAESTQLSSLSLSRLEGNNAEESKRILLEACAQDGGFFYLDLRDHKQLLVGYEALL
EIKQYFNEPLDQKMKDDRKSDTIGYEPVATSAGVLDGLPDYYESFKVSWNQLRDHVQ
ELPTVVETNIEVFDRFAKYVHSILLMILSRLSQTMRNNDNRFEYSYHRDSIATRTNLTFL
KYPKQDTTEHGVGHNKHTDVGTLTFLLSGQRGLQRLTPEGWCHVEPRSGFAVVNVGD

SLRFLSDCVLSSVIHRVLPVGAHQTEDRYTLAYFLRPEDDAVFKDINGNLVSARSWHDR
KFDHFRASHNQQKNDTILMGGMEENQKFLQYKFQA

Codon-optimized NHI 107 (Diox4) sequence:

ATGGCCCCTACAAAAGACTCTGTTATCCATATGGGTGCCGAGTCCTGGGACGAAATA
AGCGAATTTGTCACCAAAAAAGGTCATGGGGTGAAAGGATTGTCTGAACTGGGCAT
TAAGACATTGCCTAAACAGTTTCATCAGCCGCTGGAAGAACGCTTTAGTGAGAAGAA
AATCCTGGAACGTGCAAGCATACTCTTATTGATATGTCTAAATGGGATTCACCTGAA
GTCGTGAAATCCATATGTGATGCGGCGGAGCATTGGGGATTTTTTTCAGATTGTGAAC
CATGGCGTGCCATTAGAAACACTGCAGCGTGTGAAAGAAGCGACCCATAGATTCTT
CGCGCTACCAGCAGAAGAGAAAAATAACAGCAAAGAGAACAGCCCTATTAACAA
TGTCCGCTTTGGTTCAAGCTTTGTCCCGCATGTGGAAAAAGCCCTGGAGTGGAAG
ATTTTTTAAGTATGTTTTACGTTAGCGAGGAAGAGACGAATACATATTGGCCTCCGAT
TTGCCGCGATGAGATGCTGGAGTACATGCGCTCATCTGAAGTGTTAATAAAACGGCT
CATGGAAGTTCTGGTCGTTAAAGGCCTCAAAGTAAACAAATTGATGAGATACGTGA
GCCGATGCTTGTGCGATCGCGTCGTATCAACTTAAATTATTATCCGAAATGTCCTAAC
CCGGAATTAACCTTGGGGGTGGGTCGGCATAGCGATATTTCAACATTTACGATTCTC
CTGCAGGATGAAATTGGCGGCCTTCATGTTCTGTAAATTGGATGATACAGGTAATACT
TGGGTTACGTTACGCCGATCTCAGGTAGCTTAATTATTAATATCGGAGACGCACTG
CAAATTATGTGCAACGGTCGTTATAAGAGCATAGAACATATGGTGGTTCGCAAATGGC
ACCCAAGATCGGATTTCCGTCCCATTTTGTGAATCCAAAACCCCAGGCAATTCTC
TGCCCGTTCCCGGAAGTTTTAGCAAATGGGGAAAAGCCGGTATACAAGCCAGTGTT
GTGTAGCGATTATTCCAGGCACTTTTATACTAAACCACATGACGGTAAAAAAACCGTC
GACTTTGCCCTAATGAATTAA

NHI 107 (Diox4) protein sequence:

MAPTKDSVIHMGAESWDEISEFVTKKGHGVKGLSELGIKTLPKQFHQPLEERFSEKKIL
ERASIPLIDMSKWDSPEVVKSICDAAEHWGFFQIVNHGVPLETLQRVKEATHRFFALPA
EEKNKYSKENSPINNVRFGSSFVPHVEKALEWKDFLSMFYVSEEETNTYWPPICRDEM
LEYMRSSEVLIKRLMEVLVVKGLKVKQIDEIREPMLVGSRRINLNYPKCPNPELTGVLG
RHSDISTFTILLQDEIGGLHVRKLDDTGNTWVHVTPISGSLIINIGDALQIMSNGRYKSIEH
MVGANGTQDRISVPLFVNPKPQAILCPFPEVLANGEKPVYKPVLCSDYSRHFYTKPHD
GKKTVDFAALMN

Codon-optimized NHI 108 (Fum3p) sequence:

ATGAACAAGGAAAAAGTACCGCAGAACGCCGTACCGAATGGTAGGACGAAACTCC
GTCAGGTGACGTCTGCAACTCCTCTCGATGAAGTTTTTCAATACTGGGAGGAAGAC
GGTGCCATTGTAATAAAAGGCCTGTTGACTTCGGCCCAGGTTGAACAGCTGAACCA
GGAGATGGGCCCAATCCTGCAGAAAGTTGCCATTGGAGGCCATGCATCAGATGTTT
GGTTACAGAATTTTCATGGGATGAAGACGAAACGTGCAGGCGATCTGACCAATAAC
AGTGCTGTTTTTCGGGATCATTTACTAGATAATGACTTTATTCATGCCGTCTCTCAAC
GTTGCTTCGCCTATAGGGGAAAAATGGGCCCGGATGCGTATTGGTTAGGTTCCGCG
AGCACTATCCATGTTGGCCCGGGTCAAAAACCACAAACCCTCCATCGTGATCTTGG

CAGCTATCCTATCTTTTGGATGCTAGGACCTCAGGGCCCCGGAATCCCAGATTAACCTT
TTTAGTGGCAACAACCTGATTTACAGAGGCTAATGGCGCTACGAGGATTATCCCCG
GCTCACATAAGTGGGAATTTAATCAGCATGGCGATCGCGATATGACAATCCCGGCAG
AAATGAAAGCAGGCGATTGTCTGCTGATTTACAGGTAAGGTTATTCATGGAACCGGAG
GAAACAAAACGGATCAGGAGCGCGGCTGCCTCGCCGTGACGATGTGCGCGAATTT
CCTAGCACCTGAGGAGGCACATCCGTTTATTGTATCTATGGGTACCGCTAAAAAACT
TCCTGTCCGTTACAGCGATGCTTGGGCTTTCGGTCACAGTGGCCACAGAGTTCTC
CGGGCTTATGGACGAAAGATTATTCTGAGCTGGCTTTCGACTTAGGACTGGATGATT
AA

NHI 108 (Fum3p) protein sequence:

MNKEKVPQNAVPNGRTKLRQVTSATPLDEVFQYWEEDGAIVIKLLTSAQVEQLNQEM
GPILQKVAIGGHASDVRLQNFHGMKTKRAGDLTNNSAVFRDHLLDNDFIHAVSQRCFAY
RGKMGPDAYWLGSASTIHVGPQKQPQTLHRDLGSYPIFWMLGPQGPESQINFLVATTD
FTEANGATRIIPGSHKWEFNQHGDRDMTIPAEMKAGDCLLISGKVIHGTGGNKTDQER
GCLAVTMCANFLAPEEAHPFIVSMGTAKKLPVRSQRCLGFRSQWPQSSPGLWTKDYS
ELALHLGLDD

Codon-optimized NHI 109 (PODA) sequence:

ATGGAAACGGCGAAACTTATGAAACTGGGCAACGGTATGTCAATTCGGTCGGTTCA
GGAACCTGGCCAAATTGACGCTGGCTGAAATACCGTCGCGCTATATTTGCACCGTTG
AGAATTTACAGCTGCCGGTAGGTGCATCTGTTATTGATGATCATGAGACCGTTCCGG
TAATCGATATAGAAAACCTTATTAGTAGTGAACCGGTACAGAAAAGCTTGAACCTGGA
CCGCTTACATTCAGCGTGTAAGAATGGGGCTTCTTCCAAGTGGTGAATCACGGCG
TTGATACTTCATTAGTGGATAATGTTAAAAGCGATATTCAAGGTTTTTTAATCTATCGA
TGAATGAGAAAATCAAATACGGTCAGAAGGATGGGGATGTTGAGGGGTTTCGGACAG
GCATTCGTAGCAAGTGAAGACCAGACTTTGGATTGGGCGGATATTTTCATGATCCTG
ACTTTGCCGCTGCATCTGCGGAAGCCCCACCTGTTTAGTAAACTGCCGTTACCCCTT
GCGCGAGACCATCGAATCCTATTCGAGTGAAATGAAAAAATTATCGATGGTCCTGTT
CGAAAAAATGGAGAAAGCCTTACAGGTTACAGGCGGTTGAAATCAAAGAAATTTCTG
AAGTCTTTAAGGACATGACCCAGGTAATGCGCATGAACTATTATCCACCTTGCCCTC
AACCGGAATTAGCAATAGGCCTTACACCGCATTCTGATTTTGGCGGTCTCACTATTC
TTCTCCAGTTAAATGAAGTCGAAGGCCTGCAAATCAAGAATGAAGGCCGGTGGATC
AGCGTTAAACCCCTTCCTAATGCATTTGTAGTAAATGTTGGAGACGTTCTGGAAATC
ATGACGAATGGTATGTATCGTTCGGTAGATCATCGCGCGGTGGTGAACCTCTACCAAA
GAACGCTTGAGTATTGCTACATTTTCATGATCCCAACCTTGAATCAGAAATTGGCCCA
ATCTCTAGCCTTATTACACCAAATACGCCAGCACTCTTTCGTAGTGGCAGCACATATG
GCGAACTGGTTGAAGAGTTCCATAGCCGCAAGTTGGACGGTAAATCCTTTCTAGATA
GCATGAGAATGTAA

NHI 109 (PODA) protein sequence:

METAKLMKLGNGMSIPSVQELAKLTLAEIPSRYICTVENLQLPVGASVIDDHETVPVIDIE
NLISSEPVTEKLELDRLHSACKEWGFFQVVNHGVDTSLVDNVKSDIQGFFNLNMNEKIK

YGQKDG DVEGFGQAFVASEDQTL DWADIFMILT LPLHLR KPHLFSKLPLPLRETIESYSS
EMKKLS MVLF EKMEKALQVQAVEIKEISEVFKDMTQVMRMNYYPPCPQPELAIGLTPH
SDFGGLTILLQLNEVEGLQIKNEGRWISVKPLPNAFV VNVGDVLEIMTNGMYRSVDHRA
VVNSTKERLSIATFHDPNLESEIGPISSLITPNTPALFRSGSTYGELVEEFHSRKLDGKSF
LDSMRM

Codon-optimized NHI 110 (BX6) sequence:

ATGGCCCCGACCACAGCGACGAAAGATGATTCTGGATATGGCGATGAACGGCGCA
GAGAACTCCAGGCATTCGACGACACAAAATTGGGTGTCAAGGGATTAGTGGATAGC
GGAGTGAAAAGCATCCCTAGCATCTTTCATCACCCACCGGAAGCTCTGTCCGATATT
ATCTCTCCCGCTCCACTTCCGTCATCGCCTCCAAGCGGGGCCGCGCCATTCCGGTTGT
GGATCTTAGCGTCACGCGCAGGGAAGATTTGGTCGAGCAGGTGCGGCATGCGGCT
GGCACCGTTGGCTTCTTTTGGTTAGTAAACCATGGCGTCGCGGAGGAACTGATGG
GGGGCATGCTCCGCGGGGTACGCCAGTTCAACGAGGGACCGGTAGAAGCAAAGC
AAGCACTGTACTCAAGAGATTTAGCTCGTAACCTGCGATTTGCGTCGAACTTCGACC
TGTTCAAGGCGGCCGCCGCGCAGATTGGCGTGACACACTGTTCTGCGAAGTGGCACC
GAATCCACCACCCCGTGAGGAATTGCCTGAACCCCTTAGGAACGTGATGCTGGAAT
ATGGTGCTGCGGTTACGAAACTGGCCAGGTTTGTATTTGAACTACTTTCCGAGAGT
CTGGGAATGCCATCGGATCACTTGTACGAGATGGAATGTATGCAGAATCTGAATGTC
GTCTGCCAGTATTATCCCCCCTGTCCGGAACCACACCGCACAGTGGGCGTAAACG
CCATACGGATCCGGGTTTTTTTCACAATTTTACTTCAAGATGGCATGGGTGGTCTTCA
AGTGCGTCTTGTAATAACGGCCAGTCAGGTGGCTGCTGGGTGCATATAGCCCCTA
GACCAGGTGCTCTCATGGTTAATATAGGCGATCTGCTTCAACTGGTCACAAATGATC
GCTTCCGCGAGTGTGGAACATAGGGTGCCCTGCAAACAAATCAAGTGATACCGCCCGC
GTGTCGGTGGCTTCCTTCTTTAACACCGACGTGCGGCGCAGTGAAAGAATGTATGG
TCCTATTCCGGATCCGAGCAAACCGCCTCTCTATCGCAGTGTACGAGCTCGTGATTT
CATTGCAAAATTCAACACTATAGGGTTGGACGGCAGAGCCTTGGATCATTTTCGGCT
TTAG

NHI 110 (BX6) protein sequence:

MAPTTATKDDSGYGDERRELQAFDDTKLGVKGLVDSGVKSIPSIFHHPPEALSDIISPA
PLPSSPPSGAAIPVVDLSVTRREDLVEQVRHAAGTVGFFWLNVHGVAEELMGGMLRG
VRQFNEGPVEAKQALYSRDLARNLRFASNFDLFKAAAADWRDTLFCVAPNPPPREEL
PEPLRNVMLEYGAAVTKLARFVFELLSLGMPSDHL YEMECMQNLNVVCQYPPCP
EPHRTVGVKRHTDPGFFTILLQDGMGGLQVRLGNNGQSGGCWVDIAPRPGALMVNIG
DLLQLVTNDRFRSVEHRVPANKSSDTARVSVASFFNTDVRRSERMYGPIPDPSKPLY
RSVRARDFIAKFNTIGLDGRALDHFRL

Codon-optimized NHI 111 (BX13) sequence:

ATGGCTCCCACGGCAGCAAAGGACAGCGGTTCCGGCCGACAGGTGGCGCGAGGTT
CAGGCTTTCGAAGATTCCAAGTTGGGCGTGAAGGGGTTAGTTGATTCAGGCGTCAA
ATCAATTCCGGCGATGTTTCATCACCCCTCCTGAATCCCTGAAAGATGTCATCTCGCC
TCCGGCCTTGCCGTCATCTGACGATGCGCCGGCGATTCTGTTGTTGATCTGTCCG

TAGCTCGCCGTGAGGATCTGGTCGCACAGGTAAAGCATGCTGCGGGAACAGTTGG
CTTCTTTTGGGTTGTTAATCATGGAGTCCCGGAGGAATTGATGGCGTCTATGCTTAG
TGGCGTACGCCAATTCAACGAAGGGTCTCTGGAAGCTAAACAAGCTTTATATAGTAG
AGATCCGGCCCCGCAACGTGCGTTTCGCTTCGAACTTCGATCTTTTTGAAAGTGCGG
CGGCCGACTGGCGAGATACTCTATTGCAAAATTGCTCCTGATCCGGCTCCTCGC
GAATTAGTACCCGAGCCACTACGTAACGTCATGATGGAATATGGAGAAGAATTAATA
AACTGGCACGTAGCATGTTTCGAGCTTCTGTGCGAGTCTTTAGGCATGCCTAGTGAT
CATCTACATAAAATGGAATGTATGCAACAACCTTCATATTGTCTGCCAATATTACCCACC
GTGCCCTGAACCGCATTAACTATCGGGGTTTCGCAACACAGTGACACCGGCTTTT
TCACTATCTTGCTCCAGGACGGTATGGGAGGTCTACAAGTACTGGTCGATAGAGGA
GGTGGCCGTCAGACCTGGGTTGACGTAACACCGCGCCCTGGTGCCCTTATGGTTA
ATATGGGTAGTTTCTCCTCAGTTGGTCACTAATGACCGCTACAAAAGCGTAGACCATA
GGGTGCCAGCTAACAAATCAAGTGACACAGCTCGGGTGTGAGTTGCTGCCTTCTTC
AACCCGGATGAGAAGAGAACGGAAAGGCTCTATGGCCCGATCCAGATCCAGCA
AACCTCCTTTATATCGTAGCGTTACCTTTCCGGATTTTATCGCCAAATTCAATAGTATT
GGTCTGGATGGTCGTGTTCTGGACCATTTTCGACTTGAAGACGATGGTCCGACCCG
ACTGGCCGCACCTGCCCATCACGTGTAA

NHI 111 (BX13) protein sequence:

MAPTAAKDSGSADRWREVQAFEDSKLGVKGLVDSGVKSIPAMFHHPPESLKDVISPPA
LPSSDDAPAIPVVDLSVARREDLVAQVKHAAGTVGFFWV/VNHGVPEELMASMLSGVR
QFNEGSLEAKQALYSRDPARNVRFASNFDLFESAAADWRDTLYCKIAPDPAPRELVPE
PLRNVMMMEYGEELTKLARSMFELLSESLGMPSDHLHKMECMQQLHIVCQYYPPCPEP
HLTIGVRKHS DTGFFTILLQDGMGGLQVLVDRGGGRQTWVDVTPRPGALMVNMGSFL
QLVTNDRYKSV DHRVPANKSSDTARVSVAFFNPDEKRTERLYGPIPDPSKPPLYRSVT
FPDFIAKFNSIGLDGRVLDHFRLEDDGPTRLAAPAHV

Codon-optimized NHI 112 (HPPD) sequence:

ATGTGTTTATCTCTGGCCAGCACCGCCCAGCGCAATACCCAGTTTAGAAGCCGCGT
CCTGGTACTTGCTGAGCTTGTTAAAAGTATGGGTCATCAGAACGCCGCGGTGAGTG
AGAATCAGAATCATGATGATGGCGCAGCAAGCTCGCCCGGCTTTAAGTTAGTGGGG
TTTAGCAAATTTGTCCGTAAAAATCCCAAATCAGATAAATTAAGGTTAAACGCTTTCA
TCACATTGAATTTTGGTGTGGAGATGCGACAAATGTTGCCCGGAGATTTTCCTGGG
GTTTGGGTATGCGCTTTTCGGCTAAAAGTGACCTGAGTACGGGAAATATGGTTCAC
GCAAGCTATCTTCTGACCAGCGGAGACCTGCGATTTTATTTACTGCTCCATATTCTC
CATCTCTTAGCGCCGGCGAAATAAAACCGACAACGACCGCCTCAATTCCGTCTTTC
GACCATGGGTCTTG TAGATCGTTCTTCTCCTCTCATGGCCTGGGAGTGCGGGCCGT
CGCGATTGAGGTTGAAGACGCTGAATCCGCTTTCTCGATATCAGTTGCAAATGGGG
CTATTCCGAGCTCACCGCCTATCGTGCTGAATGAAGCAGTGACCATCGCTGAAGTC
AACTATACGGTGATGTTGTCCTGCGTTATGTAAGTTATAAAGCAGAGGATACGGAAA
AGAGCGAATTCCTGCCGGGCTTTGAGCGTGTAGAAGATGCCAGTTCTTTTCCACTC
GATTATGGTATTCGCCGACTGGATCACGCGGTGGGCAATGTTCCCGAACTGGGTCC
AGCCCTTACCTATGTGGCGGGCTTTACGGGTTTTTCATCAGTTTGCTGAGTTTACCGC

CGACGATGTGGGGACCGCGGAAAGTGGTCTGAACTCGGCGGTTCTTGCAAGCAAT
GATGAAATGGTCCTGCTTCCGATAAATGAGCCTGTGCATGGGACCAAGCGTAAGAG
TCAGATCCAAACATATCTAGAGCACAATGAGGGAGCTGGGCTGCAACACCTGGCCC
TTATGTCCGAAGATATTTTTAGAACTTTACGGGAAATGCGCAAGAGGAGTAGTATAGG
TGGTTTTGATTTTATGCCTTCGCCTCCCCCTACTTACTATCAAACCTAAAAAACGT
GTGGGGGATGTGCTGTCTGATGATCAGATAAAAGAATGCGAAGAGCTGGGTATACT
GGTTGACCGGGATGATCAGGGTACTTTACTACAGATCTTCACTAAGCCGCTTGGTC
GTCGCTACTTATAA

NHI 112 (HPPD) protein sequence:

MCLSLASTAQRNTQFRSRVLVLAELVKSMGHQNAAVSENQNHDDGAASSPGFKLVGF
SKFVRKNPKSDKFKVKRFHHIEFWCGDATNVARRFSWGLGMRFSKSDLSTGNMVHA
SYLLTSGDLRFLFTAPYSPSLSAGEIKPTTTASIPSFHDHGSCRFFSSHGLGVRAVIEVE
DAESAFSISVANGAIPSSPPIVLNEAVTIAEVKLYGDVVLRYVSYKAEDTEKSEFLPGFER
VEDASSFPLDYGIRRLDHAVGNVPELGPALTYVAGFTGFHQFAEFTADDVGTAEGLNS
AVLASNDEMVLPPINPEVHGTRKRSQIQTYLEHNEGAGLQHLALMSEDFRTLREMRKR
SSIGGFDFMPSPPTYYQNLKKRVGDVLSDDQIKECEELGILVDRDDQGTLQIFTKPL
GRRYL

Codon-optimized NHI 113 (KthP) sequence:

ATGACAACGGCCGATGAATTCGCCTTAAGCGACGAACAGCTGGACTCCTTTTCGACG
CGACGGTTTTTTAGGCCCTTTGACTATCTATCCTCCGGATGAAATGGCGGAACTCTG
GAAATCAGTCCAGCGTCAAGCATTAGATCGAACACATGCAGCTTATCCGGAAGTGG
ATGCGGGTATGGGCGCCCCCTAATATATTCAATTATGATAGACATCTGGATATAGATCTG
TTGGCAGAGCACGCTTGTCATCCTAAAATTGTTGGCGCGGTTGGCTCAATTCTGGG
CCGCGACCTACTGTGTTGGAGGTCAGAATTCTTCCCAAATATCCTGGTGATGAGG
GCACAGATTGGCATCAGTCAGATACCTTCGCAAATGCCTCCGGTAAGCCACAATTG
CTATGGCCGGGTGAATCCGAGGAATCTTTCGGCGCCGGCACGATCACGGTGTGGA
CCGCCTTTACAGACTCAACCCGTGAAAACGGTTGTCTTCAGCTCATTCCGGGAACA
CATAATAAAATGAATTATGATGAAACGAAAAATATGGATTATGACCAAGAACGTATCAA
TGCCTCCGTAAAAGATGGTGTAACCGTGGTTTCTTTGGGTATGACTATCGGCAGCT
CCAAATTGATCCAGATTGGACTCCGGATGAAGATGATGCCTTTTCGTTAGTCATGGA
AAAAGGACAGTGTGTTATATTCTGGTCTACACTAATGCATGCAAGTCTGCCGAACAC
TAGTACGGGCCGGGATTACCGTATGGGTTTTGCTACGCGTTACGTTCTACGGCGG
TTCGCGTGTATCCGGATACAGATCATATTGAAGAGTACGGTGGGAATATCTCTCTAGA
TCGTTGGGGAGCTATGTTGGTGAGCGGCCGTGACGAACACGGCCATAATAAAGTG
GTGGATCGGACGCTCCGTGGGACTCCAGTGGGGCCTGCAGCGGCTAGACGTCCG
TAA

NHI 113 (KthP) protein sequence:

MTTADEFALSDEQLDSFRRDGLGPLTIYPPDEMAELWKSQVRQALDRTHAAYPEVDA
GMGAPNIFNYDRHLIDLLAEHACHPKIVGAVGSILGRDLLCWRSEFFPKYPGDEGTD
WHQSDTFANASGKPQLLWPGEESESFAGAGTITVWTAFTDSTRENGCLQLIPGTHNKM

NYDETKNMDYDQERINASVKDGVKRGFFGYDYRQLQIDPDWTPDEDDAFSLVMEKG
QCVIFWSTLMHASLPNTSTGRDYRMGFATRYVPTAVRVYPDTHIEEYGGNISLDRWG
AMLVSGRDEHGHNKVVDRTLGRTPVGPAAARRP

Codon-optimized NHI 114 (WelO5) sequence:

ATGAGCAATAACACAGTTTCTACAAAACCGGCGCTACATTTTTTAGACATCAACGCTA
CTGAAGTAAAAAATATCCGACTGCCATACAAGATATTATTATTAACCGTAGCTTCGAT
GGGATGATAATTCGCGGAGTCTTCCCCCGGGATACCATGGAACAGGTGGCACGCT
GCTTGGAGGAGGGTAACGATGGAGGGATGAAATCAATTCTTAATAAGAACGAAGAAT
TCGGCACCAAAGTTGCCCAGATTTATGGCCACGCCATTGTGGGACAGAGCCCGGA
TTTAAAGATTATTTTGCATCGTCGGCAATCTTTCGCCAGGCTTGCCGAACGATGTTT
CAGGGAAGCCCTGACTTTGAGGAGCAGGTGGAATCAATATTTTATTCTCTGTCTGG
GTTGCCCGGTGGAAATTCCAACCTGGCCCAGAAGGCCAAACATATACGCCTGCAACTA
TCCGTCTTTTACTGGAGGGGCGCGAGATCGCCGTGCACGTCGGTAACGATTTCTTA
CTCATGCCGGCTGCCAATCATCTGAAAACACTGCTGGATTTAAGTGATCAACTGTCTG
TACTTTATACCATTGACCGTACCTGAGGCAGGTGGGGAATTAGTCGTTTATTCTCTG
GAATGGAACCCACAGGAAGCAAGCAAATACGCACAAATGCAGGAGTATATGGATGA
TGTTGAATTCAAGATTAAGAGTAACCAGAGCCAGAGCGTAGCCTATGCACCGGGGCC
CTGGTGACATGTTACTCTTTAATGGGGGCCGCTATTACCATAGAGTTTCAGAAAGTTAT
TGGAATTCTCCTCGGCGTACAATAGGCGGTTTCCTGGCATTCTCGAAACAACGAG
ATAAGATATACTACTGGTCTTGA

NHI 114 (WelO5) protein sequence:

MSNNTVSTKPALHFLDINATEVKKYPTAIQDIIINRSFDGMIIRGVFPRDTMEQVARCLEE
GNDGGMKSLNKNEEFGTKVAQIYGHAIVGQSPDLKDYFASSAIFRQACRTMFQGS
PDEEQVESIFHSLSGLPVEIPTGPEGQTYTPATIRLLLEGREIAVHVGNDFLLMPAANHLKT
LLDLSDQLSYFIPLTVPEAGGELVVYSLEWNPQEASKYAQMQEYMDDVEFKIKSNQSQ
SVAYAPGPGDMLLFNGGRYYHRVSEVIGNSPRRITGGFLAFSKQRDKIYYWS

Codon-optimized NHI 115 (AmbO5) sequence:

ATGAAAAACAACACTCGTAATTTCAATATTGGCAACGTGATCCACGGTAAACGGCTG
ATTATCACGGAAGAAAAAATGATGAGTAATAATGCCGTGTCGACTAAGTCAGCACTG
AATTTTCTGGACATTAATGTAACGGAAGTTAATAATTATCCCACTGCTATTCAGGATAT
TATTATTGATCGTCGTTTTGATGGAATGATCATAACGGGGGGTTTTGCCCTTAGATAGC
ATCGAACGTGTGATCCGTGCCTGGAAGACGAAGATGAAGGGGGTATGAAACTCAT
TTTTAATAAAAAACGAAGAGTTTGGCACGAAGGTTGCACAGATTTATGGTCATGTTATC
GTTGGTCAGAGTCCAGACCTAAAAGACTACTTTGCGAGTTCCGCAATTTTTAGACAA
GCTTGTAGAGCCCTGTTTCAGGGTAACCCAGATTTTGAAGAACGCGTCGAATCCGT
GTTTCATAGCCTGTGTGGGTACCTGTAGAAATCCCCACGGGCCAGAGGGTCAAT
CATATACCCAGCCACTTTACGCCTCTTGACCGAAGGACGCGAAATTACTGTCCATG
TGGGTAACGATTTCTGCTTATGCCTGCTTCAGAACATTTAAAGACACTGTTAGATTT
TTCCGACCAGCTGAGCTATTTTATCCCTTTATCCGTCCCACAAGCTGGGGGCGAATT
AGTCGTCTATAATTTGGAATGGAATCCTGAGCAGGCTGAACAGTCTGGTGACCTGC

ACAAGTACATGAACGACGCAGACAGCCGCTTTCAAAGCCAACAAAGCCAGAGTGTT
GCTTTTGC GCCCGGACCAGGTGACATGATCCTGTTCAACGGTGGCCGCTATTATCA
TCGTGTTAACCAGGTGATCGGAAATTCGCCGAGACGCACCATTGGTGGTTTCCTGG
CTTTTAGCAAAGAGAGAAACAAAATTTACTATTGGTCTTGA

NHI 115 (AmbO5) protein sequence:

MKNNTRNFNIGNVIHGKRLIITEEKLMSNNAVSTKSALNFLDINVTEVN NYPTAIQDIIIDR
RFDGMIIRGVLP LDSIERVIRLEDEDEEGGMKLIFNKNEEFGTKVAQIYGHVIVGQSPDL
KDYFASSAIFRQACRALFQGNPD FEERVESVFHSLCGLPVEIPTGPEGQSYTPATLRLL
TEGREITVHVGNDFLLMPASEHLKTL LDFSDQLSYFIPLSVPQAGGELVVYNLEWNPEQ
AEQSGDLHKYMN DADSRFQSQQS QSVAFAPGPGDMILFNNGGRYYHRVNQVIGNSPR
RTIGGFLAFSKERNKIYYWS

Codon-optimized NHI 116 (DAO) sequence:

ATGGTCGAAATTCCAGCTATCGATCTGCGCCTTGCGGGTGGCGGCGGTGGCGCGG
AAGAGACCGCACGCCTTCGCGATGCCTGTGCCCGTTTAGGATGTTTTCTGTGTCTCC
GGGCATGGCGTACCGCCGGGCCTGCAGGCTGAGATGAAAGCGGCCGTCAGGGCA
TTGTTTCGATCTGCCAGACGACGCAAAAAGGCGTAATGCGGATATAATTCCTGGTAGT
GGGTATGTCCCTCCTGGTACCGCCAACCCTCTATACGAAGCCTTTGGGCTTTGTGA
CGCTGCCGCTCCTGCTGATGTAGATGCGTTCTGCGCAAGACTCGATGCACCGCCG
CACGTCCGGGAAACCGTGAAAGCATACGCGGAACGTATGCATTCCCTCATTGTTGA
TGTCGCTGGAAAAGTAGCTGCGAGTTTAGGTCTCCACGGTGCCTCTTTTCAGGATT
GGCCTTGTCAGTTTAGAATGAATCGCTATAACTATACACAGGATTCAGTTGGCTCAC
CGGGCGTTCAAGTTCACACTGATTCCGGTTTTCTGACAGTTCTGCAGGAGGATGAA
TGTGTGCGGAGGGCTTGAAGTCCTAGATCCGGCGGCAGGCGAGTTTGTACCGGTAG
ATCCGCTGCCGGGATCTTTTGTGGTGAACGTTGGGGATGTTGGTCAAGCATGGTCC
AACGGTCGGCTGCACAATGTTAAGCATCGTGTGCAGTGTGTGCGCCGCTGTCCCAC
GGGTCAGTATTGCTATGTTTTTGTGGCGCCAAAAGATGACACGGTTAGTGACCCG
GGGGAAC TTGTAGATGGTGAGCACCCGCGAAGGTATCGGGAATTTAAATATGACGA
CTACCGCCGTTTACGCCTCTCCACCGGGGAGCGTGCAGGTGAAGCACTAGCGCGT
TTGGCCGCATAA

NHI 116 (DAO) protein sequence:

MVEIPAILRLLAGGGGGAEETARLRDACARLGCFRVSGHGVPPGLQAEMKAAVRALFD
LPDDAKRRNADIIPGSGYVPPGTANPLYEAFGLCDAAAPADVDAFCARLDAPPHVRET
VKAYAERMHSLIVDVAGKVAASLGLHGASFQDWPCQFRMNRYNYTQDSVGS PGVQV
HTDSGFLT VLQEDEC VGGLEVLDP AAGEFVPVDPLPGSFVVNVGDVGQAWSNGRLHN
VKHRVQCVA AVPRVSIAMFLLAPKDDTVSAPGELVDGEHPRRYREFKYDDYRRLRLST
GERAGEALARLAA

Codon-optimized NHI 117 (M2H) sequence:

ATGGTAGCACCTAGCCGCCTACCGAGTCATGAAGAACAGAGCGCAGCGGCAGCAG
CCGATGGCAGCGCGACACCCTCACAAGGAATTCGGTGGTTGATCTGGGGGTTCT

GATTAACGGTGCGGCTGATGAACGGAGCCGTGCTATTCGTGATCTAGGTCGCGCCT
GTGAAGACTGGGGCTTTTTTCATGGTTACCAACCATGGTGTACCGGAGGCCTTACGA
GAAGCGATCATGGATGCATGCAAAGAACTGTTCCGTTTGCCTTTGGAGGAAAAGAA
AGAATACATGCGTGCAAACCTATGGATCCTATAAGGATTGGGACCGGGTTTTATTCT
GTCGTTGACGCAGTGCCCTGTCGCAGAGACTATCTCAAATGTTCTCACATCCCGA
GTTTCACTGTCCGGAGAAACCGGGCGAAGTTACGGGAAATTGCTACTGAATATGCGA
CCTGCACCCGCGCCTTGCTGCTGGAATTAACCAAAGCTATATCTGAATCACTTGGCT
TGGCAGGGGGCCGCCTGTCGGAGGGCGCTAAACCTCGAGTCGTGCTTTCAGATCCT
TGTTGGCAACCATTATCCGGCTTGTTCAAGACCCGATGAACAAGCAATGGGGTTGA
GCGCGCACTCTGATCATGGGTACTGACCCTGCTTTTCCAGAATGGAGTGGATGGG
CTGCAGGTAAACATGATGGCGAATGGTTGCTCGCGAAACCACTGCCTGGCTCATT
TTTCGTAATCGCTGGCGATCAGCTTGAGATCGTCACCAACGGTAGATATAAAGGTGT
GCTGCATCGTGCAGTCGTCGGCGGTGAACAGTCTCGCATGAGCTTCGTGTCACTG
ATAGGTCCATGCATGGATACGGTAGTAGAGCCGCTGCCGGAATGGCAGCCGATGG
TCGTGGCCTGGAATTTCTGTTGGATCAGATACAGAGATTATATGGAATGCAACAGTC
TAATAGCATAAACGAAAAACGGCTTTAGATATCGTTCGGGTTATGCATCAAGCTGGC
TAA

NHI 117 (M2H) protein sequence:

MVAPSRGPSHEEQSAAAAADGSATPSQGIPVVDLGVLINGAADERSRAIRDLGRACED
WGFFMVTNHGVPEALREAIMDACKELFRLPLEEKKEYMRAKPMPIRIGTGIFYSVVDA
VPCRRDYLKMFHPEFHCPEKPAKLREIATEYATCTRALLLELTKAISESLGLAGGRLSE
ALNLESCFQILVGNHYPACSRPDEQAMGLSAHSDHGLLTLFQNGVDGLQVKHGEW
LLAKPLPGSFFVIAGDQLEIVTNGRYKGVLRHAVVGGEQSRMSFVSLIGPCMDTVVEPL
PEMAADGRGLEFRGIRYRDYMEMQQSNSINEKTALDIVRVMHQAG

Codon-optimized NHI 118 (EcdG) sequence:

ATGGCTTCAATCTCATACGATGGCCTGTTACGAGGCGCGGCAAAGGACATCCAGAC
CCTGACTGAAGCCTCGCTGGTGCATGGGTACTTTAATCTCGAGCTAGACTGTCCTG
AAGGTAAACAGTTAAGAGAAGATGTGCTGTTTCTGGAGTCCTTCACCAAAGAAATTT
TTGATACCCCGTCTCCCCAGAAAACCATTTATGATTTTAAAAAACTCGGCAGGTTCC
GTACTACCGGTTTCAAGCCATTGGGTATCGAAGAAGGCGCGGAAAGGTAAATCGGAT
GGTTTTGAAATGTTTATGCTACCGCAGAACGAGCTGCTTTTACCTTCCCACCAGGAT
AACTTCAATCCCCCTCGGCCGTTTTTAGTCACCGGGCAACCCTGACAAGATGTAT
GTCCAATTATGATGCGGCAAGCCAGCTGATTCTTAGACGCATTACGGAATCACTGAA
TCTGGATAATGCATTGTTGGCTGCTCACAATCCTAGTGAACCCTCAGTAACTAATT
GGGTTTTTTTACGTTATCCGCCACAGCCTGCGACTTCAGAGAATTGCGGGCATATCG
CACATACTGACGTTGGCACCCTGACGATCCTTGCAGCGACACAGCGGGGTCTGCA
GGTGATAAATTCTGAGACCCAGGATTGGACCTTTGTTGATCCGCATCCGCAAACG
AATTTCTGCTAGTCCAATTTGGAGATTGTCTGAAATTTTAAGCGGCGGTTCGTGTGG
TGCCGTCGATTCATCGCGTTATTCCGTCCGATAATCCCGAAGAAAGGGAAGGTACG
AAATATACCCTTGCATATTTTGTAAGACCTAACGAGGAAGCGGTTATCAAAGATGATC
GTGGCGAGGAATGGGTCTATGGTGACTATCACTGTCGTAAATTTGGTGCATTTGCG

CGTCCACTCAAAGAGGGGCGATCGTGACCGGATGCCAGATAGGCCTGTGGGCGAAT
ATGATATGATTAAACATTCGCAAATTTAAGGGTCTGGCTGACGGAGTCAGTGCGGCTT
AA

NHI 118 (EcdG) protein sequence:

MASISYDGLLRGAAKDIQTLTEASLVHGYFNLELDCPEGKQLREDVLFLESFTKEIFDTP
SPQKTIYDFKKLGRFRTTGFKPLGIEEGAKGKSDGFEMFLPQNELLLPSHQDKLQSP
SAVFSHRATLTRCMSNYDAASQLILRRITESLNLDNALLAAHNPSEPSVTNLGFLRYPQ
PATSENCGHIAHTDVGTLTILAAATQRGLQVINSETQDWTFVDPHPQNEFLLVQFGDCLK
FLSGGRVVPsiHRVIPSDNPEEREGTKYTLAYFVRPNEEAVIKDDRGEWVYGDYHCR
KFGAFARPLKEGDRDRMPDRPVGEYDMINIRKFKGLADGVSA

Codon-optimized NHI 119 (AniG) sequence:

ATGGCGTCTATTAGTTATGAGGGTCTTCTGAGAGGAGCAGCTAAGGACATTCACGC
CCTTACCGAAGCCGCATTAGTGCATGGATACTTTAACCTCGAGCTAGATTGTCCAGA
AGGACAACAGCTCAGACAGGATGTGTTATTTCTAGAATCTTTTACCAAAGAGATCTT
CGATACACCGTCCCCCAGAACTGTGTATGATTTTAAAAAACTTGGTAGATTTTCG
CACCCTGGTTTCAAACCACTAGGTATCGAGGAAGGGGCTAAAGGTAAGAGCGATG
GCTTCGAGATGTTTCATGTTGCCTCATAATGAGCTGCTGCTGCCTACGCATCAGGATA
AGCTGCAGTCCCCATCTGCCGTCTTTGCCACCGGGCAACATTAAGTAGATGCATG
AGTAATTACGAGGCAGCATCACAGCTAATTTTACGTAGAATAACGGAATCGTTAAACC
TGGACAACACTCTGTTGGCGGCGCACAATCCAAGTGAGCCATCCGTCACCAATTTG
GGTTTTTTACGTTATCCTCCGCAGCCTGCGACCAGCGATAATTGTGGACATATTGCG
CATACCGATGTAGGGACCTTAACGATTCTCGCTGCAACCCAACGCGGTTTACAGGT
TATTAATTCGCAGACACAGGACTGGACGTTTGTGATCCGCACCCTCAAACGAAA
GTTTACTCGTGCAGTTTGGTGATTGTCTGAAATTTCTGTCAGGAGGACGTGTTGTAC
CTTCTATCCACCGGGTTATCCCGAGCGATAAACCGGAGGAACGGGAAGGCACTAAG
TACACACTCGCTTATTTCTGTCGCGCCCGAACGAAGAAGCTGTCATTAAAGACGGGCG
AGGCGAAGAATGGGTATATGGCGACTATCATTGCCGTAAATTTGGGGCTTTTGCACG
TCCTTTGAAAAAGAAGGTGATAGAGATAGGATGCCGGATAGACCTGCTGGCGAGT
ACGATATGATTAAATATTCGTAAGATAAAGGGCTTATCTGAGGGCGTGTCCGCCGCTTA
A

NHI 119 (AniG) protein sequence:

MASISYEGLLRGAAKDIHALTEAALVHGYFNLELDCPEGQQLRQDVLFLLESFTKEIFDTP
SPQKTVYDFKKLGRFRTTGFKPLGIEEGAKGKSDGFEMFLPHNELLLPTHQDKLQSP
SAVFAHRATLTRCMSNYEAASQLILRRITESLNLDNTLLAAHNPSEPSVTNLGFLRYPQ
PATSDNCGHIAHTDVGTLTILAAATQRGLQVINSQTQDWTFVDPHPQNESLLVQFGDCLK
FLSGGRVVPsiHRVIPSDKPEEREGTKYTLAYFVRPNEEAVIKDGRGEWVYGDYHCR
KFGAFARPLEKEGDRDRMPDRPAGEYDMINIRKIKGLSEGVSA

Codon-optimized NHI 120 (PhqC) sequence:

ATGTCTAAAACCAACCGAAGTGAAAGTGGTTGAAGTCCAGCTGGAAGACCCGCTGC
CGGGGATTGTAGACGCGTCACGTTTTATCTCCGGTTCACCAACTGAACAACGCGCT
TTCGCGGTTGAGCTGGTGGATTCCGTTTCGACGTTGCGGATTTGTAAAGGTGATCAA
TCATGGGCTTTTCGGACGAACCTCATAGATGAATTATTCGCCTGGTGTCAAGTCCTCTCA
CGTAGTACAAAACGAAAGGTTTTTTGCAATTGACCCAGAGCAAAAGTTGGCGGTAG
TCAACCCGCCAGGACCGTCTCCACAGCGAGGCTGGTCTTGTGTGGGAGCGGAAA
AGGCCAGCCGTTTATTTTCCCGTGGGCAGACAAGTTTGGATTAAACAGACGCCCGC
CGAAACCAGGAACACTTCGACGCCGGATCTCCGAGCGATACAAAATGGCCTAGTAG
ATGGCCGGATGAGGCGGTCATACCCGGTTTCAAAGCATTCTCTAGAAGACTTTTATGT
GCGGTCTCATCAGGCAGCTCTGCTTATACTGGAAGCTCTGGAAATGGGTTTAAACC
TGCCGGCTGGAGTTCTTAAGAGCCGGTGTGGGGGCTGCGCGTCGGAAGTGAAGATT
AAATAACTACCCCGAAATTGATATTGAAGAACTGCGGCGTGGAAAGATTAGCCGCAT
TCATCCACATGCAGATCTCGGTGTTATTACGTGCCTTTTTCAAGACGTTTGGGGGG
ACTGGAATTAGAACATCGTAGCCATGCTGGTCTTTCTGCTGTTCCACCAGGGG
CGAGATCAGAGATGGTAGTAAATATTAGTGAGACATTCCAAGTGTGGACCAACAATG
TTATTACCGCTGGCATAACATCAGGTGACAGTCCCTCCGGAAATGAAAACACGCACC
GAAGGACGTATTAGCGCTCGCCGCTCATGCGCCTTTTTTTTAAAAGCTAATGGAGAT
GCGTCTGTTGCCCCCTGCCACAGTTTGTACACAAGAACGTCCGGCTGCATATTC
AGAAATGACGGCTCTTGATTACCACCAGAAACGGTTAGCAACAGCTTACTGA

NHI 120 (PhqC) protein sequence:

MSKTTEVKVVEVQLEDPLPGIVDASRFISGSPTEQRAFAVELVDSVRRCGFVKVINHGL
SDELIDELFAWCQSSHVVQNERFFAIDPEQKLAVVNPPGPSPQRGWSCVGAEKASRLF
SRGQTSLLDLDARRNQEHFDAGSPSDTKWPSRWPDEAVIPGFKAFLDFYVRSHQAA
LLILEALEMGLNLPAGVLKSRCGGCASELRNNYPEIDIEELRRGKISRHPHADLGVITC
LFQDGLGGLELEHRSHAGSFLPVPPGARSEMNVNISETFQLWTNNVITAGIHQVTPPE
MKTRTEGRISARRSCAFFLKANGDASVAPLPQFVTQERPAAYSEMTALDYHQRLATA
Y

Codon-optimized NHI 121 (ImqE) sequence:

ATGACGATGTTGTCTGACCTGCCAAAGATACCTACCCTGGATTGGGCTGATTTTGCC
GAGGGTGATACGGATCAGCGTTTAAACTGGCACAGGGTCTGGTACAGGGTTTTAA
ACGCTTTGGCTTTGTAAATTAGTGAACCATGGTCTGTCTGATGAACTGATTCAGCA
GTTGTTGCGCGAGGTTAAACGCTTCTATCGTCTGCCTGACGAACTGAAACAGAAAG
CTGCGCACCCGCCCGGGCCTAATCCTCAGCGCGGTTGGTCTGGCATTGGAGTTGA
ATCCACGAGTAAGTTGTATGGTGAACAAACCGAGCGGCCTTCTGGTAAGTTAAAAG
ACGCCAAGGTCGGGACAGATTTCTCAAGCAGTAACTCTCCCGAGAGCTGACCCA
CATGAAAGAACATTATGACATTGGACCACCGACAGACACGCAGTTTCCGACCCGCT
GGCCAGATGAGCAGGACATCCCAGGATGGCGGGCGTTTATGGAGAGCTATTACGC
CCGTGGGCAGTCTTTCTGTTTAGACTTAATGGAAGCGTTAGAAATCGGCTTAGAACT
CCCTAAGAACACACTGCGTTCCATGTGCATACCCGATGGATCCGAGCTTCGGCTGT
TACACTATCCTGAGATTCCTGCAGCCGAATTGAGAAGTGGTGACACGGCGAGAATT
TGCCACACACCGATTTTGGACTGATCACACTGCTTTTCCAGGATGGAGTGGGTGG

TCTGGAAGTTGAAGATCCCCTCCAGCAGGGGCATTACATTGAAGTTGCTCGGGAGC
AGCCTTATGAAATGATTGTCAATGTTAGCGCTACCTTTGAGCGTTGGATGAATGGTG
TAATTAAAGCGGCGGTACACAGGGTAAATATAACGCCAGAAGGCCAAACACGTTCGAG
GATGCAGTTGTGCCTGAACGCTGGTCAGCAGCTTATTTTTTTAAAGCTCACAAAATG
GCGCATGCTGGTCCTCTTCCAGCGTTCGTTACTCCCGAACGCCCGGCCTTATATGA
TAACATAACAGCACTTGAGTTTCAGAAACGGCGTACTGATCTGGTATATACAGGCCA
GCAGCTAAAAGTTGAGGAAGCAGCCTGA

NHI 121 (ImqE) protein sequence:

MTMLSDLPKIPTLDWADFAEGDTDQRLKLAQGLVQGFKRFGFVKLVNHGLSDELIQQL
FAEVKRFYRLPDELKQKAAHPPGPNPQRGWSGIGVESTSKLYGEQTERPSGKLKDAK
VGTDFFSSSKLSRELTHMKEHYDIGPPTDTQFPTRWPDEQDIPGWRAFMESEYARGQS
FCLDLMEALEIGLELPKNTLRSMCIPDGSELRLHYPEIPAAELRTGDTARIWPHTDFGLI
TLLFQDGVGGLEVEDPLQQGHYIEVAREQPYEMIVNVSATFERWMNGVIKAAVHRVNIT
PEGKHVEDAVVPERWSAAYFFKAHKMAHAGPLPAFVTPERPALYDNITALEFQKRRTD
LVYTGQQLKVEEAA

Codon-optimized NHI 122 (UcsF) sequence:

ATGGGCGTCCCCTCCTGGACGTGTCACAGCTGCAGGCGGGCCCAGAAGCCCGT
AAACAATACTTACAAGCCCTGGTCCAGAGTTTTTCGGGACTATGGCTTTGTCCGTCTT
ACCAAACATGATGTTCCGGCTAAGCGGGTACAACGCATATTCGACTTAAGCACCCA
GATGTTTAATCTTGATATCGATAGCAAATTAGAGTTCGCGAATATTGCGGATGGCAGT
CCACAGCGTGGGTATTCAGCTGTGGGCGTAGAAAAAACCGCATCACTGCATGGCAA
TCTGATAGGCAGACGTGTGGATGAGAACTGACAGACGCTCGGGAACACTTTGATT
GCGGATCCCCACTGGACAAGTCGTTTCGCAAATCGTTGGCCTGAGAACTGCAGGG
TTTTCAGCAGGAATTGGAGTCTTTTTATTTTCTGAACAGGTAACAGCTGGGAT
ATTGGGCAGCTTGGAAGAAGCTTTAACTGCCCCCTGGTACGTTGAACAACATGA
TTACGAAAGAGAACAACGCTTCTGAGCTGCGACTCAACCACTACCCGCCTGTCCCT
GCAGGCACGCTGAGAAATGGTAACGTAGCACGGATCTGGCCGCATTTTGACCTGG
GCGTCATTACCTTGTTATTTACTAGTGCCGTTGGGGGATTGGAAGTTGAGGATAGAA
ATGCACCCGGGCCACAGACTTTTATACCCGTGGAACCAGAGACCGAAGCGGAGTT
GATTGTCAATATCTCAGAAACCTGCAGCGGTGGACAGATGACCATTACCTGCCG
GGCTGCACAGAGTTACAATACCGAAAGATCTGGACACCGAAATACAGAACGATGCA
AATGTAGAAATTCCAGGTCGTTATAGCATTGCGTATTTGTGCAAGGCCGACCGCGAG
GCAGATGTTGGAACCTCTGCCCGTTTTCCAGACGGGTGAAGCTCCGAGGTATAAAGC
CATGACGGCTTCTGAATATCATCGATCTCGGTTGCTGACCGCGTACTAA

NHI 122 (UcsF) protein sequence:

MGVPLLDVSQLQAGPEARKQYLQALVQSFRDYGFRVRLTKHDVPAKRVQRIFDLSTQMF
NLDIDSKLEFANIADGSPQRGYSAVGVEKTASLHGNLIGRRVDEKLTDAREHFDCGSPL
DKSFANRWPEKLQGFQQUELESFYFELEQVTAGILGSLEEALNCPPGTLNNMITKENNA
SELRLNHYPVPAGTLRNGNVARIWPHFDLGVITLLFTSAVGGLEVEDRNAPGPQTIFP

VEPETEAEELIVNISETLQRWTDHLPAGLHRVTIPKDLDTIQNDANVEIPGRYSIAYLCK
ADREADVGTLPVFQTGEAPRYKAMTASEYHRSRLLTAY

Codon-optimized NHI 123 sequence:

ATGGGCTCGTTGGAAGTTCCATGTATTGACCTGAGCGAGAATGATACTAGTATCGTT
GTTAAAGAATTACTGGATGCGTGTA AAAATTGGGGTTTTGTATCCTTGAAAAATCATG
GCATCCCGCTGGACGAAATTGATCGGACTTTTAAACTTGCAGATAAATTCTTTGATAT
TCCAGTCGAAGAAAAACAGAAATACCTGTTTAAAGGTGGTCGTCTGCACTCAGGCT
ATACTGGTCACTTTGGTGAAAAGCTCGATATGGAACATCAGTCAAGGGGTGATCTGA
AAGAAAGTTACGACTTGGCAGGATTCCCAGATCCTAAACTTGAGAACCTCTGTCCCT
TTATCGCTGAACACATGGATGAGTTTCTGCAATTTTACGCGCCATTGCTATAAGCTTAC
CTTAAGATTGTTAGATTTTTTTTGCTATTGGATTCCGGTATCCCCCAGATTTTTTTTCAA
AATCACACTCTTCAGAAGAAGACGTGCTGCGACTGTTGAAATACTCAATACCAGAAG
GTGTTGAACGGCGTGAAGATGACGAAGATGCCGGTGCCCATTCAGATTATGGCTCA
ATCACTTTACTGTTTCAGCGCGATGCAGCTGGGTTGGAAATACGCCCCCCTAATTTT
GTGAAAGACATGGATTGGATAAAAGTGAATGTGCAACCTGATGTTGTCCTGGTGAAT
ATTGCGGATATGCTCCAATTTTGGACAAGTGGGAACTAAGGTCAACAGTTCACCGT
GTCCGCATTGATCCGGGAGTAAAACTCGTCAGACTATCGCGTACTTTGTTACTCCC
GATCCTGAAACTCCACTTTACCTCTGTTTGAAGAAAAGACAGGCAAGGATATTGAA
ACCGTAACCGCCGGTGAATGGATTGATGGCCGGATCAATTTTACATACGGGTATAGT
GCCCCGCCGAAAGGGTATCTCGGAAGCCAGAACGATGGCATTGTGGCTTGA

NHI 123 protein sequence:

MGSLEVPCIDLSENDTSIVVKELLDACKNWGFVSLKNHGIPLDEIDRTFKLADKFFDIPV
EEKQKYLFKGGRLHSGYTGHFGEKLDMEHQSRGDLKESYDLAGFPDPKLENLCPFIA
EHMDEFLQFQRHCYKLTLRLLDFFAIGFGIPDPFFSKSHSSEEDVLRLLKYSIPEGVERR
EDDEDAGAHSDYGSITLLFQRDAAGLEIRPPNFVKMDWIKVNVQPDVVLVNIADMLQ
FWTSGKLRSTVHRVRIDPGVKTRQTIAYFVTPDPETPLSPLFEEKTGKDIETVTAGEWID
GRINFTYGYSAPPKGYLGSQNDGIVA

Codon-optimized NHI 124 (ANS) sequence:

ATGGCCACATGCTGGCCCGAGCCGATTGTAAGTGTACAGTCGCTCAGTCAAACCG
GAGTACCAACGTTCCGAATCGGTACGTTAAACCGGCCCATCAACGCCCCGTATTT
AATACGACACAGAGCGATGCGGGTATAGAGATACCTGTGTTAGATATGAATGATGTG
TGGGGAAAACCGGAAGGGTTGAGGCTGGTTCGCTCAGCTTGCGAGGAGTGGGGG
TTCTTTCAAATGGTCAACCACGGTGTACCCATTCTGTTAATGGAACGTGTGAGAGGA
GCCTGGCGGGAGTTTTTTGAACTCCCCTTGAGAGAAAAGCGTAAATACGCAAATTC
GCCTGATACGTACGAAGGATATGGAAGCCGACTGGGTGTGGTGAAAGACGCCAAA
CTGGATTGGTCGGACTATTTCTTCCTGAATTATCTTCCAAGCAGCATCCGAAATCCAT
CGAAATGGCCAAGTCAACCTCCTAAAATTCGTGAACCTATCGAAAAATACGGCGAGG
AAGTGAGAAAACCTCTGCGAGCGGCTCACCGAACTCTGAGCGAATCGTTGGGACT
CAAACCGAATAAACTTATGCAGGCTCTGGGCGGCGGAGATAAAGTGGGTGCCTCG
CTGAGAACCAATTTCTATCCGAAATGCCCCAGCCGCAGCTGACACTTGGTCTGTC

CTCACATAGTGATCCGGGTGGCATTACTATCCTGCTGCCGGATGAAAAAGTTGCGG
GCCTGCAGGTACGCAGAGGCGACGGTTGGGTCACGATCAAATCTGTCCCGAATGC
GCTGATCGTGAATATTGGTGATCAGCTCCAGATTCTGAGCAATGGTATATACAAATCA
GTTGAACATCAGGTTATCGTCAATTCAGGCATGGAAAGAGTCTCTCTGGCATTTTTC
TACAATCCACGCTCTGATATCCCGGTTGGTCCCATTGAAGAGTTAGTAACCGCAAAT
CGTCCGGCTCTGTACAAACCTATCAGATTCGACGAATACCGGTCACTGATTCGGCA
AAAAGGACCTTGCGGCAAGAATCAGGTGGACAGCTTGCTTTTGACTAGATAA

NHI 124 (ANS) protein sequence:

MATCWPEPIVSVQSLSQTVPTVPNRYVKPAHQRPVFNTTQSDAGIEIPVLDMNDVW
GKPEGLRLVRSACEEWGFFQMVNHGVTHSLMERVRGAWREFFELPLEEKRYANSP
DYEYGYGSRLGVVKDAKLDWSDYFFLNLYLPSSIRNPSKWPSQPPKIRELIEKYGEEVR
KLCERLTETLSESLGLKPNKLMQALGGGDKVGASLRTNFYPKCPQPQLTLGLSSHSDP
GGITILLPDEKVAGLQVRRGDGWVTIKSVPNALIVNIGDQLQILSNGIYKSVEHQVIVNSG
MERVSLAFFYNPRSDIPVGPIEELVTANRPALYKPIRFDEYRSLIRQKGPCGKNQVDSLL
LTR

Codon-optimized NHI 125 (VrtI) sequence:

ATGGGTGCACGCTCTAAAGAGGCTAGACACCGCTGGTTCAGCCGCCTACCTCCTG
ATGCATCGAGCTCCTTTCTGCCATGCAAAAGACCGAAATCTGTTGCATTTGTGCTAT
GGATCCGACCGAGTTGCTTTTTGAGGGAGTCTTTACCGGCCGAACCTCAGTGGGCT
CCCAGGTCTGCCCCCTCCCGCCCCAGGCTCCGACTAACACCATGAACTGTGGGTTG
CCCGAGGCAGCCCTTAGTGTCATTGATTGGGGTCGCCTGAAAAGTGGTGATGTGAA
CGAAGGTGCGCGCTTGCTGTCTGCCTGTGATGATCAAGGTTTTTTTTTACTTAGACCT
GTCTTCTGAGCCGTCTTTCCTGCATGACCACAAAAGCGTCCTGCATTTTATGGATCA
GTATTTCCATCAAGGGCTGGCGGATAAGATGAAAGATGATCGCCAGAGTGACACCC
ACGGCTACGAACCAGTCGCCACCAGTACAGGCGCGCTGAACACCCTGCCGGATTA
TTATGAATCATTGAAAGCTAGTCGCGATGAGCTGCATGGAGATGGACGTAATTTAGC
GCCGGCAGTGTGTGACCGCCAAGATTTATTTCTTAGATTTTCCGACATGATGCATCA
AATGGTTATCGCCATACTTCAAGAGTTAGACTGCCAGCTGGGCTTTGGCGGTGATC
GGGCTTCTTTTCAAGATTTCCATCGGAAAGACGCTGAGTCCCTTACGACATTAAGCA
TGTTTCGGTATCCTAAACAGGAAACACTGGATCTAGGAGTAGGGCATAATAAACATA
CTGATATAGGCACATTAACCTTTCTGCTGTGTGATCAGTGGGGCCTGCAGGTCCTGT
CAAAAGACCCTGCGGGATGGCGATTTGTGCGACCGAGGGAAGGTCACGCAGTGAT
TAATGTTGGCGACACACTGCGCTTTCTATCCGGTAACCGCTTTCGGAGTGCGGTTT
ATCGTGTAATTCCAACGCAGCGCTTACAGCATGAAGATAGATACTCGATTGCCTACTT
TCTGCGTGCCGCTAATGACACTCAGTTCACCGACTCAGCAGGACGCCAGGTTTCA
GCTAAGCAGTGGCACGATGAAAAATTTGACGTATTCAGAGAACTCACGAGGAGCA
GGAAAAAATGCCAATTCTAACCGGGGGAATGGAGCGGTTAGAAAACCTGCCCGGG
ATATGGTGCGGAGTCCGCTTAACGGATGGAATTTGTCATCGCCTCGGTGCGGAAGA
CTGCTGA

NHI 125 (VrtI) protein sequence:

MGARSKEARHRWFSRLPPDASSSFLPCKRPKSVAFVLWIRPSCFLRESLPAELSGLPGLPLPPQAPTNTMNCGLPEAALSVIDWGRLKSGDVNEGARLLSACDDQGFFYLDLSSEPSFLHDHKSVLHFMDQYFHQGLADKMKDDRQSDTHGYEPVATSTGALNTLPDYYESLKASRDELHGDGRNLAPAVCDRQDLFLRFSDMMHQMVIAILQELDCQLGFGGDRASFQDFHRKDAESLTTLSMFRYPKQETLDLGVGHNKHTDIGTLTFLLCDQWGLQVLSKDPAGWRVAPREGHAVINVGDTLRFLSGNRFRSAVHRVIPTQRLQHEDRYSIAYFLRAANDTQFTDSAGRQVSAKQWHDEKFDVFRETHEEQEKMPILTGGMERLENLPGIWCGVRLTDGI
CHRLGAEDC

Codon-optimized NHI 126 (GA2ox3) sequence:

ATGGTTGTGCTCGCGGGCCCTCCAGCTGTAGATCATATTCCACTGCTTCGCTCACCAGACCCGGGCGACGTGTTCAGCGGTGTACCGGTCTGAGACTTGGGTTCGCCAGGCGCGGCAAGGGCAGTAGTGATGCATGCGAGAGATACGGTTTTTTTAAAGTTGTATCACGGCGTGCGACAGATACCATGGATAAAGCCGAATCTGAGGCGGTGAGATTTTCTCAGACCCAACCGGACAAAGACAGGTGAGGTCCCGCGTATCCTTTTGGTTACGGCAGCAAGAGAATCGGCTTTAATGGTGACATGGGTGGCTGGAATATCTGTTGTAGCCCTAGATGATGCCTCTCTGGCGGATGCTTGCACTGTCCCAAGCTGCGCAGTATTTAGGGCGGCATTAAATGAATATATTAGTGGCGTTAGGAAAGTCGCCGTGCGCGTTATGGAGGCGATGAGTGAAGGCCTGGGTATTGCCCAGGCAGATGCGCTGAGTGCCTGGTAAGTGCCTGAAGGTTCTGATCAGGTATTCCGCGTTAATCATTACCCCCCATGCCGTGCCCTGCAAGGCTTGGGATGCAGTGTTACGGGTTTCGGGGAGCACACAGATCCAGCTGGTGAGCGTTCTGAGAAGTAACGGGACATCAGGCCTTCAGATTGCTTTAAGAGACGGTCAGTGGGTCTCGGTGCCTTCGGACCGGGATTCATTTTTTGTGAATGTCGGCGATTCTCTGCAAGTCCTTACCAACGGCCGCTTTAAGTCAGTCAAACATCGCGTAGTTGCGAACTCGCTGAAATCACGCGTGTCCTTCATCTATTTTGGCGGCCCTCCTTAGCCCAGCGTATCGCTCCGTTGCCTCAACTGTTAGGCGAAGGAGAACAGTCATTATATAAAGAGTTCACGTGGGACGAATACAAAAAGGCAGCCTATAAATCACGTCTCGGAGACAACCGCTTAGCACAGTTTGAGAAAAAATAA

NHI 126 (GA2ox3) protein sequence:

MVVLAGPPAVDHIPLLRSPDPGDVFSGVPVVDLGSPGAARAVVDACERYGFFKVVNHGVATDTMDKAESEAVRFFSQTPDKDRSGPAYPFGYGSKRIGFNGDMGWLEYLLALLDDASLADACTVPSCAVFRAALNEYISGVRKVAVRVMEAMSEGLGIAQADALSALVTAEGSDQVFRVNHYPPCRALQGLGCSVTGFGEHTDPQLVSVLRSNGTSGLQIALRDGQWVSVPSDRDSFFVNVGDSLQVLTNGRFKSVKHRVVANSLKSRVSFIYFGGPPLAQRIAPLPQLLGEQEQSLEYKEFTWDEYKKAAYKSRLGDNRLAQFEKK

Codon-optimized NHI 127 (GA20ox5) sequence:

ATGTGTATTTATGCCTCCCGTCAGACCGTCTGCCCTTATTTGACTCCCTTTAAGGTGAAACGTCCCAAGTCACGAGAAATGAATAGCAGTGACGTAACTTCTCGCTGCTGCA
GAGCCAACCGAATGTTCCCGCGGAGTTTTTCTGGCCTGAAAAAGACGTTGCGCCTCCGAAGGTGATTTAGATTTACCAATTATTGATCTGAGCGGTTTCCTGAACGGCAACGAAGCGGAGACACAGCTGGCTGCCAAAGCAGTTAAGAAAGCGTGTATGGCCCATGG

TACTTTTCTGGTCGTAAATCACGGCTTTAAAAGCGGTCTTGCAGAAAAGGCGCTAGA
AATTAGCTCTTTATTCTTTGGACTTAGCAAGGATGAAAAATTAAGGGCGTACCGTATC
CCAGGCAATATCTCGGGCTACACCGCGGGGCATAGTCAACGGTTTTTCGAGCAACCT
GCCTTGGAACGAACTTTGACCCTGGCATTAAAAAAGGGCCCCCCCCACGTTGTGG
AAGATTTTTTGACATCCCGTTTAGGTAATCATCGCCAGGAAATAGGGCAGGTCTTCC
AAGAGTTTTGCGACGCTATGAACGGTCTGGTAATGGATCTTATGGAGTTGCTGGGA
ATTTCTATGGGACTAAAGGACCGTACATATTATCGTAGGTTTTTCGAAGACGGCTCAG
GAATTTTTAGATGTAATTACTATCCGCCTTGTAAGCAGCCGGAAAAAGCCCTGGGTG
TTGGTCCGCATAATGATCCAACCGCTATAACCGTACTGTTACAAGATGATGTAGTAGG
ACTAGAAGTTTTTCGCGGCGGGGTCTTGGCAGACGGTTCGCCCACGCCCGGGTGC
TCTGGTCGTAAACGTCGGTGATACGTTTATGGCTCTGTCCAATGGGAATTATAGAAG
CTGCTACCATCGTGCCGTCGTCAATAAAGAAAAAGTGCGTCGCTCTCTTGTATTTTT
TAGCTGCCCCGCGTGAGGACAAAATTATTGTTCCGCCTCCGGAAGTGGTCGAGGGC
GAGGAAGCATCACGTAAATACCCGGACTTTACTTGGGCTCAACTCCAGAAATTTACT
CAGTCGGGCTATCGAGTGGATAATACTACGTTACACAATTTACGCTCCTGGCTTGTT
TCAAACAGCGATAAGAAATCTACTTAA

NHI 127 (GA20ox5) protein sequence:

MCIYASRQTVCPYLTPFKVKRPKSREMNSSDVNFSLLQSQPNVPAEFFWPEKDVAPSE
GDLDLPIIDL SGFLNGNEAETQLAAKAVKKACMAHGTFLLVNHGFKSGLAEKALEISLFL
FGLSKDEKL RAYRIPGNISGYTAGHSQRFSSNLPWNETLTLAFKKGP PHVVEDFLT SRL
GNHRQEIGQVFQEFCDAMNGLVMDLMELLGISMGLKDRTYYRRFFEDGSGIFRCNYY
PPCKQPEKALGVGPHNDPTAITVLLQDDVVGLEVF AAGSWQTVRPRPGALVVNVGDT
FMALSNGNYRSCYHRAVVNKEKVRRLVFFSCPREDKIIVPPPELVEGEEASRKYPDFT
WAQLQKFTQSGYRVDNTTLHNFSSWLVSNSDKKST

Codon-optimized NHI 128 (GA2ox1) sequence:

ATGGTACTGCTCTCCAAACCCACTTCAGAGCAGTACACTTACGTTTCGCAACAATATG
CCCATTACATTTAGCTCTAGCATCCCATTGGTGGATCTCAGTAAACCAGACGCGAAG
ACTCTTATCGTAAAAGCCTGTGAGGACTTTGGTTTTCTTTAAAGTGATAAACCATGGCA
TCCCTTTGGATGCCATATCACAAATTGGAGAGCGAAGCCTTTAAGTTTTTTAGTCTGC
CGCAGACTGAAAAAGAAAAAGCTGGTCCAGCCAATCCATTTGGATATGGGAATAAAA
GAATTGGTTTTAAATGGGGATATAGGTTGGATAGAATATTTACTTTTAACGACGAATCAG
GATCACAACTTTTCACTGTACGGAGAGGATATAGATAAGTTCCGGGGTTTACTGAAA
GACTATAAATGTGCAATGCGTAATATGGCCTGCGAAATCCTGGATCTCATGGCCGAA
GGTCTTAAGATTCAACCTAAAAATGTGTTTTCAAATTGGTCATGGATAAACAGTCTG
ATTGCCTGTTTCGCGTCAATCACTACCCAGCCTGCCCGAGCTGGCAATCAACGGC
GAGAACCTGATTGGGTTTTGGTGAACACACGGATCCTCAAATCATCAGTATTCTCCGT
AGTAATAATACGTCGGGGTTTTAGATATCGTTACGTGATGGTTCTTGGATTTAGTTT
CGCCTGATCATTCTTCTTTTTTTATAAATGTCGGGGATTCTCTCCAGGTCATGACCAA
TGGTCGTTTTCAAGAGCGTTTCGACACCGCGTTTTAGCTAACGGCATCGATCCAAGAT
TGTCATGATCTACTTTTGCGGCCCACTGTCCGAAAAAATTGCACCGCTGCCTA
GCCTTATGAAAGGCAAAGAGAGTCTCTATAAAGAGTTTACGTGGTTTCAATATAAATC

GTCTACCTATGGCAGCCGTTTAGCGGATAACCGGCTGGGCAACTATGAACGTATTG
CGGCCACCTAA

NHI 128 (GA2ox1) protein sequence:

MVLLSKPTSEQYTYVRNNMPITFSSSIPLVDLSKPDAKTLIVKACEDFGFFKVINHGIPLD
AISQLESEAFKFFSLPQTEKEKAGPANPFGYGNKRIGLNGDIGWIEYLLLTTNQDHNFSL
YGEDIDKFRGLLKDYKCAMRNMACEILDMAEGLKIQPKNVFSKLVMDKQSDCLFRVN
HYPACPELAINGENLIGFGEHTDPQIISILRSNNTSGFQISLRDGSWISVPPDHSSFFINV
GDSLQVMTNGRFKSVRHRVLANGIDPRLSMIYFCGPPLSEKIAPLPSLMKGKESLYKEF
TWFEYKSSTYGSRLADNRLGNYERIAAT

Codon-optimized NHI 129 (GA2ox1 2) sequence:

ATGGCCGTGCTCAGTAAACCCGTAGCTATTCCCAAAAGTGGTTTTTCACTAATTCCG
GTAATTGATATGAGCGATCCCGAGAGCAAACATGCCTTAGTTAAAGCATGTGAAGAT
TTCGGGTTTTTTAAAGTGATTAATCATGGTGTATCAGCCGAGCTGGTCTCAGTTTTG
GAACATGAAACAGTGGATTTTTTTAGCCTGCCTAAATCTGAAAAGACACAAGTGGCC
GGTTATCCGTTTGGCTACGGCAATTCGAAAATTGGCCGGAACGGAGACGTTGGGTG
GGTAGAGTACCTGCTGATGAATGCCAATCATGACTCAGGTTCTGGACCCCTTTTTCC
ATCACTTTTAAAGTCTCCCGGGACTTTCCGTAATGCCCTGGAGGAATACACCACAAG
CGTGCGGAAGATGACGTTTGTGTGCTGGAAAAAATCACGGACGGTCTCGGCATCA
AGCCTCGCAATACCTTGTCAAAGCTCGTTTCCGACCAGAATACGGACAGCATATTAC
GTCTGAATCATTATCCGCCTTGCCCACTGAGTAATAAAAAACAAACGGTGGTAAAA
ACGTGATTGGTTTTGGCGAACATACTGATCCACAGATAATTTCCGTGCTTAGATCCAA
TAATACGTCTGGCCTGCAGATTAATCTCAACGATGGTTCCTGGATTTCCGTTCCCCC
GGACCACACGTCTTTCTTTTTTAATGTAGGGGATTCTCTTCAGGTAATGACCAATGG
AAGATTCAAGAGCGTGCGCCATCGTGTATTGGCTAACTGTAAAAAAGTCGCGTTTC
GATGATTTATTTTGTGCTGGGCCATCGCTGACGCAGCGTATTGCTCCGTTGACCTGCTT
AATCGATAACGAAGATGAACGTCTGTATGAAGAATTCACATGGAGCGAGTATAAAAAT
AGTACCTATAATTCACGCCTGTCAGATAATCGGCTGCAGCAATTTGAGCGGAAAACC
ATCAAAAATCTGCTGAATTAA

NHI 129 (GA2ox1 2) protein sequence:

MAVLSKPVAIPKSGFSLIPVIDMSDPESKHALVKACEDFGFFKVINHGVSAELVSVLEHE
TVDFFSLPKSEKTQVAGYPFGYGNKIGRNGDVGWVEYLLMNANHDSGSGPLFPSLL
KSPGTFRNALEEYTTSVRKMTFDVLEKITDGLGIKPRNTLSKLVSDQNTDSILRLNHYP
CPLSNKKTNGGKNVIGFGEHTDPQIISVLRNNTSGLQINLNDGSWISVPPDHSTFFFN
VGDSLQVMTNGRFKSVRHRVLNCKKSRVSMIYFAGPSLTQRIAPLTCLIDNEDERLYE
EFTWSEYKNSTYNSRLSDNRLQQFERKTIKNLLN

Codon-optimized NHI 130 (GA3ox2) sequence:

ATGCCGACGCCGAGTCACCTGTCTAAGGATCCACGTTATTTTGATTTCCGCGCCGC
ACGTCGTGTACCTGAAACGCATGCCTGGCCCGGTCTTCACGATCATCCCGTAGTCG
ATGGTTCTGGTGCCGGTGGCGGTCCCGACGCAGTTCAGTTGTGCGACATGAGGGA

CCCGTGTGCAGCGGAGGCAGTCGCACTGGCCGCACAGGATTGGGGTGCTTTTTTG
CTGGAAGGGCATGGTGTACCCTTGAGTTGCTGGCAGGCGTTGAAGCAGCCATTG
GGGGCATGTTTCGCATTACCAGCATCCGAAAAGATGCGTGCAAGTTGCCCGTCCTGG
CGACAGCTGTGGTTACGGCTCGCCCCCGATCAGTTCTTTTTTTTCCAAATGCATGTG
GTCGGAAGGTTATACTTTTACGCCAGCGAACCTGCGGTCTGATCTGCGGAAGCTTT
GGCCGAAAGCCGGCCATGATTATCGGCACTTTTTCGCGAGTAATGGAAGAGTTCCAT
CGCGAAATGCGAGCATTAGCAGATAAATTATTAGAGTTATTTCTGGTAGCGTTAGGAC
TGACCGGTGAGCAGGTGCGGGCTGTTGAAAGTGAGCATAAAATCGCGGAGACTAT
GACAGCCACCATGCACTTAACTGGTACCCAAAATGCCCAGATCCAAAGCGTGAC
TGGGCTTAATCGCACATACAGATTCTGGGTTTTTTTACATTTGTTTTGCAGTCCTTAGT
GCCGGGTTTACAGTTGTTTCGCCACGGCCCCGATCGGTGGGTGACCGTACCAGCT
GTGCCGGGCGCTATGGTTGTGAATGTTGGGGACCTGTTTCAGATTTTGACCAACGG
ACGTTTTTCATTCTGTATATCATCGCGCTGTTGTCAACCGAGATTCAGACCGTATTAGT
CTTGGCTATTTTCTCGGGCCGCCCGCTCATGTTAAGGTGGCCCCGTTGCGTGAAGC
ATTGGCAGGTACCCAGCAGCATATCGGGCCGTGACCTGGCCGGAATACATGGGT
GTGAGAAAAAAGCTTTTACAACCTGGAGCCTCAGCGCTGAAAATGGTCGCCATTTT
TACTGATAACGATGCCGCGAACGATACAGATGATCTGATAAGCTCATAA

NHI 130 (GA3ox2) protein sequence:

MPTPSHLSKDPYFDFAARRVPETHAWPGLHDHPVVDGSGAGGGPDAPVVDMDRD
PCAAEAVALLAAQDWGAFLLLEGHGVPLELLAGVEAAIGGMFALPASEKMRVRRPGDSC
GYGSPPISSFFSKCMWSEGYTFSPANLRSDLRKLWPKAGHDYRHFCAVMEEFHREMR
ALADKLELFLVALGLTGEQVAAVESEHKIAETMTATMHLNWYPKCPDPKRALGLIAHTD
SGFFTFVLQSLVPGLQLFRHGPDRWVTVPAVPGAMVVNVGDLFQILTNGRFHFSVYHRA
VVNRDSDRISLGYFLGPPAHVKVAPLREALAGTPAAYRAVTWPEYMGVRKKAFTTGAS
ALKMVAISTDNDAAANDTDDLIS

Codon-optimized NHI 131 (GA3ox1) sequence:

ATGCCATCGTTAAGCGAGGCTTATCGCGCCCACCCTGTACACGTAAATCACAAACAT
CCGGACTTTAATTCATTACAGGAATTACCAGAATCATACAATTGGACGCATTTAGATG
ACCACACGCTGATCGATTCTGAATAACATTATGAAAGAGTCGACCACAACCGTGCCG
GTGATTGACTTAAACGATCCCAATGCATCTAAACTGATCGGGTTAGCATGTAAACTT
GGGGCGTTTATCAAGTGATGAACCATGGTATTCCTTAAGCCTGTTAGAGGACATTC
AGTGGCTGGGACAAACATTATTTTCTCTGCCAAGCCACCAGAAACATAAAGCCACC
AGATCTCCAGATGGCGTATCTGGCTATGGGATTGCCCGAATTTCTTCATTTTTCCCG
AAGCTGATGTGGTATGAGGGGTTCACTATTGTGGGTAGTCCGTTAGATCACTTCCGC
GAACTGTGGCCGCAGGATTATACACGGTTCTGTGACATAGTGGTACAATATGATGAG
ACTATGAAAAAGTTAGCCGGAACGCTTATGTGTTTGATGCTGGATTCTTTAGGCATCA
CGAAAGAGGATATCAAGTGGGCGGGTTCTAAGGCTCAATTTGAGAAAGCATGCGCA
GCGCTCCAACCTGAACCTCCTACCCTAGTTGCCCAGATCCAGATCACGCCATGGGGCT
GGCACCACACACGGATAGCACTTTCCTGACGATTCTCTCTCAGAACGACATATCGG
GTTTACAGGTTAATAGGGAAGGATCGGGTTGGATCACAGTACCGCCGCTGCAAGGC
GGCCTGGTGGTGAATGTTGGCGATCTCTTTCACATACTCAGCAATGGTTTATACCCG

AGTGTGTTACATCGGGTTCTGGTAAATCGTACGCGGCAACGCTTCTCTGTGGCTTAT
CTCTATGGTCCGCCGTCCAACGTGGAAATCTGTCCCCATGCAAACTGATTGGGCC
GACGAAGCCCCCGCTGTACCGCTCAGTCACATGGAATGAATATCTCGGCACTAAAG
CCAAGCACTTTAACAAAGCGCTGAGCAGTGTGCGTCTGTGCACCCCAATTAATGGA
CTGTTTCGATGTGAATGATTCTAACAAAAATTCTGTACAGGTTGGGTAA

NHI 131 (GA3ox1) protein sequence:

MPSLSEAYRAHPVHVNHKHPDFNSLQELPESYNWTHLDDHTLIDSNMKESTTTVPVI
DLNDPNASKLIGLACKTWGVYQVMNHGIPLSLLEDIQWLGGTLFSLPSHQKHKATRSP
DGVSGYGIARISSFFPKLMWYEGFTIVGSPLDHFRELWPQDYTRFCDIVVQYDETMKK
LAGTLMCLMLDSLGITKEDIKWAGSKAQFEKACAALQLNSYPSCPDPDHAMGLAPHTD
STFLTILSQNDISGLQVNREGSGWITVPPLQGGLVNVGDLFHILSNGLYPSVLHRVLVN
RTRQRFSVAYLYGPPSNVEICPHAKLIGPTKPPLYRSVTWNEYLGTKAKHFNKALSSVR
LCTPINGLFDVNDSENKNSVQVG

Codon-optimized NHI 132 (OsGA3ox1) sequence:

ATGCAGATCATGACATCATCGTCTACCAGTCCAACCTCTCCAACCTCCCCTCTGGCG
GCCGCGGCTGATAATGGTGTAGCCGCTGCCTATTTCAATTTCCGTGGTGCAGAGCG
GGTCCCTGAGAGTCATGTGTGGAAAGGTATGCACGAAAAAGATACGGCACCCCGTAG
CTGCCGCTGATGCGGACGGGGGTGATGCAGTGCCGGTTCGTTCGATATGTCAGGGG
GGGACGATGCTGCGGTGGCCGCAGTTGCACGTGCAGCTGAGGAATGGGGAGGTT
TTCTTCTGGTTGGCCATGGTGTAAACGGCAGAGGCGCTGGCACGCGTTGAAGCACA
AGCCGCCAGGCTCTTCGCATTGCCTGCGGATGACAAGGCGAGGGGTGCCCGACG
CCCGGGGGGAGGCAATACCGGTTATGGCGTACCGCCGTATCTGTTGAGATATCCCA
AACAGATGTGGGCTGAAGGATATACCTTTCCGCCGCCCGCAATACGCGATGAGTTT
CGTCGTGTGTGGCCAGATGCAGGTGATGATTATCATCGTTTTTTGTAGTGCCATGGAA
GAATACGATTCTTCTATGCGTGCTCTGGGTGAACGGCTGTTGGCGATGTTCTTTAAA
GCATTGGGGCTGGCAGGCAACGATGCTCCGGGGGGCGAGACCGAACGTAAAATTC
GTGAAACCTTAACAGTACCATACATCTTAACATGTTTCCGCGGTGTCCCGACCCTG
ATCGAGTGGTTGGTTTAGCCGCACATACGGATAGCGGCTTTTTTACGTTTATTCTTC
AGTCCCCAGTGCCAGGACTGCAATTACTGCGCCACCGCCCTGACCGTTGGGTAAAC
AGTTCCTGGAACGCCGGGAGCCCTGATAGTCGTAGTAGGCGATCTATTCCATGTGC
TGACCAATGGACGTTTTTCATAGTGTTTTTACCAGGGCTGTTGTGAACCGCGAGCGC
GATCGCATTAGTATGCCCTACTTCCTGGGCCCCGCCAGCCGACATGAAAGTCACGCC
CTTGGTGGCAGCTGGAAGTCCAGAGTCAAAGCTGTCTATCAGGCCGTGACCTGG
CCGGAATATATGGCAGTCCGCGATAAATTATTTGGGACAAACATCTCTGCCCTATCTA
TGATCCGGGTGCGGAAGGAAGAAGATAAAGAAAGTTAA

NHI 132 (OsGA3ox1) protein sequence:

MQIMTSSSTSPTSPTSPLAAAADNGVAAAYFNFRGAERVPESHVWKGMHEKDTAPVA
AADADGGDAVPVVDMSGDDAAVAAVARAAEEWGGFLLVGHGVTAELARVEAQAA
RLFALPADDKARGARRPGGGNTGYGVPPYLLRYPKQMWAEGYTFPPPAIRDEFRRVW
PDAGDDYHRFCSAMEEYDSSMRALGERLLAMFFKALGLAGNDAPGGETERKIRETLT

STIHLNMFPRCPDPDRVVGAAHTDSGFFTFILQSPVPGQLLLRHRPDRWVTVPGTPG
ALIVVVGDLFHVLTNGRFHSHVHRAV VNRERDRISMPYFLGPPADMKV TPLVAAGSPES
KAVYQAVTWPEYMAVRDKLFGTNISALSMIRVAKEEDKES

Codon-optimized NHI 133 sequence:

ATGCTGGATCAAAC TACTAGCATTCTTAGTGAAGAGACATTAAACGGCCCTGAGACA
GTAGTTTTGAAAGAACCGTTCCCTATTCTGATCGCGTCTAATCAGCTCCCGGCCAAT
TTGGCTGAAGAAATTGACCGCGACTTCCCGCAATACACCGGAGCAGGGTATCTGCC
ACATGAAGAAAAAGACTGCGGACCAACAATCAATACTATCGTTAGTGAAATGACCTC
ACGTGAGTTTGCCAATTCCTTAGGCAAGCACCTCGGAGTCCCTAATCTGGGTGATTA
TCCTACAATGGTGAGCATATGTCGTAGCTTGAATAAAAAACATGGAAATATCCACACA
GACTCGAATTCTAAAATCGTCACTTGCCTGCTGTACTTAAACCCGGGTTGGATGCAA
AATAGCGAGGGTTGTCTGAGGTTCTTGAGACGTATTGATAGCTTTGAAGACATGGT
GGCGCCTGAAATTCGTCCGGTGTACGGTTCATTGGCGGCTTTTCGTGAGCTGATA
ATTCGTTCCATGGTCATCTGCCATACGAAGGCGAGCGGCGCGTTATTCAAGTTGCAT
GGTTAACGTCTGAGGAGGAAAACTCCGTAAAACGAAGCGGGGCAAAATGAGCCG
CTTTCTGAAATGGATGACATCTAGCTTGGGGAAATAG

NHI 133 protein sequence:

MLDQTTSILSEETLNGPETVVLKEPFPILIASNQLPANLAE EIDRDFPQYTGAGYLPHEE
KDCGPTINTIVSEMTSREFANSLGKHLGVPNLGDYPTMVSICRSLNKKHGNIH TDSNSK
IVTCLLYLNPGWMQNSEGCLRFLRRIDSFEDMVAPEIRPVYGS LAAFRRADNSFHGHL
PYEGERRVIQVAWLTSEEEKLRKTKRGKMSRFLKWMTSSLGK

Codon-optimized NHI 134 sequence:

ATGGCCACCGCGGCCTATACAACCTTTACGCTGGGTGATACACTTACAGAAGAGCA
GAAGGCATTCTTTGAAAAACATGGGTATATTCAC TTTTCGAATGTGTTGGATGCAGC
AACCGTGCAGTCTATCATAGATGCCAGCGAAAAAGTGCAGGAGAAATGGATTT CAG
AAAATGTTGAAAAGATCAACGGTGTGCCGATAAAATACGGCACCGATCTCAACGGAA
ATAAAATCGTTCAACGTTTTCGCCTTTATAAATCAGCATACTACTGTTTTTAAGCGAACTG
CTAAAGGATGCACGTATTCAATCACTGCTCGAGCTTATCGGCCCAGGTGCTAGAATT
GGTGAGAATGAGAAGGACGGTATGGTCTTCAATCATTATGTTAACGGTCCGGAGAG
TAAGTTCACTAAGATGGGTGGCACACGGATGGACTCCGTGATATCTTCATGGGCG
GCCGACTGAATCCGATGTTGAATATGGGACTGCATCTTAGCACCTGCAGCCGGAA
AACGGTGGCCTGCGTATCATACCGGGGCACACATAAACAGGGTCTATTTTCAATGCTA
TTTAAAAAACGGTATTTTATAGATCATCGTCCGGATAAAAATGAAATAGCCATTATGCC
GAAAGCGGGGGATCTAACGGTGCATGACGGCCGCCTGTGGCATCGCGTTGCCCA
GAGCAGTGTCTGTTGGTGAAGCCTCACGGCGTCGCGTCATTTACGTGCCGCTGATT
GCGGGTAAGTACGAACCCAAAAATGAAAACAGCCCTACGCTGTTCTATCAACGCTTT
GCAGGCATCGTGAAATAA

NHI 134 protein sequence:

MATAAYTTFTLGDTLTEEQKAFFEKHGYIHFSNVLDAATVQSIIDASEKVQEKWISENVE
KINGVPIKYGTDLNGNKIVQRFAFINQHHTTVLSELLKDARIQSLELIGPGARIGENEKDG
MVFNHYYVNGPESKFTKMGWHTDGLRDIFMGGRLNPMLNMGLHLSTLQPENGGLRIIP
GTHKQGLFSMLFKKRYFIDHRPDKNEIAIMPKAGDLTVHDGRLWHRVAQSSVVGESR
RRVIYVPLIAGKYEPKNENSPTLFYQRFAGIVK

Codon-optimized NHI 135 sequence:

ATGGCGACACGTCATCGCCGTCGTGGAGGGAGCGCTCCGTCTTGGGCAAAACCA
GGTAAACCTGGTGAAAGACCGGGAGGACCAAAGAAATCACGTGGTAGAACGTCTT
GGAAAAGTCTGTTAATTTGGGGTGTTTTCGGGGTAAGTCTGGGACTGATGGCGGGG
TATTATTTATGGGGCGAACTGATTACCGACGACTCGGTAAGTGAAGTATTAGCAGCG
CAGCGTGATGCGGTGGCGCAGAGATTCTTTCATGTGCCGTGCTCACAGGATTATGA
ATCCCTCAAACAATTTGAAGCGTGCAACCCCGCGCAAATGTGGGCGCGCTGTAACAG
ATTCTGTTATCACCTACAGGAAGCCGAGAAAATGCGTCGGCTAGCAGAAGCAGGG
CTGTCACTTGGGGGTTCCGATGGCGGTGCTAGCATCCTCGATCTCCACAGTGGGG
CTCTATCTATGGGTAAAAAATTTGTGAACATGTATCGCTTCTTTGGAGACAACTTAA
AGATGTCATGTCAGATGAGGATTTTAATCTTTATCGCGAAGTCCGCCTAAAGATACAA
CACGAAATTGCGCGAACATTCAATATTAGCGTGTCAAGTCTGCACCTGACGAAGCC
TACATTTTTTTCACGGATGAACAGTAGTGAAGCGAAGACAGCCCATGATGAGTATTG
GCACCCGCATATCGACAAAGTGACCTACGGGTCATTTGACTACACGAGCCTCCTTTA
CTTATCAGATTATTCACAGGATTTTGGGGGCGGCCGGTTCGTCTTTATAGACGAGGG
GGCCAACCGCACAGTCGAGCCGCGAACGGGCCGGCTGAGCTTCTTTACAAGTGG
TTCAGAAAATCTGCACCGCGTGAAAAAGTAAGCTGGGGTACGAGGTATGCCATAA
CTATCTCGTTTACCTGTAATCCGGAACATGCAATTGGGGATCCTACGTGGACATAA

NHI 135 protein sequence:

MATRHRRRGGSAPSWAKPGKPGERPGGPKKSRGRTSWKSLLIWGVFGVTLGLMAGY
YLWGELITDDSVTEVLAAQRDAVAQRFFHVPSCSDYESLKQFEACTPRKCGRAVTDVS
ITLQEA EKMRRLAEAGLSLGGSDGGASILDHSGALSMGKKFVNMYRFFGDKLKDVMS
DEDFNLYREVR LKIQHEIARTFNISVSSLHLTKPTFFSRMNSSEAKTAHDEYWHPHIDKV
TYGSFDYTSLLYLS DYSQDFGGGRFV FIDEGANRTVEPRTGRLSFFTSGSENLHRVEK
VSWGTRYAITISFTCNPEHAIGDPTWT

Codon-optimized NHI 136 sequence:

ATGAATCATCCAAATCGTGATAAAATTGCTGACCTAATTTTTCTGAAACTTAAAGACAA
TGAAGAAGTCCTGAAGAAACACTTCGCACACACCTCCGAAGGCATCGGCTATTTTT
ACCTGGACGATCTGCTGCCGAAACATCTAACCGACGAAATTTTTGATAAATTTCCGA
GCACAAAAGATATTAAAGTCAAACGTAGCTTACGGGAATATAAATATGTGGCAGCTCA
AATGAATCGATATCATCCACTGCTGGAGGAAACCATTTATGCCTTTCAAGACAAAAG
AATCGTGGATCTCATCAGTAAGATCTGCGGTTACTGCAGCGTGAAGCCGGATGGTG
ATCTGTACGCAGGGGGTATTTTCGATGATGGGCAAAGGAAATTATCTGAATCCGCATC
TGGATAATTCTCATGACAAAGACGTAAAGTTATGGAGAGTGCTGAATCTGCTGTATTA
CGTAACACCCGACTGGATGCCCGAAAATGGTGGCAACCTGGAGCTATGGCCTAAA

GGCTTAAAAAGTGAACCAGTGAGTATCAATTCCCGGTATAATCGTCTGGTCGTTATG
TCGACCCATAAAGATAGTTGGCATTCTGTTGGCAAGGTGAAAGTCGACAAAGTCAG
ATGTTGTATTTCAAATTATTATTTTAGTACGGAACCGGTAGATGCCAAACGAAGTTTCC
ATGTCACGACTTTCCGTGGTTGGCCTGGCCAATTTTTTCGAGATAAAATTCTTAAAT
AGACTCATCTATACGTATGGGCGTACGTAAATCTTTAAAAAAGGTATTCGCGAAAAT
CCACACGTCTACAAAAAGGACGATTAA

NHI 136 protein sequence:

MNHPNRDKIADLIFLKLKDNEEVLLKKHFAHTSEGIGYFYLDDLPLKHLTDEIFDKFPSTKD
IKVKRSLREYKYVAAQMNRYHPLLEETIYAFQDKRIVDLISKICGYCSVKPDGDLYAGGIS
MMGKGNYLNPFLDNSHDKDVKLWRVLNLLYYVTPDWMPENGGNLELWPKGLKSEPV
SINSRYNRLVVMSTHKDSWHSVGKVKVDKVRCCISNYFSTEPVDAKRSFHVTTFRG
WPGQFFRDKILKIDSSIRMGVRKIFKKGIRENPHVYKKDD

Codon-optimized NHI 137 sequence:

ATGACTGAATCTAGTCTGCATGACCTCTTCTCGGGTTTGATAGACGATCTGGCATCA
CAGGGATGGTCACAGCGTGCTCTTTTTGCGCCTGAGGTACTCACACGTGAATTAGC
CGTAGAATGTCGCACACGTGCGCAGAATGGAGAGCTAAACGCCGCCGGGGTAGGA
CGTGGCGGCACCCAGCAGGTTCAAGGAAGGGATTTCGTGGTGATCGTATTCAATGGT
TAGAACCCGGTCAGTCACAGGCCTGCGACCAATATCTGCAGCTAATGGATGGGCTG
CGCCAGGCACTTAATCAAGCTCTATACTTAGGCTTAGAGGATTATGAGTGTCATTTTCG
CTTGCTATGCCCCAGGTGCATTTTATCAGCGACACTTGGACAGGTTCCGAGATGAT
GATCGTCGTACCGTGTCCGCGGTTTTTTATTTGAACGAAGAATGGCAAGCCGAACAT
GGTGGCGCGCTGCGTCTGTATTTGGCCGACGGTTCGCGAACATGATGTACTGCCCC
AAGCCGGTACCCTGGCGTTATTCCTGAGCTCAGAGATGCCACATGAGGTACTGCCG
GCTACACGAGAGAGATTGTCACTGACAGGTTGGTTTAGACGTCGCGGAGGGGCAG
TACTGTAA

NHI 137 protein sequence:

MTESSLHDLFSGLIDDLASQGWWSQRALFAPEVLTRELAVECRTRAQNGELNAAGVGR
GGTQQVQEGIRGDRIQWLEPGQSQACDQYLQLMDGLRQALNQALYLGLEDYECHFA
CYAPGAFYQRHLDRFRDDDRRTVSAVFYLNEEWQAEHGGALRLYLADGREHDVLPQA
GTLALFLSSEMPHEVLPATRERLSLTGWFRRRGGAVL

Codon-optimized NHI 138 sequence:

ATGGATCCATCTCATATGAATTTGCCAGTTATTGACTTAGACGTTTATCTGAATAAACC
GCGTGATTGCGCTGAGGTGCGCCAAGAATGTGCAAAGGCAGCAGATGCTCTCATT
CTTATGGCGCCCTTGTTCTTCATGATTCACGCGTAGACTCTAAAGACAATGATACGTT
CCTGGATCTCCTGGAGGATTATTTTGTCAACCGTCCGACGTAATTCGCAACGATGA
GCGCCCCGAAGTGAAGTATCAGATTGGAGTTACATTGGAAAATACTGAAAAACCGAA
ATGCGCAGTAGACGAGCCTTGCCCTCGATGTAGTTAGACGTCTTCATCCTAGTCAAC
GTCCACTCGATATTTCAAGGTCATCAACCTGATCCGAAATGTCGCTTTTTTTGGCGTAT
GGCTGACCGGCCACCGTACGAGACAGATTTCCGTCACTGAATGCACCGAACGTG

GTACCGGATGCTCCGCACATCAAACCGCGATGGACACCCACCATGGACATGTGGG
GTACGTCTATGAAAAATGCCGTTAGCAAGTTATCAGAAATGACTGCAGTGGGGTTAG
GCCTTCCCGCAGAGTATTTTTCTGACGCGGCAAGATACGGGCCGCATCTCTTGGCG
CCTACAGCATCTGATCTCGAGAAATATGGGGCGAAAGATACAATCCTGGCCGGTTTT
CATACCGACCTGAATTTTTCTGACAATTCATGGCCGTTTCGCGGTATCCAGGCCTGAAC
ATTTGGGCCCCGAATACGGGGGACCGCATTGCCGTGAAAATTCCGCCGGGGGAATT
ATCTGCTTGTACAAGCCGGCAAACAGCTAGAATATGCAACGGGTGGTCTGGTGAAG
GCCGGATACCATGAAGTGGTGATTAAACGACAAGACGATTGAAACGATAGAAAAGAG
GAAACAACAATTTCTGATCGCCCTCTGGTGCGCATTAGCTCCACGTTATTTTGGCA
CCTTAATAGCGATTTTGATCTGGCCCCCGTCCCAAAGCTTGCCGAACGTGCTAAACA
GGTGCGCGACGAACAGGCACGACTGGGAAGGGATGAAGGTGAACCATTACATAC
CCACCGACGAAAGTAGGCCACCAGGTGGAGGGAGAATTAAAGCATATCGCACTGAT
GGTTTGA

NHI 138 protein sequence:

MDPSHMNLPVIDLDVYLNKPRDSPEVRQECAKAADALITYGALVLHDSRVDSKDNDTF
LDLLEDYFAQPSDVLRNDERPELSYQIGVTLENTEKPKCAVDEPCLDVVRLHPSQRPL
DISGHQPDPKCRFFWRMADRPPYETDFPSLNAPNVVPDAPHIKPRWTPMDMWGTS
MKNAVSKLSEMTAVGLGLPAEYFSDAARYGPHLLAPTASDLEKYGAKDTILAGFHTDLN
FLTIHGRSRYPLNIWARNTGDRIAVKIPPGNYLLVQAGKQLEYATGGLVKAGYHEVVIN
DKTIETIEKRKQQFPDRPLVRISSTLFWHLNSDFDLAPVPKLAERAKQVRDEQARLGRD
EGEPFTYPPTKVGHQVEGELKHIALMV

Codon-optimized NHI 139 sequence:

ATGGCTGCAGAAACCTTACTTGGAATGAAGTCAGTCCTTTTGGCTCCTTATCAT
GGGCTCCAGATCTTTACCGGCACGAAGGATTTTCGGAGCCCCATACTGGGGAGCG
AGAGATTAAATAGAAAAGGTTTGCATATCTGGCGCGTTAAGACTGCGTCGCGATTGG
CTGAGTGGCGTCGGCGTCGGCTGAAACATCTCCTTCCCGAAGCGGAACGAGCCTT
TTTTGCGGAAAATGGTTACATAGAACGACGCAATCTCTTGGCCGAAAACGAATTCG
GCAACTGGTGGCAGAAGTAGAAGCCCTGCAAGCGCCAGCTCGTGAAATGCGTGAA
GGCGGCGCTGTTACACGTCGTATTCCGTTGACACCCGACGTATTAACCCGTAGCCC
GGCGCTCGCAGCATTCAATAAAATGAAGCCTGGACCGCCCCCATTTCGCTATGTGG
GGGGCTTTAATGTAGAACCGGTACTTTTGATTCAAACAATATTTGGAGAGCCGAGCG
CCCGGCCGGGGGAAAAAGACCCACAGACGGATTTACATATGGATACTTTTCATTCAA
CTGCAAAGGCATGGTTCTTCCTTTACGACGTACCGGAGGACGAAGGCCCATTCACC
TACGTAGCTGGGTCCCATAGATTAAGCGACGTCTGGCGTGGCAAAAACGGAT
GTCCGTTCTAGCGGCTGCTAGACACGGGGGCGGGGCATTTTCGGATCCCGGCCGC
ACAACTGAAGAGATTACACATGCCTGCTCCACGAAATTCGCGGTCCCTGCAAATA
CCCTTGTGGTCGGTGATACCTTTGGGTTTCATGCCCGTGGTTTGAGCGTGCGTAAA
TCTATCCGAGTTGAATTATACGCAAGCCAACGTCCAAATCCTTTTCTGCCATTTATTC
ACCTGGACAGTGCGTGGCTCCCGTTTGTGTCCGGGCGCAAAGAAGTGATCAGTTG
GTTTTTCGAAGATTGGCTGGTAAAGTTAAACTGCAACGACTTATCTGGAGACCTGT
CGGCCGAGTTAGCGCCAGGCAAACAGCGCCGGAACAAGGGTAA

NHI 139 protein sequence:

MAAETLLGKLKSVLLAPYHGLQIFTGTKDFRSPILGSERLNRKGLHIWRVKTASRLAEW
RRRLKHLLEAERAFFAENGYIERRNLLAENEFRLVAEVEALQAPAREMREGGAVT
RRIPLTPDVLTRSPALAAFIKNEAWTAPIRYVGGFNVEPVLSIQTIFGEP SARPG EKDPQT
DLHMDTFHSTAKAWFFLYDVPEDEGPFTYVAGSHRLTKRRLAWQKRMSVLAAARHGG
GAFRIPAAQLKRLHMPAPTKFAVPANTLVVGDTFGFHARGLSVRKSIRVELYASQRPNP
FLPFIHLDSAWLPFVSGRKEVISWFFEDWLVLKLLQRLIWRPVGRVSARQTAPEQG

Codon-optimized NHI 140 sequence:

ATGCCCCCGAAAACGTCTAAGTACCCTGCCCCGCAGAAAGTTACTTATACCTCAAAA
GACATACCGATACCGGATAGTTTCCTGAGTAGTCCAAGTACCACGCCGATTACCTCT
ACTCATATTGACTTCGCGAACAGTCCGCTGCCTCAATATGATGGTCATACCGCCATT
GTGCTGGATAACGTTCTGTGCGCTGAAGAGTGCAAAGAGCTACTTTCGTTGGCGGA
GCAATCAGTTGAAGGTGATGAAGCTTGGCAGCCGGCTCTCGTGTCCGGGGGTAAAT
GGGTACGAGGCCCGTGCTCCGGGCTATAGGGAATCAGACCGTATTATCTGGGATCA
ACAGACTATCGTAGATAGGTTATGGGAACGGTGCTTGGAAGCAGACGGATTACGCG
ATTTACTCGCAGTTGCCCCGCATGAGACATGGATGAAAGGAGGTAAATGGGTCTTTT
CACGCTTGAACGATCGTATGCGTTTTTTTGAATATTCTCCCGGGCAGTTTTTTAAACC
GCATTGCGATGGCGCCTATTACTATACCGAAGGTCCGGGCAAAGAATTTGAGACTTT
CTACACCCTACACCTTTATCTGAACGATTCCGTAGAGAATGACCCGACTAGCGACCT
CCAGGGCGGGCGCCACATCGTTTCTCGATCGGAAAGGTGAAAAACGTGTGGATGTG
AACCCGAAGGCCGGCTCAGTTCTCATTTTCCAACATAAAGGCTTATTCCACGAGGG
TGCGTTGGTGAAAAAGGGGATCAAGTACACTATGCGAACTGATATCTTGTACGAATG
GATCCCGGACAAAGATGCCGAGGAGAAACCTGAGACGAAAGCACCTTGGTGGGAA
TGA

NHI 140 protein sequence:

MPPKTSKYPAPQKVITYTSKDIPIPDSFLSSPSTTPITSTHIDFANSPLPQYDGHTAIVLDN
VLSPEECKELLSLAEQSVEGDEAWQPALVSGGNGYEARAPGYRES DRIIWDQQTIVDR
LWERCLEADGLRDLLAVAPHETWMKGGKWVFSRLNDRMRFLKYSPGQFFKPHCDGA
YYYTEGPGKEFETFYTLHLYLNDSVENDPTSDLQGGATSFLDRKGEKRVDVNP KAGSV
LIFQHKGLFHEGALVKKGIKYTMRTDILYEWIPDKDAEEKPETKAPWWE

Codon-optimized NHI 141 sequence:

ATGCCTAGTCGCCGTCTGAAGTCCGAGAGTGTTGCAGGCGCGGGGGGAAATCGTG
CACGTGCGACTAGATCGCATCGTTCCATCCCCTGGCGTATGCGCCGCCCGTGCTG
GACATGGTCACCGAACCCTAGTGCACGGTCGCGACGTTCCATGGTCGAAACTTCA
GCTGATCTGAGTGGGGACGTTAGTCGAAGTATACCGCTACTTGTCCGTGACCTGCC
GCGTGGATACCCCGCTCATGACACGGCCTTTTCGAGCCGTCATGGTCTGTCATGCA
AAGGCAGGACCATGGACGTAAATCGGCAACAGTTCTTAGAAGATGGTTACGTTATAC
TGCGCCAGGTAATACCACCAGATCAACTCGACAGCCTGAGGCACTCGTATGAAATT
ATGGTGGACAGGCAACGTGCTACTTGGGCCCAGGAGGATCCACCGGACGGAGTG

TGGGGGCGTGCGGCACAGCCCAGGTAAATCTGACATCCCTTGCGGATCAGATCG
ATGAGTCAACAGCCTCAACAATCGAGATATGGCTGCATGAAAATACGCAGGGAGCT
AGCAGCCAGCTTCTGGGTGTTGAAGATGCAGCCGTCACGGAAATGATGCTCATGTG
TTCGCCGGTTTTCTGATCACGGACCCGCACGATGGCATCGCGACTTCGCCCCCTGCC
CATAGTTCCCCTGTGATGGGGTATGCAGAAGATATTCTGGATAATGGACCCCGGTAT
GTGCAGTGGAAATTTATCCCTGTACGATGATGACGTAATGTGGGTCGTTCCAGGCTC
ACATGTTCCGGTGTCTGACCTCGGACGAGAACGCCCAACTAGAGCGCGATGCTCAG
GCTCCGCTGAGTAGTGGAGTACAAACGCACCTCAAAGCAGGGGACGGTGTAGCGT
ATATCCTTCCGATACTGCACTGGGCATCAAATTATAGTACTCGTATGCGGCGTACAAT
CCATGGTGGCTTTTCAATGTTCACTCATTATCCGAACCTATCATACTTAAAGCAGCTT
TCACCACAGGCCCGAGAGACCTTTGGTCGTTGGGTGAAGCGTTCGGACGATACGA
TGACTCGGACTGAAATTGCATTGCGTGCCGCGTTAGAAGCGGATGGTGCAGCATAT
CAGCAGGCCTTACAGGATCTTCATCCTGAAAGCGGCAGTATGGCAATGCGGCAAAG
TACGATTTTGCTTAGCAAGTCCGCCAAACGTATTCAGGATCTGAAGCGTCCAGCGA
GCGGGGTCTCGGAAGAAGAAGTGTCTTATGCGACGGGCATCCACCCTATGACCAT
GCAGTGCGGCCAGCCAATGGCTGATCGGTTTTCTGTGCGCCGAGGCAGGTGCGCT
GTGGGAGCGGTTTTCTGTTGGGTGACGATCGTCTGCGCGGCGATCAAGACGCAACT
TGTCCTGGTTTTTCAGGGAGGACCCACTTCATATTTTTTTAATGATGTACCTGCCGAA
CTCACAGTTGATAACTTCATCGCCCAATGGTCATAG

NHI 141 protein sequence:

MPSRRLKSESVAGAGGNRARRTRSHRSIPWRMRRPCWTWSPNPSARSRRSMVETS
ADLSGDVSRSIPLLVRDLPRGYPAHDTAFSSRHGLSCKGRTMDVNRQQFLEDGYVILR
QVIPPDQLDSLRSYEIMVDRQRATWAQEDPPDGWVGRAAQPRNLNLSLADQIDESTA
STIEIWLHENTQGASSQLLGVEDAAVTEMMLMCSPVSDHGPARGWRDFAPAHSSPVM
GYAEDILDNGPRYVQWNLSLYDDDLWVVPGSHVRCLTSDENAQLERDAQAPLSSGV
QTHLKAGDGVAYILPILHWASNYSTRMRRTIHGGFSMFTHYPNLSYKQLSPQARETFG
RWVKRSDDTMTREIALRAALEADGAAYQQALQDLHPESGSMAMRQSTILLSKSAKRI
QDLKRPASGVSEEELSYATGIHPMTMQCGQPMADRFSAEAGRLWERFRWVDDRRLR
GDQDATCPGFQGGPTSYFFNDVPAELTVDNFIAQWS

Codon-optimized NHI 142 sequence:

ATGTCTACAACACAAACCCAGACGGTTACGACAACGGTAGAGGCCCCGAAACCTAA
ATTGAGATATCTACATATTAGTGATGGGAAAGACGCAATTCTGAAAGTCATGCAGGA
GGACGGTGGCGTGGTGATTCGTGAATTCTTAACGGCGGAGCAGACCAGGCAAATT
AATCGCGATATTGATGCAGTTATCGATAAAATAGTGGATGGGGGAAAACATGCGGAT
AGTAAAATGCGAGATTTCCACGGTCTTGTGACCAAACGTATGACAAATCTGCCCACA
CATAGTAAAACCTTTCGCGACGAAGTGCTCAATCACAACTACTACATGAGATATGC
GAGGATATTTTTAGGGCTGACTCCGGTGATTACTGGATGAACACAGCACAGGTGATA
GATATCGGTCCAGGCAATGTGGCGCAACCTCTTCATCGTGATCAGATGCAATACGCT
GTCTTTTTCGGACGTTGGTTCTAAAACTAAACATGAAGCCACTATAAATTTTTTTGTTG
CGCTGACTGAATTTACAGATGAGAATGGAGCCACACGCATTATTCGGGGGAGTCATA
TATGGCCTGATCATCGTGATTACGGTACCCAAGAGCAGACTATCCCTGCCTTAATGC

ATGCCGGGGACGTGACCCTCTTTAGTGGCAAAACCTCACACGGAGGTGGCGCAAA
TCGCACAAAAGACTTTTCGACGCCGTGGAATAGCGCTCAGCATGCAGGCAAGCTACT
TGACACCGGAAGAAGCGTACCCATTTATAGTTTCCTCGCGAAATCGTTGAAACTATGA
CACCGCTGGCGCAACGAATGATAGCTTGGCGTTCTCAATATCCAGTTGACTCTGGG
GGCTTATGGCAATCAGACTACTGCGAAATTGCCGACGTTTTAGGACTGAAGGCAGC
TCCACCCGTGGCGTAA

NHI 142 protein sequence:

MSTTQTQTVTTTVEAPKPKLRYLHISDGKDAILKVMQEDGGVVIREFLTAEQTRQINRDI
DAVIDKIVDGGKHADSKMRDFHGLVTKRMTNLPTHSKTFRDEVLNHKLLHEICEDIFRA
DSGDYWMNTAQVIDIGPGNVAQPLHRDQMQYAVFSDVGSSTKHHEATINFFVALTEFTD
ENGATRIIPGSHIWPDRDYGTQEQTIPALMHAGDVTLFSGKTSHGGGANRTKDFRRR
GIALSMQASYLTPEEAYPFIVPREIVETMTPLAQRMIAWRSQYPVDSGGLWQSDYCEIA
DVLGLKAAPPVA

Codon-optimized NHI 143 sequence:

ATGAATGTGCTGCGTATCGATTTTGAAAAATCGGATGCGGTATCATTATTCGCCTCAT
CCCTTCATCAGACCGGTTTTGCGGTTCTGGAAAATCACCCGATCGACATACAGTTG
ATTGATGATATATACAAGGAGTGGATGACCTTTTTTCACTCTGAAGATAAATTTAACTA
TCAATTCATAGTAGAGACACAAGACGGATATTTTCTGCAAGTATTTCTGAAAAAGCC
AAGGGTGCCGAACAGAGAGATCTTAAAGAGTTTTATCAATACTATCCGTGGGGGGCAA
TATCCGAAGAAGTTGGGTGATAATACAAAAAACTGTATCAGCAGCTGAATCAGTTG
GCTGCGACTTTACTTTTCGTGGCTTGAAGATGAGCTGCCAGCCGCGATTGCATCGAA
ATTGTCCATGCCTCTGTCAGCAATGATAGAGCACAGTAATCAGACTATGTTAAGAATC
TTACACTATCCGCCCTTATCCGGAAACGAACCGGGCGGGGGCCGTGCGCGCGGCAG
CGCATGAGGATATAAATTTAATAACCCTGCTTGTAGGGGCGACATCGAGTGGTCTTC
AGGTAAAGGACAATCACGGTAATTGGCACGAAGTTCCGTGCGCAAAGGAATCGATC
GTAATTAATATCGGTGACATGCTGGCTCTGGCGACGGATAACTACTACCGCTCTACA
ACGCATCGCGTCATAAATCCTGATGCAAACCAGGAAGCCCGCTTGAGCATGCCTTT
GTTTCTGCACCCTGACACGAAAGTTCGTTTATCCCCGGAAAAGACTGCCGGCGAAT
ACCTCCACGAACGGCTCGTCAATTGGGAGTCAAATGA

NHI 143 protein sequence:

MNVLRIDFEKSDAVSLFASSLHQTGFAVLENHPIDIQLIDDIYKEWMTFFHSEDKFNYQFI
VETQDGYFPASISEKAKGAEQRDLKEFYQYYPWGQYPKNLGDNTKKLYQQLNQLAAT
LLSWLEDELPAAIASKLSMPLSAMIEHSNQTMLRILHYPLSGNEPAGAVRAAAHEDINL
ITLLVGATSSGLQVKDNHGNWHEVPCAKESIVINIGDMLALATDNYRSTTHRVINPDAN
QEARLSMPLFLHPDTKVRLSPEKTAGEYLHERLVELGVK

Codon-optimized NHI 144 sequence:

ATGACGACCCCGACACAGACCAGTGCCGATGAACTGGGTACACCGTATGGGGGGGC
TCACCCCAACGGCAACCGCTGATCTGAACCGCGATGGCTTTGTCCACCTGTCCGG
CGTGCTATCTCCCGAAACGATAGCGCGTTACGAGCCGACCATAACTTCAGAAAGTCA

TCCGTCTTAATACTCAACATCTGCCTCTGGCGGAACGGGATACCTACGGCAAAGCAT
TCCTTCAGGTTTCTAACCTCTGGCGCGAGAACGAACGTGTGAAGGAATTGGTGT
TCGCCTCGCTTAGCAGCGATTGCAGCCCGCTTACTTGGAGTTCATGCTGTCCGGCT
GTACCATGATCAGGCGCTCTATAAGGAGCCTAGCGGTGGCATCACTCCGTGGCATG
CTGATCAATACTATTGGCCACTTTCTTCAGATCGTACAATTACGTTATGGCTCCCGTT
ACAGGAAACTGGCTCCGACCTGGGTCCTTTAGCCTTCGCTCGCGGCTCCCACCAT
TTTTCTTCAGGACGTGATCTGCCAATTTAGACGAAAGCGAACGCGTTATCGAGCA
AGCGGTTGCAGAACAGGATTTTGAGGATGTCGTGAACCGTTTGTCTTAGGCGATG
CATCTTTTCATCATGGGTGGACATTCCATCACGCAGGCCCAACCGTGGTGCAGTA
CCGCGTCGCGTAATGACTGTAATTTATATGGATGCAGATATTCGTGTTACCGAGCCG
ACCAATGCACACCAAGTGAACGATCGTGCATGGATGCCCGGCACGGGCATTGGCC
AAGTCCCTGATACTCCGCTGAACCCAGTACTGTTTGACGGCCGGAGTTCATGA

NHI 144 protein sequence:

MTTPTQTSADELGTPYGGTPTATADLNDRDGFVHLSGVLSPETIARYEPTITSEVIRLNT
QHLPLAERDYGKAFQVSNLWRENERVKELVFSPLAAIAARLLGVHAVRLYHDQALY
KEPSGGITPWHADQYYWPLSSDRITLWLPLQETGSDLGPLAFARGSHHFSSGRDLPI
SDESERVIEQAVAEQDFEDVVEPFALGDASFHHGWTFHHAGPNRGAVPRRVMTVIYM
DADIRVTEPTNAHQVNDRAWMPGTGIGQVPDTPLNPLFDGRSS

Codon-optimized NHI 145 sequence:

ATGAACTCCCTGTTTGAACCAATAATCGACGGGATTCTAGCGGAAGGTTATGGTATT
GTCGATAATTTTCTTACAGCCAATGAGGTATCCGCACTGGCTAAACGCCTGCACGAA
CGTCGTGAGGCTGGTCAGTTTCGTGCAGCAGGGATAGGAAACCAGCAGCGCACC
GTCGAAAACACCATTCGAGGTGATGAAATCCTGTGGCTGGAAGAGGCATCAGCGA
CCCCAGAGGAGACAATGTTTCTGCAACGTATAGGTGAATTTGTTGAATATGTTAACC
GTACCTGTTATTTGGGCCTGCGGGATTATGAGTTTCATTACGCATTGTACCCCCCAG
GTACCTTTTATAAACGGCACCTTGACCAGTTTCGTTCTGATTCCCGTCGGAGATTGT
CAGTTATCTGCTATTTGAACACGGATTGGCAGGAAACAGACGGAGGACAGCTGGCC
CTCTTTCTTCCAGAGTCTGATGGTAGCACAGAACACGAACTGACTATCCAGCCTATT
GGTGGCCGTCTCGTGTGTTTTGAAAGTGGTCGCTTAGAACATGAGGTGCGGCCTG
CAGGTCGTGAACGTCTTCCGTAACAGGCTGGCTGAAAACGGCGTAA

NHI 145 protein sequence:

MNSLFEPIDGILAEYGIVDNFLTANEVSALAKRLHERREAGQFRAAGIGNQQRTVENT
IRGDEILWLEEASATPEETMFLQRIGEFVEYVNRTCYLGLRDYEFHYALYPPGTFYKRHL
DQFRSDSRRLSVICYLNTDWQETDGGQLALFLPESDGSSTEHELTIQPIGGRLVCFES
GRLEHEVRPAGRERLSVTGWLKTA

Codon-optimized NHI 146 sequence:

ATGTCACGGGTTTTAACCGATACCGCCCTGGCACAGTATCGTGACCAAGGCTACTA
CAGTCCGTTGCCAGTGCTGTCGGATGATGAAGTTGCGCGCCTGCGCGGAAAGTTA
GAGGATTTTGAATCGGCACAGGGTCACCCGATAGAGGGCGCTCAGCGCTCCAAA

GTCATCTCCTGTTTAAATGGCTAGATGATTTGATGCGTGAGGCCCGCATTCTGGATG
CAATAGAAGACCTGATCGGCCCGGATTCTCTCTGTTGGAATTCCATATTTTGGATAAA
GGAACCCAAGAGTCCCAGCTATGTTTCTTGGCACCAAGACTTAAATATTGGGGTCT
GGACTGTGACGACCTGGTTACTGCCTGGGTTGCTCTGTCTCCGGCATCTGTGGAAT
CGGGTTGTATGCGCGTCTTGCCAGGTTACATAGGAATGAAATGTTACCGCATGAA
GATATTTTCGATGCAGAGAACATGCTTACCCGGGGACAAGAAATTGCTGTAGAAATG
GATGAGGGTGCTGCAGTCACCATGGCACTACAGGCAGGCCAAATGTCTATCCATAA
CGTTAGACTGGCGCACGCAAGTGGCCCGAACAATCAGCGGATCGGCGAATCGGT
GTGAGCTTCCATTATATGCCGACAAGAAGTAGGCAACTGGTTGGTGAATGGGATAG
CGCTGCGCTCGTAAGGGGGGAAGACCGTTTTCCACCATTTTGTGCGGCCCTGTC
CCATCCTGTGATTTGGATCCGGAGGCGGTAGCGTTTCATGAGAAAGCCTCAACAGC
GGTACGTGACATTCTTTTAAAGGTGCTCACCGCGTTCGCCAGACTCTTTAA

NHI 146 protein sequence:

MSRVLDTALAQYRDQGYYSPLPVLSDDEVARLRGKLEDFESAQGHPIEGAQRSKSHL
LFWLDDLMREARILDAIEDLIGPDSLCLWNSIFWIKPKSPSYVSWHQDLKYWGLDCD
DLVTAWVALSPASVESGCMRVLPGSHRNEMLPHEDIFDAENMLTRGQEIAVEMDEGAA
VTMALQAGQMSIHNVRLAHASGPNNSADRRIGVSFHYMPTRSRQLVGEWDSAALVRG
EDRFHHFVAAPVPSCDLDPEAVAFHEKASTAVRDILFKGAHRVRQTL

Codon-optimized NHI 147 sequence:

ATGGATGATGAAGAGGAAGAATTTATTCCACCGCCTCCGCCACCAGGGCCTCCCCC
CCTGTAAAGAGAGGATCAGCTCCTGCATTTAGCGCGGCAGGGATGGCTTTTTCTAG
AACTTCCGGATGCTCTGAGCCAGTCCATGACTGATCTGCTGCGGCATTCTTCGCAG
TATTTTGATGCGCCGGATATTGAAAAAAGAGCTCTACCCAAGTAAATTAGGGACC
GAGTTTGGCTATTATCCAATTGCTGAAGAAAAAGAATACATTACCTTGCGCTGTCGG
ATTCACACCGATCCGAACGCTAAAGCGAAACCGGCGGCAAACTCGCTGCCTCAC
TTGAAGCTTCGACGGTGGACGCCTGGCACCACGCAGGAGTGTTATTATGGAGGATT
TTATGTGATATTGCCAGAGCTAGCGACTTGGATGTTTCCGTGTGGAACGATATCCTA
GACGGAACACTGGATATGCCCCGATAGCGAAGATCAACTGACATATGCTTTGATGCGC
CTTTTTCGTTATTTTCCTTCTACAGGCCACGCAGAAGAACACACTGACTTAGGTCTG
CTGACCTTATGCATAGGTGATGGGACAGGACTGCAGGTCTTAGATAGGTTCAACAG
CGATCAAAAACCCGCTTGGGTGGATGGTCCAGTCGGTACTCACACAGCAACGGTAT
TAGTCGGACAAACATTAAGGGCACTCTCTGCACGAACATGACCGCCGGGGCACAT
CGCGTTGTTGGAAATAGTCAGGGCCGCCAGTCGGTGGTTTTTTCGCTGCGTCATTC
AACCCGCCATGACGTTGATTTTCACTGTTTGGCGGGGAAGGCAAACTCCATCCCA
CGGAACGTGGAAAACCATCCAGGCAGGTAAGGTCAATATTAACACCGAGAAGGAA
AAACGCGATGCGCAACGGGCACGTTTTAGAACAAACGCGCCCAGGCGCCGAAGCC
GAAGCGCTGGAGCATGCCACCCGTGGTCAGGGATAA

NHI 147 protein sequence:

MDDEEEEFIPPPPPGPPPLLREDQLLHLARQGWLFLPELDPDALSQSMTDLLRHSSQYF
DAPDIEKKELYPSKLGTEFGYYPIAEEKEYITLCRIHTDPNAKAKPAAKLAASLEASTVD

AWHHAGVLLWRILCDIARASDLDSVWNDILDGTLDMPDSEDQLTYALMRLFRYFPST
GHAEETHDLGLLTLCIGDGTGLQVLDRFNSDQKPAWVDGPVGTHATVVLVGQTLRALS
ARTMTAGAHRVVGNSSQGRQSVVFALRHSTRHDVDFSLFGGEGKLHPTTELWKTIQAGK
VNINTEKEKRDAQRARFRTRPGAEAEALEHATRGQG

Codon-optimized NHI 148 sequence:

ATGGATTATGGCTATGCCGCAGAAGAACCGGCTGGGGATGCACCCACTGCATTTCTG
TGAAGCCGAAAAAATAACCAGCTATACCGTGAGCAGCAAATGAAGATGAAGAACG
GTAAATTACGTGCCGGCAAATTAGTGACCCGGCCACAGATATGTCAGAAGTCCTG
GATTTGCACCCCGACGCGGCTGGCAATGGCTCATTGAATGAAGCGGGGGCCACCA
GCTCTTCTGGCCAGTTCACAGCAGATGCCCTGCAGCGCGGTGAAGTTGTGAGGCA
TGTCGTTCCAGGATGTCCAGGGGCAGTATATACGTTTCGCGCAGCATGCAGGGTTAG
TATTTCTGCCGGCTGCACTTCCCGCGCAACAGCAGGCTGCCTTAGTGGCAGCCGC
ACTGGAAGATTATTGTCAGCCTCCGGCACGGACTAACCATACTCGTCTGTATGGTCC
GCTTCCGGGTCTGTGGCGGGCCGCAACAGAACGTCTGCGTCTAAATTGGACGCGT
CGCGTCGAAGAGCCTGCGGCTCCACAGACTGGCGCTGCTGCAGGCTCAAGGGGT
GGTGCGGATGAGGGTGAAGAAGAAGACGGTGGCGGTGGATGTGCTGGCCCGTCA
TATGAGCAGTGCTGGTCTCGCGACGGGCCTGGCCCTGCCGCAGAACAAATTGCTGC
GCAAGCTGAGATGGGCAACACTGGGGCCACAATTTGATTGGACCGAACGGCAATA
CGATTTCACTGGAGCCTATCGCCAGCTGCCCCCTTCCCTGTCCGATCTGGCAAGGC
AGATGGCTGCAGTAGTGATGCCCTGCAGGCTGCGGGTATGCAGCTGATGCCGGC
AGCAGCGGAAGCGGAAGTCCCTCAACAGCCGGCAGCACCGCGCGTACAGGCTAC
TGAGCCTTCGCAAGCTGCAGCTGGTGCCGTTTCGGCGGGACTGGCACCGCCTACT
GGCGCGGCCCCCGGCGGCCCTCGTGGCTACGAACCTGATGCAGCAATTGTAAATT
ACTATCAGATCGGTGATGTCCTAGGTGGCCATGTGGATGACGTTGAGTCAGATCTC
GCACAGCCGATCGTCTCTGTGAGCCTCGGTTGTCCGGCGCTGTTTTTAATGGGAG
GCCGAACGAAAGCAACTCATCCGTCAGCCCTACTTTTACGTGGTGGTGTGACTC
GTGCTTGCGGGCCAGGCCCGCTCTTGCTATCATTAG

NHI 148 protein sequence:

MDYGYAAEEPAGDAPTAFREAEKKYQLYREQQMKMKNGLRAGKLVTRPTDMSEVLD
LHPDAAGNLSLNEAGATSSSGQFTADALQRGEVVRHVVPGCPGAVYTFQAHLVFL
PAALPAQQQAALVAALEDYCQPPARTNHTRLYGPLPGLWRAATERLRLNWTRRVEEP
AAPQTGAAAGSRGGADEGEEDGGGGCAGPSYEQCWSRDGPAPAEQLLRKLRWA
TLGPQFDWTERQYDFTGAYRQLPPSLSDLARQMAAVVDALQAAGMQLMPAAAEAEV
PQQPAAPRVQATEPSQAAAGAVSAGLAPPTGAAPAAPRGYEPDAAIVNYYQIGDVLGG
HVDDVESDLAQPIVSLSLGCPLFLMGGRTKATHPSALLLRGGDVLVLAGQARSCYH

Codon-optimized NHI 149 sequence:

ATGTCCACGTCTGAGGCACTGGTAGCAGAACAGGTTATAGACACAGGCCGCTATCC
GTTGTCAGAACAGGAGGTGCAGCCTGGCGGGAAGCAGTGTCGGCAACCCATCG
CGAATTAAGGGAAAGTGTTGTAGTGTTCTGCCAGACTTCGTGCGCGCCGAGCTG
ATTGGTGCGCTGCGCGCAGAATGCGTCCAGGTGGCCCCATTGGCACACTTTGACG

TCGAGACAGTGAACGCATACAATATCGCCTTAGATACACCGCTTCCAGAAGACCATC
CCGGGCGGACAACAATGGAGCGGGGGAATGCGTTTCGTTCGCACGCGACAGAATAC
CGGCACATTATTTGATTCAGCAGCTGTACGGTTCGGTCTGTTTCAAAGATTTGTAG
CCGACTGCTTTGAACTGCCTCAGGTGCATGAGCTCGCGGACCCTCTGTCCGGGTT
AGTCTTAAACGTTGTATCTCCCGGATTATCACACCCTTGGCACTTCGATACTAATGAA
TTCACGGTGAGCATGCTTACCCAAGAGTCAGAGAGTGGAGGCGTGTTTGAATACTG
CCCGAATATAAGGAGCGCGGCGGCGGAGAATTTTGATGACGTTTCGTGCGGTTCTG
GCTGGTCGCGGTGATCACTTGATACGGCGTTTATCCTTACGGCCAGGCGACCTCCA
GCTGTTTAAAGGACGATATAGTTTACATCGCGTTTCAACAGTTGATGGGGAAACGGC
ACGCCACTCCGCAATATTTGCGTACTCGGAACGCCCGGGCGTGATTGGCTCGGTT
GAACGTACCCGCCAGTTGTTTGGGAGAGTGTTGCCGGATCATTTAGCCGCCGCGG
GTAACGCAGTACGTGGGGATCAGCTCCTTGATTAA

NHI 149 protein sequence:

MSTSEALVAEQVIDTGRYPLSEPGGAAWREAVSATHRELRESGCSVLPDFVRAELIGAL
RAECVQVAPLAHFDVETVNAYNIALDTPLPEDHPGRRTTMERGNFAVARDRIPAHYLIQQ
LYGSGLFQRFVADCFELPQVHELADPLSGLVLNVVSPGLSHPWHFDNEFTVSMLTQE
SESGGVFEYCPNIRSAAAENFDDVRAVLAGRGDHLIRRLSLRPGDLQLFKGRYSLHRV
STVDGETARHSAIFAYSERPGVIGSVERTRQLFGRVLPDHLAAAGNAVRGDQLLD

Codon-optimized NHI 150 sequence:

ATGTCCTCGCTTGAGGAACAGCTGCTGGGCTTGCGCGACTGTATACAAAATAAACC
CCCGTATTGCTCTGGTACCCTAAAGTTGCCTAGTGAAGATTTCTCTTGTAATATGG
GAAAGGTGATGATGTTTCGTCTGTTGATTTATCTACGGCTACCGAGGAGTCGGCAAA
ACACCTGGCAGAGAGTTGTGACAGTGCGACTTTTGGGTTGAACAACCAGGACGTAT
TAGACGAGAGTTATCGTAAAGCTGGAAAGCTGGATCGAAAACACTTTAGTGCGGCC
TTTGACCTGGCCTCTACCGGCCTGTTGGGCATCATTGAAACCGAGTTGATCGAACG
CAATAAGGAATCCCCTTCAATAAGAGCTGAACTGTATAAACTTAATGTTTATGGACCG
GGGTCGTTTTTCAAAGCTCACCAAGGACACCCCGCGGTCAACAGATATGTTTGGCAG
CTTAGTGGTGGTGTATCCAACAGTGACGAAGGGGGGGCGCTGGTATTGAGGCAC
GGCGGCAAAGAATGGACATTTGATTCGTCTCGGTATCATAGCCGATCAAAAAGAACC
GCGCCTAGCATATATAGCATTTTTTAGTGATGTGCAACATGAGGTGCTGCAGGTTCA
ATCAGGTTATCGCATTACCATCACATATAATCTGTACTATAATAGCCCGCAGCCCAGC
GATTTACCTGTGCGGCCGTTGACCTTTGAATCTAGTCTCAAAGCTGCTCTGCAGCA
CCTACTTGATGATCCAACGTTTTTACCCGAAGGTGGTCATCTGGGCTTTTGTCTAAG
CCATCAGTACCCGGTTGAAAGCGATCGCGGGGCAGGTGCAAAGCTCTGAGCGAA
GTATCCGGCATGTAAAGGGATCTGATGCGTCCTTGGCTTCGGTTTTTACAGCGCT
GGGACTTAGAAGCAGACTGGAATTCGTCTGGAGGATAACGAGGTCTGGATTGAG
AGTGAGGAGGGCGGATCAACTCACATGATTGCGTATGTTTTATTTGATGAATATGCG
CCGGATATAGAAGAAACAACGGTAGAAAGTCAGCTGTTTCAAGTTCTGCGCGACAT
CGGTGGCAAACCTGGCGACCAGAATTCGCCCGCTCTACCCAGGCAGGAACGCGATT
GAACCCGCTGTACATGTGCATTGGGTGGTCAGTCCAAGTAGCAATACAGGTTTTAA
TTCAAACCCGATACCTCACATATGGGAATGAGGCTTTACCTGGAATGCAGTATACC

CATCTTTGCATTTTGGCTGATGTGGGGGATTCCAGCGAACGACGTCGTTTCATGGTAT
AGTCGTGTGGGCGCGCGAAGATAA

NHI 150 protein sequence:

MSSLEEQLLGLRDCIQNKPPYCSGTLKLPSDFLLYYGKGDDVRRIDLSTATEESAKHL
AESCDSATFGLNNQDVLDESYRKAGKLDRKHFSAAFDLASTGLLGIIETELIERNKESPS
IRAELYKLNVEYGPSSFFKAHQDTPRSTDMFGSLVVVYPTVHEGGALVLRHGGKEWTFD
SSRIIADQKEPRLAYIAFFSDVEHEVLQVQSGYRITITYNLYYNSPQPSDLPVRPLTFESS
LKAALQHLLDDPTFLPEGGHLGFCLSHQYPVESDRGAGAKALSEVSGMLKGSDASLA
SVFTALGLRSRLEFVVEDNEVWIESEEGGSTHMIAYVLFDEYAPDIEETTVESQLFEVLR
DIGGKLATRIPLYPGRNAIEPAVHVHVWVSPSSNTGFKFKTRYLTYGNEALPGMQYTH
LCILADVGDSSERRRSWYSRVGARR

Codon-optimized NHI 151 sequence:

ATGTGGCTGAGTAATAACCGTAAACCAGCAACTACGGGGCCACCTGTGATTTTAGA
GACTTCATATACGAGCAAAGAGGTGCCCATACCAGATACATTCCTTACGACTCCGCC
GCCTGATGCCGAGCCGATCACCGCCAATATTATCGATTTTTCTTCATCATCGCTGCC
GGAATATAAGGATTATTACGCGGTTATATTAGATAACGTGTTGAGCCAGTCGGAATGT
GCCCAGTTATTATCGCTGGCGGAACAGTCCGTTGAAACAGGTGAAGCCTGGAAACC
GGCATTGGTTAGTGTTGGTCCGGGTCGTGAGGCTTTGATGACAACTATCGTAACT
CGGATCGCATCATTTGGGACAATGATGTTATCACGTCACGCCTCCTGGAGCGGTGC
TTTCAGGCAGACGGAATTCGTAAACGTCTTTCTGTAATCGCCGGCGAACAGTATCG
CGGGATTCTTGGGGCGTGGGCACTGGAGAGTGCACAAAGCTGGCAGGTAGTCAA
GCTAAATGAACGCATGCGCTTCTTAAGGTATACTAACGGGCAATTCTTTAAAGCACA
CTGTGATGCGCCGTACACGACCGGCAATCAGTGACCTTTTATACTGCAACTGTA
CCTATCTGATGGAAAAGAAGACGAATCAAAACGCTTGGTGGGCGGTGCTACCACCT
TTTGGAGTCGCGATGAGCGTCGCCGCTTGGATGTTTCATCCCAAACCCGGGCGGGT
CCTGATTTTTTCAGCATAGGGGATTATATCATAGTGGCGATCAAGTACTCCAAGGGGTT
AAATATACGATGCGTTCGGATATTCTGTACAAACCGGAAACACAGGGGAAATGA

NHI 151 protein sequence:

MWLSNNRKPATTGPPVILETSYTSKEVPIPDFTLTPPPDAEPITANIIDFSSSSLPEYKD
YYAVILDNVLSQSECAQLLSLAEQSVETGEAWKPALVSVGPGRREALMTNYRNSDRIIWD
NDVITSRLLERCFQADGIRKRLSVIAGEQYRGILGAWALESQSWQVVKLNERNMRFLR
YTNGQFFKAHCDAPYTTGNQCTFYTLQLYLSDGKEDESKRLVGGATTFWSRDERRRL
DVHPKPGRVLIFQHRGLYHSGDQVLQGVKYTMRS DILYKPETQ GK

Codon-optimized NHI 152 sequence:

ATGACCCTGTGCCGTATCTCAGCCTCGGCTATTCTGTCGTAAATCGTATGACGCTT
TGCCGTTTATTTGCTCCGAGCTACCGTGTGCGTGTGAGCTGTTATTCGGTGGGTAA
CCGCGCCATGTCTTGCTCCCGATCATCGGAGCTGATGAGTGTTTCCCCACCATTAC
AACCGCAGAAGTCAGCCGATTCTGCAAGTAGCAGTAGTGGTCCCAAGATCGGGGG
TTGCCTGGAAAACGAAAGCTCAGATGACTGGAATAGCCATGAGAAATGGTTCTCCC

TGCGCAATCCCCAGATCCAGGACGATTATCGCGCCTATCCTATGCCAACGCCAGGA
CGTATTTTTAGTCCAAAACGCGTAGTGAATAACGATTTGCACAATGAAACCTCACCAA
GCTTCCGCCCCCTTCAATATCTGCTACCCGGAAATGCGTATCTCCGGGCGGGGCACC
CCGGTTAAATTAATGCCAGCTTGTTTACCCAGAACAAGCAAAAGCGGATGGAGAA
CGAATGCCTTAAGAACGGCATTGAATGGCATAAACTAGGCCCTGGAATGATCCTGTT
AAAAAGTTTTTTAGGTCACGATAATCAGATCGAAATAGTGCGTATTTGTCAAAAACCTG
GGGGCGGGTCCTGGCGGCTTTTATCAGCCGGGCTATTCCGACGGTGCTAAGCTTC
GCCTAAAGATGATGTGTCTTGGGAAAAATTGGAATCCACAGACAAGCGCATAACGAG
GATACATGTTTCGACGGGAGTAAACCGCCGGACATTCCGAACAAATTTAAGGATCTG
GTACTACGGGCCATCACATCAAGTCATGAGTTACTGAAGCAGGAAAATCGCTTCGC
GGACGTAAAAAAAATTTTACCTAGTATGACACCAGACCTATGCATAGTAAATTTCTATA
GGAATACTGGTTGTCTTGGCCTGCACCAGGATAAAGATGAAAGTAAGGAATCCATTG
GTCGGGGTTTACCAGTAGTTAGTTTTAGCATTGGCGACTCAGGTGATTTCTTTATG
GTAAAAACGCGATGAGAAAAAAGCGTCTCGTATAAAGTTGGAATCGGGCGACGTA
CTGATTTTTTGGTGGAAAATCCCGGGATGTATTTTCATGGCGTACCTTGTATCCACAGG
GATACCATGCCCAACTGGTTACGTGATGAAAGCCGTCTATTTCCGGGCGCCTGAA
TCTGACGTTTCGCAAGTATTGA

NHI 152 protein sequence:

MTLCRISASAILSLNRMTLCRLFAPSYRVRVSCYSVGNRAMSCSRSELMSVSPPLQP
QKSADSASSSSGPKIGGCLENESDDWNSHEKWFSLRNPQIQDDYRAYPMPTPGRIF
SPKRVVNNDLHNETSPSFRPFNICYPEMRISGRGTPVKLNASLFTQNKQKRMENECLK
NGIEWHKLGPGMILLKSFLGHDNQIEIVRICQKLGAGPGGFYQPGYSDGAKLRLKMMC
LGKNWNPQTSAYEDTCFDGSKPPDIPNKFKDLVLRITSSHELLKQENRFADVKKILPS
MTPDLCIVNFYRNTGCLGLHQDKDESKESIGRGLPVVSFSIGDSGDFLYGKKRDEKKA
SRIKLESGDVLIFGGKSRDVFHGVPCIHRDTMPNWLRLDESRLFPGRNLNLTFRKY

Codon-optimized NHI 153 sequence:

ATGTCAGATAAAATGAACCTTCCTATCATTGATCTGTCTGGATATCTGAATCCGGAGT
CGCTGGAGGATCGTGAGCGTGTGATCGCCCAAGTGCGCGATGCATCCCGGCAGTA
TGGTTTTTTCCAGGTACGCGGTCATGGAGTGCCCCCGAGCCTCCAACACGATCTGA
TTCGATCAATGGGTAATCTGTTTCAGTTTACCTAAAGAAAAGAAGTTAGAAATGTCTTT
TCTCAAGAACCCGTGTAGGCGGGGATATGAAGCGGCGGGTATGTCTCTGCGAGAA
GGGGATCTACTTCCTGACGCCAAAGAATGTTTTTATATCGCCCGCGATGATCCGATT
ATCGAGCTTAGTGGCTTCTATGGTCCCAATCTGTGGCCTAATCTGCCAACCGAAGAT
TTTCGCGACCCGGTTTGGAATATTATGAACAGACTAGCGAACTTGGTAAGAAGATT
TGGTCTATTTTGTAGAGGGGCTCGGTCAACCGCCCAGTTTAGTGAGAAATTTGC
ACGCCGCGCGATTGTACCGATGAAGATGATTCGCTATCCCCCGCAGTCAATTACCT
GCCGGGCCAATTTGGCATTGGCGCGCATACCGACTTCGGTGGCGTCACGATTCTC
TTCCAACAACAGGTAAAGATGGATTAGAAGTGTGGCATGAAGGCAAAGAGACGTG
GATCGAGGTTCCGGCTCTGGAAGATGTTTACGTCATTAATTGCGGTGATATGATCCA
ACGATGGTCCGGAGATCGGTACAAGAGTGCGCGTCACCGTGTAATTAATAAGTCCC
AGGGCGAACGGTTATCCTGCGCTACGTTTTGGCATGGCGACATTAACGCCACTAAT

CCTTTAAATCCCGACGATCTTAATTCAGAAACAGTTGGCCAGCTGCTGGTGAAGAG
ATTTAGAAACCAGTATAGTATGACCGAAGAATCTATTGCGCAGGTTGGTGCGGCGTA
A

NHI 153 protein sequence:

MSDKMNLPIIDLSGYLNPESELEDRERVIAQVRDASRQYGFFQVRGHGVPPSLQHDLIR
SMGNLFSLPKEKKLEMSFLKNPCRRGYEAAGMSLREGDLLPDAKECFYIARDDPIIELS
GFYGPNLWPNLPTEDFRDPVWKYYEQTSELGKKIWSILLEGLGQPPSLVEKFARRAIVP
MKMIRYPPQSITLPGQFGIGAHTDFGGVTILFQQPGKDGLEVWHEGKETWIEVPALED
VYVINCGDMIQRWSGDRYKSARHRVINKSQGERLSCATFWHGDINATNPLNPDDLNSE
TVGQLLVKRFRNQYSMTEESIAQVGAA

Codon-optimized NHI 154 sequence:

ATGCGTGGAGTAGATTTTTACACAAAGCGGGCCAAGGATATGTTGATCTGCCTCC
CCGTCTTGTGCATTAGATGACCTGCCCGAAGTTCGTCGTCATTAGATGGCTTAGC
AAGACTGCGCCGCAGGCCTGGCCCTGATGCTAGTGCTCGCACCACTGCCGCATTA
GCAGCATTGTTATTGGAATAACACGCTCAGGCGGCCAGAGCCGCAGGCGATTTACC
GGCGCTGATGGATCGCAGGGTGCACGATGTAGTGGAATGGCTGACTAGGCACCCC
GCACGGAGACTAGATGTTACGCGAGCGGCGGCGTCAGCGGAGTTATCAGCAGATC
AGTTTTCAAGGCTGTTTCGCCGCGAGACCGGGCAGTCACTGAGAGCCTACCAAATA
GCCGTGCGTATTGATCGCGCGCGGGAACCTCCTCGCCGAATCGGGTATGACAGTCT
CCCAGGTAGCGCGCGTTCTCGGTTATGCAGATCATCGCCTTTTCGCCAGACAGTTT
AAAGATCACACCGGCACCGCACCGGCATCCGGCGGAGCTCCGAGAGAGCGTACA
CCCGATCGGTCATCAGCCCGCAATCCACGTCTCGCTCCGTCTCCTGCGGGATTG
CATGGGCATATAGACGACCGATGACATATATCGTTCCTGCAGATCTGTACCGTGCGG
ATCGGCTGGCTCCGCTGCTGGATAGCATTAAACGAAATCGGTGCGGCAGAGACGGA
TGCCTATCGCTCTCTTGGGTTTCTCGCAGTTAGATCCCTGCTTACCGATCGCGATGT
TCGGGGAGTGTTAGACGGACTGGCCGTCGTAGCGCGGCCGCCGAGCCCGGCCTC
AGTGGAATTTGAGGAATGGGCGAGACCGGAAGAACGTGACCGCGATGAACTTTTA
GATGGAGTACGCAAACTACAACATTTTTGTGTCCATGAACCGCGGCTAGCCGAGCT
CGCACGGCACCCGGCTATCCTGGCGACCGTTGCCAGATTTCTCGATGCTGAACCT
GTTTTGATCCAGGATATGGCGCTTTTGAAACCACCGGGACGCGGTGCGGAAAAACC
GTGGCATCAGGACAAAGCTTTTTTTGATATTCGCTCGGTGCACCAGTGGTTGGAG
TTTGGATTGCTCTCGATGAAGCCACTATCGATAATGGATGCATGCACATTCTGCCTG
GAACACACACTGAAGGTCCGGTGGTCCACTTTGTCCGCAGAGATTTTCAGATTTGC
GACACGCAAGTCCAGACACACCGTGATACAGCCGTTCCACTTCCGCCTGGTGGCG
CCCTGTTTCTGGACGGATTACTGCACCACGGGACCCCGCCAAATCTGACGGACAC
TCGTCGGCGGGCAGTTCAGATGCACTATGTTCCGGCCGGGACCATGCGGACACCG
CAGGAAGATAGACTGGAGGTTTTTCGGCGCTGATGGTAAAGATGCCACTTGTTAA

NHI 154 protein sequence:

MRGVDFSHKAGQGYVDLPRLVHLDDLPEVRRHLDGLARLRRRPGPDASARTTAALA
ALLLEIHAQAARAAGDLPALMDRRVHDVVEWLTRHPARRLDVHAAAASAELSADQFSR

LFRRETGQSLRAYQIAVRIDRARELLAESGMTVSQVARVLGYADHRLFARQFKDHTGTA
PASGGAPRERTPDRSSARNPRLAPSPAGFAWAYRRPMTYIVPADLYRADRLAPLLDSIN
EIGAAETDAYRSLGFLAVRSLLTDRDVRGVLDGLAVVARPPSPASVDFEEWARPEERD
RDELLDGVRLQLHFCVHEPRLAELARHPAILATVARFLDAEPVLIQDMALLKPPGRGRE
KPWHQDKAFFDIPLGAPVVGWVIALDEATIDNGCMHILPGTHTEGPVVHFVRRDFQICD
TQVQTHRDTAVPLPPGGALFLDGLLHHGTTPPNLTDTRRRRAVQMHYVPAGTMRTPQED
RLEVFGADGKDATC

Codon-optimized NHI 155 sequence:

ATGATTCAGCTCCCATTAATTGTTCTGTTCAATATGATGACCAGTTTCTGAGCCAGA
AAGAATCAACAGCCCTGTACCAAAAACCTGAAGCTTTGTATTGCGACTGCACCTCAGA
AAATCGATCTCCCTAACGGGGAACACATTCTCCTGGAAGCCCCGAAGACACAGTTC
GCACTGCCTGAATTCATTGCCACCGAAAAAATGCATAAGGCCCCAGGGCGAAATACA
AGTCATGTTCCCAGAGCTGGAACGTATTAAGCAGAAGCTGGAGACACTTACTCAGA
GGCGGTTAGATGTCTGTGTTGCAATTTATTATTCAAGCGGAGCGGTTGGCGTTGACT
ATCATTCTGATTTGAGCGCCTTCGGTGATACTTCTTGCATCCCAAGCATCTCGCTCG
GTGCGACCAGGACGTTTAGCCTCCGGGAAAACATTAATCACGCCAATTCATATGACC
TGGAGCTGGTACACGGCTCGTTAGTTATTATGGGAGAAAATTGTCAAGAACATTATG
AGCACGCTATTCTTGCTGATCCAAGCATTCAAGAAGACAGAATCAATCTCACATTTT
GTACATTCGGCGGTCTGAACTAA

NHI 155 protein sequence:

MIQLPLNCSVQYDDQFLSQKESTALYQKLKLCIATAPQKIDLPNGEHILLEAPKTQFALPE
FIATEKMHKAQGEIQVMFPELERIKQKLETLTQRRLDVCVAIYYSSGAVGVVDYHSDLSAF
GDTSCIPSISLGATRFTSLRENINHANSYDLELVHGSLVIMGENCQEHYEHAILADPSIQE
DRINLTFRTFGGLN

Codon-optimized NHI 156 sequence:

ATGCGCCTTAAATTGAATGAGCTCCAGGATCAGTTTGAAGAAGTTGGAGCCATTTCG
CATACCGAACTTTCTTTCAAATCCGACCTAGACACGATAAAAGAACTCTATTCAGAA
CTGAAAATAAAAACTTAAAGGAATATACTCAAATGTTAAAGATAAGAAGCCGGAAC
TCAACTACAAAATAAATGAGACGTTGAAGTCGTGTTACAAAAAGGCAATAGATCAGC
ACTTTATCGACTATCAAATTGGCGGAGGCGCCTTTCTTATAAAGGGCACTGGGGAG
GGGAGCGAATCAAGCCTACACCAGGATTGGAATATTGTAGACGAATCACAATATAAA
TCGGCCGCTATATTCTGTCCAATCCAGGACGTTGATGAGAAGAATGGCTGTATTCAA
GTTGTGAAAGGCAGTCACAAATGGTTTAATAATATCAGGAGTTTCAATATCAGTAGCA
TATTTTTGAACTTTAACGACGTAGAGAAACAGCTGATTCCCTTCCCGGCAAAGGCAG
GTGATGCGATTGTGTTTAGGCATAACGTGTTTCATGGCTCTAAGCCTAACTTCACCA
ACGATATTCGCATTGCAGCTTCCATGTCTATAGCCACCAAGAACAGCCCGTTGATAC
ATTATAAAAAATCAGGAGATAATGTGATTACGTTTCGTGTTAACGACCACTTCTTTAAC
GAAGAAGTTCAGCAGCTGTACCAGAACAAGGAGATAAATATTGATATTATAGACGAAA
AACCCATTTCAGAATTTCAAATTCTGGATCAGAAAACCTTTCGCGAATCATTATAAAAA
GAATAAATCAAAAGGCATCGTGAATCGAATTAAACACATCTTGTTCCGCTAA

NHI 156 protein sequence:

MRLKLNELQDQFEEVGAIKIPNFLSKSDLDTIKELYSELKIKNLKGIYSNVKDKKPELNYKI
NETLKSCYKKAIDQHFIDYQIGGGAFLIKGTGEGSESSLHQDWNIVDESQYKSAAIFCPI
QDVDEKNGCIQVVKGSHKWFNNIRSFNISSIFLNFNDVEKQLIPFPAKAGDAIVFRHNVF
HGSKPNFTNDIRIAASMSIATKNSPLIHYKKSGDNVITFRVNDHFFNEEVQQLYQNKEINI
DIIDEKPISEFQILDQKTFANHYKKNKSKGIVNRIKHILFR

Codon-optimized NHI 157 sequence:

ATGAACTTACATAGCATCGATGATGGGTTTACACATGCCGAGTGTTCTGCGATCATT
CTGCCGTTGCAAGTGCTCCAGCGAGAGAAGCTCTGCTGGTTGGTCAAAATAGGGA
TCATAATCTGCGTCGAGCTAAACTGGTCTGGCTCGATGAAATTGATGGTATGGCTTG
GGTGATGGAACGTCTGATTGATGTAGTACGTACAAGTAATAGGAATTGGTTTGATTTC
GATCTTCGAGAGTTTCGAGAGTCCCCTCAAGTCGCGAGCTACGATGCTACCGATGG
TGGTCATTTTACGTGGCACAGCGATATTGGTGATGGTCCCATGGCCCATAAACGCAA
GCTGACCCTGGTTGCTCAACTGTCTAAGCCGGGTTTCATATGATGGTGGCAACCTCG
AAGTAATGCCTGGCGCACACATTATTGCCGCTAATCGCACCCAAGGAAGTATCACCA
TCTTCCCTTCCCTTCACTTGTCATCAGGTCACCCCAGTCACCCGTGGCACTCGGAAT
TCCCTGACTGTGTGGGCGCATGGGCCGAAATTCCGGTGA

NHI 157 protein sequence:

MNLHSIDDGFTHAECSAITAVASAPAREALLVGQNRDHNLRRAKLVWLDEIDGMAWVM
ERLIDVVRTSNRNWFDLREFAESPVASYDATDGGHFTWHSIDGDPMAHKRKLTL
VAQLSKPGSYDGGNLEVMPGAHIIAANRTQGSITIFPSFHLHQVTPVTRGTRNSLTVWA
HGPKFR

Codon-optimized NHI 158 sequence:

ATGGCATCTGACCTCAAAGACTTTTATACGCGTTTACGATGGCGTGCTGGATCCCAAT
CTTTGCAACAACGCCATCAAAGTGTGATGAAACACCAGATGCCCAGGACCGCTG
GGATAATCAGCATAAACCACAGTTCACGCAGATGAATATAACTATGTTATCCGAACAG
CAGAGAGACCCTAAATGGGGTGTGATCCATAACAACATTATAGCATCAATTCAGACC
GTTAGCGAATACTATATGCGAGATACTGGATGTTCCCCGTTCTGGCCGCCGAAGAAC
TCTATAGAGCAAATTCGTATGAAAAAATATACCGCTGAATCAGGTGACCGGTTTGATC
TGCATATAGATGTTGGAGATTACGCCACTGCCCGCCGGTTTTTAGTGATGTTTTCTA
TTTAAACGATGTTGAAAAAGGTGGTGAAACGTCGTTTCCGGCGATTGAACTTGATAT
TAAACCGAAACAAGGCTCGGTCTTGTGTTTTCTCCCGTGTGGATGTATCCACATTT
AGGCAAACAGCCGATTTTGAATGATAAATATATCGTCGGCACCTACCTTCATTATCAG
TGA

NHI 158 protein sequence:

MASDLKDFIRVYDGVLDPNLCNNAIKLFDETPDAQDRWDNQHKPQFTQMNITMLSEQ
QRDPKWGVHNNIIASIQTVSEYYMRDTGCSPFWPPKNSIEQIRMKKYTAESGDRFDLH

IDVGDYATARRFLVMFFYLNDVEKGGETSFPALIELDIKPKQGSVLCFPPVWMYPHLGKQ
PISNDKYIVGTYLHYQ

Codon-optimized NHI 159 sequence:

ATGGCTCAAGCTCTGGATCTGGTTGCCTATGAGACTCTTGAAGAACAGGTCTGAAGC
AATGTATCGTGATGGCTTTGCATATTTACCGGACGTTCTCAATGCTGACGAGGTGGC
AGCGCTGCGCGCCCAGATGGACGCACTTACACCGAGACCCGAATCATACGATAAAA
ACATGACTGCGGAGGAGGACGGGTTTATCAATCGTCACGTTAACAATGCCTTTAACC
GGCATCCCCACTTTCTGGGCTTTCTCGATCGGGAAGCGGTAGTCGATATCGCAGAA
GCGATCCATGGGGACGATTGTCATTGCTTAGGAATGACTGCATGGATGACTGGCCC
TGGTCGTCCGGACCAGGCACTGCATACAGATTGGTTACCGCTAGAACTTCCACCAG
ACATCCTTGCCGACCCCAGAGTGCGTACGCCTATTTTTATAACCACCGCGCACTATT
ATCTTGATGATCTGTATGAAGAATTAGGACCAACCAATTTTATCCCGGGCTCGCATCT
GTCCGGTTGTAAGCCTGACGGGGCTACAAGTTGGCAGGGCCAGGAAGAAAGAAG
CATTATGTGCAAAGCAGGAGATGTTGTGATTTTCCGTTCCGAGGTTTGGCATCGCG
GGACTGCAAATACCTCTGACCGCACGCGTTTCCTGCTGCAGGTACACTACTCCATG
CGGATGATCACCCAAAAGTATCCGCCATACATGGGACGCTTTAAGTTTGACCCCGC
GATTCTGGAAGCCGCAAATGAACGGCAACTTCGACTTATGGGCGACCATAAGAAGA
GCAACTATGATTAA

NHI 159 protein sequence:

MAQALDLVAYETLEEQVEAMYRDGFAYLPDVLNADEVAALRAQMDALTPRPESYDKNM
TAEEDGFINRVNNAFNHRPHFLGFLDREAVVDIAEAIHGDDCHCLGMTAWMTGPGRP
DQALHTDWLPLELPPDILADPRVRTPIFITTAHYLLDLYEELGPTNFIPGSHLSGCKPD
GATSWQQQEERSIMCKAGDVVIFRSEVWHRGTANTSDRTRFLLQVHYSRMITQKYP
PYMGRFKFDPAILEANERQLRLMGDHHKKSNYD

Codon-optimized NHI 160 sequence:

ATGCTGTCTAAAGAACAGGTCACCCATTTGAAACCTTTGGATTCTGGTACTGAGA
AACGTACTIONTAGAGACGAGGTGGACATTATGATAAAGGAATCGGAGGAAATATTT
TCAGAGCTACGCCAGGGGAAACCGTTACGGCCCAAGAAAGAGAAGCTGTGCAGC
CTTTTTTCGAGAGAAAACCTTTTTACTCTATTGCTTGCAGGACGATCGTATTTATAG
TATCGGAGAATCGATTCTGGGCTCTGATTTTATGTTGGTTGTTACAGAGGGCAACTT
ACATGTAGGTGACACGCCGTGGCATGCGGGAGAGGAGGCAAGGGTTCTACGCACC
GTTAAAATAGGTTTCTATCTGGAACCGTTAACAATTAACACCGGTAGCCTACGCGTG
ATTCCTGGCACGCACAAGATTAGTAGCCAGATTATTTTAGTATTCTCAAAACAGCAA
ACAAAACAGTGACTTTATGCCCTTCGGCGTCTCACCCAAAGAAATCCCCTCGTAC
CCTATTCAAAGCGATCCGGGTGATCTGATAGTATTACCGAATCTGTTGTCCACGCA
GCTTTTGGAGGTAGGGATGGGCGGCACCAACATGCTATCAATTTTTGTGAGTATCCT
AAATCTGAAGAGCTGATAGCGTTTACCAAAGACTGGTATTCGAGAACCGTTAACATAT
TTCGACCTCCGATTTCAAATATAAATAGCGACAATGCCAGATTACGACGTATGTCTGA
AGGCTGGCTTCAGCTAGGATTTGAACCAGTGAACATTTGA

NHI 160 protein sequence:

MLSKEQVTHFETFGFLVLRNVLSRDEV DIMIKES EEIFSELRQGKPFTAQEREAVQPFFE
RKPFLHSL LADDRIYSIGESILGSDFMLVVTEGNLHVGDTPWHAGEEARVLR TVKIGFYL
EPLTINTGSLRVIPGTHKISSPDYFSILKTANKNSDFMPFGVSPKEIPSYPIQSDPGDLIVF
TESVVHAAFGGRDGRHQHAINFCEYPKSEELIAFTKDWYSRTVNIFRPPISNINSDNAR
LRRMSEGWLQLGFEPVNI

Codon-optimized NHI 161 sequence:

ATGGTAGAAAATTCGCAGCAGCTGTCCTCGCAATACGACGAGCATGGATACTTCGT
CATTCGTA ACTATTTTAATGAGGCCCAAATTGCAAGCCTCAGAAAAGTTGTGCTTAAA
TTTCACGAAAGTTGGAAGGCTGATAATGAGGAGTTTACCAGGAAGAGGCATTTAAT
TCCTCCTTAATTACAGGTT CAGAATATCTGCCTACCGAAGACCGCAGGGTTCTTTT
ACTTTATATCCAGCAAAAAGGTTATGGAAGTTGTGCGATGCCGTAATACCTAACAAACC
GGCTTTTATGAATACCCAATTATTTTAAACCCGGTAAATCCTCAACAGAAAGATTTT
GGCACCGCGATTGCCAGTACGATTATGATATTGACGATCAGATGAAAGTTATTATGGA
AACGCAGGTTCTGCATCTGCGGGTGCCACTTTTTGACGAGCCGGGCATGGAGCTG
ATCCCTGGTACCCATAAACGGTGGGATAATGAGGAAGAATATAACGTTCCGCCAGGAA
GAAATGGTAAAGTATCGTCTGATGATATTTCCGGTGGCAAGCAAATTCCGCTGGCG
GCGGGTGATCTATTAGTCTTCAGTGCGGATATGATCCACCGCGGGCGTTACGGTCT
AGATCGTCTGGCGTTAGACATCCTCATCTTTGATAGCGCTGCTGACTACGTTGATTA
CGTTGATGACGATTGCCTTCCTACACCAGCAATGTTAAGCAATATAAGCGACCCGCG
ACTGTTTATGAACACGCTGCACTTGAAGTCCATGCAATACTCCTGA

NHI 161 protein sequence:

MVENSQQ LSSQYDEHGYFVIRNYFNEAQIASLRKVVLKFHESWKADNEEFYQEEAFN
SSLITGSEYLPTEDRRVLFNFISKKVMEVVDAVIPNKP AFMNTQLFFNPVNPQQKDFW
HRDCQYDYDIDDQMKVIMETQVLHLRVPLFDEPGMELIPGTHKRWDNEEEYNVRQEE
NGKVSSDDISGGKQIPLAAGDLLVFSADMIHRGRYGLDRLALDILIFDSAADYVDYVDDD
CLPTPAMLSNISDPRLFMNTLHLKSMQYS

Codon-optimized NHI 162 sequence:

ATGAAA ACTGACGCGCGCGCCCTGGATAGCGCGCTTGAGCAGTTTCGTGCCGAAG
GCTATACCATTATCCGTAATTTATCC CAGCAGATGAGGTGGCGACCTTGCGGGCCG
AAACCAAAAAATTATACGAGACTGCGATCGCGCATCACGCGACCTACAAGCATGGG
AACCTTACCTATGAGATCTTACCGGAGGCCCATTTCCGGTGCTCGCTATGTCATCAA
GCATATTGGTTCGCGTGGGCCAGTGAGTATTTTGATAAATTTCCGGTCACATCCGGCA
AATCTTGAGTTACTGGAACCGCTGATTGGTAGGAATATTAAACAGGTAACGCAACAG
ATCCATTGGAAGCCGCGGGAGCCTCTCTGACCGGATACCGATTTACCAGGACCT
GCGCTTTCGGGAGTCGAAGGAAGCATTTGAGGATGTGGTGCGCGATTCCGGTTACC
ATTGGTGTGCTATCGATCCGGCAACCAAAGATAATGGATGTCTGAGAATCGTCCCC
CGGTCTCATACTAACGGTTATTTGGGCCTATCAGATAACGGCGAAGGGAGCATTATG
AAAGGGCTGACCCATAACGATGAGCTGCTGGCCGTCGGTTTAAATCCTGACGACAT

ACTGGATGTTGAGCTGGAACCAGGGGATGCTGTGGTTTGGGGTCTTCTGACGGTG
CATGGTTCCCTGCCAAATTCCTCCGCAAACGATCGAGCCTTTGCTTTAAGTTCTTAC
GTGCGTGGCGAAACGTCCCAACGTGGTGAGTGGGCATTTAAAGATGGTGTGGGAA
CTCGTCTAGGTGCAACACCACAGCTGTGTAAAAATGAACGCCTGTTTGATAACCTTG
AACCACATTATGATGAAACTAAATGGTTCCTGTAA

NHI 162 protein sequence:

MKTDARALDSALEQFRAEGYTIIRNFIPADEVATLRAETKKLYETAIAHHATYKHGNLTYEI
LPEAHFGARYVIQAYWFAWASEYFDKFRSHPANLELLEPLIGNIKQVTQQIHWKPPGA
SLTGYRFHQDLRFRESKEAFEDVVRDSVTIGVAIDPATKDNGCLRIVPRSHNTNGYLGSL
DNGEGSIMKGLTHNDELLAVGLNPDDILDVELEPGDAVVWGLLTVHGSPLNSSANDRA
FALSSYVRGETSQRGEWAFKDGVGTRLGATPQLCKNERLFDNLEPHYDETKWFL

Codon-optimized NHI 163 sequence:

ATGCGGGTTCTTCTGGCCGATGAGCCTGGGTTCATGAAGGGCTCGTGCAAGCAG
ATTCCACCGCGAAGCCTCAGTTACCGAGATCACCTCCTATTTGGGCGGGTTCAAGA
CAGGAAATTTGTGAGAATTTAGAATACTTCCGCTCATATCAGGGTGGTGTCTTACTTCA
AAAATGATATAGTTCGGGGCTACCTGCTGGGGGCTTTTTCGGGCAAGCCGTGATCTT
TTCTGCCATGATGGGAAACTCATTATCTCGCACGGTGGTGGAAAAAGTGAAAACTTT
GTAGGAAGCAAAGAAGGCCCGCCAGCTGCGTAGCGCGCAGGACCAGACTACGTCT
GACACATCTGTGCGTGCTCTCCTGCGTAACTATAAAGAAGGACGTCCGTTAGTGTTA
TTAGCAGATGATCAGTACACCCTGTTTCCTTATGATCTGTCAGCATCAGGTTATACGT
ATGTGGTCCTGGGTATCTATTGGATATCCCATGCTTGGGCCGAATGCCAGCCGACC
CTGACTAACAGTACATGCGTAATCCGTTGGAAATTCGCTTTTTCAGTGGTGGCAGGAT
CAGGGCTCCCCGTGGTGGCTGACTCCGGAGGGGGTTCGTGGCTTCATTACCGGAG
CCATTAGTCGGGAAAACAGATCCGGATTTTCATTGTACCCAGTGCCTATGGGAGTCA
CCAGTTGTATACAAACAGAGTGGGATGTGTCTGATTCCGGGGCTGCGCCGGTTTTTG
GAAGATAAATGGCAAAGAACCTGAAAGCCTGGAGTATAGCGTTGAATTTCTGCGTCT
GCAACCGAGAACTTTTCGAAATCTTACCGACGCTCACTCCAGCCGCTGGGACCCAC
CAGATTACTTCATCTCTGAGCTGCCCAGGCTGGCATTGCACTGATTGCGGTCTGTCT
ATCTTCTCGTTTCAAGTGGGAGTGCTGGGAGTGCGCACATTGCCAGGCAAACCAA
CCTATTAAGTGGGAAATACGCCATGCCAAAGATTTTTGGCATTGAGACCAACCAAT
TATTTTACCGATCTACGCATTGCCCGAAAGTCCGGTATAACCAAAGCCTCCCGGAT
GTCATAGATATGGGTGGGGGTAGGGGATTTATGACTCGCCAAACCTTTGTACTTCCA
TCCGACCGCGGAAAGATTCATCTGATAACCACAGGCCCACTGTGCAACCGAGAAGT
GGACGAAATTTTCCAGGGTTATCAGAAGCAAGCGTCTTGTGGCGAACTGAAACTTC
AACGATATCCCTTACGCAGCGTGCGGCTCTTTCATCCGGCTATCCGTGGCACACTG
CTGGCCAACTACTTTTCCCAAATTCGGGCGAACCGTATAAATACGTTGGTGAAACC
GCAAACCTCTGTGCCTTTAGACGAAGCACCCAACTGTGTGCAGGCAGCCCTGGACG
TTATTAATAAGCGGGTGGATCTGGCCGTAAAGCAAAAATCTCAGTTCAATGAAGTCC
TTACAGCGGCGTATTTGGCTACCAAAAAATGTCTTTTCATAGTGATGACGAAAAAG
GATTAGGTCCGATCGTTGCCTCCCTGTCCCTTGGCAGCCCTGCCGTGATGCATTTT
AGACACCACACAAGTGGAGCTGGGCAAAATCAACCTAACGAAATCGTCATGAGCTT

AATTCTACGCCACGGTAATGTGCTTGTATGGAAGGATGCGGGGTACAGATACACTA
TGAGCATAACAGTTATACCGACCGATTTCCGTATAGCAGCCACAGCACGTTGGATCAA
CCCATCTTAA

NHI 163 protein sequence:

MRVLLADEPGFHEGLVQADSTAKPQLPRSPPIWAGSRQEICENLEYFRSYQGGVYFKN
DIVRGYLLGAFAASRDLFCHDGKLIISHGGGKSENFVGSKEGRQLRSAQDQTTS DTSV
RALLRNYKEGRPLVLLADDQYTLFPYDLASGYTYVVLGIYWISHAWAECQPTLTNSTC
VIRWKFAFQWCEDQGSPWWLTPEGVVASLPEPLVGKTDPDFHCTQCLWESPVVYKQ
SGMCLIPGCAGFWKINGKEPESLEYSVEFLRLQPRTFEILPTLTPAAGTHQITSSLSCPG
WHCTDCGRLSSRFKWECAHCQANQPIKWEIRHAKDFWHLRPTNYFTDLRIARK
SGITKSLPDVIDMGGGRGFMTRQTFVLPSPDRGKIHLITTGPLSNREVDEIFQGYQKQAS
CGELKLQRYPLRSVRLFHPAIRGTLANYFSQNSGEPYKYVGETANSVPLDEAPNCVQ
AALDVIKKRVDLAVKQKSQFNEVLTAAYLAHQKMSFHSDDEKGLGPIVASLSLGSPAVM
HFRHHTSGAGQNPNEIVMSLILRHGNVLMMEGCGVQIHYEHTVIPTDFRIAATARWIN
PS

Codon-optimized NHI 164 sequence:

ATGAGCGGTTCGCGATTTATTAGGCTTACCGCTTGCCGCCCTTGCGGTATTTACCAGC
GCGAAATCTTTTCGCGATAATCCAGTGCTGGGGAACCGCTGGCTGAATCAGCGGG
GGCTGCATGTTCTGCGCTTGAAGCTTGCTGCCGGCCTCGCAGCCCGCCGTAGACG
CCGCATTTCCCGGCGTATCCCAGCGAGCTTGCTGCATCAGTTCGAACAAAACGGTT
TCATTTGTATTGAAAATTTCTGCCGCAAGCTGAATTCGGAGCCTGCAGAAAGAAG
TGTTAAACCAGCCATGGGATAGATATGATATGACTCAAGGCACAACAACACCCGCC
GAGTTTTTTTAGATGGTGTGGAAGTGAACGGTTATCACCGGCGCTGCACAATCTG
ATATCTCGGCGTGATCTGAAAGATCTCATTGCTATGTTGCCGGTACTCTTGCTGAA
CCTGTGTTTAGCCTGCAGGCGATATTTCTGGTGGGACGGGTAAACACCCCTGACCC
GCAGGCGAGCGTCCACAGTGACACATTTCACTCTACAGCCAAAGCTTGGCTGTTTC
TTGAGGACGTTTCAGGATGAGGCAGGACCTCTGTCATATGTGCCTGGCTCTCATCGT
TTAACTAGCCAGCGTCTGGCGTGGGAGAAAATTCAGTCCTTGACAGCAGCTGAATC
GGCAATTACTTATCATGCCCGTGGTAGCTTTCGCGCCGCGATGAAGGACCTAAATG
CGATGAATTTGCCGTGCCACACCGTTTTGCTGTACCTGGCAACACGCTAGTGATC
GCGGATACACACGGCTTCCATTGCCGTTACGCCACTAGAATACAAACAACACGGGT
GGAAGTGTATGCGAGTCTTCGTCGAAATCCTTTCGTGCCGTTTGGCGGTCTGGATA
TACTGTCGTGGCCGTGGTGCCGCGAAAGGTCAGGCTCTCTTTACTTAAAAGCGATG
GAGTTCGGTAGAAGGTTTCGGTTCAATTCGTATGCCGTGGAAGCAAGTTGGGCATGG
TCTCCTGAAGCAGAGCTAA

NHI 164 protein sequence:

MSGRDLLGLPLAALAVFTSAKSFRDNPVLGNRWLNQRGLHVLRLKLAAGLAARRRRRI
SRRIPASLLHQFEQNGFICIENFLPQAEFRSLQKEVLNQPWDYDMTQGTTRRVFLD
GVELKRLSPALHNLISRRDLKDLIRYVAGTLAEPVFSLQAIFSGGTGKHPDPQASVHSDT
FHSTAKAWLFLEDVQDEAGPLSYVPGSHRLTSQRLAWEKIQLTAAESAITYHARGSFR

AAMKDLNAMNLPCHRFVPGNTLVIADTHGFHCRSATRIQTTRVEVYASLRRNPFVFP
GGLDILSWPWCRERSGSLYLKAMEFGRRFGSIRMPWKQVGHGLLKQS

Codon-optimized NHI 165 sequence:

ATGTACCAAATTTCTAATAACATCTATTGCCAAAAAGACATTTTAGATCTGGAGATCCC
CACCAAACCTTCTCACCAACCCATACTATGACTATCCGTATCTGATCATAGAGAATTC
TTTTCTCAGAAAATTCTGAAAGAGCTGTGTGAGATGTTAAAATCCAATTCGGATGTCTG
AAGATGCCAAAATTGCAAAAATTAACGATCTGAACATCTTAGACAAGAAATTGGATAA
GTCAATCCGGAAAACGAAGATACATAAATTACCTAAACGTTATTTAAATATTTATGAGA
AAAAATTCATTTTTTCATCAGAAAAAAATTGAGGAGTTTTTTAAATTAGCGCTCACCACT
AGTACCAAGGTGCAAGTTTTACAGTATACTGAGGGATGTTTTTACAAGGCTCACAGC
GACGACTCGAATATGATCGTAAAAGATGATAAATTAGTGGGGTTTTTGCCGGTGGCC
CTGCAGAGAAAAATTACCACCGTTTTATTCTCGACGACGAATATGAGGGGGGCGA
ACTGGTGTTTAATTATCTGTATGACAAAGATGGAAATGTGGTTCAACTGAAAGGGCG
GAGCGGCGATATGATTGTTTTTCTGTCAAACCCAGTTTATACCCACGAGGTTAAAGA
GGTTATTTCAAGGCAACAGGTTTACTTTGGTGCAATGGCACGATGCCATCATCAACTG
A

NHI 165 protein sequence:

MYQISNNIYCQKDILDLEIPTKLLTNPYYDYPYLIENFFSQKILKELCEMLKSNSDVEDAK
IRKINDLNILDKKLDKSIRKTKIHKLPKRYLNIYEKKFIFHQKKIEEFFKLALTTSTKVQVLQ
YTEGCFYKAHSDDSNMIVKDDKLVGFLPVALQRKITTVLFLDDEYEGGELVFNYLYDKD
GNVVQLKGRSGDMIVFLSNPVYTHEVKEVISGNRFTLVQWHDALIN

Codon-optimized NHI 166 sequence:

ATGCTAACGCCTGACGAAATTGGGCGTCTGCGAGATTTTTGTGATGAATGGTTCGG
GGCAGCAGACACCGACGAGATGCCGGCCTCAGTCTTCCTGCGTACCCCGGAACTG
GCTCGAATTCCTTTACGTGAAGACGTAGTGGCGCTTCTTAAGACTGTGTATGGCGAA
TCCTATGTGCTTTATCCTAATTTTATAGTAAGGAAAAACCTGTATGTCGGCTGGCACA
TTGATCCTGCATTGCGAGGTCCGGATAAGCGCTATGTTTGAAACCTGGGTTTTTAC
ATTTCCAATGTGTTATATATTTACAGGACAATGACCGCGAATTGGGCGGCGGGCTAG
ATGTTATATCAGGTTTCGCATCGTCCGGTGCTTCGCTTCATATCAGGACGCAGTCCCT
TTGGTTATTATGGCGTTCAGTTTGCGAGACGGTTACTTATGCCCCGCGCGAAACATA
CCCTGCGCATCAGAGCAGGGGACCTCGTGATATGGCATGGGCGCGCAGTGCATCG
GTCGACTCCAATGCGTCGCCAGACTCGAGAAGCAAATACGCTCTCTTTTCTCTAC
AGGACAACGTGACCGCTTCGCTACGAACCAAGTTTTTGGCTGACATGGTTGGCCATC
GATACCAGTTAAAAAAGGGGCGACACAATACAGTCCCCGATACGCTGAGCTGCCT
GACCTGCACTATCCAGACGCATTCCCTCCGGAAATGGTGGAAAGTGCAACAAAACA
TTCCGTGGAAGTTGTCACACTTTAA

NHI 166 protein sequence:

MLTPDEIGRLRDFCDEWFGAADTDEMPASVFLRTPELARIPLREDVVALLKTVYGESYV
LYPNFIVRKNLYVGWHIDPAFAGPDKRYVWKPGFLHFQCVIYLQDNDRELGGGLDVISG

SHRPVLRFISGRSPFGYYGVQFARRLLMPRAKHTLRIRAGDLVIWHGRAVHRSTPMRR
QTREAKYALFFSTGQRDRFATNQFLADMVGHRYQLKKGATQYSPRYAELPDLHYPDAF
PPEMVESATKHSVEVVTL

Codon-optimized NHI 167 sequence:

ATGGCACCGGCAACAGAAGCGGCCCTACAGCAGACCCGGCGGGCGGGCGGCTTTG
GCAGCAGTCGAACGCCAGGCAGCTCGCGCAGCATATTTGCGAGACGGTCGTCTGT
TATTTCTTGAACGTTTCTTGCCAGAAGCTGCATTGCGCCCGTTACAGGAGGAAGCA
CAGCGTTTGAAACCTAGATTACATCGTAATTATATACCTCGTCATAAAAAGGGGGGCG
CCGTGGGTATCCGACATTACGTGCAGAAGCGCCCGCCATCTTAGCGTTGTACCGG
AGCGCGGGCGCTTTTGATTTTGTGCGGGCGTGACCGGGGAGGCAGTACAGCATT
GTCCGGAAGATGACCCCCATGCATGTGCTCTTTACTATTATACTGAACCTGGGGATC
ATATCGGCTTTCATTACGATACCTCTTATTATCGGGGGCTGCGTTTTACCTTGCTGGT
TGGCTTAGCGGACCGTTTCATCGTCGCGACTGGTTTGCAGGCTTCACACGCGCGAC
CCGGCGCCGGAAGAAGAGGTGGCTCTGGCTACACCGCCGGGTTGTCTGGTTTTGT
TTGATGGAGATGCACTCTATCATGCAGTTACGCCTCTTGGGCCGGGGGAGGAGAG
GATTATGCTGACACTGCAGTACGTCACCGATCCCCGGATGGGTCTTGCCCATCGTT
TCGTTTCCAACATGAAAGATGCTATAGCCTATTTTGGCCTCCCGGCTTTACGCAGAC
GCCGACCATAA

NHI 167 protein sequence:

MAPATEAAPTADPAAAAAALAAVERQAARAAYLRDGRLLFLERFLPEAALRPLQEEAQRLK
PRLHRNYIPRHKKGGAVGYPTLRAEPAILALYRSAALLDFVAAVTGEAVQHCPEDDPH
ACALYYYTEPGDHIGFHYDTSYYRGLRFTLLVGLADRSSSRLVCR LHTRDPAPEEEVAL
ATPPGCLVLFDG DALYHAVTPLGPGEERIMLT LQYVTDPRMGLAHRFVSNMKDAIAYFG
LPALRRRRP

Codon-optimized NHI 168 sequence:

ATGGCCCCACAGCGCCGAGGTGCCCCGAAAGCTGAAGGCAGCGGTGCGGCCGA
GCGTGGTCGACCCTCTTCTACAAAGAAAGATCAAGTCCCCCGTGAGGCACAGCGT
CCATGGCTCAAGACCGTAGGTTTAGGAGCAGGACTGGTCCTTGTGGCGTTACTTCT
GTGGAACAGTCTGGGCACTGACGATGGTATCGCAGAAGTTCTGGCACTGCGAGGA
GAAGTACTTGCGGGCCGCTTCATTGAAGTTCCGTGCAGTGAGGATTATGACGGCCA
CCGTGCGTTTGAAGGATGCACCCCGCGAAAGTGTGGTCGAGGAATAACCGATATT
GTTATAACAAGGGAAGAGGCAGATCGTATCAGAAGTATCGCCGAAAAGGGCCTTTC
TTTAGGAGGCTCCGATGGCGGCGCTTCCATTTTGGACCTGCACAGTGGGGCACTAT
CGGTGGGGAAACACTTTGTGAATCTTTATAGGTACTTTGGCGATAAAATACAAAACAT
TTTTTCCGAAGAAGACTTTCAGTTGTATCGCGATGTTAGGCGTAAAGTTCAGCTCAC
GATCGCAAATGCATTTGGTATTTAGCTTCCAGTCTGTACTTAACGAAGCCGACATT
CTTAGTCGTATTAATTCTACCGAAGCGAGAACTGCGCACGATGAGTACTGGCATGC
ACATGTTGATAAAGTAACTTACGGCAGCTTTGATTATACATCTCTTCTCTATCTGTCAG
ATTATCTTGAGGACTTTGGAGGTGGGCGCTTTGTTTTTCATGGAGGAGGGTGCTAAC
AAAACAGTAGAGCCTCGCGCAGGCCGAGTTTCTTTTTTTACGTCCGGAAGTGAGAA

TTTGCATCGGGTTGAAAAAGTGAGATGGGGCACGCGGTATGCTATAACTATCGCCTT
TACTTGTAATCCAGATCACGGTATCGAAGACCCGGCCCTCACTTAA

NHI 168 protein sequence:

MAPQRRGAPKAEGSGAAERGRPSSTKKDQVPREAQRPWLKTVGLGAGLVLVALLLW
NSLGTDDGIAEVLALRGEVLAGRFEVPCSEDYDGHRRFEGCTPRKCGRGITDIVITRE
EADRIRSIAEKGLSLGGSDGGASILDLHSGALSVGKHFFVNLRYRYFGDKIQNIFSEEDFQL
YRDVRRKVQLTIANAFGISASSLYLTKPTFFSRINSTEARTAHDEYWHAHVDKVITYGSF
DYTSLLYLSDYLEDFGGGRFVFMEEGANKTVEPRAGRVSFFTSGSENLHRVEKVRWG
TRYAITIAFTCNPDHGIEDPALT

Codon-optimized NHI 169 sequence:

ATGGCGACCAGCTATCCCACATTCACGCTGAGTGAACAACCTACCGCGGAACAGCT
GGACTTCTTTAACACGCATGGTTTCATCCATTTCAAGAACTTTATTAAGCCCGAGACC
GTATCATCGATTATCGATGCTTCGAAACAGGTTGAACAGAAATGGATTGAACAGGAC
ATTAATAAATCAATGGCGTTCCTATTAAGTACGGTAAAGACTTGGATGGGTCAGCC
ATTGTGCAGCGCTTCGCCTTTATAAATCAACAACACCAGACCCTGAGCGGTCTGTTA
CTGGATCCTCGCTTTAATGCCTTACTTCAACTGGCCGGAGATGGAGCTCGGCTTGG
AACGGAGGAAAAAGATGGGATGGTATTCAATCATTATATAAACGGCCCGGATTCTAAA
TTAGCAAGATGGGCTGGCATACTGACGGTCTGAGAGATATCTTTTATGGTGCTAAA
TTAAACCCAATGCTTAATGTAGGCATTCATTTATCGACCTTAAAACCGGAAAATGGGG
GTCTGAAAATCATCCCTGGCACCCATAAGCAGTCTATCTATCAAATGCTTTTTAGAAA
GAAGTACTTCTTAGATAATAAACCGGATGCAGAAAGAGGTGAGCATACTGCCGGAGG
CCGGAGACCTGACTATTCATGATGGGCGACTGTGGCATCGCGTCGCCGAGAGCGC
CATTAGAGGTGAAGAAAGCCGTAGGCGTGTGATTTATGTGCCAATCATTGCTGGCAA
ATATGCACCTAAGAATGAGAATAGTCCTACCGTATTTTATCAGCGGTTTGCCGGTATA
GTCAAATAA

NHI 169 protein sequence:

MATSYPTFTLSEQLTAEQLDFFNTHGFIHFKNFIKPETVSSIIDASKQVEQKWIEQDIKKIN
GVPIKYGKDLDGSAIVQRFAFINQQHQTLSGLLLDPRFNALLQLAGD GARLGTEEKDG
MVFNHYINGPDSKFSKMGWHTDGLRDIFYGAKLNPMLNVGIHLSTLKPENGGLKIIPGT
HKQSIYQMLFRKKYFLDNKPDAEEVSILPEAGDLTIHDGRLWHRVAESAIRGEESRRRV
YVPIIAGKYAPKNENSPTVFYQRFAGIVK

Codon-optimized NHI 170 sequence:

ATGACAACGGACTATTGCCCCCATGGTCGGGACTATTATAGAAGAATTGGATTTGGC
AAGGCTGAAATCGTCGTTACAGGTTCTAAACGCGCCGTGCTGGTCGCGATGTTAGC
AGGTCCGGATGGACAGGCAAGGCGTGAAAGCGCCGTTCGCGGCCCGCATAAGGCG
CCATAATCGAATTGGTTTTGTAGTGCACGCGCCCCCACTGATATACGCTCCCTGGC
ACGTAGCGGCGTCGAAGCCCTACGTGCGGGGACGCCAGAGCTGCAAGAGAAAG
CTTCGAACAGATAGTTGCTACGGGTGAGGCAGATGCCAGTGCCTGCGTTGGGCTG
GCATATGCGTGTGCTCCTTGAAAGACAATGCCGCTTCGAAAGCCGCGTTAGACAA

AGCACTGGCCTTAGAACCGCGAAACTTGCGTGCACTTATACTGAAAGCAGACTATTT
TGCAGAAGAAGGTGATGCGCGAGCCGCAAGTGCCTTCTATCTTGCCGCGGTAAAG
ACCGCACCGCCAGCTGATCAACTGCCACCTGACCTTAGAAATGAAGTGGGTGCGC
CAAAAGCAATGTGTGATAGGTACGCCGCGCAATTTGAGGCGTTTCTCAAAGATCGT
CTCTTAGGGGAACGCCTGGCTGATGGGCGTGACGCGCGCCGCTTTACGCACTCTT
TAGATATTCTGTTCCGTAAAAAAGATTTATTTCCAGGATCCCCGATACTATTTCTTC
CCGGGTTTACCGCAAATACAGTTTTATGATAGAGAGGACTTTCCATGGTTAGATAAAA
TAGAAGCAGCCACAGCAGATATCCGCGCCGAAGTATCGAGGTTTTAAAGAAGAA
TCTACCTTTAGTCCTTATGTCCAAGGTGAGTCTCGCCGCCACATAATGAACAAGAG
GGGATGCTCAACAATCCCGCGTGGTCCGGCATTATCTGTGGAAAGACGGAGCAGT
TGATGCTGATCATGCCGCTCGCTGCCCTGGTACAATGAAGGCCCTGGCCGAGGCG
CCGCTTACTCATGTTACGGGCCGTAGCCCGGCCGTTCTTTTTAGCCTTCTCCGTCC
CGGTACCCACATCCCCCACACAATGGTTTTGTAAACACGAGATTAATTTGTCATTTA
CCTCTGATCGTACCCGGAAGTTGTAGTTTGCGGGTGCGAAACGATACCCGTGATCT
GGTTGAGGGAAAAGCGTGGCTTTTTGACGATACGATGGAGCATGAAGCATGGAAC
GACTCGGATCAGACTCGTGTTATCTTGCTATTTGAAATATGGAGACCGGAGCTAACG
GCAGAGGAGAGGCGACTGGTGTCCGCGATGTTTGAAGCGATAGATGATCATAGCG
GTGAAAAAGCCGCGTGGGGGATATAA

NHI 170 protein sequence:

MTTDYCPHGRDYRRIGFGKAEIVVTGSKRAVLVAMLAGPDGQARRESAVRGRIRRH
RIGFVVHAPPTDIRSLARSGVEALRRGDARAARESEFQIVATGEADASACVGLAYACRS
LKDNAASKAALDKALALEPRNLRALILKADYFAEEGDARAASAFYLA VKTAPPADQLPP
DLRNEVGRAKAMCDRYAAQFEAFKDRLLGERLADGRAARRFTHSLDILFGKKKIYFQ
DPRYYFFPGLPQIQFYDREDFPWLDKIEAATADIRAELIEVLKEESTFSPYVQGESSRPH
NEQEGMLNNPAWSAFYWLKDGAVVADHAARCPGTMKALAEAPLTHVQGRSPAVLFSL
LRPGTHIPPHNGFVNTRLICHLPLIVPGSCSLRVGNDTRDLVEGKAWLFDDTMEHEAW
NDSDQTRVILLFEIWRPELTAEERRLVSAMFEAIDHSGEKAAWGI

Codon-optimized NHI 171 sequence:

ATGCTGACAATTACGACTGTTGAGGAACTGACCGCCGCGCAGTTAGACGATGTCAT
TCATGCAAGGACTCTTGGTATACTGATAAAAGGTTTCGCCCCGGCAGACACCGTAG
CTCTTGCGTTAGAACGTCTGTCCCATCATGAATTACGTGGTGCATTTTCTGAACAGA
CCGAATTCGTACGCCTTGGTAAAGCCTATATCGAGATACGGGACGAAGCCTCCAGA
GCTGAATATCACGGGCAGGCGATAGCGAATATAAGAAAGATCCGCAGTGCGTTTGG
CCCACTGGCGTCGCCTATTGATCATCTGCGCTTGTTATTAGACGAAGTGTGGCCCA
AAGGAGCCAGACTCCTAGATGTGAACGGCCGAAAATGTTTCGTTGGGATTGCACGG
TTTCAGGGTAACAATGTTGACCTGACACCGCATACCGACGATTTAGCCCGTAATGCA
CCGGCCGATCACCAGCCTAGACTCTTGACTCAACTGTCCACGAACATCTACCTACA
GATTTCCCGAGGATGGCGGCCGAAGTAGAGATTTGGAACCTCCATCCGGATGAAGCC
GAATATGAACGATTACGTGGGCAGCGTGCTTATGGTATCGAACGCCACCTATTACCT
CCTCCTGATCTCGTGGTTAAGCCAGAGGCGGGAGATCTGATTTTTTTGAACCCACG

TTTAATTCACGCGGTGCGTCCTTCCGCCACATCAACCCGCGTTACACTCGGTGTATT
TATAGGTTATTTTGGAGACGATCAGCCTCTCGCCTATTGGTCGTAG

NHI 171 protein sequence:

MLTITTVEELTAAQLDDVIHARTLGILIKGFAPADTVALALERLSHHELRGAFSEQTEFVRL
GKAYIEIRDEASRAEYHGQAIANIRKIRSAFGPLASPIDHLRLLLDEVWPKGARLLDVNG
RKCFVGIARFQGNVLDLTPHTDDLARNAPADHQPRLLTQLSTNIYLQIPEDGGELEIWN
LHPDEAEYERLRGQRAYGIERHLLPPDLVVKPEAGDLIFLNPRLIHAVRPSATSTRVTL
GVFIGYFGDDQPLAYWS

Codon-optimized NHI 172 sequence:

ATGATTCAAATCAGTAATGAAATTTTTTTCGACAAACGCCTCCAAGAATGGGATATTG
CGAATAAAATCTTGCCCAATCCATACTATGATAAACCGTTTCTGATTATACCTAATTTTC
TGGATAGCGCCCTGGCACATGAAATCGCTGATACTATTTACCAAGAGCAATATGCTC
AAAAAGCTCAGATTAAAAAATGCTTCTGCAATCAGTTGTTGAGCCAGATGTTAATGA
AACGATCAGAAAGACAAACCTCTATACATTGAATCCATTTACACGCGCGTTATATGAA
ACACTGTTTAAACTCCACCAGCCACAGATAGAACGTTTCTTTAATTTGTCCTTGACC
CTGGCCACGCCGATTCAAGTTTTAGAAATACACGCAGGGCAGCTTTTATATCAAACAT
GCGGATGATTCTAACGAACTGATCGATAAAGAGGGTAGTACAGTGGGTTTCACCTG
CGTTGCACCCCAACGTAAATTAACGACGGTTTTATTTCGCGACTAGCTTTTCATGAAGG
GGTTGTCGCACAGGATGATAACAGCATTTTTCAGGTGGGGAAGTCTGTTTAACTA
CCTGTATGATAAGGACGGTAACGGCATAGCTTTTAAACCACGCGCGGGCGATATGAT
ACTCTTTCCAGTAATCCATATTTTAGCCATGAGGTCAAAAAGGTTACATCCGGTTAC
CGGTTAACTCTGGTCCAGTGGCATAATGCTATTGTGAGCGGCTGCTGA

NHI 172 protein sequence:

MIQISNEIFCDKRLQEWDIANKILPNPYDVKPFLIIPNFLDSALAHEIADTIYQEYQAQKAQ
IKKMLLQSVVEPDVNETIRKTNLYTLNPFHTALYETLFLKLHQPQIERFFNLSLATPIQVL
EYTQGSFYIKHADDSNELIDKEGSTVGFVCVAPQRKLTTVLFATSFHEGVVAQDDKQHF
SGGELLFNYLYDKDGNIGIAFKPRAGDMILFPSNPYFSHEVKKVTSGYRLTLVQWHNAIV
SGC

Codon-optimized NHI 173 sequence:

ATGAACGAACACTACGATATCAATCAGCACGGTTCCAAAGCGAAACGTCTACGCCC
CTCAGAGGAAGCAAAACAGATTGCCTCAACCGCTCATACAGATGATAATCAGGAGA
GCACTGAGTTCAAGCTGGCCGTA CTGCGCATCTCTGCATCCGGATAAGTCGCCCCGAA
GTTCACTTAGATTACCTTCTGGCCTATCAAGGAAGCGCCTATAAAGCTTCCCAGGCT
CTGTCTGGGCAAAGCAGACCACGCAGTTAAGCGTAAAAGGCCGTCAACGATAGCATA
CCAAAGTAGCCTTGACTCGTTTGCTAGTAGCCGGGGACCGGCCAACGGCCCTGCG
ACAGGAAGCGGCAAACTGTTAACAAAAAAGGGCAAAACGCTGCATCTGTACACCCC
ACGTGAGATAGAGGAAAATACTCCATGTTCTATTATACATAATTTTCTTCTACTGCAC
AGGCTGATGCGTTATTGAAAGAACTATTGGAAGAAGCACCGAGCATGAAAAGAGGG
ACATTCCAACGTGTTTGAACGTACCGTTCAGAGTCCTCACACCTGGAAATTCTATGTG

GATACGCTTGAAGATGTGAAAGTGCAAAAAACAGAATATGTGTATGACGGTATATATG
AAGCGGACGTCAGTCAAACAACCCCGGAAATGCTGAAAGTCAGTAAAATCGTGAAG
CAGACGGTAAACAAAGAGGTGGAACGCCGTATGCGTGATTTTCAGCCTGAGGGCA
AAAAATTACGCTTTTCACTCTCCGACATCCTGGGAGCCTAATGCAAGTTTTGTAACT
GCTATGACGGAGCAAAAGAAAATGTTGGTTGGCACGCAGATCATTTGACATATCTGG
GTCCCCGTGCTATAATAGGGTCCTTATCACTGGGTGTGGCGCGCGAATTTTCGTGTA
CGTCGGATCGTCCCGCAAGTGAAGCGGCTAGCGCCGATGAACAGGGTCAGATCG
CTATCCATCTGCCACACAATCACTCCTTGTTATGCACGCAGAGATGCAGGAAGAAT
GGAAACATTCAATCGCAGCGGCTCAGACAATTGAACCTCATCCGTTGGCCGAAAAC
AAGCGCCTTAATGTTACCTACCGATGCTACCAGCCTTATTTAAATCCGAAATTCACCC
CACGTTGCCGCTGTGGCGTCGCGTGTGTACTGCGATGTGTACAGAAAAGGCAAGT
GACCCGTGGCCGGTACATGTGGATGTGTTACGCGAACTATACCCCGGCCAGAAAG
GATGCAGCTATTTTGTGGGCGGAGTTTGACGAGGATGGTCGCCCGCCTTGGGC
CGAAGGTTACCTAGGTAACGCCAACAAGCCTGAACCAGGAACAGGCAGATGGGAT
GAAGATTCCACGCTACCAGCATAA

NHI 173 protein sequence:

MNEHYDINQHGSKAKRLRPSEEAKQIASTAHTDDNQESTEFKLAVLASLHPDKSPEVH
LDYLLAYQGSAYKASQALSGKADHAVKRKRKPSTIAYQSSLDSSFASSRGPANGPATGSG
KLLTKKGKTLHLYTPREIEENTPCSIIHNFLPTAQADALLKELLEAPSMKRGTFLFERT
VQSPHTWKFYVDLTEDVKVQKTEYVYDGIYEADVSTTPPEMLKVSKIVKQTVNKEVER
RMRDFQPEGKKLRFQSPTSWEPNASFVNCYDGAKENVGWHADHLTYLGPRAIIGSLS
LGVAREFRVRRIVPQVEAASADEQGQIAIHLPHNSLLVMHAEMQEEWKHSIAAAQTIEP
HPLAENKRLNVTYRCYQPYLNPKFTPRCRCGVACVLRCVQKRQVTRGRYMWMCYAN
YTPGQKGCSYFVWAEFDEDGRPPWAEGYLGNANKPEPGTGRWDEDSTLPA

Codon-optimized NHI 174 sequence:

ATGGCAACCCAGACTAGTAAGAATGAATTTTCTGCTGCAGATTTGCTGAATAGTGCT
CTGACATTTATTAATCCGATTGTCACCGCACCCCTTTAGTGCGATTCAGAATCTTTTTG
ATTATCTGGGAAAAAATCCGCAAACCGCTGCTGCGCTCAATAAAACATACAGCTTAA
GAGGGATATTTAAAGCAGCTGCGACTACTAATCCAGCCTGCGACCAGAAATTAACAA
TTGATCTAAGCCCGACTAGGATTGCCCGAATTCGAAGCGCCATCAAATGAAGTGG
CTCCGCATGGTTTAGTGAGATTTTAGCTTTCTTTGACGCTATCAGTCAACATTACGT
TGTGCAGATTTTGACTTTACTGTCCACGATCGCAGGGCGCGATCTGATTTCTTTACA
TGCGAATTTTAACGTTAATTTTCGTATCATCGACTACACTACAGCAACAGCTTCCCCG
CAGTCCCTGAATGGATGCGGAGCGCATACCGATTATGGTACGTTTTCAATTATTTTC
AGGACGGTAATGCCGGCTTAGAGATGGAGGCACCGGAAGCGCCTGGCACATGGGT
CTCTGTTCCGGGTAACGCGACGGTGCTGCTGTGCGGTTGGTGTGCGGTCGTTCTT
AGTGGCGGAAAAGTGATGGCAGTGCGTCACCGTGTCCGTCTGTGTACCGGGTGTTT
GCAGGCTTTCTGCTGTTTTATTTCGTAGCGCCTGATTTAAACGTAAACTCGCGCCAG
CCGAACGAGTAGACGCGTTTCAAGTATCCGGTTAATCAGGGACTTTTTGATGTGAGA
TGGTTCAAAGAAGAAATGGGAAAAAAGTGGCGGTATCGGGAGGGAAATGGGAAGT

TGGAGGATGACGGCTTAGAGCAGGATCATGACATCGGAGATTTGATTTGGAAGAGT
TTCTAA

NHI 174 protein sequence:

MATQTSKNEFSAADLLNSALTFINPIVTAPFSAIQNLFDYLGKNPQTAAALNKTYSLRGIF
KAAATTNPACDQKLTIDLSPTRIARIPSAIKIELAPHGLVEILAFFDAISQHYVVQILTLLSTI
AGRDLISLHANFNVNFRIIDYTTATASPQSLNGCGAHTDYGTFSIIFQDGNAGLEMEAPE
APGTWVSVPGNATVLLCGWCAVVLSSGGKVMVRHRVRRVPGVRRLSAVLFVAPDLNV
KLAPAERVDAFSDPVNQGLFDVRWFKEEMGKKWRYREGNGKLEDDGLEQDHDIGDLI
WKSF

Codon-optimized NHI 175 sequence:

ATGATCGAATCGTTCGCCAGGATGGTTTTGTGTACTCCCGGGTGCTCTTCAATA
GAAGAGGTTACGGGCCTGAACGAAGCTATAGACGACCACCAGCTGCAGTTTCCAG
ATGGATGGCCAGACCGCGGCGAGGGTGGTCGCCGTCAGTGCGTTTCTATCCTCCT
GAATATGCCTGTCTTTGATCATAGTTTACTACATCCCGAAATTCTTCCGCTGGTTAGC
AGACTGGTGGGTAAAGAACTGGTGGTAGAAGAGCATAGTGTAAATGGTGCGGGCGC
CGATTGCGGGTAATCCGCCAGTGTCAAAATGGCATCGAGACCGACCTAATAACCCG
GATCATGAATTTGGTCTAGAAGCGTTAAGCTTGGTGTATTATTAACGGACGTCGATG
AGACTACCCATTGTTTTTCAGTTGTTCCCGAGACCGTGGAACCAAACGTGGAGAA
AATTTGCCCGGTTGTGACGGCAGCAGTGCCCGCGATGTGCTGGGGCCTGCGGGC
ACTGCGTTACTTTTTCAATGCAGGGTCCTGTCATGCAGGACGCCTGAGAACAACAAC
CAGCGAACGCCGCACAATTCATATTTATTTCCGGTCACGCTTCACATGCTCCGTTATC
AAATCACACACCTATGCCTCGGAGGCTGGTTGAACATCCAGATGAAGACGTTCCGCC
GTCTGTTTAGCCAGCCGAATGAAGTTACTCGTTCTTCCTTATGTCCGACCGTCCCGT
GA

NHI 175 protein sequence:

MIESFAQDGFVLPGLALSIEEVTGLNEAIDDHQLQFPDGPDRGEGGRRQCVSILLNM
PVFDHSLHPEILPLVSRLVGKELVVEEHSVMVRAPIAGNPPVSKWHRDRPNPDHEF
GLEALSLVYYLTDVDETHCFVVPETVETKRGENLPGCDGSSARDVLGPAGTALLFNA
GSCHAGRLRTTTTERRTIHIYFGHASHAPLSNHTPMPRRLVEHPDEDVRRLFSQPNEV
TRSSLCPVTP

Codon-optimized NHI 176 sequence:

ATGGATATAGGCGTCCCCGTCAAAGAGCTGGGTGATATAGAAGTGACACCCCTGAT
CGACGCTATTATGTCTATAGACGACGAAGCGTGGTTAGCAAATAATCATCGTCAGAAT
GCGTATGAGGTGCATGCCAGACGCAGTCTTTAGTGATGCTATTTGTGATACTAAA
GTTTGGCCGACAGTTAAAGTCACTAAAGAATCAGCCTGGGATGAGCTCTCCGAAGT
GGCGCTTCCGATCATGGATTGATTCTTGAGAAATATTATCCTCCGGGCGGGGACTGT
CATTCGTGCCATGGCAGCGAAGCTGGTCAGCGGCGGAGTGATTAAGCCGCATGTA
GATAGTCATCAGAGTTTTTCATGTGGGCCATCGCATCCATATACCGATTACGGCAAATC
CACGCGTTCGGTTTATGATCGATGGTAAACCCACCGTTTCGAGATTGGCAAAGTG

TACGAACTGAATAATCAAATTCAGCACTCTGTTCATGAATAAAGGGAAGGACGACCGC
ATTAATTTTATTTTTGACTATATTCCGCCTGTTGAGCTCGCAAACTTAATAGCTAA

NHI 176 protein sequence:

MDIGVPVKELGDIEVTPLIDAIMSIDDEAWLANNHQRNAYEVHAQTQSLVMLFVDTKVW
PTVKVTKESAWDELSEVALPIMDSILEKYYPPGGTVIRAMAAKLVS GGVIKPHVDSHQS
FHVGHRIHIPITANPRVRFMIDGKPHRFEIGKVYELNNQIQHSVMNKGKDDRINFIFDYIP
PVELAKLNS

Codon-optimized NHI 177 sequence:

ATGAAAAATGAAATTATTCTTAGTGATTCCCTTGCAGCAGAACGACCTGACTCGCCTG
TTCAATGATGAGGCACTCGCTATTCATGTAAAAAATATGTCGATTACATATTTCCGA
CAAACCTTTCTGACTTTTTTCTGTCTCACGAAAACCTTAGAGTTGCACGCCCATGACTT
GAAAAAAGGCGATAAAACAATTTTTGTGGATTATGGTGTGGATCGCGTAGGCACGAG
CTATAACTACCTTTGGGAAACCGAAAGATAGCGATT CATATAAAAAATATTTGAAA
ATGCCCTGTCTGGCGATTAGGAATGTTCTGTAATTTTTGCGCTCCAATGTTAGCTCCGT
TCGATAAACTGAGACTGGAGCTGGATGAAGTTTGGTCTGCTGGCGCCTCCATTGCT
AACTTTGAAGGGAAGAAGATGCATGTGGGTATTGCGCGCGTGATGAAACGCCCCG
AGTTATCGTTTATGGTCGAAAAACAGCCCCACTTTGACGGATTACAGCAGCAGTCAG
TCAATTTACTGGGTCAGTTCAGTGTTAATATTTATATT CGAATGCCGGTCAACGGGGG
CGAACTGGAGCTGTGGGATGTGCCAGCCATTCCGATTACAGAGCTGATTGAGGATA
ATGCCGAAAATGATTGGCGCGGTACATTACCCCTAGTACGTTAATCAAACCCGAAC
AGGGCGATCTTATAATTATAAATAACCCGTAAACCGCACGCAATTCGTAGCTTCTCGGA
CGGTTGCCGGATTTCTCTGCAGAGCTTTATCGGACTGAGCCTTAACAAACATCTTAT
GCTGTGGAATTGA

NHI 177 protein sequence:

MKNEILSDSLQQNDLTRLFNDEALAIHVKKYVD SHISDKLSDFFLSHENLELHAHDLKK
GDKTIFVDYGVDRVGTSYNTTFGKPKDSDSYKKYFENALSAIRNVNFCAPMLAPFDK
LRLELDEVWSAGASIANFEGKKMHVGIARVMKRPELSFMVEKQPHFDGLQQQSVNLL
GQFSVNIYIRMPVNGGELELWDVPAIPITELIEDNAENDWRGTLPPSTLIKPEQGDLIIINT
RKPHAIRSFS DGRISLQSFIGLSLNKHLMLWN

Codon-optimized NHI 178 sequence:

ATGGAAAACGACAAAGTCAACGAAGCAGCTACGGGCCTAACTCCTGAAGAAGTGG
ATCATTTTATAAAACATGGTTACGTACTGCTGCGGAATGCGTTTAGTACAGACACCGC
AGCCGCCTGCCGTGAATTTCTCTGGGCGAGGATAGAGCAAGATGGTGTGAAACAG
GACGACTGCAGTACCTGGCCAGAAAAACATTGGATTTCTGAGAGTTACTCTGATGC
TACTGGTGAACCATGGACGGAGGTTTTGACTCCCCGCCTGAAATCAGCTATGGACC
AGCTTTGTGGAAAAGACCGCTGGAATGAGTCGGACCTAGTTTGCGGATGGTGGGT
TATCACATTTCTGGCCATGCCATGCTTCCTTGGGGTCCTGCCGGCCATTGGCACG
TTGACGGAGCTCATTACATACATAAACTCGATTCCAAGGAAAGCGGTCTGCTTCCGA
TTTTTATCTTCTCTGACATCAACCCCGGTGACGGGGGAACGGCGTTAGCTCCAGGA

AGCCACATGCATGTGGCCCATATTTTACAAGATGCGATCCCGCATGGAGGCTTAAAA
GGAGGAAAGGTCAGTGCGAGCGCGAAGTCTTGGGTTTATCAACACAAAAAGGCTT
GGGTTGAAGTCCAAGGTCGGGCAGGAGATATCATGCTGACGCATCCCTTTCTGATG
CATGCACGCAGCAAAAATTGTGGTAGTCAGGTCCGTTTCATGTGTAATCCAAATGTC
GGGCTCAAGGATCCGATGCAATTCGAACGTGACGACCCCGCCGATTATTCACCCGT
AGAAGCCGCTATTGTGGAGGCTTTAAGACAGCCGGTGTGCGCAAAAGAAAAGAAAAC
GCGGTTTGCACATATA

NHI 178 protein sequence:

MENDKVNEAATGLTPEEVDHFIFKHGYVLLRNAFSTDAAACREFLWARIEQDGVKQDD
CSTWPEKHWISYSYDATGEPWTEVLTPRLKSAMDQLCGKDRWNESDLVCGWWVIT
FPGHAMLPGWGPAGHWHVDGAHYIHKLDSKESGLLPFIFSDINPGDGGTALAPGSHMH
VAHILQDAIPHGGLKGGKVSASAKSWVYQHKKAWVEVQGRAGDIMLTHPFLMHARSK
NCGSQVRFCNPNVGLKDPMQFERDDPADYSPVEAAIVEALRQPVVSQKKRKRGLHY

Codon-optimized NHI 179 sequence:

ATGAATTATATCAACTTCCAATCCGTAGATGATTGTTTAGCCACTCTGTCGGAGACAG
GCTTCGTTAGAGTCCCGAACTTTCTTGACGAGCACACGGCAACCACCTTAGAGAGT
ACGCTGAAAGAATTAAATTTCAACACCGCCGCGATAGTCAACGCCCGTCCCCATGA
ATTCACAGCGAGTGAATTGCAGAACAAAACCAACCAGGAGAAGCAGCAATTGTTTT
CCCATATCTATGAACAGGCCTCGCAAGGTATTGGCTTTGTTTACGGACGGCACGCA
CTGTGCAATACTACAAACGAAGAGCTGATTGATTTTAAGAAGCATCTGAACTCAAGC
GAACTTTTAGAGCGAATGTCTCGGGCCTCCCAGCAAAAAATTATCAAAGCGAGTGC
TCAAGCTACGTGCTATCAGAAAGGTGATTTCTCACACGTCATAACGATGTGATACAT
AGCGAGGGACGGGTATATGCCTACGTTCTGGGTCTGACAGAACAGTGGCACCCAG
ATTGGGGCGGTCTGCTGCAGTTTTACGAACCGGACGGGACGCCAACGAACTCGTA
CGCGCCGCAGTTCAATTCACCTACTATTTTTGACGTAACGAAATTCACTCGGTGAG
CTATATCACCCCTTCGCTAAGTCAAACGCCTGTCAATTACAGGTTGGTTCAGAAC
CAAATAA

NHI 179 protein sequence:

MNYINFQSVDDCLATLSETGFVRVPNFLDEHTATTLESTLKEINFNTAAIVNARPHEFTA
SELQNKTNQEKQQLFSHIYEQASQGIGFVYGRHALSNTTNEELIDFKHLNSSELLERM
SRASQQKIIKASAQATCYQKGDFLTRHNDVIHSEGRVYAYVLGLTEQWHPDWGGLLQF
YEPDGTPTNSYAPQFNSLTIFDVTKIHSVSYITPFAKSKRLSITGWFR TK

Codon-optimized NHI 180 sequence:

ATGAATGAGATTCTGTCCTCGGAACAAATTGAAATTTTTTCATCGCGACGGCGTGGTC
GTAATCCCGAACTTTTATAACATGGATAAAATTACGCCCATTCAGAAGGGTATCTATGA
CATTATCGGTCAAATAATAACCCGTGAAGAGATCTCCCTCAAACAGAGCCCTTTTAA
CCCGGATACTTTTGATCAGCATTATATCGACTTAATTGGAATCAATCGCGATTGGGGC
GGCGAGATTTATGATGCGGTAAACAGATTCCGGCTTTTATTGCGCTTGTGGCGGAC
GAGTCGCACGAAAAGTTATTTAAACAAATTCGCTGTACCCGCAAACCGGGGATCGC

CGGGGGGGGATATGGTATTCGCATTGATAACCCAAATGAAGATAAGTTCAGAGCAAT
GTGGCATCAGGAGTACCCAGCGCAGTTGCGCAGTGTGGACGGGTAGTTTTCTGG
TCGCCATTAGTGCCTATCACGGAAGAAATTGGTCCAGTAGAATTTTGTCCAGGATCC
CATCATGAGGGTCCGCTGCCGGTATGTTACGCTGACCCGGAGCACACAGGCCGCA
CCGGAGCCTATTCACTGAAAATCCTGGACGAGGCCGTGCACCTGAACAAGTACCG
GAAGATAGCGCCGCTGACCAGCCCCGGGGGACCTCGTGATAATAGATTTTCTAGTTC
TCCACGCAAGCGGCGTCAATAGATCACATCGCGCCCGTTGGTCCATGCAGTTTCGG
TATTTCAACTTTGAGGATCCCATTGGACGCAAACATGGATGGAAAGGCTCCTTTGCG
GCGGGCACCGATTTTCGTAAGATTCATCCGGAACATTTGCAGAAAAACCGCTGCA
GTAA

NHI 180 protein sequence:

MNEILSSEQIEIFHRDGVVVIPNFYNMDKITPIQKGIYDIIGQIITREEISLKQSPFNPDTFD
QHYIDLIGINRDWGGEIYDAVKQIPAFIRLVADESHEKLFKQIRCTRKPGIAGGGYGIRIDN
PNEDKFRAMWHQEYPAQLRSVDGLVFWSPLPITEEIGPVEFCPGSHHEGPLPVCYAD
PEHTGRTGAYSLKILDEAVHLNKYRKIAPLTPSGDLVIIDFLVLHASGVNRSRHRARWSMQ
FRYFNFEDPIGRKHGWKGSFAAGTDFRKHPELFAEKPLQ

Codon-optimized NHI 181 sequence:

ATGGAGGATCAGAGTGAGTCCTCCCAGAACCAGAGCACTTCGCGGGCGCAATAGGC
CACCGCGGCCTCCGGTCTTAGGTGTGGGTGACCGATTGGGGGCCGGGGACTCTT
ACATAGTCAACGATTTGTTGCCGAGTGACATCGCGGATAATGTATTTCATAAGCTCAA
GGAAGAAGTAAAATGGCAGGTGATGCATCATCGCGGTGGTGAAGTTCCCCGCCTT
GTGGCGGTGGAAGGAGAAGTTGGCCAAGACGGTAGTTTTCCGGTGTATCGCCATC
CGGCTGACGAAAGTCCGCCACTGCTGCCTTTCTCGCCGACTGTTTCATTAATACGG
GAATATGTCCAGAAAGTTGTGCAGCATCCTGTTAATCACGTACTAATCCAGTTCTACC
GTAGTGGAAGATTACATCAGTGATCACAGCGATAAACGATAGATGTTGTACGCG
GGAGCAACATAGTTAACGTTTCCATGGGAGCGCAACGCGTTATGACGTTGAAATTAA
AAAAAGATAAGCACAAGGGAAGTGATATCGACGCACCTCATGAGGGTGAGATTCTG
CCAACACAGGCAAGCAATGTACCGGCGCCTCCGAGGCCATCCCCAAAAAATTCCGTT
GCCACATAATTCAATGTTGGTTATGGGTCTCGAAACAAATGCAAAGTGGTTGCATGG
AATAAATCATGATAATCGTCCGTTTCAGACGAAGAGTCCGGAGGAACAGCGCGAAG
AGGGTGGCAGAATTTCTCTGACTTTTCGACATATTGGTACCTTTTTGTCAAAGGACG
AGGCATTTATCTGGGGCCAAGGGGCGAAGGGCAAACGCGAGAAGAAGCGGGTAA
GGTGATATTTACCAGGATGAAGTGGAAAACTTCTGATAGCGTTCGGTGATGAGAA
CCAGCAGTCGGATTTGATTGGGACCAGGCATATGGTCCTGGGTTTGACGTATTGC
ACCTGACAAGTAAAGAAGGTAGCGGTGGGCCTCCAAGTTAA

NHI 181 protein sequence:

MEDQSESSQNQSTSRNRNPPRPPVLGVGDRLGAGDSYIVNDLLPSDIADNVFHLKE
EVKWQVMHHRGGEVPRLVAVEGEVGQDGSFPVYRHPADESPLLPFSPTVSLIREYV
QKVVQHPVNHVLIQFYRSGKDYISDHSDKTIDVVRGSNIVNVSMGAQRVMTLKLKDK
HKGSDIDAPHEGEILPTQASNPAPPRPSQKIPLPHNSMLVMGLETNAKWLHGINHDN

RPFQTKSPREEQREEGGRISLTFRHIGTFLSKDEAFIWGQGA KGK TREEAGKVIFHQDEV
EKLLIAFGDENQQSDFDWDQAYGPGFDVLHLTSKEGSGGPPS

Codon-optimized NHI 182 sequence:

ATGATTGATGTAGATAGTTTTTTGGCCCGCGGTTATGTCCGTGTTGAACAGGCTTTTA
GCAGAGAAAGTGCGGCCGCTTGTAGAGATATTCTATGGCGCGATACAGGATGTGAT
CCGGATGATCCGGCGACATGGACCCGTCCAGTTGTACTGCTGGGAGACCACGCGG
AAGAACCCTTCCGTGCCGCGGCCAATACCGGTCCGCTGCGGGCGGCTTTTCGATGC
GGTTGTAGGTAAGGGCGCTTGGCTCCCAAGAGGTGGCCTTGGCACCTTTCCGGTC
CGCTTCCCCAGTGATCAGCCACCGGGTGATGATGGTTGGCACATTGACGCTTCTTT
TCCTGGAGACGATCCAGCCGACTTTATGTCTTATAGAGTTAATGTGGCCTCTAAGGG
GCGAGCCTTACTGATGCTATTTCTGTTCAGCGACGTCGGGGAAGATGATGGCCCGA
CTCGAATTCGTGTTGGCAGTCATCTGGACGTCCCTCCTATTCTGGAGCCTGCCGGA
GAGGCTGGACTGGCATT CATGGATCTCGCTGCTAAAGCAGTTCCGGCAACGGAAC
ACCGTCCACTAGCCTCCGCTACCGGCCGGGCTGGCGATGTGTACTTGTGT CATCC
GTTTCTGGTG CATGCTGCACAAGCACATCGAGGTACTACCCCGCGCTTTATGGCGC
AGCCTCCACTGTTCCCCGCGGGGCCCTTACCGCCAAGCAGCCCAGTACGCGTAGC
TATCGACCGTGGCTTAGGTCGTAGTTGA

NHI 182 protein sequence:

MIDVDSFLARGYVRVEQAFSRESAAACRDILWRDTGCDPDDPATWTRPVLLGDHAE
EPFRAAANTGPLRAAFDAVVGKGAWLPRGGLGTFPVRFPDQPPGDDGWHIDASFP
GDDPADFMSYRVNVASKGRALLMLFLFSDVGEDDGPTIRIRVGSHLDVPPILEPAGEAG
LAFMDLAAKAVPATEHRPLASATGRAGDVYLCHPFLVHAAQAHRTTPRFMAQPPLFP
AGPLPPSSPVRVAIDRGLGRS

Codon-optimized NHI 183 sequence:

ATGGCCAAGCGCAAATTAGCTCAAGAGGGGGCCGGTCGCAAAACGGACCAGGAAAG
GGGGCGAAAAAGAGGCAGTGGAAGTGTACCTCCAAATGGCGCCCGGGAACCGG
TGTGCGGCGAACCACCAGCTTGGGCCGAGTGCCGTCCTGATCTTTGCGATGCACT
GCCGTGGTTCCGGTCCGTACAGGGTGGCGCTTATCATGTTGGTGA ACTCTCATTCG
GTTGCTTGATCGATGCGGATTCCGGTAGTCGTGCTCACGTAGATGATGAAACTATTA
TAACAAGGATAGGCGGGGGGATGCGAAAAAGATCCTAACGGGAATTTGATCCTGCTG
AAGGACCAGGACGACAGCGATCGCGCAGTCGCATCCTATATCAACTCACAAGCGGT
TAAACTGCCGGTGGGCCTTATTATTGGCGATCGTAACCCCGTGCTAGGTCGCCAATT
GCCGCATCGGTATAATGTAATGGGTACTTCCGCATTACGCACATTTGGTACGAAAAA
GTCGGCAAGCGGACGGGTGCTAAAATCAGATTTCAAAGCTTGATTTAGAAAAAAG
GTCGTGGTGGGCGGCGAAAGGTTCTCCCGATCCTCCGCCGGTCTCAGAGCGCGA
ATTTCTGCCACCTGAAAGTCAAATATGTCCGGAATGCACTGTAAGTAGTCCCCGCGT
TTACAATGAAGGTTGGATGTGTCTCCAGCCTTCTTGCTCACAATTCTGGTCTATCAAT
GGAAGTCCGCCGCCGTCTGACCTTACCTATCATCCGCGTTTTCTGTGCGGCGCGCG
AGCCTCCAGATGAGGAAATTAGGCCCCAGTATTCCTTAGTCCCGGATCTCTTATCCA
CAATTCCTGAAGAAGACCGTGATGCGGGTTTATCGCGTATTGCCTGGAAAGGTATTG

TCTGCCCCGACTGCCACAAATGCATTTACGCGAGATTTTGGCGCGGATGGAAGTGC
ACCGATCCGCTGGACAATAAAAGTAGTAGCCGCACTTCGACGAGTAATAACAACCTCC
CCGACTGGATCTACCTCTCCGTGCACTTTCGAAAAAATGATGCCAATGAGGCCGGT
CTCACTCCGAAGCGTTCGTGTCCGATTTTCGAAATTGGCGCCATTACGCGCGCTGTTT
TCGTTAATTCAAAACCTATTCAGCCAAAACGGGATTTCTCGGGCCCTTATGCTAAATA
TACCTATGAACTGAAAGATATCGGCACAGTCACTCATTTATCGCCAACCGGGAGGT
ATTAAGCCGTCCTAATGGGCCAAATGACTTATTTGAACAGTTGCAACTGGTGGACCT
GGGGCTGCGGCGTTACCCCTGCGAGCAGAGTGTGCGCAGCAGTGGCCGGAACGTT
GACTAGCCACTTTGCCGTTAACTACGGTATGCCGTATAAGTATGTGGTCTCTGTCTGA
CTCAAAAGGCTTCGATGAGGCTCCTCCAGAAATCATGCGTGCTTTAGGCCGCTGA
CCTGGGCAACTGAACAGGCGGTGACGGCAACCGGTGATGAATTTTTACCGCCAAA
CGAGTTACTGGCCCTGGCCTACTTCGAAGAAATGTCAATTGGTTATCACGATGATGG
TGAGAGTTCCTTAGGCCCTACCATAGCGACGTTGTCATTAGGTGCAAAAGCAACTAT
GAAAATACGTTTAAAAGATAAGTACTTCAGAGGGTGTTCGGCATCAAAGAACTTCT
GCCGGAGGACATTGTTCTGCCTGGCTGCGAGAAATACGATGAACGCAAAGAACTAA
AAGCTAAATTTGCTAATAAAGAGATAACTGAAAAAGAATATAACGAACGCAGACTGGA
GATTATCAATCTATGAAGAGGCGCGAGGGCAGTCCCGTTATCAGCCTCGAAATTCA
TCACGGTGATTTAGTTGTAATGCATGGAGCTGATATGCAGAAATATTATGAACATAGT
GTGATCCCGGAGAATAAATTACGTTTTCGCTCTGACCTCACGTTATATTAAACCTGACC
AAGTTGAACAAAAAGACCTGCACAAAGGTAATTTACCCTTGGGCCGGATGAAGTTT
ATCATGGGCAGTAA

NHI 183 protein sequence:

MAKRKLAQEGPVAKRTRKGGEKEAVEVSPPNGAREPVCGEPPAWAECRPDLCDALP
WFRSVQGGAYHVGELSFGCLIDADSGSRAHVDDETIITRIGGGCEKDPNGNLILLKDQD
DSDRAVASYSINQAVKLPVGLIIGDRNPVLGRQLPHRYNVMGYFRITHIWYEKVGKRTG
AKIRFQKLDLEKRSWWAAKGSPDPPPVSEREFLPPESQICPECTVSSPRVYNEGWMC
LQPSCSQFWSINGSPPPSDLTYHPRFLSAREPPDEEIRPQYSLVPDLLSTIPEEDRDAG
LSRIAWKGIVCPDCHKCISRRFWRGWKCTDPLDNKSSSRTSTSNNSPTGSTSPCTFE
KMMPMRPVSLRSVSDFEIGAIQRAVFNNSKLIQPKRDFSGPYAKYTYELKDITVTHFI
ANREVLSRPNGPNDLFEQLQLVDLGLRRYPLQQSVAAGTTLTSHFAVNYGMPYKYVV
SVDSKGFDEAPPEIMRALGRLTWATEQAVTATGDEFLPPNELLALAYFEEMSIGYHDDG
ESSLGPTIATLSLGAKATMKIRLKDKEYFRGCSASKKLLPEDIVLPGCEKYDERKELKAKF
ANKEITEKEYNERRLEIIKSMKRREGSPVISLEIHHGDLVVMHGADMQKYEHHSVIPENK
LRFALTSRYIKPDQVEQKDLHKGNFTLGPDEVYHGQ

Codon-optimized NHI 184 sequence:

ATGGAATCCTTTAATGAATATCACATTGATCCGAAACAGTTTCCCTTTCTGAAAAATTT
CCAGGACAACCTGGCAGGTGATCCGTGACGAATATACCTCATTTATCAACAACGCATC
TAATGAAGAATTGAAATTTACTTATGATGTTTTAGGCCCGAAAAGTCAGACGATAAAG
ACCAAAGGCAAATCAAATATAGCGCCTTCGGCATTCTGTTTCAAGGTATGTTTCATTG
AAAAGTACATTCAGGCACATCAGATTAAATACCCGGACTACGGCCCGGACGAAGCC
TCAAAGAAAGCGCTGGTTTTGCGGGAAAAATACTTTACCAATTTGGCCAATGTAATTA

AAGATGTAAATCTCATAGAAGATGATATCATCCGTAATGTATATTATGGGACCTTTTCAT
CCCGGTCTTGATATTAAATTACATGTAAATTATAACCCGCATACTAATCGTGGATATCT
GGGTCTGATTGTACCTGAAGGCGATGTGGCGATGAAAATATGCCACGATCAACTGT
ATTGGCATGAAGGGAAATTTCTGGTACTGGATCATTCTTACCCTCATTGCCCCCATAA
CTACACATCCTATGACCGCACGGTACTAGTAGTCGATTTTTTTTAAGCCCGATAAGCCA
AGAGATGAAGTTATAGAATTCGAAAAAGAACAGGTTACGCAGAGAATGCAAGATAAC
CCATACAGCTTGGGCGTATTTGGAAAAAGCGATAAAGCTAAAGAGGAGGAGGACTTTATT
AAATATGGATTAGCTCACCAGCTTGAATGGGATAAGGCTTTGATTGA

NHI 184 protein sequence:

MESFNEYHIDPKQFPFLKNFQDNWQVIRDEYTSFINNASNEELKFTYDVLGPKSQTIKT
KGKSKYSFAFGILFQGMFIEKYIQAHQIKYPDYGPDEASKKALVLRKYFTNLANVIKDVN
LIEDDIIRNVYYGTFHPGLDIKLHVNYNPHTNRGYLGLIVPEGDVAMKICHDQLYWHEGK
FLVLDHSYPHCPHNYTSYDRTVLVVDFFKPKPRDEVIEFEKEQVTQRMQDNPYSLGV
FGKSDKAKEEDFIKYGLAHQLEWDKALI

Codon-optimized NHI 185 sequence:

ATGCAGTTAGACAAACAGCAAATAGACTTTTTTTGATGCGTTCGGCTATCTTGTCGTAC
GCCAGTTACTGACCCCAGAGGAAACCGAGCGTGTCATTGATGCATTTGAGTGGTCT
ATACAAAATTGGGGTGGCGGGACCGATCACGATGGTTCCAAACGTACGATGTTTGG
CGGACCAATTGAACACTCCCCTGATTTGTGCGCTTTAATGGATCACCTGGGATTCT
GGGCTTGATTGGTGGTGTAAACAGGTGAGAGATTTAACTATTGCGGCGGTGATGGCA
ACTACTATACGGGCAATACCCGGTGGCACCTGATGGTAACTGGGGCCAGGCTTGG
GCAACAAAGACTGCATTTTATCTCGATGAAGTGGGAGCCGATTCCGGTTGTCTGCG
TGTGATTCCTGGGTCCCATCATCCGGATCACTTCATCCGTAAAGAAGGTATTCATCC
CCGCGATTCTCTCGAAATGTTTGGGGTACCACCGGAAGATTTCCCCGGTAGCGTGG
CGCTGAGTACGTGCCCAGGAGATGTGGTTATATTCAATCATGATCTGTATCACGCGA
GTTTTGGCGGCGGTAACAGGCGCCGTATGTTTACTATGAACTGCACCCGTCATGCC
GAAACACCTGACGAGATGGACTTGCTGCGCGAGTATGTTGCGGTTTATTCTCCGGG
TGGTTATGATATAGATACCGGCGCGGGCATGTACTTTCCGACGATGTTACATACCGC
AGATGATGCTCGGATGACCCATCTGCAGCAGGCTCGTGATATGCATGACGAGCTGT
ATCCGCAGTACGCTCGCGACGCAGGTGAACGCGATAGTCACAGAGGCCGCATGCG
CTAA

NHI 185 protein sequence:

MQLDKQQIDFFDAFGYLVVRQLLTPEETERVIDAFEWSIQNWGGGTDHDGSKRTMFG
GPIEHSPDLCALMDHPGILGLIGGVTGERFNYCGGDGNYYTGNTRWHPDGNWGWQAW
ATKTA FYLDEVGADSGCLRVIPGSHHPDHFIRKEGIHPRDSLEMFGVPPEDFPGSVALS
TCPGDVVIFNHDLYHASFGGNGRRRMFTMNCTRHAETPDEMDLLREYVRVHSPGGY
DIDTGAGMYFPTMLHTADDARMTHLQQARDMHDELYPQYARDAGERDSHRGRMR

Codon-optimized NHI 186 sequence:

ATGTTAACTCCAGAAGTTACGTAAAAAAGGAAGCGCAGTACTAGTGAAACTGAAGGT
GATCAGGAGTATACTCATGGTATAGCTGGTGCCGTTATACTGAAATCATCCCCGACT
CAAGACAATAAAAAACAGAAGTTGTTAAAAATTGATATCCGACCTCTTTGAACTCGG
GTTTAGAACAGAATCACCGGGCGCCGACAACTCGTATAGCAGCCTTTTTTCTGAC
ACTGACAATGACAGCCTTTTTGGAGACCTGACCGACTCATCCACAACAAGTCACTG
CGAAGATGACACGGTTGCGTCCCGCACGGCACCATCAATCATGGGAATGTTTTTCG
AACCTACCATTCTGCTTCCCCCGAACTGGCCGACACAGTGATGACCTTCTGCATG
AATACATACTTTCGTGCGGCCCGAAGACAACCAAGCGATGTTATTTGGGCGGCTATGT
TCGCCGGACCCCTCTGAACCTCTGGATGTTAATAAGGGTTTGCCTGAAGTTCTGCT
GGACTTACTGGAATCAGTGCGGGTGCGTCTGGAACCGGTTTTACCAACTGACAAGT
ATGAGCTCCTGTTTCCCAAATGCCCTACCATGGCGCGTCAGGCTATTATTAATCTTTA
TCAGCCAGGAGAGGGAATTACCCCCCATGTTGATCTGTTGAGTCGATATGGTGACG
GTATTATCGGCGTCTCTTTAGGTTCTGGCTGCGCAATGCGCTTCGATAAGACGGCAA
CAACAGATAATAGTTTTCCAAGTGAAGGTGAGCGGCATGACCTGTATCTGCCAGAAA
GGTCCGTAATTGTGCTGTGCGGAGGACGCACGTTACCAAGTGGACGCATGGAATTGAT
AAAAAGACACGTGACTTTGTTGCGAACGATACTGATTTCGACCCAAGGCGCATGGGT
TGAGCGATCTGTTGCTTAAGCGTTACATATCGGTGGCTGTTACCAGGTGCGGACG
TTGTAGGCGAAACAGCAGATTAA

NHI 186 protein sequence:

MLTPEVTLKRKRSTSETEGDQEYTHGIAGAVILKSSPTQDNKKQKLLKIDIPTSLNSGLE
QESPGADNSYSSLSFSDTDNDSLFGDLTDSSTTSHCEDDTVASRTAPSIMGMFFEPTIRL
PPELADTVMTFCMNTYFRRPEDNQAMLFGRLCSPDPSEPLDVNKGLEPEVLLDLLESVR
VRLEPVLPTDKYELLFPKCPTMARQAIINLYQPEGITPHVDLLSRYGDGIIGVSLGSGC
AMRFDKTATTDNSFPSEGERHDLYLPERSVIVLSEDARYQWTHGIDKKTRDFVANDTD
STQGAWVERSVRLSVTYRWLLPGADVVGETAD

Codon-optimized NHI 187 sequence:

ATGTTTTTCTCCACGACGTACCAAGCACTGCGCGTTTATACTACAACCGGCCTATAC
AACCGCCTTCGTGCGAACAATGATCCGTTACCGCTGAGCAAGGGGGTTTCCCGA
AAGAACCACCAGCCACAGACCCAGAGCAGGCGATGACCCCTACCGACAATCCAAC
TATTTCTGCTCTGACTACTGAAGAACTGGCTTTCTTTAAACAGTTCGGATACCTTATC
AAACCTAAAGTGCTGAATGCGGCTACCTGTAATGAACTCGTCGACTTGATGTGGCA
GAGCGCCCCAACTGCTCTGAACAGATTCGATCCCCGTACCTATCAGACGATTCCTA
AGTCGGAATGGTCAAGCGATTCCCTTCGCTTTGTTCAAGATGATAAATGGCAATTC
GTGCCCTCGGAACTGACCAGCCCCTGATCGATGCGATGACACATCCGCAGCTGTG
GCAATGGGGAGAACAGCTGTTGGGAAAAGGAAATCTACGTGCACCAACACTCGGG
GGCCAGCCCATGGGGTCACGCGGTCCGGCCTGGCCTGGGGGTCCGGTTGATCCG
CAGGACACAGAAGGCGTTAGAGGAATCTATGCGACACTGCCGAATCCCAGTTTAGA
AGGGGCGCAAGACTCTTTACATACAGACGGCCACCCATTTTCATGTTGGATGGGTGT
GTTTATTGGAGGACTGTCCACCGGAGTCAGGCGCTTTTAAAGTTTGGCCGGGTCT
CACCAGCGTTTTTATCCCTTATTTCCCATGCCTTACGATCAAACAAGAATCCCCTTT
ATGATCATCTTCCTAGCCATAAAGGCATTTTGCATCCTGCGCCGTATTTAGCAGAAGT

CAAAGCTGTCGAAACCGATACGGACCCGGTTGATGTTTGGGGGTCACAGGGCGAT
GTGATACTTTGGCACCATCGTCTTGGACATATGGCGGGTCACCACAAAGGCCATCA
AGCATCTATTAGACAGGCTCTCTTATTTGATTACAACCATATAGCGCTAGATGCGATG
CGTTGCGAGCCGACTCCTTGCGATATGTGGCAGCACTGGTCGCCGGAGCTGCGCG
CAGCGCAGGTTACTACCTTCTCGGACGCACTGATGAGTGCGCAACGTCTGGCTGC
CGAAGGTCAGAATCGCCCGTAA

NHI 187 protein sequence:

MFFSTTYQALRVYTTTGLYNRLRRNNDPFTAEQGGFPKEPPATDPEQAMTPTDNPTIS
ALTTEELAFFKQFGYLIKPKVLNAATCNELVDLMWQSAPTALNRFDPRTYQTIPKSEWS
SDSLRFVQDDKWQFRALGTDQPLIDAMTHPQLWQWGEQLLGKGNLRAPTLGGQPMG
SRGPAWPGGPVDPQDTEGVRGIYATLPNPSLEGAQDSLHTDGHPFHVGVWVCLLEDCEP
PESGAFKVWPGSHQRFYPLFPMFYDQTRIPFYDHLPSHKGILHPAPYLAEVKAVETDT
DPVDVWGSQGDVILWHLHRLGHMAGHHKHGHQASIRQALLFDYNHIALDAMRCEPTCD
MWQHWSPELRAAQVTTTFSDALMSAQRRLAAEGQNR

Codon-optimized NHI 188 sequence:

ATGACAGATCATCAGAATAGCGCTTTTCAGCCGCTGAATGAAGTGTTTGAACCTCCT
CTGCGCCCAAGTTAAATTCCCCCTTATCTTACCGGCACACGCTCCACATCTTAGCAAT
CAGGGCTGGAGTACATTAACATTCTCCCCGACGGATCCGATTCATATTTCTAGCCAA
AAATTACTTCAGGCTAGCCGTAGCTTTTTTGTCTTCCGTTGGAATACAAAACGAGAT
TTCTTACAGGCAAGGGGACGGAGGAAGGGTGGAATTGCGTAGAAGGTGAAAAGGA
GTTTATTACATTAAGGGAAGTGAATAGCACCCCGCCGGAAGTATTAGATGCAACAAA
AGAGTTCTGGGAAATTACCGGAGATGTACTTAATAAAATTCTTGGCGAAGTAGCTTC
GAGCTTAGGGATGCGGAAAGAATCTCTGACTCAATATTCGGAACCCTGTAGCAAATT
ACTTGGAGAACGGACTGCCTCAATGATTCGCCTGTTTAGGTATGAAATGGATGGAGT
CGGAAATAAAGTGGTATGTGAGCCGCACCGTGACCTTGGCTTACTGAGCCTTAGCA
TTTCAGACGTTCCGGGTCTGGAAGTATTTGATAAGGATTTTAAACGGAGCTTTCCAA
TTGAACGCAGCTACGAAGGGCGGGCGGCAGGCACCGTGCTGGTCGGTCGTGAAC
TTGAGTTTCTGTCAAATGGCCGATATCTAGCAGGTGGACATAGCGTACATATGCATC
CAGAAACAGTAACGCGAAATGAACCGGATGGGGAGGAGAACGGTAATGAACGCCA
GATGCCGGCCGGCAAACATTATAGATATTCAATTGTGTTTGTCTGCGCGGCCATGA
GGAAGTTCGCAATCGACACCGATAAGCTACGTACCTCAATTACGGGTCGTTGGAAAA
AACCCATGAGATCCCTAAAAATGGGGAATCTGTACCGGCGTTTTATGTCCAAACAG
TGAATATTAATGCCGAAATTGAAGAACGCCAGGAACAGAGAGAACGCCTGCATGAG
AAGAAGGTAAAAAGTCTGACAGGCGATTAA

NHI 188 protein sequence:

MTDHQNSAFQPLNEVFELPLRPVKFPLILPAHAPHLSNQGWSTLTFSPDPIHISSQKLL
QASRSFFDLPLEYKTRFLTGKGTEEGWNCVEGEKEFITLRELNSTPPELLDATKEFWEI
TGDVLNKILGEVASSLGMRKESLTQYSEPCSKLLGERTASMRILFRYEMDGVGNKVVC
EPHRDLGLLSLSISDVPGLEVFDKDFKRSFPIERSYEGRAAGTVLVGRELEFLSNGRYL

AGGHSVHMHPE TVTRNEPDGEENGNERQMPAGKHYRYSIVFVLRGHEELAIDTDKLR
TSITGRWKKPMRSLKMGNLYRRFMSKHVNINAEIEERQEQRERLHEKKVKS LTGD

Codon-optimized NHI 189 sequence:

ATGGCCACAGAAAATAGTAAGGTGGTCGATCTAAATATCAAAAAAGAAGATCGAATTT
TGGACTTCAGTGATTTCCAAAAACAGGAAATCAAATTTGACATTGAGAACTGCAGG
AAGCTTATCATCAGATTGTGAAAATTAAGAAATTTGAAGATGCCGGGGTTACACATTT
CGGGGCTATCTCTCTTACCCAAATTCCTGGAGATCCGGATTCTATTAAGGGCAACAA
AGCCCGAGGCGTTTACTGGACGAAACCTGATAAAAGCGGTAAAGAAGTCTCTCGCG
ATGAAATGATCGATGAAGCTTCATATTCGGAATTTATAAAAGACTATGAGAACACATAT
TTTAAAGAGGTATACGATGTTCTCAGTAAAAAATATAAGTTAGGCCGCGTACGAATTC
TGCTGAAGGAACCGAGATCAACGTTGTCGTGGCATCGTGATCCTGAACCACGGCT
GCATATTCCAATCATTACAAACCCGGGATGCTTAATGGTTATTGACAATGTGGCAAAA
CATATGCCAGCGGACGGTAGCGTTTGGGTCACAAACAATACGAAATATCATAATGCC
TTTAACGGAGGTGAGGAAAATCGTATTCACCTGGTTGCTTGCGTTCTGGACTATAAA
TTTAATTAA

NHI 189 protein sequence:

MATENSKVVDLNIKKEDRILDFSD FQKQEIKFDIEKLQEAYHQIVKIKKFEDAGVTHFGAI
SLTQIPGDPDSIKGNKARGVYWTKPDKSGKEVSRDEMIDEASYSEFIKD YENTYFKEVY
DVLSKKYKLGRVRILLKEPRSTLSWHRDPEPRLHIPITNPGCLMVIDNVAKHMPADGSV
WVTNNTKYHNAFNGGEENRIHLVACVLDYKFN

Codon-optimized NHI 190 sequence:

ATGTGGCGCAAGAGTGTGCGCTCCCATATCGTGGGAAAAGTTGAGCTGGATAAAGC
ACGCCTGCAGCATGATTTGGAGGCTCTGGCTGCGGTACCGAGGGTGGAGGAAGA
GTATGATGAATTTTCTTCGGGTTACTGGAAGAACTTGAGCCTTTGGAATTCATCCGG
AGAAGCCGATGATACGATGTATCGTGATATTCAGGGGTCAGCAAAACCAACTGCACA
CGCCGCGAAAGCCCCCTATTTAGACGAACTGATACACACTGTGTTTGATAGCAAAAT
TGTTAAAATGGCCCGTGACGCAATTTGGTAGACGCAATGGTGATCCCGCATCGTG
ATTTTATTGAACTAAATAAGGATAATGATCAATACTTCCGTACCTTTATGGTTCTTGAG
GATAATGGATCCGCTTTCCATTTCGGACGATGACACGGTTATTCACATGCGTCCAGGT
GAAATTTGGTATCTGGACGCAGCAGCTCCACACAGCGCTGTAAATTTTTCATCTGAT
TCACGCCAGGCCCTGTGCGTCGATTTTGCATTTGAAGGTAGTTTTACCGAAGATCAA
ATATTTGCCGATAAGAGTTTCTATCGCCCAGATCTGGAACCGGAAATTGTAGTGCGT
AAACCGTTTACTACGGATCACCGTGACAACTGGTACAGTTGGGCGGGATAATCGA
TAATGATAACTTTAAAGATATCCTCTTCTTGATGTCGCGCGTTCACTATCGTTACGATG
TTCCTGCAGCAGAAACCTACGAATGGTTCGTTGAGGCGTGTCGCTTGGCAGATGAC
ACTACACTAACCGCAAAGGCAGAGGGTGTGCGGGATTACATGATAGGCCAGCGTG
CTCTGGGAGAACGTCTTGTGGCGGCAGCCTAA

NHI 190 protein sequence:

MWRKSVRSHIVGKVELDKARLQHDLEALAAVPRVEEEYDEFSSGYWKNLSLWNSSGE
ADDTMYRDIQGSAPTAHAAKAPYLDELIHTVFDSKIVKMARARNLVDAMVIPHRDFIEL
NKDNDQYFRTFMVLEDNGSAFHSDDDTVIHMRPGEIWYLDAAAPHSVNFSSDSRQA
LCVDFAFEGSFTEDQIFADKSFYRPDLEPEIVVRKPFTTDHRDKLVQLGGIIDNDFKDL
FLMSRVHYRYDVPAAEYEWVFVEACRLADDTTLTAKAEGVRDYMIGQRALGERLVAAA

Codon-optimized NHI 191 sequence:

ATGAGTAAAGTTGAAAATCATCACCTGCTGAGCGCCGTCCAGATGGCGCAATTTGC
GGTCAATGGTTTTCTGCAGCTAGAGAACTTAGTCCCCCAAGAACTGAATGAGGCCG
TTCACGCAGAACAGCAGGCATGGAAGGGCCCGGGTTCTTATTGGAGCCAGTCGAA
GCTGATTAAAGATGTCTTTGAACTGCCGCAAGTAAAGGGTGTCTTGCAGAGCCTGG
TAGGTGCTGCACCTGTTTATGATCACAGTGCATTACACATAGTATCCCCACAGCACC
ATCATGCTCAAACTATCACGCGGATTCCGTAATCGATACGCGTCCGTTTGCTTTTG
ATATCCAGGCATTTTACTTTTACATGACACTCCAGAAATTATGGGGCCAACACTTAT
CCTGCCAGGATCACATCTGCACAATAAAGTAAATACAGGATCCATCTCCCACTATAAA
AATATCCTGGGACAACGTAAATTAGTGAGCAAAGCCGGCACAATTGGTTTTCTCCAT
CATGCGATCTGGCATTGTGCACAGCCAAATTATACCGATGAGGCACGTTATGTTTTTA
AACTCCGTCTGCGTCCAGGCCAAGAACAACGGTCGCTGTTTAACATTGCTGATTATA
ATGGACCCGAAGTGGCTCAGGTTCTTAACAATTATCACGACTGGGCTGGTAATGATG
CGCGGCTGAATCAGGTAGCCGCAGCAAAATTCTATCGGTATTTGTGTGGTGATGAC
CGTGTTGACTTTTCATTCGAAGGCATCTTCACTCGCATGGGCATATGA

NHI 191 protein sequence:

MSKVENHHLLSAVQMAQFAVNGFLQLENLVPQELNEAVHAEQQAWKGPGSYWSQSK
LIKDV FELPQVKGV LQSLVGAAPVYDHSALHIVSPQHHAQNYHADSVIDTRPFAFDIQ
AFYFSHDTPEIMGPTLILPGSHLHNKVNTGSISHYKNILGQRKLVSKAGTIGFLHHAIWH
CAQPNYTDEARYVFKLRLRPGQEQRSLFNADYNGPEVAQVLNNYHDWAGNDARLNQ
VAAAKFYRYLCGDDRVD FSFEGIFTRMGI

Codon-optimized NHI 192 sequence:

ATGATCGATCCCATTTTACGCAACTATTATGCCGAACAGATCTTGAACAAACTGGCC
CAGTTTAAATTTGATTTACAGCAGGAATTTGCCACCGACAACCGTATTAATACCTGCT
ATTTAGATGATCTGCTGAATGTAGATGATGTGATTAAGATTTATAATGCCTTTCCTGAT
AAAAAATATCTCCTGCAACTGAAGGACCTTCGAGAATATAAATATGTGGGTATACAGC
TCAACAAATTCAACCCAATCCTAGAAGAAATTGTGTATGCGTTTCAAGACGCCCGTG
TGGTTCAGCTGATTGCGGAAATTACTGGCTTTGAACAACCTTATGCCGGACGAATACC
TGTATGCCGGCGGTGTGTCACTGATGGAACACGGCTGTTTTCTGAATCCTCACCTT
GACAATAGTCATGACAAGGATATGATTAACCTATCGTGTGCTTAACCTGTTGTATTATGT
TACGCCGTCTTGTTGGAGACCTACGGGGGCAATCTAGAACTTTGGGATCAGGATC
TAAACATCCTTG TAGAACCATTCACTCGAAGTTTAATCGCCTGGTCATCATGGTTAC
GAATAAAACCTCTTTACATAGTGTCTCCCCCATCAACCATCACGGACAACGTTGTTG
CGTTAGCAATTATTACTTTAGCCCTAAACCCGCCGATAAGCAGAACTACTATCATGTG
ACGAGTTTCCGTGGTCGGCCTGAACAGAAACTGCGTGACATTGTACTGCGAGGAG

ACGCGCGCCTGCGCAAGCTGGTACGCAAAATATTTAAAAATCGCATAAAAAAACCGC
ATTTTTATCGTAAATAA

NHI 192 protein sequence:

MIDPISRNYAEQILNKLAQFKFDLQQEFATDNRINTCYLDDLLNVDDVIKIYNAFPDKKY
LLQLKDLREYKYVGIQLNKFNPIL EEIVYAFQDARVVQLIAEITGFEQLMPDEYLYAGGVS
LMEHGCFLNPHLDNSHDKDMINYRVLNLLYYVTPSWLETYGGNLELWDQDLKHPCRTI
HSKFNRLVIMVTNKTSLSHSVSPINHHGQRCCVSNYYFSPKPADKQNYHVTSFRGRPE
QKL RDIVLRGDARLRKLVRKIFKNRIKKPHFYRK

Codon-optimized NHI 193 sequence:

ATGACAGATAGAGAACAGCTGCACCGTGACGGGTACGCACTTTTACGCCAAGCTGT
GCCAGCAGAATGGCTGGACGAACTACGTACCTTATTCGATGCGCGCATCACCCCTT
CGCATCAGTGGCCTGTGCCACGTGGTGCAGACTGGCACCATAGTCGTCTTGACGA
TCATGCTATGATCCAGGCTGTATGTCGCCTTCCACAGCTGCTGGCCGTAGTAGGAG
AACTGATCGGAGAACGTTTTTTTTTGGCCCAGGTGGAGGGTTCGTGAGCCACTGGC
GGGGGGGGGACATCAACAACTGCATCGTGACCTTTCGATCCAGCGACCGGGTGAT
ATAGCAAATGCGATGGTCTTCTTTGACGATTACGGGCCCCGATAACGGGGGCTACTCG
CATTGTGCCTGGAAGCCATCGCCCGTATGCCGACGAGCCGCCTTTTGA CTTTAATG
ATGAAAGTAGAAGCGTCCAGTTAGCCGGTGCTGCGGGAGACATTCTGGTGTT CGA
CGTGGACCTGATTACGCTGGTAGTTTAAATCGCCTGGGTACCAGGCGCCGCTCAA
TTCTGATTTCTTATTTTGC GGAACCTTTGTATGCAAGTTATCTTGAAACGCGATCATT
GCGTGGTATTCGTATGGATGCTTCAGAACGATTTGAACCGGCGAATTTTTCACTGTC
ACCTGCTTAA

NHI 193 protein sequence:

MTDREQLHRDGYALLRQAVPAEWLDELRTLFDARITPSHQWPVPRGADWHHSRLDDH
AMIQAVCRLPQLLAVVGELIGERFFLAQVEGREPLAGGGHQQLHRDLSIQRPGDIANA
MVFFDDYGPDNGATRIVPGSHRPYADEPPDFDNDESRSVQLAGAAGDILVFDVDLIHA
GSLNRLGTRRRSILISYFAEPLYASYLETRSLRGIRMDASERFEPANFSLSPA

Codon-optimized NHI 194 sequence:

ATGACTATCACGACACCTCCTCCAACAGGGAGACGCGAATGGATACGGGATAGCGA
TTGTGACTTGGACGCATTCAGAGCCTCGGTTGATCGATCTACCGATCTGGCGGACT
ACCCCTTCGCACATTCAGTAGAACAGACGTCTTTTATATCGGTCCGATAGCTTAAT
TCCTCACCTCGATGATGCACAATCTCGTCGTGCGGTCCAGACGGAACCTGGTTCGG
GCGTTAACGGATGGACCGGGAATTGTCGTTTTT CAGAATGCATTTAGCGATCTGGCA
GTGCTTGATCGTGCTACGGAACAGTTCGACTTACTTATTGCGCAGCAGCATGCTAGT
GGTGGGGTTGTCGGTGACCACTTTGGTAAAGCAGGAGCTAACGATCGCATTGGA
CGCTGCTCAGAACTGGCCTTAGGGGCTCCTGAGGTTTTTGCAGAATATTATGCAAA
CGATATACTTGCGCTTATTTGTCAAAGCTGGTTAGGCCCCCTATATCAGGTTACCTCT
CAAGTGAACGTGGTCAATCCAGGGGGAGCGGCTCAGGTGCCGCACCGTGATTATC
ATCTTGGAATCGTTCCTCGTGAAGAATTAACGGAATACCCCGCACATCTTCACAGAA

TGTCGGCGGGCGTTAACTACAAGGTGCGGTGCGCCATTGCGATATGCCGGTCTGA
AAGCGGTCCTACCCTGTATCTGCCTTATTCTCAACTGTTTGAGGCCGGTTATCTGGC
ATTTTCCCGCCCAGAGTTCGTAGAATTTTCCGCGATAGTCATGTACAACTGCCGTT
GCGAAAAGGAGATGCGGTCTTTTTCAACCCTGCCCTTTATCATGGAGCTGGACGTA
ATCGGTCTGACGCAATCCGCCGTATGGCAAATCTGCTGCAAATCTCGTCACCGTTC
GGTCGGGCGATGGAAGTCCTTGACCGTGAAGCCATGGCTAATGCTGTCTACCCCG
CTTTGTTAGCACGTCACTCTGCGGGGGCCTCCGAGCGGACGCTGCGCAACGCAG
TCGTTGCCACAGCAGAGTGTTATCCCTTCCCCACGAATCTCGATCATGATCAACCG
GTACATTCTCTGGCGCCTGCGACGCAAGTTGATACCGTTTGGGAAGCATTGAGAGA
GAATGCGGACCCCGCGGTGCTCGCCGAACGTTTAGCAGCTCAGACTACACGTCGG
AGACCGTAA

NHI 194 protein sequence:

MTITPPPTGRREWIRSDCDLDAFRASVDRSTDLADYPFAHSVEQNVLLYRSDSLIPH
LDDAQSRRAVQTELVRALTDGPGIVVFQNAFSDLAVLDRATEQFDLLIAQQHASGGVVG
DHFGKAGANDRIWNAQAQKLALGAPEVFAEYYANDILALICQSWLGPLYQVTSQVNVVN
PGGAAQVPHRDYHLGIVPREELTEYPAHLHRMSAALTQGAHAHCDMPVESGPTLYLP
YSQLFEAGYLAFSRPEFVEFFRDSHVQLPLRKGDVFFNPALYHGAGRNRSDAIRMA
NLLQISSPFGAMEVLDREAMANAVYPALLARQSAGASERTLRNAVAVATAECYPFPTNL
DHDQPVHSLAPATQVDTVWEALRENADPAVLAERLAAQTTRRRP

Codon-optimized NHI 195 sequence:

ATGCAGTCAGATCTGAGCAAACATGCCTCGACAAATACCGCGAGTTCGACTCGTATT
AATGACCAGATAGATTTTCCCGAATGTGCGCGTGAGCTGATTCATTCAGGGTGGTCA
ATTAACAAGCTGCCGATAGCATTACAGGCTCACTTCTGGGATGCACTGGATCTGTAC
GCCAATGTGGGTTCGATGTTAAATCGGAATTTAGCTTCCCTGACCATACAGATGGT
TTCCTGCCATTTGGCATGGAATACGCCAAGGCTACTCATCAACCGGATCTGTGCGA
GCGTTATTGCTACTGGCACAAAGATCGTCGTCGGCACGAGGCCCATGCGTTTTCTG
GTAGCGAGTTTTATCGCGCTATCTGCGGGTATGAATCAGGAATCTCTGAAGTCGCAC
AGGGCGTTCTGGATAGTATATGTGGCTTTTTCAATGTTTCTGATCCAGTGGATATACG
TAATAGTTTCATATATTCAATTATGTGCTTATCATAAGCCGCCCGCCGCTGATCGG
GAATACCTTCAGAACCGTCACGAAGATGGACACTTACTGAGCATTATTAAGGGAAAT
CGGGATGGCCTGGTTATTTTCCCGGGGCGAGAGACTGGTTGTGCGACTGGCCG
ACGATGAAATGATCGTAATTACAGGTTCTGCTGCTGACGCTCTTATCAGATAATAGGAT
CCCGTATATGGATCATGCTGTGACTAATCCATGCGTTCCGGTTGCACGCTTAAGCAT
AGTTTATTTTCGTCATCCAGATCTGACACGTAAATACACATCGTTTATGAACTGCAAG
CAACTGGACTTAGTGGCCGTGGCGAATGAGAGCCATCAGGCGTTCGGTAACAATC
CTTTCTCAGCAGCCGCGTAG

NHI 195 protein sequence:

MQSDLSKHASTNTASSTRINDQIDFPECARELIHSGWSINKLPIALQAHFWDALDLYANV
GSDVKSEFSFPDHTDGFLPFGMEYAKATHQPDLCERYCYWHKDRRRHEAHAFSGSE
FYRAICGYESGISEVAQGVLDISICGFFNVSDPVDIRNSSYIQLCAYHKPPRRPDREYLQ

NRHEDGHLLSIIKGNRDGLVIFPRGERLVVRLADDEMIVITGSLLTLLSDNRIPYMDHAVT
NPCVPVARLSIVYFVIPDLTRKYTSFMNCKQLDLVAVANESHQAFGNPFSA

Codon-optimized NHI 196 sequence:

ATGAAACACTTGACGAAAATTACAGATTACAAAGTCGATATCGAGAAATTGAAATCTG
TTTACTTTAACACAATAGAAAAAATCATCGAGTGGAGCAAAGATGACCCGACTCTCTA
TGACTTTAATGCAATTTGCGTAAACCAGATTCCGAGCGATCCACTATCTATCCGTGGT
GGCAACATCCGCGGTCTATATTGGACGTATCCAAAAGATAGCTGGGAAGAGGAAAA
ACGTTTGAACAAGATCGATGAAAACCAGTACACGGAAGTTTGCAAACCCTTTAAAAA
TACTTATGTAGAAGAGATCTACAATGAAATCTCTCAGCGTTGGAATATCGGTTCGATTC
AGGTTTCTGATGAAGCCCCCAAGAAGTTGTCTTTCATGGCACCGGGATCCAGAAAA
AAGATTACATATTCCACTGATCACCAATCCGGGATGTCGCATGGTGATTGAATCTGAA
AGCTTCCACATGCCAGCCGATGGATCAGTTTATATTACGGATAATACAAAATATCACA
ATTTTTTTAACGGCGGCGAAATAGACCGAATCCATCTGGTCGCGACTCTGCTTAAC
TAA

NHI 196 protein sequence:

MKHLTKITDYKVDIEKLKSVYFNTIEKIIIEWSKDDPTLYDFNAICVNQIPSDPLSIRGGNIR
GLYWTPKDSWEEEEKRLNKIDENQYTEVCKPKNYVEEIYNEISQRWNIGRFRFLMK
PPRSCLSWHRDPEKRLHIPLITNPGCRMVIESESFHMPADGSVYITDNTKYHNFFNGG
EIDRIHLVATLLN

Codon-optimized NHI 197 sequence:

ATGACCGCTGCGAAAACGCGGACCGATTATGCTGAGTACACGGACTGTACCCCCCT
GTTAGACGACCGCAAGGAACTGGATCGTTTTTATGACGAGCACGGTTATCTGTTTTT
ACGTGGTGTTCGATCGCGCACTTGTGAGAACCGCTGCTGAACAGATGCTTCATG
GACTGGTGTGCTGGGAGCTGCGGATCCGCACGCTACTCTGGATGAATTTACGATC
GATTCCTTTGAGGCCGTGGACGAAGTTGCTATGCATGGCCACATAAAATACGATGAA
TTTTGGAATTCAGCCCCGACGACCCGACTGTTTGAACAGATATTCGGCGAGGAGGT
TTTCGTTTTTTCGAAGTACCACCATCCGATATTATCCATCGCAGGCTGGATCAGAGGA
TCCAGCCTTTTCGTATCTTACTCCGCTACACCAGGATGGGTCTATATTGGACCTAAT
AAAGACTTCCGTACGGTCTGGGTCCCGTTAATTGGAACAACAGAAGGAACAGGGG
GAGTTGCGTTAGCTGATGGGTCTCATCGTCATGGACCGCGGGATCATGTTGTGAAT
GACTCCTTTAGACGGTTCGGGCACCCGGTGCGGGGGATTCCGCCACATTTTGTAG
GTGAAGACGAGCCACTGCTGTTTTCAGCGATGGAACCTGGTGATGTTCTTGTATTT
CATGCACACATGTGTCATAAAAGCATTCCGAATCTGGCTACAGCTCCGCCGCTAATG
CGGATGTCCATGGATACACGTGTCCAGCCGGCAGCATCTCACAGAGGATACAATGC
ACTCACTCCATGGCCAGAATCCGCAAAGGACCCGTCTAAAGGCATAATGTCAAAAAT
TACAGGTACCCCTACTGAGATAGAGTGA

NHI 197 protein sequence:

MTAAKTRTDYAEYTDCTPLLDDRKELDRFYDEHGYLFLRGVLDRLVVRTAAEQMLHGL
VSLGAADPHATLDEFTIDSFEAVDEVAMHGHIKYDEFWNSAPTTRLFEQIFGEEVFVFR

STTIRYYPSQAGSEDPAFSYLTPLHQDGFYIGPNKDFRTVWVPLIGTTEGTGGVALADG
SHRHGPRDHVVNDSFRRFGHPVRGIPPHFVGEDEPLLFSAMEPGDVLVFHAHMCHKS
IPNLATAPPLMRMSMDTRVQPAASHRGYNALTPWPESAKDPSKGIMSKITGTPTEIE

Codon-optimized NHI 198 sequence:

ATGTTTAAATGGTTCATCAAGATACTCAATTTACTGCGTGGTATAGTCGAAGTGCGTA
GAGGTTTCGTAGAATTCGCCAAGACGGGTAACACCCCTCCGGAGGCTTATATTCAA
ATGATTAATCTTTTCTGTGCGACAGGTGGCCTCAGTAATGATTTGATTCATCAGATGA
TTAAGAGTCCGAAGCGTAAGTTTCCTGTGACCTCAGGTATTCTGGGCAATTTTACAG
AAAGCGAACTATCGAAGGTTACTATGACGATTAAAGAGAAAGGTTATTTTGTATTCTGA
AAACGTTCTCTCTGACGAAATAGGGAATTACCTGTATGAACCTGGGTGTAATACGGA
ACTTTATCAACGCCCGTTAGATTCCGAATCGTACAAAAACAAACCAATTTATAGCAAA
TTCAATCCCTCTCTGGCACCAGCGAGCATACGGTACGATTTTGACGAAGGAATGTTA
ATAAACGATCCCATTATTCAGTCAATAATGACAGACTTTTCGGTATTGTCCATAGCGC
AGAGTTATTTAGGCTGCTTGCCGAAAGCTGATGTTACGGGTATGTGGTGGCATACTG
ATTCAGCAAAGAGCCAAATGCCGAAGCGGCAACTATGTGGCATTTTGATATGGACC
GCGTTAAATGGCTGAAAATTTTCTTCTATCTTACAGACGTCACTCCGGAAACAGGCC
CACATTGTTTTATTGAAGGTTTCGCATAGAACCCGTGGGATTCCCAAACATTTTTTAAA
ATATGGTTACTCTAGGCTGTCAGATCGCGATGTTGAAGACTACTATCCAAAAGAGAA
ATATATAGAGTATAACGCCAAGAAATTCACGGTGATTGTAGAAGACACACGTGGTTTA
CACAAAGGCAGAGCAGTTACGAATGGCTCCAGACTTATATTCCAGACACAGTTTTTCC
GATCACCTGTTCCGGTGGTACGTACTCGAGTAAGAAAATAAACCGCTTTGCGAACGC
TAAACAGAAGAATTTATTAAACTCAACAAAGATATTTATGAACGCTTTCTTTAA

NHI 198 protein sequence:

MFKWFIKILNLLRGIVEVRRGFVEFAKTGNTPPEAYIQMINLFCATGGLSNDLIHQMIKSP
KRKFPVTSGILGNFTESELSKVTMTIKEKGYFVFENVLSDEIGNYLYELGCNTELYQRPL
DSESYKNKPIYSKFNP SLAPASIRYDFDEGMLINDPIIQSIMTDFSVLSIAQSYLGCLPKA
DVTGMWWHTDFSKEPNAEAATMWHFDMDRVKWLKIFFYLTDTVTPETGPHCFIEGSHR
TRGIPKHFLKYGYSRLSDRDVEDYYPKEKYIEYNAKKFTVIVEDTRGLHKGRAVTNGSR
LIFQTQFSDHLFGGTYSKKINRFANAKTEEFIKLNKDIYERFL

Codon-optimized NHI 199 sequence:

ATGAATATAGCTCAGTCCACAATAGCACCCGCTGACCTTTCTAGTGTCTCACTGCAG
CGCAACCCTGTTTTGGTAGTGGAGAACTTCTGGTCGTCGGATGAACGACGCTTCTT
CCGGGAAAAAATGAACGGTGCAAGTTGGAAGTCACTTTCAGACCTTCCCCACGTAA
GAGCCGACTTCCCAAATTCCGGTAATTGGGCGAAAGCGGAGCTGGGGTCTGAGGA
AGGCCGGCGGTTTTTGTGCGCGCCTCGAGCTGCCGTGTATTCGTGATCATATTGAAA
GTTTTCCAAATATTATAGGTCGTCATGTCGGTTTTTAATTACTACTCTTACGCCGCTGG
CGATTGCCTGTTAACCCACGACGACACCGACCAGGGTCGTCTGGTGGAGGGAAGA
CGCGCGCCTAAGAGACGGATTGCCGTTGTGACATATGTACACGAGGAGTGGCAGC
CCGACTGGGGCGGTGAACTGATTATCTACGAACGGCGCGCTGATCGTGCCGGGGA
GCCCGTAAACTTAATACCCACCCATTGCATTGAACCCAGGCCGGGTAGTTTAGTTAT

GTTTACAGTTCCAAGATTTTCATCGGGTGTGTGCGCTAGATCCGACGGCTGGAGAAC
ATCGCCGTCTGTCTATTGCAGGATGGTTCATGACCGAACACTCCTAA

NHI 199 protein sequence:

MNIAQSTIAPADLSSVSLQRNPVLVVENFWSSDERRRFFREKMNGASWKSLSDLPHVRA
DFPNSGNWAKAELGSEEGRRFLSRLELPCIRDHIESFPNIIGRHVGFNYYSYAAGDCLL
THDDTDQGRLVEGRRAPKRRIAVVTYVHEEWQPDWGGELIYERRADRAGEPVNLIPT
HCIEPRPGSLVMFTVPRFHRVCRVDPTAGEHRRLSIAGWFMTEHS

Codon-optimized NHI 200 sequence:

ATGTTGGATATCTCGCGCATTGGTCGACAGGCACTTGCTAGTGAGCCTTTTGGGTG
GGCCTTTGTGGATCGCCTCTTCAGTTTCGGGGATGCAGCCGCACTGGCCGCCTCA
TTTCCGAGAGATCATTTCAGACAGTTGCAGGCTATGATGGTGAGAAATCGTACGAA
TACGTGGCCCGCAGTCTCGTGCATATGGGGGCACATGTCCCCAGCTTCGCAGAAC
ACCTCAGTCCTGCCTGGAAACATTTAGCAAGTGAAGTGTAAAGCTCTGCATATCGCG
CGGCAATGACCCGTCTAACCGGTGCGGATTTAGCGACGGCCCCGATGGAGATCAAT
GTCGTGCATTATGGGACGGGTGCGTGGCTCGGACCGCATCTTGATTTGAAAGAAAA
AATTGTTACGCATGTTCTGTATTTTAATGAGTCCTGGAAAAAAGAAAACGGCGGCTAT
CTGAGCATCTTACGGAGCGCTGACCCTAGCGATATTGTGTCTGAAATTATGCCGATA
GTGGGGAATTCGGTAGTTTTAGCCCGTTTACAGACGCGTCGTGGCACGCCGTGAGCC
GTGTAAGTGAAGGTTGTCGGCGCAGCCGCCGGTTCGATGAACGTCATATTTTCATCTA
CCCGGTAGTGTCAGCACTATTTGGCCACCTGGCCGCACCGCAGAACTCCATGATTA
TACAGGTATTTAG

NHI 200 protein sequence:

MLDISRIGRQALASEPFGWAFVDRLFSFGDAAALAASFPRDHFKTIVAGYDGEKSYEYV
ARSLVHMGAAHVPSFAEHLSPAWKHLASDLLSSAYRAAMTRLTGRDLATAPMEINVVHY
GTGAWLGPLDLKEKIVTHVLYFNESWKKENGGLYSILRSADPSDIVSEIMPIVGNVVL
ARSDASWHAVSRVSEGCRRSRSMNVIFHLPGSVSTIWPPGRTAELHDYGTI

Codon-optimized NHI 201 sequence:

ATGAACGCTCAAGATCATGACGAAGATACGGATCGAGATGCCTGCAGCTCACCTGA
TAGCCTGTTCGATGGGGAAGTGGACGCGTGTAGTCTGGACGGAGCCATTACACTG
CTGCCCCGCGCGCCGTACAGCACCGCCAGTTCCGGGTCTGCTATTTTACCCACATAT
CCTAATACAAGAAAGCCTGGCCAGAGATGTATATGCGTTTTGTCGAAGAACATATTTT
ACGGCCGCTGGTGCGGACCAGGTTATGCTGTTTGAACGTGCGCCTGCCGCCAG
GGTCGCAGCGAGCGGCAAGAAGTCGATCAGAGGCCCGCCGTCAGGTTTACCAGCG
ATTTTGCTATCACTTCTTCGTGCCATTTTACAGAACTCACTGGCTTTGGTCCTGCCTCCT
GATGTTTCATGCCCTTTTGTTCCTTCGCGAGCGCCCAAGCGCGCACGCCAAATTATCGTA
AATCTTTACGCCCCAGGAGAGGGTATATCAGCGCATGTAGATCTTTTGAAACGCTAT
GGCGATGGTATCGTGGGGGTTTCCTTTGGGTGAGGCTGCGTGATGCGCTTTAGTG
ACGTGGGTGATGACGCGGCAGCAAATGAATCTTACAATCCTGGCACAAAGAAAGAT
GATGGTGGTGAACGGGAATTTTACGACGTGTATCTACCGGAGCGCTCCTTCTATGT

GATGATGGGGGATGCACGTTATAGATGGACTCATGGTATCGAACGCCGCCGTGAAG
ATTATGTGGAACAGAGGACGGAGATAAAGCGGAATGGATCGGACGCGGAGAACG
TCTCTCAGTGACCTTTCGGTGGATGCTGGAGGGTGGGGATGTTCTCTGA

NHI 201 protein sequence:

MNAQDHDEDTRDACSPLDGLDACSLLDGAITLLPARRTAPPVPGLLFYPHILIQ
ESLARDVYAFCRRTYFTAAGADQVMLFERAPAAQGRSERQEVDQRPPSGLPAILLSLL
RAISESLALVLPDPVHALLFSAAPKRARQIIVNLYAPGEGISAHVDLLKRYGDGIVGVSFQ
SGCVMRFSDVGDAAANESYNPGTKKDDGGEREFYDVYLPERSFYVMMGDARYRW
THGIERRREDYVETEDGDKAEWIGRGERLSVTFRWMLGGDVL

Codon-optimized NHI 202 sequence:

ATGCTTCTTGATACCTATTTCTATCACCTGCCTCGCGCTATCCCATCCCATACCTGTG
AAGACATCATTGAATTTGGGAAATCTCTTAATCCAACCTCAGAGCCGTACCATGTCCA
CAAAAGATATGCTTTCTGACGAGGAAAAAACAGGAAATTAAAGATACCCGCAACA
GTAAAGTCGCATGGGTGTATCATGACAATCCTTGGCTGTTTCGGCAGTTAACCCCGA
TTCTAGAGTACGCGAACAAAAGTTGGGGGTTTAATATTTACGTTACGAGAATATCCA
GTTCACTGAATACGAGCCGCGTGGCCACTATACATGGCATAATGATGCTATCCAGAA
CCCGATGAACCTAAAAACATGATGAGAAAATTGAGCATGGTGGTACAATTGTCTAA
ACCGGAAAAATATGAAGGTGGCGGATTTCTGTTTTAACCTACGTGGTCTGGACTCAC
AGGTCGACGACAACATTATGAGCCCGCCTCCAGAATTTAAACAACAAGGCTCAATAA
TAGTGTTTCCTTCCTTTCTGTGGCATAAAGTGGAACCTATTACGAAAGGCATCCGTC
ATTCCTTGATTATGTGGGCTATTGGCGAAAAATGGAAATAA

NHI 202 protein sequence:

MLLDITYFYHLPRAIPSHTCEDIIEFGKSLNPTQSRTMSTKDMLSDEEKKQEIKDTRNSKV
AWVYHDNPWLFRQLTPILEYANKSWGFNISRYENIQFTEYEPRGHYTWINDAIQNPMN
LKNMMRKLMSMVVQLSKPEKYEGGGFRFNLRLGLDSQVDDNIMSPPEFKQQGSIIVFPS
FLWHKVEPITKGIRHSLVMWAIGEKWK

Codon-optimized NHI 203 sequence:

ATGTCGGATCAGGCGCGTGAGGAGGCACTGGCGCAGGCCGCTCTGGTTGCTTTAC
GAGGAGGTAATGCTGCTAAAGCCAGGGCCACTCTGGCGCAAATGGCCGCACCTCC
TCCGATGTTATTGGCCCAGGTTTGTAACCGTTTAGGTGACCGGGATGGCGAAGTCG
AGGCACTGCGAGCCATATTGGCTGGGGACCCTCGAAATTTACCTGCTCTCTTGGCT
ATGGGACACAATGCTCAAGCACGAGGCGACGATCGTGGCGCGATTTTCATGGCGTC
GCACCGCACTGGCGCAAGCAGCGGCCCATGGAGCCCCACCTCAGCTGCAGCCTT
TATTACAACAGGCACAGGGAAGCATTGCACAGAGCAGCCAACAGTTTGAGGATCAC
CTGACGGCAGCCATCAGAGATCTGCCTCCCCCTTCCACGTATTGCGCTTGCAACGGA
TCTGCTTCTGGGAAAGCGTGAGATTTATCTTCAGCAACCGTCTATGTTTTATTTCCC
GGCCTCCCCCAGCGAGCATTTTACGAAAGGTCCGATTTTGATTGGGTGGCTCCTAT
GGAAGCGATGACTGATGCCATCGTCGCAGAACTAGCTGCAGTGCGGGCCGGTGCG
CCGGATTTTGCCCCGTATGTGCAGACAAGTAAAGAGCGCCCCGCCCGAACAATAA

GCTGCGTGACGATCCGTCCTGGGGCGCATACTATTTCTGGCAGTCAGGAGCTCCG
GTTGCAGATCACGCGACCCGCTGTCCAGCTGTGATGGCCGCGCTTGATCATGCTC
CAATGCCTGTTATCGAAGGTCGCTCACCCACAGCACTGTGGTCTCTGTTGAAACCA
GGAACATCATATCGCGCCGACACGGGTTATTGAACACTCGGCTGATTTGTCACCT
GCCATTACTGACGCCACCGGATTGCGCCTTACGTGTCGGTGCTGAGACCCGTCGG
TGGCATCGCGGTGAGATGTTGATTTTCGATGATTCCATCGAACATGAAGCTTGGAAT
AGATCGGCCGATACTCGCGTCATTTTACTGTTTGAGGTTTGGCGCCCTGAGATCGTA
GCGGAAGAGCGGGCCGCGTTGACACTGCTGTTCCAGGCTATCGACCAGTACGGC
CCGGCGCAGATCGACACCGGCGGGTGA

NHI 203 protein sequence:

MSDQAREEALAQAALVALRGGNAAKARATLAQMAAPPPMLLAQVCNRLGDRDGEVEA
LRAILAGDPRNLPALLAMGHNAQARGDDRGAISWRRTALAQAAAHGAPPQLQPLLQQ
AQGSIAQSSQQFEDHLTAIRDLPLPRIALATDLLLGKREIYLQQPSMFYFPGLPQRAF
YERSDFDWVAPMEAMTDAIVAELAAVRAGAPDFAPYVQTSKERPAPNNKLRRDDPSWG
AYYFWQSGAPVADHATRCPAVMAALDHAPMPVIEGRSPTALWSLLKPGTHIAPHHGLL
NTRLICHLPLLTTPDCALRVGAETRPWHRGEMLIFDDSIHEAWNRSADTRVILLFEVW
RPEIVAEERAALTLLFQAIDQYGPAQIDTGG

Codon-optimized NHI 204 sequence:

ATGGGTGCGGAGCATTCTAATGCCCTTCCTCTGGGTTACGAACTAGTTAAGGGGTG
CCTCCCACCAGCTCAGTGCCATGCCATATGCGAGGAATTATCATCGCATCACGTCTG
TGCGGGTACGGGGGGGATTAGAAAACGCTGAAAAAAATTCACGGGGGATCCGCGAT
CTGGCACATTGTGCACACCTGCTTTCTTTGGCAGCTCAGTACTTAAATGGCCCCGGC
GCAATTAGTTCGGGCTATTGTTTTCAATAAAACCGTTGACAACAATTGGTTAGTGACT
TGGCATCAGGACAAAACGGTATGTGTATCAGCCAAATTCGACGCCCCGGATTGGGG
ACCGTGCTGAGAAGGACCACACTCTGCACGTGCAAGCGCCGCTCGCAGTTCTT
AATAACATGGTTACGCTGCGGATCCATCTGGACCCAGCGGATATTAGCAGTGGTTGT
CTTAAAGTCATCCCGTCAAGTCATCAGGCCGGTCTGCTGAGTCAGAAAGATATAGAA
CAAATTGTCCGACAGCAGCCTGAGGTGGTATGCGAGGCCGGCGTTGGAGATGTCC
TTGTTATGCGTCCTCACCTATTACATGCGTCATCAAAGCTCAAATCCGTCCCAAC
GCCGGGTTGTCCATCTAGAGTATAGTGGGTATTGTTACCAGACCATGTGTCATGGG
CTTAG

NHI 204 protein sequence:

MGAEHSNALPLGYELVKGCLPPAQCHAICEELSSHHVCAGTGGIRNAEKKFTGIRDLA
HCAHLLSLAAQYLNGPAQLVRAIVFNKTVDDNNWLVTWHQDKTVCVSAKFDAPDWGPW
SEKDHTLHVQAPLAVLNNMVTMRIHLDPADISSGCLKVIPSSHQAGLLSQKDIEQIVRQQ
PEVVCEAGVGDVLMRPHLLHASSKAQNPSQRRVVHLEYSGYSLPDHVSWA

Codon-optimized NHI 205 sequence:

ATGAGCGTACAGCAAGTTAAGGAACAGGGTTTCTGCATCCTGGAACATGTTTATAGC
GGTGAGGAAGTTCAACGTATAATTGAAAAAATTGAAGGAGTTGATCCCGTAGGCC

GGCGTTTCGAAAACTAGCGATCTATTTGCAATACGTCGCTTTCTGCACGTAGTGGC
CGATGTCGGCCCCCTGATTTTCACTCCGGCGCTGCAGACAATAAAGCTCCTTCG
GTCCAGATTTCTTTCCAGTCAAGAGCATTACTTTGATAAGCCGGGTGGAAGCAATT
GGTTTGTAGCGTATCATCGTGACTTAACAATTCTGGTTGATCGTAGAGTTGAGTATGA
AGGATACAGTGGCTGGACTGTGAAAGAGGACCGTTTTGGCGTACAGCCACCGGTT
GATGTTCTCGAAAATATCTTTACTATCCGTATCCACCTGGATGATACCGACGAATCGA
ACGGTGCACTTCGGGTGGCTCCGGGCTCACATCTCGAAGGTGTAGTTCGTCCAGA
GCTGACAGATCTCAGTGAAGAACAGGTGTGTGCGTGCCGAGAGGAGGCGTGATG
ATTATGAAGCCGCTCCTTCTGCATGCTTCCGGACGGACAGTTTCGGAGCGTAATAG
ACGCGTCATTCACATCGAATTCAGTAATCGTGCGCTGCCAGGTGGTTTAGAATGGG
GAGAAAAAAAAGAAACAGTATAG

NHI 205 protein sequence:

MSVQQVKEQGFCILEHVYSGEEVQRIIEKIEGVDPVGPAPFRKTSDLFAIRRFLHVVADV
PLIFTPALQTISSFGPDFFPVKSIYFDKPGGSNWFVAYHRDLTILVDRRVEYEGYSGWT
VKEDRFGVQPPVDVLENIFTIRIHLDDTDESNGALRVAPGSHLEGVVRPELTDLSEEQV
CRVPRGGVMIMKPLLLHASGRTVSENRNRRVIHIEFSNRALPGGLEWGEKKETV

Codon-optimized NHI 206 sequence:

ATGCTGAAAGAAAACTTGCACGTGGACTGAAAGTTCTTACTGATAAACGCTACAGG
CAATTCTATGCTCAGAGACAGATTTTAGGTGTTCTTCTCGGGAACGCAAGGCCAAT
TCACTAGCATCCCGCCTTCCCGTTTTTGGAGGCACGTGGTACAGGCGAGACCTCTGC
ACAGACAGCTATTCTTAAGGATCGCGGTTATCTGTTCTCAATAACTTGATTAAGCCG
GACCAGCTTCAGGCAATGCATGCCTTTTTTCAGTGTTAATGAGTGCGCGGATCCATAC
AGGCCAGAATTTGGCAAATTTGTTGCACCGGATAACGCGCCGCCGCGACACATGT
GGCGTTTTTTTCCAATGAAGCGATCATTCGTGCCCCGCACGTTCTGGATATAGCAA
TGATCCTAATGTGCTTTCAATCGTATCAGGGTTTCTGGGAGCGAAACCCACTATCTC
ACTGATCACTGCTTGGTGGTCTATGCCTCATAAAGATGGTAAAGCAGAGGAGGCGG
AATTGTTCCACCGCGATGTGGACGATATTCGGTTTGTAAATATTCTGCTACCTGAC
AGACGTTGACGAAGTGAGTGGCCCTCACATGTTTGTACCCGGATCTCAAAGTATCG
ATAGGTTGACGAAGATCAGAAGGTATCAGGACAGTGAAATCCTTGATGCGTTTGGT
GAAACCAGCGTTACGACATTTACGGGTAAAGCAGGGACAGCTTTTTTAGAAAACACT
TATGGATTCCATCGCGGGGTGCCTCCAACGCGCAAACACGGCTCCTATTTAGGT
ACTATACTCTTTGAGGAACTCGATATACGGACCAGATAAACCTGTCGGTCGGATTGG
GGCAAACGGGGTCCCCGCCGGCATTGACCCCTTTATCAACCGGGTGTACCTATCCC
CGCGCTAA

NHI 206 protein sequence:

MLKEKLARGLKVLTDKRYRQFYAQRQILGVPSRERKANSLASRLPVFEARGTGETSAQ
TAILKDRGYLFLNNLIKPDQLQAMHAFFSVNECADPYRPEFGKFVAPDNAPPQTHVAFF
SNEAIRAPHVLDIANDPNVLSIVSGFLGAKPTISLITAWWSMPHKDGKAEAEELFHRDV
DDIRFVKLFCYLTDVDEVSGPHMFVPGSQSIDRLTKIRRYQDSEILDAFGETSVTTFTGK

AGTAFLENTYGFHRGVPPTRKPRLLFQVLYSLRNSIYGPDKPVGRIGANGVPAGIDPFIN
RVYLSPR

Codon-optimized NHI 207 sequence:

ATGGAGATTCGTAAACTGATCCCGGAAGTTTATGGGGAACAAGGGTATTCGCTCCAT
CTTAAACTTTCTGAGGAGGAACTCGGTGCAATCAGAAAAATGATCCGCATGCAGTG
GCTGTACCGCCTACAGCTTATTGCCCCGAAATATACATATCAGTTCGATGAGCTTGG
AATAGAACGATATCACGAACTGGCTCATACAATTGATCACAGCCAGTCGTGGCCGAA
AACGAGCAGAGTCCTGCCTAGAGAGGCAGTGGATGTGATCCGAGCGATGGAATTTT
TTCAGAAAATGGAAAAGGAGTTTGGTGATATTAATTTGCGGACGAGGAAAAGCTG
GGGTGGGAGAACATTTATTGGCGGTTGGTGCGCCCCGGAATTCTGACTTCGGAA
CCTTACATACAGAAAATTGGTTTGTAACTCTCGGGTATTATGGCGATGAAGTGCACGA
TAAAGACTGGGAGAAAATTAATCTGGATCAGCATTTCATGCGACTCCGGGGAAAAA
TGGTTTGATTGTTGTACCGCATTCTCACCAAAAAAAGATTGGAAATGGCATGCAGA
GGATAAATATGGGCAGAAAAAGCCTATAATTGATGAAGACGTTTCCCAGTTGAACCA
GCTGCTGCTGGCTACAGAGCCCCGGGAGAGCTGTGGTATTTCACTATGACCTCCTTC
ATGGAGGGGCTGAGAATAAAGCCGATACTACACGCATCTCTACTGAGTTCACCTTCC
TTATTAAGAAAAATAAGATCGCCGGTTTAGTATGTAA

NHI 207 protein sequence:

MEIRKLIPEVYGEQGYSLHLKLSEEELGAIRKMIRMQWLYRLQLIAPKYTYQFDELGIER
YHELAHTIDHSQSWPKTSRVLPREAVDVIRAMEFFQKMEKEFGDIKIADEEKLGWENIY
WRLVRPGNSDFGTLHTENWVFNLGYGDEVHDKDWEKIKIWISIHATPGKNGLIVVPH
SHQKKDWKWAEDKYGQKKPIIDEDVSQLNQLLLATEPGRAVVFHYDLLHGGAENKA
DTTRISTEFTFLIKKNKIAGLVC

Codon-optimized NHI 208 sequence:

ATGCCTTCGACATACCTACAGTCCCTTCAAAAAGAAGGTTTCGTTGTGATCCCTAGC
CTGATTCCGCCAAGTAGTAAAGAATTTGCGACATTAAACAGGCCGCTACTACTGCG
ACGACCAACACCCGAACCGGAACGTGGCCATACTTCCGTACCGTCCCTAAGCAGTT
TCCACCCTGGCCCACAAACGTTCCACCTCCAGCAAGCGAAGGCGGTATATGGGGA
GTGCAACATCTGTTGCACCCGGACATGCCAGGTCGCGAAGAATTGCTAAGTTTTA
TTTCGATGAGAGAATTTTATCTGTAGTTGAAGAACTGCTAGGGCTCGACCTTGCCGA
AAATGATGAAAACTGGTCATGGAACGTTCACCTGTTGGTGGCCCCTGAACTC
ATGATTTTGCCTTACGCTGGCATCGTGATGATATTCCAGAGACCGCTTCCCCGGATG
AAGAAGAAAAGTTGTTAGCATCAAATCTCCGGGTGGTAGACAGTCTCACGCCCGAG
TACAATCTGGCATTGTGTGACGATGCATCTCTGATTGTTGTGCCGGGTTCACCGT
CGTGTTTCGCACGGAAACAGAACGTAACGCAGACCCGTACGAAAATGAACTGCCGG
GACAGCTAGTCGTTGAATTAAGGCTGGTGATGCAGTTTTCTATGATTCAAATATACT
CCACCGCGGCGTTTATAAAGCCAAAGAGGAGGGGGGAGAAGAATCTAGATTGACC
TTACATGGGTGCGTGGGTATAAAGAAACGGATGGTGGCGAAGGTGATGGTAGTAA
AAAAGTTCGCGCCACTGCAGTTCTACAGCATGGAGTGGGCGCATGGGTGCATCGG

GGTGATGCTGCTTTTGGGGTTGGAGGTCGGGCGGAAAAAATGCGTGCGAATCTCG
TGGCAATGGGAACGGGGGAAGGTGTTGGTTACTCGTTACAGGGGTGA

NHI 208 protein sequence:

MPSTYLQSLQKEGFVVIPSLIPPSSKEFATLKQAATTATTNTRTGTWPYFRTVVPKQFPP
WPTNVPPPASEGGIWGVQHLLHPDMPGREEFAKFYFDERILSVVEELLGLDLAENDEK
LVMELFNLLVAPETHDFALRWHRDDIPETASPDEEEKLLASKSPGGRQSHAQYNLALC
DDASLIVVPGSHRRVRTETERNADPYENELPGQLVVELKAGDAVFYDSNILHRGVYKA
KEEGGEESRLTLHGSGVIKETDGGEGDGSKKVRATAVLQHGVGAWVHRGDAAFVG
GRAEKMRANLVAMGTGEGVGYSLQG

Codon-optimized NHI 209 sequence:

ATGACCGATCCGAACACTTGTCTGTCCGATGAACAGATGCGTCATTATATCACCAGG
GGCTACGTCGTGCTGAAGACCGGACTGCCTAAAAGCTTCCACGAACAAATTTACCA
GCGCACATCGGAGGTAATGGAGAAGGAAGGCAACCCGGGTAACAACATTCTTCCG
CGCGTGCCAGAACTGCATCGTGTGTTCCGCCGACCCTACCTTGCGAGGCGCGCTTA
GCAGCGTATTGGGCCCGGATCACATCATGCACAGCCACCGTCATTGCCATGTTAATA
AGGGCCCCGGGCGATGGCGGCGGCGTGCATAAGGATAGTTACTGGGGTTATAGAAG
GGTCCGCTCGCATAGAACTAGGTGGGCCATGCTCCTCTATTACCCACAGGATTGTC
CAGAGGAAATCGGTCCGACAGGCGTAGTGCCGGGGCAGTCAAACCTATGAGCATAA
GGAGAGTTGGGAGCCGCTGGAGCAGATCCTACCATGTGTGGGCGAAGCGGGCAC
CGCTGTGCTGATCCATTTTGACATTTGGCACCGCGCTTGCCCTAATCTCACAGAGA
AGACCCGCTTCATGATGAAATTCCAGTTCACGCGGATGACAGAACCTACTGCTCCG
ACCTGGAATAATCGATCGGCCGTTTTTCTGAGGCAACGGGTCAGGCGATAGACA
CCGTGGTTTGTGGACGCGGATGTGGAATTGGCACAGAGGTGACGCGCTAGCTACG
GTTGATGGAACCGGCGCAAGTGGTGTGATGCGGTTGCTCAGTTACGCGATGGGG
ACTTAGAGGAACGTATGGCAGCAGCGGATCACTCGGTGCCGCCGGCGCAGGCGA
TGGTACTTTGGATGCCTTAAGAGCCGCCCTTGCGAGACGAAGCGGAACCGGTGAGA
TTGAATGCTGCGTATTCTCTTGCCGCGATTGGTACCCCGGCAGTAGCTGGCCTCGT
TGATTGCTTGACCGACGATATGGAGCCCGCTCGTCAGGATGCGGGCTCAGGGTCTG
GCCGCTATGGGCCCTGCCGCGGAAGTTGCGTTAGTGAACGCCTGTTCTGACGCAG
ATGAGGCGCGACGGGGATACGCGGCATTTGCATTGGGTGAAATGGGCGCTCACGT
GGTTAGTGATGCTGCTGCAGCTGTTTCGGGCCTTGCTACCGATCCGGCTGAATTTG
TACGACGTAACACAGCGGACGCCCTTGCTACTATGACTGGACACGCCGACCACGC
AGTACCTGCATTGACTACCCTGTAAAGTGATGATTCAGATCAGGTTAGATTTGACGC
GGCATATGGTTTAGCGCATCACGGTGTGGCCGCAGCTCCGGCGACGGACGGTCTG
GTTGGGGCTCTGGATGATGAAAACCGTTACGTCCGCAACCACTCAGCAGAAGCCC
TGAAGCGTATTGGGACCCCGACCGCCACCGCGGCGTTGTTGACTTTCTTGAAAC
ATCACGTTGGTGCCCCATTACCAGCAAAGAAAGCACGTTCTGA

NHI 209 protein sequence:

MTDPNYLLSDEQMRHYITRGYVVLKTGLPKSFHEQIQRTSEVMEKEGNPNNILPRV
PELHRVFADPTLRGALSSVLGPDHIMHSHRHCHVNKGPGDGGGVHKDSYWGYYRRVR

SHRTRWAMLLYYPQDCPEEIGPTGVVPGSQTYEHKESWEPLEQILPCVGEAGTAVLIH
FDIWHRACPNLTEKTRFMMKFQFTRMTEPTAPTWNNRSAVFPGGNGSGDRHRGLWT
RMWNWHRGDALATVDGTGASGVDAVAQLRDGDLEERMAAADSLGAAGAGDGTLDALRAALRDEAEPVRLNAAYS
SLAAIGTPAVAGLVDCLTDDMEPARQDAAQGLAAMGPAAE
VALVNACSDADEARRGYAAAFALGEMGAHVVSDAAAVSGLATDPAEFVRRNTADALAT
MTGHADHAVPALTTLLSDDSDQVRFDAAYGLAHHGVAAAPATDGLVGALDDENRYVRN
HSAEALKRIGTPTATAALFDFLETSRWCPITSKESTF

Codon-optimized NHI 210 sequence:

ATGAATGAACATTTATTAAATTCGAAACAGATGGCCAGTTTTGTTGCGTCAGGATATC
TGCGCCTGGATAACATGGTACCTAAAGATCTGTGCAATGCATGCCTGGACGAAATGA
AGCACCATAATGGGTATTTTGAGGTTGGTGCGCCTTTTGAAGAGATCTGGCCTAAGA
ATACAGCATTAGGTGACACCTTTCGTCTTCCTCAAATCAAAGGCCTGATCCAGTCAT
TAGTCGGACCCGACCCTCTGTATGACCATCACTTTCGCGATTTAACAAAAGCGAATA
ATACTCGAGGACCTGATATGCACCAGGATTCTGTTATCGATTTCCGTGAAAACCTATTT
TGATATCCAGCTGTCTTTTTTTCGCAGCAGACACGCCAGATAAAATGGGCGGTACTTT
TCTAATTCCGGGGACTCACTACAGAAATGTTTCGCACCTCTGAGATTACGATTTATCAA
CACATGAAAGGAAAAGTTTGGGCAGCCTGTCCTGCGGGTACAATATATGTTTGGAAT
ACGCGTGTGTGGCATGGCGCTCGGAGCAATCGGTCTGACAAAGATCGGTATATGTA
TAAATTGCGGCTCAACCCTACACAACCGCAGATCGGACTGTTTGATACCAGTGACC
TGAACGACCCATCTATCGATTGATACTGAATACAAATCATGGATGGGAAGGTAACG
AGCATCGTTATGAGCTTATGCAACGGATTAACTGTGGCGTTACGTTTCCAATCAAC
CAGACTACGATGTAGGTGAACGGTTTATGCGCCGTATTGAATACAACCCCCAGATTG
AAGCGGCGTAA

NHI 210 protein sequence:

MNEHLLNSKQMASFVASGYLRLDNMVPKDLCNACLDEMKGHHNGYFEV/GAPFEEIWPK
NTALGDTFRLPQIKGLIQSLVGPDPDLYDHHFPHLTKANNTRGPDMDHQDSVIDFRENFYDI
QLSFFAADTPDKMGGTFLIPGTHYRNVRTSEITIYQHMKGKVWAACPAGTIYVWNTRV
WHGARSNRSDKDRYMYKLRLNPTQPQIGLFDTSIDLNDPSIDSILNTNHGWEGNEHRY
ELMQRIKLWRYVSNQPDYDVGERFMRRIEYNPQIEAA

Codon-optimized NHI 211 sequence:

ATGACAGCAAGTGAGTCACCTAAATGGAAATCATCTCTGTTACAGAAACGGTTAGTC
ACTCGCAGCGCATTTTGCAACGAAGCATCGCAGTGTGCGGCATCCATATTGCGGTC
TGAGGCTGCGCGCGTTGATGGTCAGCTGTGTGATGATGTTTCGAGCGGTCCTGGCA
GGTAATGCTGTTTACATTCGCCGCTTCGTGTGCGATGAAGCCGATATGCGGCTCTAT
GAACGCCTCAAGGCAGAACTGGTAGCCGCAACCGGAGCGAACATGTCTCATGATG
GTGGTCGCATAGATTGGTCCCGCCATGAGATTTTTGAAAATCCAACTGGCATCAGC
GCGATGTTTAATGAGATTATTGATATGTTAGCTGAGTATTTTCGATTTGGACGTGTATGC
GACCAGGCTCAATTACTATCGGGATGGGCATCAATGGAAGCCGCAACATCATGATTC
TCATGCGTATGGGGGCACATCAACACACAGCGGCGAACGATTACGTGAAGATTTCA
CCGTGGGCATAACTCTGGGCGCGACCCGTTCACTGCTGTTTGTCCACGAAGCGAG

TGCCACCAATTTGACTTCCCACAGCGTAACGGTGACTGTTTCGCCTTCACTAGTG
AAGTTAATAACGCCTTTACTCATGGGGTCCCCCGGGTTAATACTCCTGTAGGCGACC
GCTTCAGCATTATTGCGTGGGGTTCGCAGACGCGCTATGAACGAACGTAATTCCGAT
CGGGCGGTGCCCTCATTGACGGTAGTGACCTTCAATCTGTAGATGATGCAATTCA
GGCCGCCCATCAGCTCGTCAGCCGTGCCTCAGCATCGACCCGCCCAACCGTCGC
ATCAACGCCGTCTACACGCATGGAACGGAATGATGGTAATAGTCATCGCAATGAATC
TAGCGCAGGTAGTTCGGTGCCGGCTAAAAAAGAAAAAGAATCGCCTGCAGTAA

NHI 211 protein sequence:

MTASESPKWKSSLLQKRLVTRSAFCNEASQCAASILRSEAARVDGQLCDDVRAVLGN
AVYIRRFVCDEADMRLYERLKAELVAATGANMSHDGGRIDWSRHEIFENPTGISAMFNE
IIDMLAEYFDLDVYATRLNYYRDGHQWKPQHHD SHAYGGTSTHSGERLREDFTVGITL
GATRSLLFVHEASGHQFDFPQRNGDCFAFTSEVNNAFTHGVPRVNTVPVGDRFSIIAWG
RRRAMNERNSDRAVPSFDGSDLQSVDDAIQAAHQLVSRASASTRPTVASTPSTRMER
NDGNSHRNESSAGSSVPAKKKKKNRLQ

Codon-optimized NHI 212 sequence:

ATGAACCAGGACACGACGACATTACTGAACCAACCGCAGCATCGGCAGCTTTCTTT
AGCGGATGAAGTTGCCGGAGCGCCTGGGTATAGCACTCGCCTGTCGCTGAGCGAG
CCGGAGCTGACGGTTATTTCGTCAATTAGTCAAGGATCAATACCTGCAGCAGATTGAA
GCCCAACCATCCTGATAAATTAGAACTGTTTCGTTCATGGTTCAATGGAGGATTATCACC
TGATATGCCACCACGTTGACCACGAGAAATTATGGCCGAAGGTGCGTCGTATTTTAC
CGCAATTCAGCGTCGAAATGATTCAGACTTTACCATTTCATGAAGGAACTGGAAAAAG
CGTATGGTGCGTTACGCTGAGCGATGAAGAGGAGATGGGATATGGAGAGATGTAT
TGGAGAATTGTTTCGTCCCGATTCTCCTACAGATGTTGGCCCAATTCATGCGGACTAC
ATGTTTTGGGAACTAGGCCACGGCAAGATGCCAGCAAACCTGTTTCAGGGTGAAAGT
TTGGCTCGCATTATTCGCAGAACGGGGAAAGTCCGGCTTCCAATTCGTGGCTGGTT
CTCATTTAGAAGATATTCCTTATATAGGTCAGAAAAGAGGGTTAATTCTGAAACCTAA
GCTTCTGGTGGATGTTAATAGCCTTGCCCTGGTGCCCTTTGTCGCCTCTGCCGGCG
ATATAATTGTGTTTCACGACCGTCTGTTACATGGCGGCCTTGTTGGTGGACAGAAGA
CCCGAATTAGTTTAGAGTTTACTATGATCATTCCACACCGTTCATAG

NHI 212 protein sequence:

MNQDTTLLNQPQHRQLSLADEVAGAPGYSTRLSLSEPELTVIRQLVKDQYLQQIEAHH
PDKLELFRHGSMEDYHLICHVDHEKLWPKVRRILPQFSVEMIQTLPFMKELEKAYGAF
TLDSEEMGYGEMYWRIVRPDSPTDV GPIHADYMFWELGHGKMPANCFRVKVLAL
FAERGKSGFQFVAGSHLEDIPYIGQKRGLILKPKLLVDVNSLALVPFVASAGDIIVFHDRL
LHGGLVGGQKTRISLEFTMIIPHS

Codon-optimized NHI 213 sequence:

ATGGCAAGTTCGGCACACAACCTGCAAACGCTGCCCACTTTACATGGCGTGACTGC
AGCGCCGCCGCCAACCCCGGCAACACAGCCAAATAGGTTGAGTACTAGCGATGCA
GCCGATGCATTAAGCCGTCTTCTGCATCGGTTACCGCCGACCTTATCTCTGCCTACT

CGCTTATCTCCGCCAACACGAGCCCGCCTTCCGTATCGTTCTCGCAGGATAATCC
AAACTTCCTGAAAGATATTACCAGCTCATCAAGTCAGTTAGGTTTTTTTTCAGTTAACT
AATCATCATCTCCCTAGCCAGCTGGCAGTTTCAGCTGAGATCGAGTCACTCTCCTTG
CTGAACCTGCCCCCGGATCAAAAACAGGAGACTTTTTCTAAAATTTGGCCTCTCAG
CTTCGAGTATGATCACGAGGATGGTAATGGCGACGGAGATGCGGAAAGTTTTTGCT
TCGATTCTAGTTGCAGTACCGAAAGCACCTCTCAAAGCCTGTCCTCACTGAAAGAAT
TTGCTCTGGCTCTGGAAAAAGTTGGTTTAGAGGTGGTTGAGGCACTTAGTTGCGCA
GTTGGATTTGAAAATCCACTGCGTGAAGGGGGGAACAAATTTTGCTCACTGATGTG
GATTTCTGAGGGGGTAGCTGGAAATAAACCAGGCTTTTCGGGGCCGTTTTTACCCATA
TATTATTGCACTGCACTATCAGATCCGCTGCCGGAAATATCTTTTATTGGCTGATTCT
GGCTGGGTCAGTGTCTCACCGCAAGTTGACTCCGTGCTGGTCACCGTAGGTGATAT
CGCACAGGTATGGTCAAATGGAAAATTAAGAAGGTAAGAGGCAGACCTATGGCGG
TGTCGGTCGATGGTGAATCAACACGCTGCATTAGCATGTCTCTGCTTCTGACATTGC
CAACGGAGAGTACTGTGAGTACACTGTTGCCAGGCACAACCACAACACCTCTAGT
TCATCAACTGACGACCACGGACAAGACAACAATGTGAAAGATTATAATAATGATGATG
ATGATGATGAGAAGGAAGCCGAAGATAATAAGAAAAATAAATTGTTTTTCGAGCTTTTC
ATTTGAAGATTACGCTTGGAGAGTTTACCATGAACGCCTGCCCTTTAAAGATCCACT
GGATCGCTTTCGCATCATCTCAAATTTATTAA

NHI 213 protein sequence:

MASSAHNLQTLPTLHGVTAAPPPTPATQPNRLSTSDAADALSRLHRLPPTLSLPTRL
PPTTSPPSVSFSQDNPNFLKDITSSSSQLGFFQLTNHHLPSQLAVSAEIESLSLLNLPPD
QKQETFSKIWPLSFEYDHEDGNGDGAESFCFDSSCSTESTSQSLSSLKEFALALEKV
GLEVVEALSCAVGFENPLREGGNKFCSLMWISEGVAGNKPFGFSGRFYPIIALHYQIRC
RKYLLADSGWVSVSPQVDSVLVTVDIAQVWSNGKLKKVRGRPMASVDGESTRCI
SMSLLLTLPTTESTVSTLLPGTTTTTSSSSTDHGDNNVKDYNDDDDDEKEAEDNKK
NKLFFSSFSFEDYAWRVYHERLPFKDPLDRFRIISKFI

Codon-optimized NHI 214 sequence:

ATGTCTATGAAGCCGAACCCTCTTCCTGGTGTCCCTAACGTTGAATCACCATTTTTT
GATCAGCTGTTTGCTGAGGGCACTACTCCTCCTGAGTTGCGTAGTATTGCTCTCAG
CCTTGACGCGATGGATATGCAGTGATTGATTTCCCTGACGAGGACATCTCAGGCA
TGGCCGATCGAATACGTGCCGATCTGCATGATCGCTATGATTGGGAGGCAAGGGCA
GCGGGGCGTGGCGCGGATATGCGTCTGCAAGATGCGTGGAATTCAATGATGATGT
ACGACGTATCGCAGTAAATCCGAATATAATCAACCTGCTTAGTGAGCTATATGGTAGG
AAGGCCTGGCCGTTTTAGACCCTAACTTTCTGTGGGTACTCAGCAGCACTTTCA
CACCGATTCTGTGCACTTTTCGTCAATGCCAGAAAGATACATGTGTGGTGTGTGGG
TTGCTCTAGAAGATATAGGACCCGACCAAGGCCCTGTCATCTACTATCCGGGATCGC
ATCGCTGGCCGATTTACACTAATGAACATATTGGTTATCGGCCGACGCGTGCTCGTA
CCACGCAGATGGTATACGAGGGGTATGGTCCCAGTTAGTTGCTGCCTCGGGAATT
CAGCCTAAAACATTAACAATTAAGAAGGGCCAAGCACTTATATGGCTTGCCAATTTAA
TGCATGGAGGAGATATTCATTTAAGTCACGAAAAACAAGATGGAGCCATGTCACTC
ATTATTTTTTCGAGGGTTGTGTCTATTATACGCCGATGAATTCGGACGTGCCGGGAG

GTCTGGTTGATATCAGGAGCCCGTATAACATCATTTTGGACACCCATGCTCAGAATG
CAAGCCTGGGAAGACCGCTGCGCCGAGAATACTTAGACGCCATCGCGGCCACGAG
CTATTTTGCCGCAGAGCCCGAAGATGATTTTGACCCTGCGGCTTACCTTCTGGCTAA
CCCGGATGTTGCTGCAGCGGGAGAGGACGCATACGCGCACTGGATCAAGCATGGC
AGAGATGAAGGCCGTCCGCTGAAGTTGATATAA

NHI 214 protein sequence:

MSMKPNPLPGVPNVESPFDFQLFAEGTTPPELRSIALSLARDGYAVIDFPDEDISGMAD
RIRADLHDYDWEARAAGRGADMRLQDAWKFNDDVRRIAVNPNIINLLSELYGRKAWP
FQTLNFPVGTQQHFHTDSVHFSSMPERYMCGVWVALEDIGPDQGPVIYYPGSHRWPI
YTNEHIGYRPTTRARTTQMVYEGLWSQLVAASGIQPKTLTIKKGQALIWLANLMHGGDIH
LSHEKTRWSHVTHYFFEGCVYYTPMNSDVPGGGLVDIRSPYNIILDTHAQNASLGRPLR
REYLDIAAATSYFAAEPEDDFDPAAYLLANPDVAAAGEDAYAHWIKHGRDEGRPLKLI

Codon-optimized NHI 215 sequence:

ATGGAACACCAAAAAAGGGGTGAGGTGGAGTCACCGTCGCAATGAGCGACAAA
AGACCTTTTATCATATTAACAATGGCCTGATCGCGGATAAAAGCGAATTGTCCGCAG
CAGAAATTACGGCTTACGCCGAACACACGCGTAATAAGTGCATAGCCCAGTTTGGT
GTAGTGAAATTAGCCAAATATAATTTAGATGTCTGCTGCGAAACGTATCAAGGTGTTA
TGCCTCTTGTTGCTATGCTGCATTACATTCGCCTAATATCGCCCTTGCTCTGGTTTA
CGCTGGCGCAGATCCGTGCTTTGCTAAGAGACACAATGGCGCAGTGGACAGTTTC
CCAGCGGCACGCGAAATACTCATGAAATACCCGCCGCCTTATATGGCTTGGTTGCTT
GTCCTGCTGGCGACAGCCCCTCGTACTGATAGCGCGTGCGGCGATTGCGCTTGCG
TGGGCTCGAACATGGTTTTGACTCCATGTGATCACGCTGTCTGCGAATTATGCTTTT
GGAAACATCTGGCAACAATGCGTGTGGATCAGGACATGACCTGCAGCTGTTGTGAT
GTCCAGCTGGTGCTGCCATGTGTTAAATCGCCTCCTGCGCCGCCAAGCCCACCGT
CCCCTATGGAACCGGAAGACATTGCGGTTGCATCCAAAGCCGCATATGCTTTACTC
CCGCCAGAGCCTCGGAAAGGTAGCACTAACGCAAAAGTTAGCAAACCTCGTGAAGC
CTCTTCCACTCCATAATGCCGTTGAGCTGTTTGTGGGAGCATCTCAGTCTCAGAGA
GATGCGAATATGTTTAAAGCCGTCCTGGCAGATAACTGTTCTCGCCTGCGGGCTCT
GGTGGCAGCTGGCGCAGATGTTGATTGCGCGAATGAGTATGGACAGACCCCTCTG
TTCGTAGCTGCTTGGTTAGGCCGTGATAGGGTGGTGGCCTTCCTCATCTCGGTGGG
TGCTTCTGCCGTCGCACAGGATAACGCCGGTACCCTTCCTGTGCAAGCCGCAGCT
GCGCATTGTCATACGGGTGTTGTGTCCCTGTTACAGTCACCAGTCGGCCTGTGTGA
TTTTAATCCAAGATGGTGTCCAGCTGACGAAGTCCCCTCACCCGCCTTCGTTGAAC
TCATTCCCGCGGATGCTTCGCATCCCGGCGCGGGATCCGGTTATTGGGACGACCT
GTTTCCGGAAAGTTTTTTAGCACGACTGGAGCATTTGCATTCAACCTTGCCGGTAGC
ACCAAAAGAAAAAGCCTCATGTTTGAATAGGAGCTATTTTTGTGATTCAATTGGTACC
GTTATGAATGCTGTAGAAGCTCGCTGCGGCCGTAGGCTGTTTCCGAATATGCGATTT
CTGCATTATGAAAGCATCGGCGGGTACTTACCAGCGCACACCGATTAAAGTCGTACT
GATGCCGATGGGGTCACCAGTACCACAACTTTTATATTATTTGACCAGCTGTAGC
TCAGGAGGTGAAACAACTTACTGAGCAGCATGGCGCCAGATCGCTCTGTTTTGGC
GCCCGTTAAGCCCAAGCGCGGCCGCTTACTGATCTTTCCGCATATTTGCCCGCAGC

AGGGTGGTCGCGTCGAATCTGTGCCCAAAGCTGCTGCTGCGCGGAGAGATGTATTG
A

NHI 215 protein sequence:

METPKKGSRWSHRRNERQKTFYHINNGLIADKSEL SAAEITAYAEHTRNKCIAQFGVVK
LAKYNLDVCCETYQGV MPLVRYAALHSPNIALALVYAGADPSFAKRHNGAVDSFPAARE
ILMKYPPPYMAWLLVLLATAPRTDSACGDCACVGSNMVLT PCDHAVCELCFWKHLATM
RVDQDMTCSCCDVQLVLP CVKSPAPPSPSPSPMEPEDIAVASKAAYALLPPEPRKGST
NAKVSKLVKPLPLHNAVELFVGASQSQRDANMFKAVLADNCSRLRALVAAGADVDCAN
EYGQTPLFVAAWLGRDRVVAFLISVGASAVAQDNAGTLPVEAAAAHCHTG VVSLLQSP
VGLCDFNPRWCPADEVPSPAFVELIPADASHPGAGSGYWDDLFPESFLARLEHLHSTL
PVAPKEKASCSNRSYFCDSIGTVMNAVEARCGRRLFPNMRFLHYESIGGYLPAHTDLS
RTDADGVTSTTTFILYLTSCSSGGETNLLSSMAPDRSVLAPVKPKRGRLLIFPHICPHEG
GRVESVPKLLLRGEMY

Codon-optimized NHI 216 sequence:

ATGAAATATTATCAGCAGCATCCGAATGCCTTTCCGCTGAATTATTTACAGGATCTGT
GGGGTGAAATACAAGCATGCCCCGACTTTGCCATTAATAATTTGAATAGGGATTTTCAT
AAATACTAAAGGCTTCTCCGTTGTATTCCAGCGCCAAGGCTTAACCGAGGTTATCCA
GAAATTTCTTACTTTAAACCGTATTTGGATGTTGCTTTATTACCAAAGTGTAAACGCAT
TTTATCTCAACCCTCTGCTGCTGAAAAGCGGGTCCCGTGTTGATCCTCATATCGATC
GTTCTTTGAGATCATATTGCAAGACCGTTGAGCCGCCAGCTTTTGTTAGCGTTCTTT
ACGTCAGAGTTCCGGAGGATATGGAAGGTGGCGAACTGGTTCTCAAAGTCCAGAA
ACGGCAAGTAGGCCAGATCAAGCCGCAAACGAATAGCCTTATCTACTTTTCAGGGTG
ATCTGACCCATTCAAGTCAACGCGGTTACGTCACACGGAAACCGGCTGAGCTTGGA
TGTGAACAATATTGCTTAAGTGAAGAGGAGCTTGAAGATATTCCGCAGTTTACCTTG
GAGTCAAGGGCAAATCAAGGCAACGGAAAAATAAAGGATCGAAATAA

NHI 216 protein sequence:

MKYYQQHPNAPFLNYLQDLWGEIQACPYFAINNLNRDFINTKGFSVVFQRQGLTEVIQK
FPYFKPYLDVALLPNCNAFYLNPLLLKSGSRVDPHIDRSLSYCKTVEPPAFVSVLYVRV
PEDMEGGELVLKLQKRQVGQIKPQTNSLIYFQGD LTHSVNAVTS HGNRLSLVCEQYCL
SEEELEDIPQFTLES RANQGNGKNKGSK

Codon-optimized NHI 217 sequence:

ATGAGCCTGAGTCACGATTTTAAAATCATTACAAAGGACTCTAATATGAATGACAATG
AAAAATATCTGTTTGATCTTAACGGGTACATTATCATTCGAGACGTACTGGACCAGAA
CGAGATAGATGAAGCTAATAAAGCTATCGATCACTATTCGAATGAGATCAAAGAACGT
AAAGGAGAGTTCTCCCTCTCGGGTGGTTCTGGCGAATTATTGGGAGATACCGGGC
GCGGCGACCTTGAGGGTGCTCTTTCTGCGCCAAAACCATCGTGATCCGTTTCG
CAAAATGCTGGCACATAGCAAGATTACCCCTTATTTATCAGAATTACTGAACCCTGGC
TTCAGGTTAGACCACAACATGGGGATTATTACGATGCGCAAAGGTGCCGAAGGACA
TATCCTGCATGGGTCCAGTGGCCCTGACTTTGATCCACATCAGTATTACATCTTTAAA

AATGGCAAGATGCACAATGGTTTAACCGTGGTAGCGTGGCAACTTTTCGGATATTCGT
GACGGCGACGGTGGTTTGGCTGTTGTACCTGGGTCTCATAAAGGTAACATAGCACC
ACCGCGAAGTCTAACGCGCTACGAGGAATATAAAGATGTTGTGAAACAAATTACTTG
CAACGCGGGGCGACGTCATAATCTTCACAGAAGCGCTCACTCACGGTACCCTGCCG
TGGAAGCGGATCATCAGAGACGAACTGCATTGTTTCGGTATTCTCCAGGAAACATT
GCCTACGCTAAAAATTATGATTGGCCGGATTCCATGATGGAGGGCTTGTCCCCTGAA
GAACGAGCCGTGATGGAACCACCGTATCATATCCGTCTGAACCGGCCGATAATTGAT
TCTTGA

NHI 217 protein sequence:

MSLSHDFKIITKDSNMNDNEKYLFDLNGYIIIRDVLQNEIDEANKAIDHYSNEIKERKGE
FSLSGSGSELLGDTGRGDLEGAISWPKPHRDPFRKMLAHSKITPYLSELLNPGFRLDH
NMGIITMRKGAEGHILHGSSGPDFDPHQYYIFKNGKMHNGLTVVAWQLSDIRDDGGL
AVVPGSHKGNIAPPRSLTRYEEYKDVVKQITCNAGDVIIFTEALTHGTLPWKADHQRR
ALFRYSPGNIAYAKNYDWPDSMMEGLSPEERAVMEPPYHIRLNRPIIDS

Codon-optimized NHI 218 sequence:

ATGTCCGACAAACAGCAAAAGTCAGATTGGGATGTATCAAAATTTTCGTACATATTGTG
CGGAAGGGGAGACCAAAGCCCTGAATCTGGGCAATCGGGGACCAATACGTTTTAC
ACCGGATGGTCTCCTAGACCCGAATATTCTTAACGCATATGAGCAATTCGGATTTTAT
GTCTTTGAAAATGTCATAGATCAAGATGAACTGGAAGAATGCCGTGGTGAAGTTGAC
CAACTATTGGAAAGAGCGCCATGGCCTCATAGAGATAGCAAAGTCGATAGGAACGG
TAAACCGGCTTTGGGCCCAGAATTTGCGGTAAATCCTTGGGTATGACCAAACCGCT
GTCCGATCCTTTGGGGGGCACGCGGGGAAAACAATGGGCGTCACCCGGTGAAGAT
GTTCAACCGGAACCGGGTGCTGACAGCCCGGCCACGTGCCGTATCTTGTAGCA
GGATGTCTACAACTTCTGCCTAGTTTTCTTCGGATCTTCGGCCATCCGGATATTCTC
AGAGTAGCAGAAGCTATTAACGGACCTGACTTCACCCCATTTACCGAAGTGCTTTTT
GTAAAAGAACCGGAGATTGGTCCATCTGTGAGTTGGCACCAGGATGGACAGATTCA
TTGGGATCATCCCCAATGGGATTGCAATATTCACGGCTATAATGTCCAAGTACAGCT
GTATGGTTCCACCCAGCCAACGGGGTATGGGTTTTGCCTGGTACCCACCGCGAA
GGGAAGGTCGATATTGCCGAACGTGTGTCTAAAAACGATGACAGTGATTGGTTTGA
GGACGCGGTACCTCTGGTCTGTAAACCGGGTGACGCTTTCATCACGAACCGTCAG
ACTGTGCATGGGAGTTTCCCTAATACCTCCAAGGACCGTCGTATCACGGTAAACTTC
GGGTTCCACCGTTATAGCAGTGTTATAGGACAGACGGGCAAACCTAAGTGGCGAGGG
CAATCAGTATACGGAAGACTATATCCGGGAGCGCTGCCGGTGTATACCTTTGGCTAT
TGATGCCCGTAGCCAAAGATTCCCTAATGAAGAGCGCTATACGTATCAGCCCTTTCG
CGGTTTAGAAGACCAATATCGTTATGGTCCAGATACGATTCGTGACATTCTCACAGAT
TACAACTTGCGAGATCTGGGCATCTGA

NHI 218 protein sequence:

MSDKQQKSDWDVSKFRITYCAEGETKALNLGNRGPIRFTPDGLLDPNILNAYEQFGFYV
FENVIDQDELEECRGEVDQLLERAPWPHRDSKVDRNGKPALGPEFAVNPWVMTKPLS
DPLGGTRENNGRHPVKMFEPEPGADSPAHPYLVAGCLQLLPSFLRIFGHPDILRVAEA

INGPDFTFTEVLFFVKEPEIGPSVSWHQDGGQIHWDHPQWDSNIHGYNVQVQLYGSTPA
NGVWVLPGTHREGKVDIAERVSKNDDSDWFEDAVPLVCKPGDAFITNRQTVHGSFPN
TSKDRRITVNFGFHRYSSVIGQTGKLSGEGNQYTEDYIRERCRCIPLAIDARSQRFNE
ERYTYQPFAGLEDQYRYGPDITIRDILTDYNLRDLGI

Codon-optimized NHI 219 sequence:

ATGGCTGTAGTTGATCATGCCCCGCGGCTACCGCAATTCGACAATCTTGACTTTGAC
AATTTCCACGACGAGGAGCTGCCACGCCGTTTGGCCGCTGGCAACGGTGAGCTG
GCTGCAGACATCGCAGCGGGCGCATTAGTTAAAAGCTTTGCTTGGCGCCTGAGTG
ATGGGAGAAGCGTTACGTATGTGGTAGATGATAATGGCATTGTAATACGGCCTGGTG
ATGATGCTGAACTGGTAGTTGAGGTTTCAGAGCAGGATTGGTTAACTATGTGGCAG
AGTTATGGACTTGGGTAGGCCTTATGTACGCGGAAGCGGCAGAGATGGTACGTGGA
GATTCGCGCCTGTTTGAAGATTTCAACCGGTTCTGTTGGCCATGTATCACGGTCG
ACCTCTGTATGAGGGATGGGAACCGACAGTCGATCTTTCTCGCTCTTTTACGCTAGA
TGATGATCACGAAGAAATGAGTCGATTCCTTGATGAGGCAGGGTTTCTACATATACG
GGGCGTATTCAGTCCTGAAGAGATTGATGCACTGCGTGCTGAGGTTGAACGCCAAC
GTTCCGAAGCTACCCCCGATGACCACAGGTCATGGTGGGCGACAACTCTGACGG
AGATGAAGTTTGTGTCGGGTGACACATATGGATGACCGTAGTGAATTGATGCTGAG
TCTGACCGATGATCGGCGTCTTGATGCCATTGGTGCACCTTGGAGGTGACGATTTCTG
CTGCTTACCCGGAACGGGGGGGATGGAGTGTCAGTTGTAATCAAATTACCGTCTATT
GTAGAGGGCTTAGCAGATCTCCCATGGCATCGTGACTGTGGTACCGGCGGGCACT
CCATTACTTGTCTACTGTCTCCATTGGTATCCAGCTGGACGAATGTACGGAAGCAA
ACGGTCAGTTACATTATCTTGCAAGGATCAAATAAATCTAGCAATAGAGCTCGCGAGG
TACGAGATGGTTGGCCGACCGTCGCTATTTCTGCAAGTCCCGGCGACGTGACAGTT
CACTACGGTCATACCATGCATGGCGCCCCGCCGCCTACAGGAGCCCCGGTCAGCG
GGGGTCGGCGTACCATTATGTTGGCTACCATAAACCCATCTGGGCGGAGTTTATAC
CGCCGGGCCAAGGTTATAACGACATTCTGTTTAAGGATGGAGGCCGTATCTTAAGC
CCGGAGGAATTTCAAGAACAGTCCAGTTGA

NHI 219 protein sequence:

MAVVDHAPRLPQFDNLDFDNFHDDEELPRRLAAGNGELAADIAAGALVKSFAWRLSDGR
SVTYVVDDNGIVIRPGDDAELVVEVSEQDWFNYVAELWTWVGLMYAEAAEMVRGDFG
LFEDFEPVLLAMYHGRPLYEGWEPTVDLSRSFTLDDDHEEMSRFLDEAGFLHIRGVFS
PEEIDALRAEVERQRSEATPDDHRSWWATNSDGDVECCRVTHMDDRSELMLSLTDDR
RLDAIGALGGDDFAAYPERGDGVSVVIKLPSIVEGLADLPWHRDCGTGGHSITCPTVSI
GIQLDECTEANGQLHYLAGSNKSSNRAREVRDGWPTVAISASPGDVTVHYGHTMHGA
PPPTGAPVSGGRRTIYVGYHKPIWAEFIPPGQGYNDILFKDGGRI LSPEEFQEQSS

Codon-optimized NHI 220 sequence:

ATGGCTGTAGTGATCTCCCCAACACCTGACCCGATCACATCTTCGTCGCCTTTCTCA
ATCTCTAAATTCATTGCTAAACTGAAGCTTCGCCGCTCTAGCAAGCAAAAAGACCAA
ATCCAGGATGAGATTTTCGCATGATCCGCGTCCTCCTCTGATACCTAGCCCTCTTCCA
TTGGTTCTTCCAGAGCACCAAGCATACTTTGTGTCAATTGGGCTGGACTACCCTGAC

CTTCCCTCGTCCTCGTCCCATCCTAGCCATCATTATCACCGACGAGTAACCGCGA
ACCGGAACCGGAACCTGAACCAGAACCTGGCCCGCATCCCCTGCAATCAGCCTAT
CTTACCCTGTTCTTGGCAGCCCAACAATTCTTTGACCTTGAAGATGAAAAAACAG
CAGTGAAGCACCGGTTGGGCACAGAGGAAGGTTGGACCAAATACGCGGTGAAA
AAGAATTTATTACACTGCGCACCCCTTGCCTATACACCAGATATCCTCAAAGAACCGG
CGAAACGTTATTGGGATTTAATGGGTAGTCACTTGTGTAGTACGCTGGGACGGATTT
CTATGTCAGTCGGCCTCCCAGGCGAGGGCGAAGGCGATGGTCTGAAGGGCTTCGT
TGGGCCCTGCAATGTCATGGGCGAGAAAGAAGAGGACAAAACCTCAACGATGCTG
CGAATCTTCAGATACGAATCTTGGGAACGAAAAATTGTGGCGGAAGCTCATGCCGA
TCTGGGCCTCCTTTCATGTGTAGTGGGGGATGTTCCAGGTCTCGAAGTATGGAATG
GACAACAGTTCGTAGATATCGAACGACTTTACGAACGTGAGCGTATAAGGAAAGGTA
CCAATGGTGTGGGCGGGATTAACGGCGATCGAGCGGGCTTTGGAGGGAAAGCCA
CACTCCTGTCGGGTCGCCAGCTTGAACGCTTTTCAAATTTTCGCTATCCTGCTGGC
GGTCATCGTGTTGTGTCTACGGGCTTCCCAGCCCGCCATCTTCCAAAAGTCTGTC
GGCTCATACCCCAGTGCCTAACGAGGCCGAACGCAAAGAGAAAAAATATCGGCATA
GCATTGTGTTTGTCTGCGTGCCACGAACCGACGCCGGTAAACAGCAGTACATTG
GAGACAGAAATCACAGGTAAGTGGGCAGAACCAATACGCGATGTAACGGCAGGTG
AACTTTATGAACGTATTCGTAACCAGCACTTTAATGTGAATATAGGTCATGAGGAACG
TGAAGCTCAACGGCGACGCGTCCGTGAAGCTAAAGCAAATGGAAAGTCCGTTGAA
GGAAGTGGCTAA

NHI 220 protein sequence:

MAVVISPTDPITSSSPFSISKFIAKLKLRSSKQKDQIQDEISHDPRPPLIPSPLPLVLPE
HQHTLCQLGWTTLTFPSSSSHPSHHSSPTSNREPEPEPEPEPGPHPLQSAYLTLFLAA
QQFFDLEDEKKQQWKHRLGTEEGWTKIRGEKEFITLRTLAYTPDILKEPAKRYWDLMG
SHLCSTLGRISMSVGLPGEGEGLKGFVGPCNVMGEKEEDKTSTMLRIFRYESWER
KIVAEAHADLGLLSCVVGDVPGLEVWNGQQFVDIERLYERERIRKGTNGVGGINGDRA
GFGGKATLLSGRQLERFSNFRYPAGGHRVVSYGLPSPSSKSLSAHTPVPNEAERKE
KKYRHSIVFVLRAHEPTPVNSSTLETEITGKWAEPIRDVTAGELYERIRNQHFNVNIGHE
EREAQRRRVREAKANGKSVEGTG

Codon-optimized NHI 221 sequence:

ATGAATTCGGCAGCCACCATAAAGGCGTGGAATTCCTCACTGAACGTTTCGGCCA
TCTTGCGGACTTCCCTGGGAGTGCTTCGGATACGGCGTTGCTGAAACAACATTTAA
ACGATCACGGTTATGTCTTACTGAGAGATGTTTTAGATGTTGATCTGGTCACTGCCG
CACGGAGCGAAGTATTCGGTAGGCTCGCGGAGCAAGGTGAAATAGCAGATCCACC
TGGCGGAGGTGTTGCAACTGGTACATCTCGCCGTATCGATCCGGCGGATGATGATG
GCGCCTTTTGGACATCGGTTTCTGAAGGTGAAGCACTGCGTCGTCTGACACATGGT
CCAGGCATGATGGCGATTATGCAAGCCACCCTGGAAGAACCAGCGCGTGCCTTTG
ACCTGATTTATTTGCGCCCCACCTGTGTGGGCAAAGCGACCGCGATGCATTATGAC
TATCCTTTTTTTGCAAGGAAGCGCCAGCCGATGTTCAACGCATGGATTCGGTTGG
TGATGTTCCAATTCAGGACGGGCCGTTAGTACTGGTTGAAGGTTCTCACCAGTTGCG
ATGATCTTATTGCACCTTTTCTTAGCATCGACTATGCTGCAGATCGCAGCGATAGTGT

AGTTCAGCAGGCCGCGTATGCCGGATCCGGCCAGTCGGATCCAATTCACCTGATTG
AGGATCGAGACACGCGCCTCTTGACAGCGGACTTTTGAACGGGCGACATGTTGAT
TATTAGTATGTTTCATCCTGCATGGCAGTCTAGATAACGTGTCTCCCACTAACCGAGTT
CGTCTCTCGTGTGACGTTCCGGTATCAGCCCGCTTCCCAACCGGCAGATGATGGTC
GTTATTTTGGGGCCATTCTTCAGGCTCAAAAGGTGGTGGATATGGAGATATGCGTG
GGGCCAGCCCCTGAATTAA

NHI 221 protein sequence:

MNSAATIQGVEIPTERFGHLADFPGSASDTALLKQHLNDHGYVLLRDVLDVDLVTAARS
EVFGRLAEQGEIADPPGGGVATGTSRRIDPADDDGAFWTSVSEGEALRRLTHGPGMM
AIMQATLEEPARAFDLIYLRPTCVGKATAMHYDYPFFAGSAQPMFNAWIPVGDVPIQDG
PLVLVEGSHRFDDLIAPFLSIDYAADRSDSVVQQAAYAGSGQSDPIHLIEDRDTRLLTAD
FRTGDMLIISMFILHGSLDNVSPTNRVRLSCDVRYQPASQPADDGRYFGAIPSGSKGG
GYGDMRGAQPLN

Codon-optimized NHI 222 sequence:

ATGACGGCTGCTGCCGTGTTAGACCGCGATGCCATTGCGCGCACCACCATGGCGC
ACGAGCCTTTTGTGTGGGGGTTAGTAGCGGACAGTCTCCCTGGAACGTCCGCGCG
AAGACGTCTCGCGGCAGAATCCCCTCAGAAGGTTTTGTACTGACTGAACGTGCTG
GCGGGACTACGGCAGGGAAAGGTTACCATACTTGAACTTGACACTGGTGCAGGG
CGGAGTTCCGCTTCCGGAAGGTATGCGTAGGCTCACACCGCTCTGGCAGGGCCTA
GTTACCAGCCTGTTAGATGATGGGTACCGAACCGCAGTGGCTGAAGCGACAGGCC
GTTCACTTGATGGTTGCGCTCAAGAGATTCGCGCTGTCCGGTATGGATCAGGCTCG
TGGATCGATCCTCATAACGGATCGCGCAGATAAAATAGTAACGCAGACCTGGTACTTT
AATGAAGGCTGGCGCCCTGAGTGGTCCGGCGCCCTGCGTATACTGCGTTCGCCAG
CAGTTGACGATGTGGCTGCTGAAGTTCTTCCAGGTTTAACAGACTCAGTTTTACTGG
TCCCTTCACCGGACTCTTGGCACACCGTGATGCCAGTGGCCGATGGTGCAGAACAA
GGATCGGCGAGTTCTGCTCGTGCAATTTTGTCTCAGGAGAGAACAACTTGGTAA

NHI 222 protein sequence:

MTAAAVLDRDAIARTTMAHEPFVWGLVADSLPGTSARRRLAAEFPSSEGFVLTERAGGT
TAGKGYHTWNLTLVQGGVPLPEGMRRLTPLWQGLVTSLLDDGYRTAVAEATGRSLDG
CAQEIRAVRYGSGSWIDPHTDRADKIVTQTWYFNEGWRPEWSGALRILRSPAVDDVAA
EVLPLGLTDSVLLVPSPDSWHTVMPVADGAEQDRRVLLVHFVSQERTTW

Codon-optimized NHI 223 sequence:

ATGGACCAGAAGGAATACCTGCTGAACGATCAGCAAATGAAAAAATTTATTTCGGGAT
GGTTATGTCACTGTGCAGACAGATCTGAGCGTAGAATTCCATGCAGCTGTTTTTTCAG
CAGACCGAAAATGTCTTCGAAATGGAAGGCAATCCTGGAAATAACCTGCTGCCTCG
CATAACCAATGATACAGGAAGTGTTTGATGATCGGTGGGTCAACGGCGCTCTTACGT
CAGTACTTGGGAAAGATTATTACCTTCAACCTCATAGACATTGCCATTACAATCCGCC
CAATTCTAATGGTCAGAATCTACACCAGGATGGCGGCAAACGCTGGAGCCACTACA
CTAGATGGCTGCTTGCACTTTATTATCCACAGGAAACCCCTGAAGAGCTGGGTCCG

ACAGGCATTATACCGAAATCGCACTATTATGGTAATCGCGACTCTATTAATGACGAAG
ATGAAATACCACTATGTGGAAAGGCTGGCACTGTGACTATTACAAATTATGACCTTTG
GCATAGGGCTATGCCAAACAGTTCGAGCAAAAAACGTTATATGATGAAGTTTCTGTT
TGCGCGTATGTCAGAACCTGAGGTGCCCTCCTGGAACAATCAAGACACAGAATGG
GCGTCTGCCGACATTTCCCAGTCAGACGCCGAGAATGACGTCAAAATGTTCCATCA
AATTTGGAAGTGGCATTGCGGCCAAACGAATGGTAACGGTCACTGCCCATCGTCTG
TCACCATGCCCCGACTCGACCAAGATTGCGGAGCTTGTTGAGGTTCTGGGCCAGGA
TAGCGAACCCAAATGCATCGATATCGCATACTGCTATTTCCGAATTCGGAGCGAATGC
TGTGCCGGCTCTGGTGAAGCAGCTGGAAAGCGAGAGTGAGGACATTCGTAGATAT
GCTTTCTGTGCTTTGTCGGCGATTGGAAAACCGGCGGTATCCGCGCTCATCACTGC
CACACAGCATCCTGATTGGTGGGTTCGGGCGTCGGCAGCCGAAACCCTGGGGAA
CATCGGGAATTCGGCACAGGCAGCTGTTCCATCCCTGATTGCGGCATTACAGGATG
AGAGTGAGCAAGTTCGACAGCTCGCTGTGAGGCCCTCGGGACCATTGGACAACA
TGATAGTACGGCTGTTCCGGACCTGGCACTCTCCCTGCAGGATGAAAACGAAAGG
GTTCAAGAAATAGTGTACTGGCACTCGCCAGACTGGGTCGCTATGCCACCAAGC
TGTGAATGATCTGCAATGGTTCTGTCTGATGATAATAGATATGTCCGCGGTGATGCA
GTGCACGCGTTGCGTAGAATCGATACGCCGGAAGCTCGCGAAGTTCTGATTCAGTT
CCTCTTAAAGAGCCGTTGGTGTCCCTTAACAAGCAAAGAATCAGGATACTAA

NHI 223 protein sequence:

MDQKEYLLNDQQMKKFIRDGYVTVQTDLSVEFHAAVFQQTENVFEMEGNPGNNLLPR
IPMIQEVFDDRWNVNGALTSVLGKDYYLQPHRHCHYNPPNSNGQNLHQDGGKRWSHY
TRWLLALYYPQETPEELGPTGIIPKSHYYGNRDSINDEDEIPLCGKAGTVTITNYDLWHR
AMPNSSSKKRYMMKFLFARMSEPEVPSWNNQDTEWASADISQSDAENDVKMFHQIW
KWHCGQTNGNGHCPSSVTMPDSTKIRELVEVLGQDSEPKCIDIAYAISEFGANAVPALV
KQLESESEDIRRYAFCALSAIGKPAVSALITATQHPDWWVRASAAETLGNIGNSAQAAV
PSLIRALQDESEQVRQLAVEALGTIGQHDSTAVPDLALSLQDENERVRRNSVLALARLG
RYAHQAVNDLQMVLSDDNRYVRGDAVHALRRIDTPEAREVLIQFLLKSRWCPLTSKES
GY

Codon-optimized NHI 224 sequence:

ATGAACCATCCTGTTGATAATCCCGAAATTCATCGTGAATCCTGGAGGAGAGACGGT
TATGCGCTGCTGCGCGGCGCGGTGCCCGGCGATTGGCTGGATGGTCTTCGTGCG
ACCTTCGATGCGGGCATTCTTTCCTCAGATCAGTGGCCTGTCCCTCGGGGACACCAC
CTGGAATCATGCTCTTGTTGACCTGGATGCACGGGTTGAGGCAGTTTGTAGGCTGC
CTGAAGTATTAGTTGTCGTTGGGGCCTTAATTGGAGAACGTTTCTTTTATCACAGGT
AGAGGGCCGTGAGCCGTTAGGGGGCCATGGTCATCAAACATTGCACAGAGATTTAT
CAGCACAACGCCCGGGTGATACTGTCAATGCCCTTATTTACCTGGACGATTATGGGC
CGGATAATGGCGCTACGCGTATTGTCTCGGGCACCCACCGGCCGGCGCCGGATAG
CCCTCCGTTTGATGACCTGGATGAGAGTGGTAGCGTTCAGTTGAAGGGTCAGGCC
GGTGATACTGGTTTTTCGATGCGGACTTGGTTCATGCTGGTAGTCTGAATCCGTCT
GGGAGTCGTCGACGTACCCTGTTGTTAGGGTATTTTGCTGAATCCCTGCATGCCCT

GCATCTTCAAACCGCACACTTGCGTAATGTTAGGATGGATACCCGGGAACGTTTCG
ATCCGGTATAA

NHI 224 protein sequence:

MNHPVDNPEIHRESWRRDGYALLRGAVPGDWLDGLRATFDAGILSSDQWPVPRGTT
WNHALVDLDARVQAVCRLPEVLVVVGALIGERFFLSQVEGREPLGGHGHQTLHRDLSA
QRP GDTVNALIYLDDYGPDNGATRIVSGTHRPAPDSPPFDDLDESGSVQLKGQAGDIL
VFDADLVHAGSLNPSGSRRTLLLG YFAESLHALHLQTAHLRNVRMDTRERFDPV

Codon-optimized NHI 225 sequence:

ATGCAGGATTTTATCGAAGTCATCGATAACGCACTGCCTGCTGACTTTTGCGATCAG
TTCATCCAGACATTCGACCAGAGCCCGCATCTCGTTGAAGGCCGCACTGGCGCGG
GTGTCGAACAGGATAAAAAAGTTAGCCATGACTTATATCTGGACCAGCATCAGGAGT
ACCAGGCCGCCCTGCAACACATTCGCGCCACAACCGCACAACACGTCCTGTCTTAT
TTTAAGAAGTATCACTTCGGTCTGATCGCCCCTGTGGCGCTGAAGGTGAAAGATCC
CGGTTCCGGTAAAGTCGTCAATCTGACACATGAAACTTCCACGATGTCGCAAAAG
GTCAAGAAGAATCTTACATGAAACTCCTGTATAGGCTCGGCAGTATCCAGGCCAG
CGGTATCGAGCGGGAATTGGTAACTATAATTACTGGCATTGCGAAGTTTATCCACAG
CCACAGAGCGTGGAGGCCTTACATCGCACTTTATTGTTTATGTACTACCTGAATGAT
GTCTGAAGATGGCGGTACGACGGATTTTACTATCAGGATCGCCAGATTAAACCGAAA
AAAGGTCGTATGGTTATTGCGCCTGCTTATTTACCCATACCCATCGTGGTACTACG
CCGAAAAGCAATGACAAATATATATTAACCAGCTGGGTCTTAATGAATACAGGCTCCA
CGCTGTATAACGCTGA

NHI 225 protein sequence:

MQDFIEVIDNALPADFCQQFIQTFDQSPHLVEGRTGAGVEQDKKVS HDLYLDQH QEYQ
AALQHIRATTAQH VLSYFKKYHFGLIAPVALKV KDPGSGKV VNLTHENFHDVAKGQ EES
YMKLLYRLGSIQAQRYRAGIGNYNYWHCEVYPQPQSVEALHRTLLFMYYLNDVEDGG
TTDFYYQDRQIKPKKGRMVIAPAYFTHTHRGTTPKSN DKYILTSWVLMNTGSTLYKR

Codon-optimized NHI 226 sequence:

ATGCTTATCAATGCTAATCAAGACGTAGCACCATATTTGGCTGACCCGCGTGTATTAG
GGACTGCTGAAGCGTTTTTTGGACCGTTTGTCCGTATCGCATCAGCAGGTAGTATTG
TGACCCACCCTGGCAATGCACGCGGGTATTGGCATGCAGATTGGCCATACAATCAG
ACCAACGCAAGTCGGATCCAAGTTCCTTATCCAGATCTGATGATGGTATTAAGCACC
CTGTGGATGTTGACGCCTTTC AATCAAGAAACGGGCGGGACGCTACTGGTACCAC
GGTCACATCGTTCGTCTAATAACCCGTCAGGCTCAAACGGCGTTGATCCGGATGCG
CCACATCCGGATGAAATCCACGCTACTGGCGCGAGTGGATCTGTGCTGGCTTATGA
CGCTCGTCTTTGGCATGCGGTGGCCCCTAATCGTTTCGAGTGAGCCACCGAGCAGC
GCAGGGGGCCGCGTTGTGAATACCACGCACTCTCGCAGTTGGAGCGGCTCGGCG
CATGCAACAGTGCCGGTCGCGCCAACCTGGCCAAATGTAAGACTGGGAGCCCGTA
GCCCGAAATAA

NHI 226 protein sequence:

MLINANQDVAPYLADPRVLGTAEAFFGPFVRIASAGSIVTHPGNARGYWHADWPYNQT
NASRIQVPYPDLMMVLSTLWMLTPFNQETGGTLLVPRSHRSSNNPSGSNGVDPDAPH
PDEIHATGASGSVLAYDARLWHAVAPNRSSEPPSSAGGRVNTTHSRWSGSAHATV
PVAPTWPNVRLGARSPK

Codon-optimized NHI 227 sequence:

ATGGACGATGATGATGCCCCAAGTGTGCGAAATCGCAGCACGTGCAACCCATTGGGT
AGTCGAGAGAGACTTTCTACCCGGAGCGCTGGCGCGGGCTGTGCGCGGACGGTA
TGATGACGTGTTTCAAGATGCGACGCGCGCGCGTGGTGAAAGGTTTTGCTGGGAT
TTGTGGCACGTTCTAAACAGTATACACTTCTACGGACACCCGCAGAAGACTTTTTT
GGCGAAGAATTACATGGTGCCTGGAGGAAATGCTTATGACATATGCTCGGGAGCG
TCTCGGATGTGCAAGCATGACCCCAATGTGGATGTCGTGCTACGTACATGGCATGC
GACAGGAAGTCCATGCGGATGTGCCACATGGCCCGTTTGCATTCGTACTGAGCCTG
ACTCGCGAATCAGGGGCAGACGGTGGTTTACCTTTAGCGGTGGCGAAACGCAAA
TCATGCGCCCAGAGAGACTTAACTATTGGCGCAATTTGATAGTAGTGAAGTTGTAG
AGCGTGCTCAGATCATGGAACTATTAGTCCACGCTTTAACCAGCTCGTTGTATTCTG
ATCCCCGTTTGCCCCATGGGGTCACGGAGGTTTTTGGCACACAAGATATTCGGGAT
GGCCGGCTGGTACTGCACGGGTGGTTCAAGGACCCGGAACCTTCATTCAGCGGTG
CATTATCTGAAGAGGATGCAGCGGAAACCCTTGAGACCGCCCTTGCGGAATTATAT
GCCCCGTTGGTTGAGCTCCCGCGTGCCTCTGGTATGGTGTGCGCCCGTATCACGA
TAACCCCTAGTGGGGATGTTGATGATCTGACTTGGACATGTGATACGTTGACGCCG
ATCCCTCTGCCGGAAGTCCAAAGCGAGACAGATATCCGCGACGCAATTATGCTTGA
TATCGCTAGTGCTTTACTCGAATTAAAGTTCCTCATGAAACCGATCACCCATCGTAA

NHI 227 protein sequence:

MDDDDAPSVEIAARATHWVVERDFLPGALARAVRGRYDDVFEDATRARGERFCWDL
WHVPKQYTLLRTPAEDFFGEELHGALEEMLMTYARERLGCASMPMWMSYVHGMR
QELHADVPHGPFVLSLTRESGADGGFTFSGGETQIMRPERLNYWRNFDSSSEVER
AQIMETISPRFNQLVFDPRLPHGVTVEVFGTQDIRDGRVLHGWFKDPEPSFSGALSEE
DAAETLETALAELYARLVELPRASGMVCARITITPSGDVDDLWTCDTLTPIPLPELPSET
DIRDAIMLDIASALLELKFPHETDHPS

Codon-optimized NHI 228 sequence:

ATGCCGGGAAGCCCTGGTATAAGTATACATACAGATGGCCAGCCGCATGGTTCAGAT
TTATTTGGGTATGAGGGGAGCTGCGCTCGATTGCTCCGCGTATTGTATTACTTAGAT
GAATTGACCCCGGATAGGGCCCCCTTTTCGCTTGATCCCGCGTACCCATCTGAGTTT
CCACGCTGATGCAAGTCCTTACGTGCGTTATAAATCTCATCCGGAAGAAATCACCT
GGTGGCGCCTGCGGGGACAGCGGTTATAGTTTCTCGATGCTGCTGCATGGAAGT
CACGCAAATCGCGACGAACAGCCACGAGAATTGGTTCAATTAGGTTATCGGCCGAG
CTGGGCCGGCCCTATCCAGCCGTTGATGAGTGGGCACCTGGCCTGGTCGAAGG
TGCGCCGGAAATAGCAAAACCGTATCTGAAACCGCTGAATACCACGCATGCTCAGT

GGGTTTCAGCCGCATAAACCTGAGGGCATGCGAACAGAAGCAAAGGGAATAAACCC
GTCGCGGTGGGGGGACTAA

NHI 228 protein sequence:

MPGSPGISIHTDGQPHGSDLFGYEGSCARLLRVLYYLDLTPDRAPFRLIPRTHLSFHA
DASPYVRYKSHPEEITLVAPAGTAVIVSSMLLHGSHANRDEQPRELVQLGYRPSWAGPI
QPVDEWAPGLVEGAPEIAKPYLKPLNTTHAQWVQPHKPEGMRTEAKGINPSRWGD

Codon-optimized NHI 229 sequence:

ATGGCATCGCAGGACGCAGGTCCGCATGTCTGGCTGAGCGGAGAAGCTGACTGTG
ATTTGGACGCTTTTCGCGCACTGGTGGCGGAGAGGACCGATCCTCGCGATTACCC
GTATGCGGCGGAAGTCGCCCATGATGTACCACTGTATGATAGCGATCGCGTAAGAG
CAGCCGCGGATCCACGCGGTTTCGTACAGAATGGGTGCGTGCCCTTTTGGATGG
CCCAGGGATCGTCGTCTTGCGCGGAGCGTTTGCCGACCCTGATGTGGTGGATCGA
GCCTCTGGAGTATTTGGCGCCCTGATTGAACGGGAACGCGCGGAAGGGACTGCTC
GCGGTGACCACTTTGCAAAGCCCGGCGCAAACGATCGTCTGTGGTTCGGCACTTGA
TAAACCGCCCTTCATGCGCCTGAAGTGTTGCGCGATTATTATGCTAATGACATGTT
GGCCCTGGTGTGCGAAGCTTGGCTGGGTCCGGGTACCAGGTCACCTCACAAATT
AACGTCGTGAACCCAGGTGGGGCTGCGCAATCTGTCCATCGCGACTATCATTTAGG
TTTTCTGAGTGACGAACGCGCAGCTAGATATCCCGCCCATGTGCATAGGCTGTCTC
CCGTGTTGACCCTGCAAGGTGCCGTGCGCCATTGCGACATGCCTGTAGAGAGCGG
ACCGACACTTTATCTGCCTCATTCTCAGAAATACGAGCCCGGATACCTGGCCTGGC
GCCGCCCGGAATTTGCTGCTTATTTTGAAGAACACCACGTTCAATTACCACTTGCAA
AAGGGGATGCAGTTTTTTTTTAATCCTGCACTGTTTCATGCGGCAGGACACAATCGTA
CCACCGATGTGCGCAGGATGGCCAACTTACTTCAGATTAGCTCGGCATTTGGGAGA
GCTATGGAAACCGTAGATAGGGAGGCGATGGTAAATGCGTTATTCCCGGTCCTGCT
CCGGCGTCGCTCCGAGGGTGTGGGTGAAGCGTGGTTACGCCGTGTAGTCGCGGC
ATGCGCAGAGGGGTACCCGTTTCCAACGGACCTGGATCTGGACCCGCCGCTCGCC
GGGTTAGCCCCTCCAAGTCAAGCAGACACTGTGTGGAGAGCTTTGACGGAGGAAT
GGAGTCCGGGGCGGCTCCGGCGTGAGCTGCGAGCAGGTGCCGAACGGCGTCGG
GCATAA

NHI 229 protein sequence:

MASQDAGPHVWLSGEADCDLDAFRALVAERTDPRDYPYAAEVAHDVPLYDSDRVRAA
ADPTAVRTEWVRALLDGPGIVVLRGAFADPDVVDRA SGVFGALIERERAEGTARGDHF
AKPGANDRLWSALDKTALHAPEVFADYYANDMLALVCEAWLGPGYQVTSQINVVNPG
GAAQSVHRDYHLGFLSDERAARYPAHVHRLSPVLT LQGAVAHCDMPVESGPTLYLPHS
QKYEPGYLAWRRPEFAAYFEEHHVQLPLAKGDAVFFNPALFHAAGHNRTTDVRRMAN
LLQISSAFGRAMETVDREAMVNALFPVLLRRRSEGVGEAWLRRVVAACAEGYPFPTDL
DLDPPLAGLAPPSQADTVWRALTEEWSPGRLRREL RAGAERRRA

Codon-optimized NHI 230 sequence:

ATGTTGCGCATGGTACGCGATCGCCCGGGTCAGATCGGATGCGAACGTATCAGAAA
TATGACAAACCATCCGACCGATGCGGAACGCTTCCTGTTTGATACCAACGGGTACC
TCGTATTAGAGGATTTTTTACCCCTGCGCTGGTGGATAGTCTGAACGCCGCCCTG
GAACGGACGATCGTACGCCGTCGTGACCCCGGTTTTTCATCGCACACATGAACCCG
CGTTCGCTGATAAACTTGATTCCGCAAATACTCGGGTAATGCATCTTCTTGCGGAGG
ATCCGCTGTTCCCTTGACATGCTGGACTACGACCCAATGATGGAGTATATCCATGGGT
TGTTCAATGAGATGCCTCACTTACATTCGACAGATGCTATCTATGAGATCGAACCGG
AGGAACATCACGGTAAGGGGTGGCACACTGACGGTATCCAAGATGGGTTCGGGA
TTTTCGCCCGCATATCCCACTGCTCCAGTTTAAAGTCGGATATTATCTGAGTGATATG
ACCGAACCTGGACAGGCAAACCTGACCCTCGTTCCGGGAAGTCATAAATCCCTCGT
GGAACCCGATTCTAAGAACGGCATGCCGGGCGCGGTACAGGTCTGTGGGCGTCC
GGGAACGGCTGTCCTGTTTCACAATGGAGTTTGGCATTCCGCTGGTCCGTTCACTC
GCCGCGGGGGCAAGAGGGTCATCCTGTACTATGGTTACGAACACCCTTGATGTTG
GCTTGCGCGGAACAGTGGCGTTATGACAGAGGATTTCTCAACAGCCTGACACCCC
GTCACCGCCGGTTTTTCCACGGCTTTGTTTTTGATCCCCCTGAATATCGTTGGGGCT
GA

NHI 230 protein sequence:

MLRMVRDRPGQIGCERIRNMTNHPTDAERFLFDTNGYLVLEDLPPALVDSLNAALERT
IVRRRDPGFHRTHEPAFADKLDSANTRVMHLLAEDPLFLDMLDYDPMMEYIHGLFNEM
PHLHSTDAIYEIEPEEHHGKGWHTDGIQDGRDFRPHIPLLQFKVGYYLSDMTEPGQA
NLTLVPGSHKSLVEPDSKNGMPGAVQVCGRPGTAVLFHNGVWHSAGPFTRRGKRV
LYYGYEHPWMLACAEQWRYDRGFLNSLTPRHRRFFHGFVFDPEYRWG

Codon-optimized NHI 231 sequence:

ATGGATGAATATGATGGTTTAACTTCATTTACTACAGCTTCTAGCACTTTAGAGGAGAT
CTTGAACGAAAACACCATCACGCTGAACCAGCCTCTTTATGTAATGGGCCAGAGTA
CCCTATTATACGCAGCAAGTATGTATGATGAGGAACTTGCCCTTAAAATAATTAAAGC
GAAGAAACGAATTCCTGTTAACATTAACGCAATCGATAATCACGGTTATTCAGCATT
CACTACGCAGCCGATGCTGATATGTATCAGCTGGTCAAAACCTTACTGCAATGCGAT
GATATAGACGTCATGTTAAAAACCGAAGACCTAAATGTAGTAGGGCAGATTCAGTCA
GGCGGTGCAACTGCATTACATCTGGCGGTTCATTCGGGGAAATCTTAAACTAGTTAAG
GACTTAGTGGAGTATGAAAAGAAGCTGGTCATGGTGCCGGATCTCGATGGAAATTTA
CCTGTGCACCTGGGCCAACTGTACTCTGTGAATAGCGATCTGATTCAGTATCTGTTG
AGTATACATAACACGAAGCTGTACGAAGAGTCGAATCTGATTACCCTGCAGAAGACA
CAGCAGTTACAGGCCAATAAGCGATATCAGGACAGCCTAAAAGTACCTTCCAATCTG
TATACACCTCATACTTTCCCAAACGTATGGACCAGTGCCGAGTGTAATAAGATACTGG
AACAGGTCCTGAGCAAGACGAGTCAGACTGGCTGGAATACGTCGCGGCACACCTC
CTACCCGACCACAGATCTGCCGAGCTACAGACTGCCTTTTCTGGATCAGTGGATAC
AAGAATCACTACAAATTAGACTCTTTCCTAAGATCATTGATGAATTTAGCTGCACCC
CTCCACTGTTTTATCTTTCCGTGACCTGTTCTATGTAAATACGAAGCAGCAGGGCC
TCATGTGCAGAACGACTTAGCACTGCATTGCGACGGTTCATACTCAGCTTTAACAT
TTTACTGAATCGTAAAGAGGAATTTGAGGGAGGAGGCACATTCTTCGCCCCCACAA

AAACTACCATACATATCCAGCAGGGCGATGCACTTGTTTCATTCAGGTAGGGTGGTGC
ACGGAGCTGCGTCAGTCGTGAGTGGTAAACGCCTTATAATAGTAGCCTTCTTAAATG
TTCGCCCATCACCTCCGTTATGA

NHI 231 protein sequence:

MDEYDGLTSFTTASSTLEEILNENTITLNQPLYVMGQSTLLYAASMYDEELALKIIKAKKRI
PVNINAIDNHGYSALHYAADADMYQLVKTLQCDIDVMLKTEDLNVVGGIIQSGGRTAL
HLAVIRGNLKLKDLVEYEKKLVMVPDLGDNLPVHLGQLYSVNSDLIQYLLSIHNTKLYEE
SNLITLQKTQQLQANKRYQDSLKVPSNLYTPHTFPNVWTSAECKILEQVLSKTSQTG
WNTSRHTSYPTTDLPSYRLPFLDQWQESLQIRLFPKIIDEFQLHPSTVLSFRDLFYVKY
EAAGPHVQNDLALHCDGSILSFNILLNRKEEFEGGGTFFAPTCTTIHIQQGDALVHSGR
VVHGAASVVSGKRLIIVAFNVRPSPPL

Codon-optimized NHI 232 sequence:

ATGCAAATAATACGTTACGCCCGTTTGCCCATTTGGCTATGATGCTCACGCGATCCAA
AATGAACTGACTGGAGGTAATCAGCAGTGGCTGCCTCATCTTAATACGTATCATTATT
CAGGCGGATGGCAGGTGTTACCTCTGAGGTCACCGGGAGGTAATCATCTGAACCC
TGTACCTGATCTCATGGATAATGCCAGCTTTCTTGACACGGATTATATGCAGTTATTT
CCTACTGTAAAAAAGCTGGTCAGTCTGCTTCAGTGTCCAGTCATGAGTGTACGTTTT
CTGAATTTACGTGCCGGTTCGGTCATTAAGGAGCACAGAGATCATCAACTTAGCTTC
GAAAAAGGGGAAGCCCGACTGCACTTTCCCGTTATCACGCATGCTGACGTGGAATT
TTATTCCGAAGATCAAAGAATCATTCTGAATGAAGGAGAATGCTGGTATCTGAATGC
GAACCTGCCTCATCGGGTGAGTAATAATTCTAGTATTGATCGTATTCATCTGGTGATC
GACTGCAAAGTAAACCCCTGGCTGACCGCGATGGTGCAGGGGGGCCCCCAGATC
GCAATCAAGGAAGAAGAGGAGGATCTGTCTCATTACCCGGCCATGATCGAGAATTT
GCGCCAGCAGGATAATGAGGCGGCCCGTCAGTTAATAATTAAGTGAACAAAAAC
TAAAGATGCAGAACGTTACGTCCAGCAGCCGCGCAAGGTAA

NHI 232 protein sequence:

MQIIRYARLPIGYDAHAIQNELTGGNQQWLPHLNTYHYSGGWQVLPLRSPGGNHLNPV
PDLMDNASFLDTDYMLFPTVKKLVSLLQCPVMSVRFLNLRAGSVIKEHRDHQLSFEK
GEARLHFPVITHADVEFYSEDQRIILNEGECWYLNANLPHRVSNSSIDRIHLVIDCKVN
PWLTAMVQGAPQIAIKEEEEDLSHYPAMIENLRQQDNEAARQLIKLEQKLKDAERSRPA
AAQG

Codon-optimized NHI 233 sequence:

ATGGAAGAGCGTTGGGCCGTAGCGGGTGCGGTGGATGAAGATGGGTGCTTAAAGG
CCGATCAAATCAAAAGTTGGAGAGAACAGGGGTTTGCTTTTGTGTCAGGCCTGTTA
CCGAAAGCCCTTCTGTCAGAACTGCGCAGCGACGCTCAATCGTTCTATCCAAATCC
AGAAGATGCAAACGTAGCTGATTATAACCACTTCGGGTCTAACGGACACTTTGTGTT
TCCATCCGATTATAGTTCTGCAAACAGTGTGTCTCTCCATCCAAACCTGCTGCGAGC
CGTTGCAGATCTCTTGGGCGTCGAAATAGCCGAATTGCGTCTGACACAAAGCGATC
TTTGGCCCAAATATGGAGGCAATGGACTGGAAGATAGGAGCGAAACAGAGATCAG

CGCATCCACTGCGATTATCCAAACCATACTTTGACGCATCCGCCAGAATGGGACCG
GCCTGAGGCAGTTGAAATCATTATTTACTTTGTCAGATGAAAGCGAGTGTCAAGGTAG
CACCGCTGTTGTGCCAAAACCTGGGATCTGACGATCCGGCCTATCGGTGGCCGATAG
TAAACACCCCCGGGGGTAGCAGGTAGCAATTACGTCGATGACAAGGCCAAAAGCCGA
GCGTTATATGAGAGAGCTCAACCCAGATGCAGCTGATTTTCAGACAAAAGGAATTATA
TGAACGCGAAGTGAAAACCCGCTATCAGATGGGTGATGTTATTTTCTATCGACACGA
TACCTGGCATCGCGGCACGCCTGTAGCCCAGGGTGCCCTTCGGCTGGTCCAGAAC
ATGACATTTAAAAAGGCTACATCGGATTGGGTAAAGTGTGTTTGCATTCGGGTTGGGCC
TGGAGTCTGTACCGTGCCGGCCACGGCCCAGAAAACTGATTGCGGAACTGAGTC
CAGATCAGCGTACCGTTCTGGGCTTTCCGCCACCAGGCCATTTTTACTGGACCGAA
CAAACCTCTGGAAGCTGTAGAGGCTCGATACAAACCATTCTGGGATTGATATGACTCCA
TACCATCAGGCCGTTAATCAGACGTAA

NHI 233 protein sequence:

MEERWAVAGAVDEDGCLKADQIKSWREQGXAFVSGLLPKALLSELRSAQSFPNPE
DANVADYNHFGSNGHFVFPSPDYSSANSVSLHPNLLRAVADLLGVEIAELRLTQSDLWP
KYGGNGLEDSENDRDQRIHCDYPNHTLTHPPEWDRPEAVEIIIIYLSDESECQGSTAVVP
KLGSDDPAYRWPIVNTPGVAGSNYVDDKAKAERYMRELNPDAAFRQKELYEREVKT
RYQMGDVIFYRHDTWHRGTPVAQGALRLVQNMTFKKATSDWVSVLHSGWAWSLYRA
GHGPEKLI AELSPDQRTVLGFPPPGHXYWTEQTLEAVEARYKPFIDMTPYHQAVNQ

Codon-optimized NHI 234 sequence:

ATGGATCAGCTGATCAGCGATAGTCTCAAGGAAACTGATGAGGCTAGCCTGAGAGC
AAAATACTCAGAGCAGGATGAGTTTCGTTATCGTTGATGAATTCCTGCCGTTGGAAGT
GCTGAGCCGCTGGGAACTTGAGCTTGCACGTCTGAAGCCACATGTGCATCGTAACT
ATTTGCCGGGCCACAAAAAAGGCGGTAGCGTCGCATATCAGACAATGAATGCCCTC
GCGCCATCTATTACTCGCGTTTACCATTCTGCACCCCTGCTGGGCTTTCTGCGACG
GGTTGTAGGTGCGGAGGTAAATGAATGTCCCTCAAGTGATCCCCATCGCTGTGCAC
TTTATGCATATACTGAGGAAGGGGATCACATGGGGTGGCACTATGATACGAGCTATTA
TAAAGATCGTAGATGGACCGTTCTGGTTCGGTTTTAAAGACGAAAGTAGTAGCCACCT
GCTTTGTCTCTTGCATACCCGTAACCTCCGACCGTGATGTAGTAAATTTAGAGCTCCA
GATCAAACCAGGCACTCTGGTCATTTTCAATGGCGATAAAGTGTATCATGCAGTTAG
CCCGCTGAAGAAAGGGGAAAGCCGTTATATTGTCAGCATGCAGTACGTTACCACGG
GGAATGAATCCTTTTATGCGTTTTATCAGCAACATGAAAGACGCCGTTGCCTACTT
TGGCCTGAGAGGCGTTTTTCGGCAAAGGTCGACTGCGTTGA

NHI 234 protein sequence:

MDQLISDSLKETDEASLRAKYSEQDEFVIVDEFLEPLVLSRWELELARLKPHVHRNYLP
GHKKGGSVAYQTMNALAPSITRVYHSAPLLGFLRRVVGAEVNECPSSDPHRCALYAYT
EEGDHMGWHYDTSYYKDRRWTVLVGFKDESSSHLLCLLHTRNSDRDVVNLELQIKPG
TLVIFNGDKVYHAVSPLKKGESRYIVSMQYVTTGKMNPFMRFISNMKDAVAYFGLRGVF
GKGRLR

Codon-optimized NHI 235 sequence:

ATGTTTCAGGATATTACCCAGAGTATTGAAGCGTGTGCAGCCTACTATGGGGATGAG
GCAGAGCAAATGAAGCAGTATTTAATTCAGGGTCAGGAAAAAGCGCTGGCACTTCC
AAACCGCGGCCCAATACGCTTCGACGAGAACGGCGACATTCATCCTGATATCCTGA
AACTTATTCAAAATATGGCTTCTATATTTTTGAAAACGCATTGGGCGAAGACGAGCT
TAATGATTTAAAAAATGATCTTGAACAGATGCGCGAGAATTTTCCGACCGAGATGGG
CGCAACTTTAGATGCACGCGGTCGTCCGGCATTGGGTTCCGGATCGTGAGGGCTTC
GCGCTGCAATGGGCTAAGCCTCTGTCAGATCCATTGGGCGGCACAGCAATGCTGA
ATGGTTCGACATCAAGTGAATTTGTTTGAACCGAAGCCAGGTGAAGGCGCCCCCA
GGCCACGCCTCTGTATTTGGGCGGTAGCTTGCAATATAGCGACGCGTGTCTGCGGA
CATATGCCACCCAGGGCTGCTCAAAATGGCGGAAGCAGTCAACGGTAAAGACTTT
GTACCGTTCCACGAGGGACTGTTTATAAAGGATGCAGGTTTAGGTGCGAGTGTTTC
GTGGCATCAGGATGGTGATACCCACTGGGATTCTCCGGTTTTTGATGAAAATATCCA
TGGCTTTAATTTTATGGGACAGGTGTATGGGAGTACCGCAGTTAACGGGGTGTGGG
TGGTCCCCGGTAGTCACAAAATTTCGCGGGTGAATATTGTAGACCTTGTTAGCAAG
GCGGGTACAGAACGCCTGCCTGAGGCTATCCCTATTATTTGCAACCCGGGTGATGT
TGTCATTAAACAGCAGACAGATCCTCCATGGCAGCTTTGCAAACACTGGGTTGGAAA
AACGCGTCACTGTAAATTTTGGTTTCCATCCAATGGCATCAGTGTTAAACGTCCGGG
GAGCAGGTCTCCATGCCGAGGCAGCAACATTCGATGAGGCATTTATAAAACACCGG
AGTCGATTGATTGGCATAGCTATCGCAGCGCGTAAACAACGGTTTCCAGACGAACT
GCCCTATGCGTATCTGCCTATTGCAAATGATCCTGAAAAACCAGTGTGGAACCAAGA
AGTGAAAGAGAGCCTGAAAAATTACAATCTGATGGACCTGTCAATTTGA

NHI 235 protein sequence:

MFQDITQSIEACAAYYGDEAEQMKQYLIQGQEKALALPNRGPIRFDENGDIHPDILKTY
KYGFYIFENALGEDELNDLKNLEQMRENFPTEMGATLDARGRPALGSDREGFALQW
AKPLSDPLGGTAMLNGRHQVKLFEPKPGEGAPQATPLYLGGSLQYSDACLRTYAHPGL
LKMAEAVNGKDFVPFHEGLFIKDAGLGASVSWHQDGDTHWDSPVFDENIHGFNFMG
QVYGSTAVNGVWVVPGSHKNSRVNIVDLVSKAGTERLPEAIPICNPBGDVVINSRQILHG
SFANTGLEKRVTVNFGFHPMASVLNVRGAGLHAEAATFDEAFIKHRSRLIGIAIAARKQR
FPDELPYAYLPIANDPEKPVWNQEVKESLKNYNLMDLSI

Codon-optimized NHI 236 sequence:

ATGTCGGCCGCTACCCTCGAGGAAGGCCCTCTGAGAGGTCCTTCGTTCTTTCTATC
TCGTACGGCCCTTCGCGCCCTGGCCTTGGCTCATAGAGACCGCTACGGACCTGCG
AAGCCATATCCTCACGTTGTAATCGATGGATTTCTGGGACAGCCTCTGGCAACTGAA
CTGGCCGAACGGTTCCCGGGGGCGACCGAAGCAAGTTGGAAAAGGCGAGATCAC
GTAGAGCAGGCGGCACGTCTGGGTCAGCTTCAACGCAAAGCTTTTGAAGATGTTTC
CGGGTGTACTACGTCATCTGCTGTCAGAACTGAGTAGCATGTCGTTTATAGATTTCTT
AGAAACTCTGACTGGTGTTTCAAGGTCTGATAGCCGACCCGCACTTTCTGTGGGGCG
GGCTTGCACTCTGACGCTGAAAGGGGGCCATCTAGCCCTGCACGCCGATTTCAATC
GCGACAGGTTCCGTGCCTTGACAAGACGTCTGACCGTGCTCTATTATTTAAATCCG

GGTTGGGAAGCTGCCTGGGGCGGTGACTTGGAAGTGTGGTCGGCCGATCTGTCC
CGCTGTGAGGCCCCGTATAGCCCCACTGTTGGACCGCCTTGTAGTAATGGCCCATGG
AGATGATTTTTGGCATGGTCACCCGTCGCCTTTAGAATGCCCGGAAGGGAGGGGC
CGCGCTGCCGTCGCCGCCTATTTCTATACAGCAGAGGAGTCACCTCATGCACCCGA
GCCACATTCCGCACTGTGGGCGCCGCCACGTAGTTCGTAA

NHI 236 protein sequence:

MSAATLEEGPLRGPSFFLSRTALRALALAHDRYGPAKPYPHVVIDGFLGQPLATELAE
RFPGATEASWKRRDHVEQAARLGQLQRKAFEDVPGVLRHLLSELSSMSFIDFLETLTG
VQGLIADPHFRGAGLHLTLKGGHLALHADFNDRDRFRALTRRLTVLYYLNPGWEAAWGG
DLELWSADLSRCEARIAPLLDRLVVMAGDDFWHGHPSPLECPEGRGRAAVAAAYFYTA
EESPHAPEPHSALWAPPRSS

Codon-optimized NHI 237 sequence:

ATGGAACAGGCGACCCAGGTGGTTCGAGAGGCCAGCGGATGGGTTCGAAAACATAA
AGACAATAGACGTGGCCCGTCTGCTGCGTGAAGAACATCTGTTAACCAACGAGTTC
GCCCAGCAACGTCCGTTCCGTTATATTGTTATTGATAATTTTCTGCATGCTGATCAAG
CAGAGCGGATATATAAAAGCTATCCTGCAATTGACGAAGCGTGGCAGAACGGCAAT
GATGTGCATACCAAAGGGAAATGGGGTACTCCGGACGTGGAAGGGACCGTAGCCG
GCGAATTTTACCGGGAAGTCAATAGTCCAGAATTCCGTACCCTATTAGGCCGAATAA
CAGGAATACCGCAGCTGCTCCAAGACCCAGACTTACAGGGCGCTGGACTTCATCA
GATCAGGGATGGTGGCTTCTTAAGCGTGCACATCGACTTTAACAGACTGCGCGGAT
CTAATCTAGATCGTCGCCTGAATCTGCTGGTTTATATGAACCCTGGCTGGAAAGAAG
AATGGGGTGGTTGCCTTGAGCTGTGGGACATGGAGAAAAACAAATGGTGTCCAG
TGTA CTGCCGTTGCTAAATCGTTGTGTGATTTTTGAACTAATGAAATTAGCTATCAT
GGACACCCTGTCCCCGTATCTAGCGGTGGCGTGA CTCTGTAATCGCTCTCTGTGTA
TTATTATACTGACGGCCGCGACGATGTGGTAGCAGACAATCATTCCACGATATATGTA
AATACACAAGGAGCTGAAGGTT CAGCGAAGCTTCTAAAAAATGGAATAGCACATTCA
GCACGTAAACTGATAAAGAACTGGGTGGCGATGGAAATTTT TAG

NHI 237 protein sequence:

MEQATQVVERPADGFENIKTIDVARLLREEHLLTNEFAQQRPFYRIVIDNFLHADQAERI
YKSYPAIDEAWQNGNDVHTKGKWGTPDVEGT VAGEFYREVNSPEFRTLLGRITGIPQL
LQDPDLQGAGLHQIRDGGFLSVHIDFNRLRGSNLD RRLNLLVYMNP GWKEEWGGCLE
LWDMEKKQMVSSVLP LLNRCVIFETNEISYHGHVPVSSGGVTRKSLSVYYYTDGRDD
VVADNHSTIYVNTQGAEGSAKLLKNGIAHSARKLIK KLGGDGNF

Codon-optimized NHI 238 sequence:

ATGACCACTACCGCTCGCTGCTCCCGAAGCACTAATACCGCTCCCGTAGAAACCGA
TCGCGATGGTAGTCGTACGATGACAGATACAGCTCAGAGCCAACAGGCCCAGCGA
GGCAAACAGGAAGAAGCCCATCTTATCTTACCTGCAGCAGAAGTCGATGCCGGTAC
CCTGAGATTTGCAACGGCTGACGATACAGAGCGAGCCCTGTGTATTGGTGCCTTTA
ATGTTGCGGTTCCGGAGGACCTTGATGTGCGCGCAGGGTTGGATTTTTGTAGGACA

TTTTACAAACCCGGCACCCGGAGATCCTGCGGATCGACATCGAGGTCACCCGGGAAC
ACGGCCATCCGGCAAGTAACTTGGGTATGAGGATCGCCCAGATCAAGTCGAGCA
GCTGCAGTTAGAATCCTTTTTGTGGCAAGAATACTTGCCTGACGAGGTAAGTACCG
TCTTACGCCGAATGCGCCAGCTCACACTGGATGTGCTGTATGGGGTGTTTGACGCC
GCTTGGGTGCCAGAAGCAGATCGCGATCTGATCACCGGCGGGGGCCCCCTCAGGAC
ACCGGTCTTTGTTATACCACCGTAAATCATTATCGCGCAGGTCTTTCAGATCGCGCA
GGTATAGTAGAGCATTCCGATTGAGGTTTCATTACTACGATTTGTACGGACCAGCCC
GGCTACGAAATCCTGCATGAGGGACATTGGCTCCCGGTTTCAGAGAAAGGCCGGGGC
ATTTACCCGTGAAGTTGGGTGATGCATTTAGGGTTCTTACCCGCAAAGTCCACGG
CCCGTGACAGCCGTGTACCATCGTGTGCCCCGAATTGCGACCCGATGCGGGCGTTTC
CGGATCGTTCATCGTTCAGTGTGTATATGGGTCCCCGCTATGACATGCCGTTATATCA
GTATGATACTGAAGGTCGCCTACGTGAGTATCAAAGTTTCAGAGATTTAGTGTTGA
AAAAGCAGGCAAAGTGGGGTATGACTTCCATTCACGCGTGTA

NHI 238 protein sequence:

MTTARCSRSTNTAPVETDRDGSRTMTDTAQSQQAQRGKQEEAHLILPAAEVDAGTL
RFATADDERALCIGAFNVAVPEDLDVRAGLDFCRFTFYKPGTGDPADRHHRHREHGHP
ASKLGYEDRPDQVEQLQLESFLWQEYLPDEVTAFLRRMRQLTLDVLYGVFDAWVPE
ADRDITGGAPQDTGLCYTTVNHYRAGLSDRAGIVEHSDSGFITTICTDQPGYEILHEG
HWLPVRERPGHFTVNLGDAFRVLTRKLPRPVTAVYHRVPELRPDAGVPDRSSFTVYM
GPRYDMPLYQYDTEGRLREYQSFRDFSVEKAGKLGDFHSRV

Codon-optimized NHI 239 sequence:

ATGCTGGTGGGTATCAGAGCGTTACTGCACAGCAGCCCCCATGAACAGTTCGAAAT
GCTGGACCCTGCACGCCGGATACGGACCCTGCTTCTCCATACCTTGTTACATACTA
CATCGTGTGATATCGATAAGGTTTACGCGGCAGCAAGTGTGTACCCATTTGCCATGA
GCAGTCTGCTTGCACTCCTCAGTCAACAGACACCGAACTTACAGACCCAAAAAGGG
CTGATTTTATTAGGTCTGCAGAATGATTTTCTCAGCCCAGATGGCAAATTGCCCGTTT
CCCCGCGTAGCGGTTATCTGGAACGTCTCAAGGAATTAGTGCCGGCCTTTTCGCGA
GTTTGGCTCTGTCATATGGGTCAGAAGTGAGTTTGAAGCTAACCGCGTGCGCAATC
CTGATGACGGCGATGGTGACACCGTTATTGCTGGTTCAACCGTAGACGGGAGCTTA
GGCCTGAAACATGTAAGCAAACGGAAAGCATCAGAGGACGCCACTTTACCGCTGAA
GAGGGCTAAACCCGCTGATGCGGAGGAGGAAGAAGAAGATCCGGAAGTGTCTG
AACCGTACATCGAATCGGGAACCATGTTGCGTCAAGGCGAGCTGGGGCGCCGAAT
ACCCGGAAGATATTCAGAACCTGATAGCCGATAGCGACATTCAAGTGACAAAACTT
ACTATAGCGCTTTTGGCTCTACTTCTTTATTACTAACGTTGAGAAGCAAAGTTATCAC
CGAGCTTTTTGTATGCGGATGCAATACAAATTTGTGAGTCTTTGCTACTGCGATGGAT
GCCGCCCGGTACGGGATACAGATAACGTTAATTGAGGATTGTCTGGGGTACCGCCG
AAGGGAGAGGCATGACGAGGCAATTCGTAAAGTAGTTGATATTATGGAATCGGATGT
TATGTCGAGTTCTAAAACAATAGATATGCTGCGTTCGCCGCCAGACGATGACAAACG
TGAAGATCATTGTTCCGATGAAGACGAAGAGAGCGCGGCAGCAACAGATGAACTG
GAAGCGGACTCTAGCGAAGAGGAAGAAGAAGAGGATTTATCCCCGACCCTGACG
CACATATTGAAAAGCAGCATTGGCCGCCTTCAGCTCGGCTCCCACTTAATGTGGAG

AATTTACGTTTCATTGAGTCTGCGTCGTAGCACAGCCGTTGCAGCTCGCAGTACTGT
GACATCCCAAGCTGTGGATCTTGAAGAAAAGACGGCCGAGACCACGGTGGATGAA
TACGAAAAAGCCATGCACGAAGCGAGAGATCGCGTTGCCCGTTATGATGCTCTTGC
CCAGCGCTCGACCCCCCTCTTTGGTATGAATAAGGAGAAAGAGTCAGCGGGTTTCG
CGGATACTGTATGACCTGCTTCCGGCAGAATTAGCCGAAACGGTTTTTGGAGAACT
GAAACCAGAAGTCCATTGGCAGCCTGCTGAGGAAGCCGCCGGTCACGCCCTCAAC
CATGTTTTGATCCAGTTGTATAGGGGGGGGACCGATTTTATCTCAGAACACAGCGAT
AAGACTCTGGATATTGCCAAAGGGTCATCAATCGTAAATGTTAGCTTTGGCGCACAA
CGTACTATGCGTCTGCGATCTAAGCGTGGTGCAACCAGTCATCTGGCTGCACCTAG
TAAACATGGGGCCGCAACCTCTCCTTTAACGCGTACGACCCACCGCATCCCCTGC
CTCACAATAGCATGATCACAATGTCACTGGAACTAATGCTGAATATCTCCATGGTAT
TAACGCCGATAAACGTCCAGCGGTTGAATTTCCGCTGCAGAAAAAGAGTATGATG
GACAACGCATATCGTTAACATTCCGTCAGATCGAGACTTTTCTGTCAGCCGATGAGC
GACTTATTTGGGGTCAAGGCGCTACCGGCAAATCACGCGCCCTTGCCCGTGAAGT
GGTGAATGGGGACGGGAAAGAATCAGAAGAACTGGTCCGCGCGTTCCGGTGCTGA
GAATAAAGCAAGCCGTATAGAGTGGGAAGTGGTTTACGGACGCGGTTCCGGATGTCC
TGCATCTCAAATAA

NHI 239 protein sequence:

MLVGIRALLHSSPHEQFEMLDPARRIRTL LLHTLLHTTSCDIDKVYAAASVYPFAMSSLL
ALLSQQTPNLQTQKGLILLGLQNDFLSPDGKLPVSPRSGYLERL KELVPAFREFGSVIW
VRSEFEANRVANPDDGDGDTV IAGSTVDGSLGLKHVSKRKASEDATLPLKRAKPADAE
EEEEDEPELFLNRTSNREPCCVKASWGA EYPEDIQNLIADSDIQVTKTYYSAFGSTSLLL
TLRSKLITELFVCGCNTNLSVFATAMDAARYGIQITLIEDCLGYRRRERHDEAIRKLVDIM
ESDVMSSSKTIDMLRSPDDDKREDHCSDEDEESAAATDELEADSSEEEEEEDFIPDP
DAHIEKQHWPPSARLPLNVENLRSLSLRRSTAVAARSTVTSQAVDLEEKTAETTVDEYE
KAMHEARDRVARYDALAQRSTPLFGMNKEKESAGSRILYDLLPAELAETVFEKLKPEVH
WQPAEEAAGHALNHVLIQLYRGGTDFISEHSDKTLDIAGSSIVNVSF GAQRTMRLRSK
RGATSHLAAPSKHGAATSPLTRTTHRIPLPHNSMITMSLETNAEYLHGINADKRPAVEFS
AAEKEYDGQRISLTFRQIETFLSADERLIWGQGATGKSRLAREVVNGDGK ESEELVRA
FGAENKASRIEWEVVYGRGSDVLHLK

Codon-optimized NHI 240 sequence:

ATGAACCTTAAGCAAATACGAAGTTCATATTGTCAGCACGGTTTTTGC GAAGTTCACA
GGATTTTCTGGAGATAAGGAAATTGCGCAGCTTACCGAAACGCTGATGCGTTTTTCAT
CGAAATTGGTGCGTCGCCAATTTAGAACTTTATCAACAGGGTGCCGTTAACTCCGCA
TATCTGACAGGTACCCAACATCTAACACTCGCAGAACGGTCAGTTTTTATTTGATTTTA
TTGGTAGCCATAAAGTTATGGAATTAGTGCAGGCTCTGCCTCTGT TAAAACCGGCAT
TTATGAACACGCAACTGTTTTTTCGACCCAGTTAACGGAGCGCAATCGAATTATTGGC
ACCGCGATCCTCAGTACCACCTCAACCTGCAACAGCAACGTCAAGCTCTGTCTGGA
CCTGAGGTTATTCATCTTCGTCTGGCGCTGAAAGACGAACTGGGCATTGAACTGGT
CCCGGGAAGCCACCGCAACTGGGATAATGATGAGGAGCTCGCCGTACGTCAGCAA
GTTGGTGGTTCGTTCAAACAGTGAACCGCTGTCAACGGGGCTCTCGCTGCCGCTTC

AACGGGGTGACCTGCTTATCTTTTCGGCAAACATGATTCACCGTGGCTTGTATGGTA
ATCAACGCCTTGGGTTTGATATGTTGTTTTGCGAAGCCCTTCCCGAATTACTGAAGT
TTGCGGACGCCAACTGCTTGCCGTCCGAGGCACACCTGCAACAACTTCAGGCACC
TATGGCATTTTTAAACACTTTAAATGTTAAAGGTCGCGGAGACTGTAAACCTGATTAA

NHI 240 protein sequence:

MNLKQIRSSYCQHGFQFTGFSGDKEIAQLTETLMRFHRNWCVANLELYQQGAVNSAY
LTGTQHLTLAERSVLDFIGSHKVMELVQALPLLKPAFMNTQLFFDPVNGAQSNIYWHR
DPQYHLNLQQQRQALSGPEVIHLRLALKDELGIELVPGSHRNWDNDEELAVRQQVGG
RSNSEPLSTGLSLPLQRGDLIFSANMIHRGLYGNQRLGFDMLFCEALPELLKFADANC
LPSEAHLLQQLQAPMAFLNTLNVKGRGDCKPD

Codon-optimized NHI 241 sequence:

GCTGAAAACGGGGGTAGACCACCGGTTTTTCAGATTCCCATGGAGGGGGGGCAGAG
CCTCACTTGCTTTCGCCGCACATCAATTGGTAGGGGTCATTACTGACCCAGCGGTT
CTTATGCACGGCGATGCGCCGGTTCGGGAAGAAGTTACCACACCGGTTGCAAGCG
CCGCCGTAGCAGCCGCTGCAGCCGCGAGTGCGGCACAGGGTCATGGCGACCTAG
TACGTCACCCGGTTGCCAGCTTGACGGCTTTCTGAGCGGCGCGGAAATAGCCTG
GCTGATGGAATTAGCCTTTAGCGCAGAAAATCGTTTCTTTCGTGCTCGTGTTAGTGA
TGAACGCGATGATTACCGGCATTCTCTGGTTCTTAGTGCTCCAGATGCTTTGCGGCA
ATTGTTTGTGGCAAAAATAACTGCCGCTATGCCGGAGGTTATGCCACAGCTCCGCTT
GGGTCAGTTCGCGTTAGGTAAAATTGACTGCCAAGTGACTGCCTCTGTTGATGGTT
CCTACTTTAAGATCCATACTGACGCGGGCGCAAATGAGACTTATAAGCGACAGTTTA
CATACGTTTATTATTTAATCGGGAACCGAAAGGGTTCCTGGCGGAGAACTGCGTA
TTTACGATGACATGGTCCGCAATGGTAAGCTAGCCTCTACGGAAAGCTTCCAGGTTA
TTGAACCCCGGCACAATTCAATCGTGTTCTTTCAGGCGGCGGTTCGGCCACGAAGTT
ATGCCTGTGCACGTCCCTTCGAAACAGTTCAGAGATGCACGCTTTACTGTTAACGG
TTGGATCGAACGTGCTTAG

NHI 241 protein sequence:

AENGGRPPVFQIPMEGGRASLAFAAHQLVGVITDPAVLMHGDAPVPEEVTPVASAAV
AAAAAASAAQGHGDLVRHPVAQLDGFLSGAEIAWLMELAFSAENRFFRARSNDERDD
YRHSLVLSAPDALRQLFVAKITAAMPEVMPQLRLGQFALGKIDCQVTASVDGSYFKIHT
DAGANETYKRQFTYVYYFNREPKGFTGGELRIYDDMVRNGKLASTESFQVIEPRHNSI
VFFQAAVGHEVMPVHVPSKQFRDARFTVNGWIERA

Codon-optimized NHI 242 sequence:

ATGCATCTGTGGAACATATTCAAACCCAAAAAGCGGAACAATTGGGAACCTGTACCG
CACCCTTCGTAAATCTGCCCCGCTGCGTGCAACCTTGCATGAAGAGGGCCTGG
CCGTGCAGCCATTCTCTCTCCGGACCAACTCCTGGCTTTGCGCCGACTGTATGAA
CAGGAACATCAGCTCGAAAATTCTGACCAGGGTGGCATGTTTTATTCCGTCTACTCT
CAGGATACACCGTACCGTCGTGTTTCATGAAGCCATTCAGGCCATACTGCAGCC
CGCGCTGGACGCATTATTGACAGATTACAGAACGGTGCTTAATTCTTTTATCATAAAA

ATGAATGGTCCTGCATCAGAGTTCGCCTTGCATCAAGACACTACGGGTCTGGACGA
GACACAGTATTCCAGTCTCTCGCTGTGGATCCCGCTGGAAGATATTACCGAACAGA
ATGGAGCATTGTGCGTTGTTAAGCGATCACATCGTCTGTTTAGTCCCTATAGAAGCA
TCAGTTTCCCTCCGCCATATGCAGGGATAAAACACACCATCAAGGATTACTTAGAAC
CTGTTTTTATGAAAGCCGGTGAAGCGTTGTTATTTGATAATCGTCTATTACATTATAGC
CTGCCGAATCGCTCAGATCACAACCGCGTTATCGTAATGTGTGGAATTTTTCCGCAG
GAAGCACCGGTCGTTACGTGTTTTAAATCTCCAGGTGACCCGCGCATCGAGCTGAT
CCAGCATGAAGACGATTTTCATGATTAACCTATCCTAACTTCTTCGTAGATTGTCATCAA
AAACCTACTGTTGGCCAAACGATCGGTTATGTAGCAGATACATACGGCCCAATGACA
GAAAAAGCCTTTCTGAGAGCCTGCCGTGAGCATGGAATCCAGAAAACAAATTATCT
GCGGAATGCGCTAAGCCAGGGTTACCTTCAGGGCGAACCTGTTTTAGAAAAAACCG
CACGCTAA

NHI 242 protein sequence:

MHLWNIFKPKKRNNWEPVPHHFVKSAPLRATLHEEGLAVQPFLSPDQLLALRRLYEQE
HQLNSDQGGMFYSVYSQDTPYRRRVHEAIQAILQPALDALLTDYRTVLNSFIIKMNGP
ASEFALHQD TTGLDETQYSSLSLWIPLEDITEQNGALCVVKRSHRLFSPYRSISFPPPYA
GIKHTIKDYLEPVFMKAGEALLFDNRLLHYSLPNRSDHNRVIVMCGIFPQEAPVVTCKFS
PGDPRIELIQHEDDFMINYPNFFVDCHQKPTVGQTIGYVADTYGPMTEKAFLRACREH
GIQKTNLYLRNALSQGYLQGEPLVLEKTAR

Codon-optimized NHI 243 sequence:

ATGCTTGCACGTAGAGTTGTTACCCGGCACCTAGCGCGGGTGGGCGCCCGAACTT
TTTCATCAGCACCCGCTTTTGTATGAAAACACACTGCTGCCATTATTTCCACAGGCGA
CACAGGAAGCCATTCAACACGGCCTGAATACCCAGGGTTTCTGCATCTTGCGGGAT
TTCGCTTCTTCTGCAATTGCGCAGGCCATGCGTACTGAAGCTGAAAGGCTCTATGC
GGAAGGTCACATGTTTCAATCGAACTCGGTAGACGCCGAAGGAAGATCGTACCCGA
AGCCGAACGTTTTTCGCCAGCGAACTTAACGGTAATGAATGGGATTTGGCACCGACC
ATTCTGCACTATACCCGTTCCGTAATGTTGCAGGCTCCGGCCATGTAAACAAATTG
TTTCCAGGGTTACAAATGAGCAGCCGTGCGTACGCCTCTAAATTGGCTGTGTCCTT
GGGCGATGGCGCCAGCTACCCGAAACATTGTGATACGGCTGGTCTTCCTGACAAG
CGTAAAGTTACCATGGTATATTATCTGAATCCAACTGGGCACCGGGGCCACGGCGG
AGAACTACGCGTTTTTCGCACCGAATGGTACCCATGTCGTCGAGCCACGTGCAGATA
CCCTGGCGGTTTTTTGGTTCGGATCTAGTCGCCCACGACGTACTGCCGTGCGAAAC
GCCTGTAGAAGATGTCGCGGCACGCAGATATGCACTGACACTATGGCTTGTACCCG
ATAATCCCAGACAAATTAATGATAAGAACCATCACTTATACCCATTGCGCCAGCACCA
TTTCCCGGATGCGGCTTAA

NHI 243 protein sequence:

MLARRVVTRHLARVGARTFSSAPAFDENTLLPLFPQATQEAIQHGLNTQGFCILRDFAS
SAIAQAMRTEAERLYAEGHMFQSNSVDAEGRSYPKPNVFASELNGNEWDLAPTILHYT
RSVMLQAPAMLNKLFPLQMSRAYASKLAVSLGDGASYPKHCDTAGLPDKRKVTMV

YYLNPNWAPGHGGELRVFAPNGTHVVEPRADTLAVFWSDLVAHDVLPCEPVEDVAA
RRYALTLWLVTDNPRQINDKNHHLYPLRQHHFPDAA

Codon-optimized NHI 244 sequence:

ATGGCCACTGAGCTGGATAAAGAACTGCCTTTATTTTCAGCCGTTTGCAACCGCCGC
GGGATTTCTTAGTGACGCGGAAATAGACCGTCTTATTGCCGAGCACGTACCACTCTT
ATCAGAGGGGCCCTTGGATTTGGGGGGACCAACGCTACCATTGCGCGCAGCCAA
GTAGTATTCTTAGGAACTGAGCCGAAATACCGGTGGCTTTACGATAGACTGTGGACC
GCAGCGCAGGAGTGCAACCGTTTATTTTTTTGTGTTGACATCGCCGGTGTGGAAGC
TAACGTGCAGTTAGCGCGATATGATTGTGGCAATCGGGGCTTCTATGATTGGCACAC
CGATTTGCGCGGGATCGCGCCGCGCCGTAAATATCTCTGTCTATCCAACCTTTCACG
TCCGGAAGATTATGATGGCGGCGACCTCGAGCTGCTGTATGGGAATGCCCCCGC
CGGCTAGATCGTACCCGCGGCACCTTAATTGCGTTTCCAAGTTTTATGCTGCATCGG
GTGACGCCCGTTACACGGGGTGCCCGCTGGAGCCTGGTTGCATGGATTCTAGGCA
ATCGATGGCGGTAG

NHI 244 protein sequence:

MATELDKELPLFQPFATAAGFLSDAEIDRLIAEHVPLLSEGR LGFGGTNATIRRSQVFL
GTEPKYRWLYDRLWTAAQECNRLFFCVDIAGVEANVQLARYDCGNRGFYDWHTDFA
GIAPRRKISLSIQLSRPEDYDGGDLELLYGNAPRRRLDRTRGTLIAFPSFMLHRVTPVTRG
ARWSLVAWILGNRWR

Codon-optimized NHI 245 sequence:

ATGGCCAGCAGTACCCAGGAGCACCATTTACACCATTTACCAACACCTTATGGCACG
ACAACCGCACCCCCCTCCAACACCGTCTGCACATAGCAATCACAATCATAACCTCCT
GTCTACGAGCGAGGCTGCAGACTCCCTGTCTCGGCTGCTGCATCGCATCCCTCCT
ACCCTGTCATTAAGTTTCCCGGGCCGCCGAGAGCCCTCCGTCAACGACGATAA
GTCCGCCATTGATTTCCCTGTCTGACGCTAAAAGTATTCTCCATAGTAACCTGTAAAG
CGCCGCAAAACAACATGGTTTTTTCCAGCTTACCCAGCATAGTATTAGCTCGCATTTA
GCGCAGTCTGCGGAATCGGAAAGTGCCAGTATCTTCAATGACGAAAAACAGTTGTG
TTTTCCGAAAAATTGGCCGCTGGGGTTTGATAACGATGATGACGATGATGACTT
TGTATGTGGACGCTCACTGTGCCTGGATGAGAGCAGTTCTATGGAGTTAGGCTTTT
CGTCAATTCATGAATTTACCAGTCAGATGGAGAACTGGGCCTGGAACCTGATTGAA
GAGTTAGCTTGTGCAGTTGGTTTTGAGAATCCTGTCGGTGAGGACCGGACACGTTT
TTGCTCCTTAATGTGGATCAGCGAATCCGAAAGCGGTTTCATCAAATATGCCGCTCTC
TCCAGGCAGGGTCTATCCTTATGTGGTGGGGCTGAATTATCAAATTCGTTGCCGCAA
ATATAGCATGTTAGCAGACAGCGGCTGGATCTCTGTGGCGCCTCAGGTGGACTCTG
TTATGGTTACTTTAGGCGATATCGCACAAAGTATGGAGCAACGGTAAAGTAAAGAAAG
TGCGTGGCCGGCCGGTCCCAATAACAAACGGAGAAATTAATTCATCCAGTAATAATA
GCCATTATGTTTCCCTGACCCTGCTGGTTACATTGGCCACGAAAAATACCGTAAGCC
CTCTTCTTCCAATTAAGCTGCCGTCTGTTAGGAGCAGTGTTGAATAAAGAAGATGATG
ACGGTTTAGGTGATAATGACTCTACAACCATAGCGGTGAGGAAGAATCCCCTATGT

TTAACTCATTTTCATTTCGAGGATTACGCCTGGCGTGTGTATCATGCACGCCTGAATAT
CAAAGATCCTTTGGTACGTTACCGTGTGTTGA

NHI 245 protein sequence:

MASSTQEHLHLPTPYGTTTAPPPTPSAHSNHNHLLSTSEAADSLSRLLHRIPPTLS
LSFPGRRQSPSTTISPPLISLSDAKSILHSNLLSAAKQHGGFFQLTQHSISSHLAQSAES
ESASIFNDEKQLCFPNWPLGFDNDDDDDDDFVCGRSLCLDESSSMELGFSSIHEFTS
QMEKLGLELIEELACAVGFENPVGEDRTRFCSLMWISESESGSSNMPLSPGRVYPYVV
GLNYQIRCRKYSMLADSGWISVAPQVDSVMVTLGDIAQVWSNGKVKKVRGRVPITN
GEINSSSNNSHYVSLTLLVTLAHTVSPLLPIKLPSLGAVLNKEDDDGLGDNDSTTIAVE
EESPMFNSFSFEDYAWRVYHARLNKIDPLVRYRV

Codon-optimized NHI 246 sequence:

ATGTTATCTAGATTGCAACCGGACCTGGCTGGACCGATGACGAAGCGTACAATGCA
GCAATCTAGTCAGGCCCGGCTGAACCACCCCTCGTAGCGGACAACCGTACATTAG
CAGGTTTCAGTTCATGAACCTGGTTGGGCCAACGCTGATGCAGATGCCTTCGCCGAG
CAGAGAGAATATCTGGCTACTCACAATGGCATGAGAGGTCTAGAAAGGCTCCAACC
AACCGATATAGAAGATGCCGTGCGCATATTCTACCGAGACGGATTTGTGGTAATAGA
AAATGCATTAACCGAAAAACAGCTGGCCGAATTAAAGGAAGCATCGGAAAGAGTCAT
TCGTGAGGTACTTGCTATGGACAAAAATCGGCAGGGCAACAGGGGTAGTCATCGTT
ATTCATTTGGCAGCGCATCTTTGACAGGCCAGCTGCTGCATGAACCAGCATGGGCC
ATGTTGGTAGATCTACCCACGGTCACCCCGATTATAACCGCAATTTTTGGCTCACGA
GACTATATTTTACGTGGTGCGGGAGGTGATTTCTGTCTTCCAGGTGCCTCAACCTAT
CAGCCTCTTCACTCGGATATGAATGACAGGATTGAATATCAAGGTAAGACATTCCGT
AGCTTCCACGACCCACGGGGCAAATTGAACTATCGTGACCTGCCCTGCCCTTATGT
GTGCTGCAACTTTCTAACATCCGACTTTACCGCCATAAATGGTCCCACCCGACAGAT
CCCAGGTACGCAGCACAGCCAACAACGCATTCCGAAATTAGCCCAAGAACCCGAG
TGGATGAAATTATCAACGGTGTGCCCCGGCCCCAGCAGGTTTCAGTCCTAATTCGGGA
CACCCGCGCATGGCATGGAGGAACGCCAACTTATCGGATCAGGTCCGCGCCATC
CCAAATACGGAATATCACGCGCCATGGTACCGAGAACCAATGCGTAAGTCAATGCCA
CGCGAGATTTATCAAAGTCTGAGCGAACACGCACAATATATAGCTCGGTACGTAGTC
GCTGAGGCGGGCGAAGCGCTCATTACGGGATTTCTGTAAGATCTGGGCACCACCC
CTCCAGGGCTCCGGGACGATGCTTAG

NHI 246 protein sequence:

MLSRLQPDLAGPMTKRTMQQSSQAPAEPLVADNRTLGSVHELGWANADADAFAEQ
REYLATHNGMRGLERLQPTDIEDAVRIFYRDGFVVIENALTEKQLAELKEASERVIREVL
AMDKNRQGNRGSHRYSFGSASLTGQLLHEPAWAMLVDLPTVTPITAIIFGSRDYILGA
GGDFCLPGASTYQPLHSDMNDRIEYQGKTFGSFHDPRGKLNYRDLPCPYVCCNFLTS
DFTAINGPTRQIPGTQHSQQRIKLAQEPEWMKLSTVCPAPAGSVLIRDTRAHWGGTP
NLSDQVRAIPNTEYHAPWYREPMRKSMPREIYQSLSEHAQYIARYVVAEAGEALITGFR
EDLGTTTPGLRDDA

Codon-optimized NHI 247 sequence:

ATGCATGCATCCCGAGCAACCGACCCTATTTTTACAGTACCCGATCTTCTTAGTCCT
GAAGAATGTGCAGCGTTTATCCGGAGAGCGAGTGGTACCGGCTTCGGTGAGGCCC
CCCTTACCGTTGGGGTTAATCGGTTTATGATGGAGAAATCCGTGCGTAATAATGAGC
GGGTGATCGAAGATGATCCCGCCTTAGCTGCACGGCTATGGAAGCGTCTTGAGCCT
CACGTCCCCGCGGTGTGGGGGTCAATGTGTGCGATTGGTCTGAACGAACGCTTCC
GTTACTATCGGTATACTCCTGGTCAGTATTTCCGCTGGCACCGAGATGGTAGCTTTG
TCCGTAGTCCAACCGAAAGATCTCTGTTACCGTTATATATTATTTGAACGACGATTT
TCTCGGTGGTACCACTGACTTTTACGGGAGAAGGCGAACTCCGTATCACACCGCGG
CGTGGGATGGCATTAAATATTTGCACATCCGATATATCATCAGGGGGCCGAGGTTGTG
AGAGGTACGAAGTATGTGTTGAGGTCCGATGTTATGTACACCCGTTTGTAG

NHI 247 protein sequence:

MHASRATDPIFTVPDLLSPEECAAFIRRASGTGFGEAPLTVGVNRFMMEKSVRNNERVI
EDDPALAARLWKRLPHVPAVWGSMAIGLNERFRYYRYTPGQYFRWHRDGSFVRSP
TERSLFTVIYYLNDDFLGGTTDFHGEGERITPRRGMALIFAHPIYHQGAEVVRGTTYVL
RSDVMYTRL

Codon-optimized NHI 248 sequence:

ATGTCGGACGCCCCCTTTGTGCGATCTCAAACGAACCGTATATGCTTTCCCCAGAGCAA
ATTACTTCCTTTGAGCAGCAGGGTTTCCTGATTCTGAGAGACTTTCTGGCCGACACA
TCATCTGTGCAAACACTGCGGCAATGGACCCAGCAGGTACATGACTGGCCTCTGGT
GAAAGGTAAATGGATGCCTTATCAGGAGAAAATCAGTGATGGTAGAATGGTTCTTAC
CCGCACGGAGAATTATTCACCATTCATCCCGGTTTTAATGCTCTGTTTCAGAGGTGA
CCGTTTAATGGGCGTTTTAAAGCAGTTATCAGGCGAAGAAATGATCCTGTTTAAAGA
AAAAATCAATTATAAACTCCCGAAAGCAGGCGGTTTTCGATGCACACCAGGATGCGC
CTGCCTATACGCATGCTGGTGCTCTTAAACACCTTACAGTAAACATTGCAGTAGACA
AAGCCACACTGGAAAATGGTTGTCTGGAAGTCGTCCCGGGAAGTCATCGCATGAA
CATCCCAGTGGGTAGTGATAATTGTATCCCAAAGGACTGGGAAGATGCTAACGAGT
GGATACTGGTGCCGTTGAAACCAGGGGATGTTCTGATTTTTTGGCAGTTATCTCGCA
CACCGTTCGGGGCCAAATTCTTCGAGCAACCCGAGAGCAGCAATATACGCAACCTT
TAATGCCGTCTCCGATGGTGGCGATCGTTTCGCTGAATATTACATAAACCGCCGCGC
AGAATGGCCGCCCATGCATGAACGCGAGGAAGGCAAAGATTACAGCCTGGGAGCC
CTGCGTTACGGTTTTTGGCAGCCCTATGACGGGAGCGACCCAGCACAGCCGCATGC
AAACGGAGTTGTTTGGTGCGACTGTCAGCCAGGCGGGTGTTAGCGCGAAAATTGC
CTAA

NHI 248 protein sequence:

MSDAPLSISNEPYMLSPEQITSFEQQGFLILRDFLADTSSVQTLRQWTQQVHDWPLVK
GKWMPYQEKISDGRMVLTRTENYSPFHPGFNALFRGDRLMGVLKQLSGEEMILFKEKI
NYKLPAKGGFDAHQDAPAYTHAGALKHLTVNIAVDKATLENGCLEVVPVGSHRMNIPVG
SDNCIPKDWEDANEWILVPLKPGDVLIFGSYLAHRSGPNSSSNPRAAIYATFNAVSDGG

DRFAEYYINRRAEWPPMHEREEGKDYSLGALRYGFGSPMTGATQHSRMQTELFGATV
SQAGVSAKIA

Codon-optimized NHI 249 sequence:

ATGACGGGCAAAGTGAGCCTTAACACCGATATTGGAGTTTTCCGTGCCAATCAGCT
CGATGAACTGGATGCTTTTTTCCGCGCGCATGGGTTTGCCATACTGAGGGGATTATA
CGATCCTGCCGACTTAGAAGCCTTAACCAAAGACTGCGTGGCTGCGCAGACCGGG
GTTATCGAAGGTTCTCTGGATGAACGCTACGGCAATTCTGTTCTGCTTGATGATGCT
GTTGATGGCAAACTCGGTTTACTAACTACGTGCAGTATATTACGGAAATTTCTTCGA
AAACTCGTAACGCTATCGTCCATCCTGCGATAGTGGATTTAATGGCACGGTGGGTTC
CAGAAGGATATCTGTTGGAGCATAGTCGCTTTGGTGTGTGTATCAAGATGCCAGAG
GGGGTCGTAATAGCGGTTACCGCAGAATCGGATGGCACAGTGACTGGCAGAGCGG
TCCGCATCGGGATGTGTGGCCTTCGGTCGCGTTTACTATTAATATTGATGCGACATC
GCCCCGAGAACGGTTTCCTTCGCGTTGTTCTGGCTCGCATAAATGGGCTACCCCCG
CACCGTTTAAAAATGTTAATAACGTTGCCGTCCCAGCAGGAGCCCCGCCGACCGGC
GGCTACACAGACGAAGCACCGCCGTTTCAAATGCCGTTAGCATTCCAGAAAGCTCC
GGGAGAAATTGGTATATATTGTGATGCCGGCGATGTTCTCTTCCATGACGCATACCT
GTGGCACTCCGCCGCGACTGCGACGAACGACCGCGCCATCCGTCGTCATGTTTCG
CGGTAGTTGGTACTCTGGTGTACAAGATGCCGTTAACGATGATTTTATCGAAGATTTC
GTAAAAAATGCGGCACGATGA

NHI 249 protein sequence:

MTGKVS LNTDIGVFRANQLDELDAFFRAHGFALIRGLYDPADLEALTKDCVAAQTGVIE
GSLDERYGNSVLLDDAVDGKTRFTNYVQYITEISSKTRNAIVHPAIVDLMARWVPEGYL
LEHSRFGVVYQDARGGRNSGYRRIGWHSWQSGPHRDVWPSVAFTINIDATSPENG
FLRVVPGSHKWATPAPFKNVNNVAVPAGARPTGGYTDEAPPFEMPLAFQKAPGEIGIY
CDAGDVLFDAYLWHSAAATATNDRAIRRHVRGSWYSGVQDAVNDDFIEDFVKNAAR

Codon-optimized NHI 250 sequence:

ATGAAAGTTCTTTACAAGGATTTTAACCAGGAAGCTTTCAGTTTCCAGAATGACCCG
GTTCTTGTTCTTGAGGAGTTCTGGAGCCCGGAAGACCAGGCGTTTTTTTTTGGATGC
AATGAAAAAGACTGCGTGGAAGAACTCTTAAAGATATGCCGGCCGTTAGCCACGCCT
TCCCGAACAGCGGTAATTGGCATCGGGGTGACGTGGGTGAGAGAGAACGCGAGG
CGTTTCTTAGTAAAATAACCCTGGACTGCATCGCCGACCATATTGATTCTTTTCCTAA
CATTAAACGTCGCCATCTGAATCTTAATTATTATTTCGTACGGCGTAGGGGACTGCCTA
CCTACTCATGACGATACGGATGAAGCCTACGTACCAAGTAACTTGCCTCGCCCACC
ATTGCGGCGTCTCGCCATGGTAGCATATTTTCACAACGAATGGGAGCCTTCATGGG
GAGGGGAGCTAATCGTTTATGGGGAACGCAAAGATAAAACGGGAAAGAAGACATTA
AATATCGTGGGTTGTGTAGCTCCAAAACACGCTCTCTCGCCATGTTTACCGTACCC
AGGCATCATCGCGTGTGTGCGCATAGATCCGATCGCTGGCGATAATAGACGCAAAAC
GATTGTCACGTGGTTCATGACGGAACATTGA

NHI 250 protein sequence:

MKVLYKDFNQEAQSFQNDPVLVLEEFWSPEDQAFFLDAMKKTAWKTLKDMPAVSHAF
PNSGNWHRGQDVGREREAFSLKITLDCIADHIDSFPNIKRRHLNLNYYSYGVGDCLPT
HDDTDEAYVPSNLPRLRLAMVAYFHNEWPSWGGELIVYGERKDKTGKKTLNIVG
CVAPKPRSLAMFTVPRHHRVCRIDPIAGDNRRTIVTWFMTEH

Codon-optimized NHI 251 sequence:

ATGAGTGCGGAAGCCAGAGGTTTAGTCCCGGAAATAAGGCGGGGTAAAGATCTATAA
AGATGTATATGCAAAACGGAGCCCGGGGCGTCCTGCGTTGGGCGAAGCACGGCTG
GAACGTGCCCCGCGCCGTGGATGGTGTACTCGAGTTTGACGGTAGTGGTGCACGTG
ATCGCGCATTGCGGATGGAGTATTTCTGCTAGAAATTCCTTCCGGTCTGGATGTAA
GCGCGGGCGACGCTTTTGCACGTCAAGTCTATGAAGGTCCTGCCAAGGCCCTTAT
GGCCGCTTCCGCGATATCGGGTCAGACAGGTTTGGTGACCCGCTGCTTGGTTTTTC
ATCAGCGTATTAATCAAATAGAACAATTCTTGCTTGAAAGACGCTTCTGGGCAACGG
CGTACCCGCCCCGAAATAGCCGCACTGGGTGAATCACTGACGAGGCTGTCACGTGA
AGTGCTGTGTTCAAGTCCTGAGTGCTGTGGGAATTCCCGAACAGGACCGTCGTCGT
GCAACCGGTGGATGTTCCGAATGTGCCGGCTCCTATCACTTAACATTTAACCATTATA
GACCGGCCAGGCAGATATTGGCCTCTCCAGCCACAAAGATGATGGATTCTTAAC
ATCCTGCGTACAACCGCCCCGGGGCTTGAAGTGTCCCGCGAGGACCATTTGGGAAA
CCGTTCCGGCCGATCCGGATTGCTTTATTGTTAATTTTGGACTCTCTATGGAAATCTT
GACAGCCGGCTCCCGCATGCCAGTTGCCGCTATTATGCATCGAGTAGCCCGTCAGC
AGGACGATAGATCATCATTCCGGCATTTCATCGTCCGGTTGTCTCCCGGGTGAAG
ATGAAGGAATATATCGGTACGCTACAGGATCCGGGCTTGAACGGGTATGCGGTTCA
CGCGAATTAATTGACGAAAACGATTACGAAATTTACGCCGGCACAGACGCGCCGGA
TGGTCCTGACACTGCTACTGCCCCAGGTTCTCCGATGAGCATCCACCGTAAAGG
GCGCGGGTCGATAA

NHI 251 protein sequence:

MSAEARGLVPEIRRGKIYKDVIYAKRSPGRPALGEARLERARAVDGVLEFDGSGARDRA
FGDGVFLLEIPSGLDVSAGDAFARQFYEGPAKAPYGRFRDIGSDRFGDPLLGFHQRIN
QIEQFLLERRFWATAYPPEIAALGESLTRLRSREVLCSVLSAVGIPEQDRRRATGGCSECA
GSYHLTFNHYRPAQADIGLSSHKDDGFLTILRTTAPGLEVSREDHWETVPADPDCFIVN
FGLSMEILTAGSRMPVAAIMHRVARQQDRSSFHGFSSSGCLPGEDEGIYRYATGSGL
ERVCGSRELIDENDYEIYAGTDAPDGPDTATAPGSSDEHPTVKGAGR

Codon-optimized NHI 252 sequence:

ATGGCGCTTTCTACAGAGAATTTATCGCAACAAATCCTTGAATTCAAAGCCGCCCTG
AAACAACAGAGTCCGGATTATAAGGCCCGGTTGAAAGTGTCACTGATGCGATGAA
AGCCGAAATTGCACGGATTAAACAGGAAGAGTCCGAGGGTTCAGCCATTCCTCAGT
TCGAATATTCGGATATTGCAGCCAGTGGCTTTAACGATGAACAACGTGCGAGAGTCC
ATCGGGCCGGTTGCTGTATCGTTTCATAATGCTTTACCTCGAGATGAAGTTAGTGCAC
ATAATGAGAATCTTTGAAATACATCATAGATAATGGTTATTATGACCACAAGAGTACC
GTAGAAGATAATTATTTTCACTGAAATCCGACAAGCCACAAATATTTGGCATTTA
CTGGTCACAGGCACAGGTCTGGGCGCGCCAGCACCAAAATATGGCCACCCTGCGT

CGGCATCTTAATCACCTCTGGCAGTGGCAGGATCCGCGTAGTGGTAAGGCATACTT
CAATCCCGATTTGGAGTCGAGTTATGCCGATCGTGTGAGACGACGAGAACCTGGAG
ATGCAACCTTAGGTCTATCTCCGCACGTAGATTCAGGCAGCATAGAGCGCTGGATC
GAGCCACACTATCGCGATGTGTATCATGAAGTATTCCATGGGGATTGGACCAAATAC
CAAGCATTTCGACGGTCGTAGTCGAGTGGATGTTGAGGAATTTCCATCTCCCGCGGT
ATGCTCGGTCTTTAGGACCTTTCAGGGATGGGTGCGGTTAACGCAACAAGGCAAAG
GTGATGGCACGCTACAGACCGTTCCGTCTACTCTGGCGATGCCTTTCATGTTACTG
CGCGCTATTCAGGACGACGTGGAAGAAGAAGATCTGTGTGGTGCCGCACCTGGCC
GTGCCTTAAGTGTGTTACAAGGAATGGCATCCCTTACTGCTGGAAGGCCTTGTCAGTA
TACCGAAAATGCAACCAGGGGACACAGTTTGGTGGCATCCGGACACGATTCACGC
CGTAGAAGATAAGCACAAATGGTGATGGATACTCTAACGTACTTTTTATCGGGGCCGC
ACCTGATTGCGAAAAGAATCGCGCGTTTCTGGCTAAACAGCGACCAACATTCTTGA
ACGGGGACTCTTGTCCAGATTTTTCGGGCCGAAAATCATGAACGCAACTATGAAGGC
CGCGCGACCGAGGCCGACCTCAGTCCCCTGGGTAGACAGCAAATGGGTTTTGAAT
AG

NHI 252 protein sequence:

MALSTENLSQQILEFKAALKQQSPDYKARFESVTDAMKAEIARIKQEESEGSaipQFEY
SDIAASGFNDEQRARVHRAGCCIVHNALPRDEVSAHNENLSKYIIDNGYYDHKSTVED
NYFSQLKSDKPQIFGIYWSQAQVWARQHQNMATLRRHLNHLWQWQDPRSGKAYFNP
DLESSYADRVRRREP GDATLGLSPHVDSGSIERWIEPHYRDVYHEVFHGDWTKYQAF
DGRSRVDVEEFPSPAVCSVFRTFQGWVALTQQGKGDGTLQTVPSTLAMPFMLLRaiQ
DDVEEEDLCGAAPGRALT VYKEWHPLLLLEGLVSIPKMQPGDTVWWHPDTIHAVEDKH
NGDGYSNVLFIGAAPDCEKNRAFLAKQRPTFLNGDSCPDFAAENHERNYEGRATEAD
LSPLGRQQMGFE

Codon-optimized NHI 253 sequence:

ATGTCTCCACGCAGATAGATCATTTTCGTACCCATGGCTACCTGCACCTGGAGGGT
TTCCACCCCAAACCTCGCGTGGCTCCGCTGCGCCAGAAGCTGCGTGACGAATTAA
AACGTCTCGCCGGGGCGAAAGGTGGTTTGTGCGGCTGTTCAAGCGGCTTCCTCTATT
CCAACAGATCGGTAAACTGTCGGCACTTGTTAACCTCCCCGGAGTGACGAAGCCT
TGGTGACCCCGGCTTTGCTGGACGTCATTGCAAACTGGGGCACCGGGGCCCTCC
TAGTGACGCGGCTGGCCATCCTGGAACGCAACTGCTCTTATCACCGCCCCAGCAG
GGTGATTGGACACTTCAAGGTCTTAAGTGGCACGTGGATCTGGCCGCCCGACCTC
AGGATCCTTTGCCTGGAGTTCAAGCGTTTTTCCTGATAGATGATGTCGCACCGCATG
GTGGTGCAACGTTAGCACTGGCTGGTAGCCACAGAATCGACACTCGTCGACCAGC
ATCGGATAGCCAGCCTGCGCTGCGGGAAGTCTGAAGGATCCGCTTGATCTTGAAC
GTCGTCTTGGTGAACAAGGGCTGGCCATTGTTGAGATGTGTGGGAGAGCTGGTGA
CGTTTTTTTGGATGGATATGCGTGTTTTGCATACGCCAAGCGTCAATGCCACCAAGCA
ACCTCGCATGATGGCAACAAGTAGATGCATCTTCGGAACCTAA

NHI 253 protein sequence:

MSPTQIDHFRTHGYLHLEGFHPKPRVAPLRQKLRDELKRLAGAKGGLSAVQRLPLFQQ
IGKLSALVNLPGVHEALVTPALLDVIKLGHRAPPSAAAGHPGTQLLLSPPQQGDWTLQ
GLNWHVDLAARPQDPLPGVQAFFLIDDVAPHGGATLALAGSHRIDTRRPASDSQPALR
ELLKDPLDLERRLGEQGLAIVEMCGRAGDVFLMDMRVLHTPSVNA TKQPRMMATTRCI
FGT

Codon-optimized NHI 254 sequence:

ATGACGGTGAGCCCAGAAGCATGGGCCGGTCTGGCGACTTTATCTACTGCGGTGG
AAACCCTTGAACGTATAGTCAGCAGTGCAGATGTGCATATGGATCGTCCACTGCAAG
TTATGGGCCAAGACGCTCTGCTCTTTGCCGCGAGCATGTATGATGAAGACCTGGCA
CTGGAAGTTCTGGCAGCTCGTGCTAGAATACCGGTTGATGTCAATGCCATAGACAAT
CATGGTTACACTGCGTTGCATTATGCCGTTGATGCCGATATGCACGCTTTGGCCCAG
ACACTGCTGGCGACTGAAGCGATTTGCGTGCGTTTACAGACGGAAGACCTCAGTG
TCGTGGGCCACATCCAGTCGGGCGGCCGTACCCCTCTGCATCTGGCAGTATTGAG
AGGTAGCATGGATTTGATGCAGCTTTTACTGGAAGCGGACCCTCTGCTTGCAACTG
TGGCGGATCTGGACGGCCATTTACCGGTGCATCTGGCTCAGTTACACGGCGGGAG
CATGGATCTTATTGGATGCCTACAGGCATTTTCATGCGGCCACTCTCTATGATGTCGC
TTCAC TTCCGGAGAGAAAGTTGGCGACTCAGGCTATTGCTGCCGCCCGCTACCAG
GCGAGCCTGTCCGTACCCGATGCGGTGGCGACTCCTCATATATTTCCAGGTATCTG
GACGCAAGCAGAATGTGAAAGAGTCTTAGGTCAATTGGAAGCGACTACACACGTTA
CCGGATGGCATAAGACACGCCACACCTCATATCCGACAACAGATCTTCCATCTTACT
GCTTACCGTTGGGTGAACACTATTGGGTTCAAGACACGCTCTCTGCGAGATTATTC
CTTCTATTCTGAGCCGTTTTCAACTTCCTGCTTCCACGCAACTGTCATTTCCGGGATC
TGTTTTATGTCAAATACGAAGCAGCCCAAGACGCCCGAGCGCGATCTAGCTCTGCAC
TGTGATGGGTCTGTTCTGTCTTTAATGTACTGCTCAACAAACGGACTGATTTTCGTA
GGTGGAGGTACTTTTTTCGCGCCCACACAGACAACGGTTCATATTGAACAGGGTGA
TGTAGTCGTTCACTCGGGCCGGGTAGTTCACGGTGCGGCACCCGTGACGGAAGGT
AAGCGTTTAATTCTAGTCGCGTTTCTGAATGTCCGCCACCGGCATGCGCGCCTTG
A

NHI 254 protein sequence:

MTVSPEAWAGLATLSTAVETLERIVSSADVHMDRPLQVMGQDALLFAASMYDEDLALE
VLAARARIPVDVNAIDNHGYTALHYAVDADMHALAQTL LATEAICVRLQTEDLSVVGHIQ
SGGRTPHLAVLRGSMDLMQLLLEADPLLATVADLDGHLVPVHLAQLHGGSM DLIGCLQ
AFHAATLYDVASLPERKLATQAIAAARYQASLSVPDAVATPHIFPGIWTQAECERVLGQL
EATTHVTGWHKTRHTSYPTTDLPSYCLPLGEHYWVQDTLSARLFPSILSRFQLPASTQL
SFRDLFYVKYEAAQDAQRD LALHCDGSVLSFNVLLNKRTDFVGGGTFFAPTQTTVHIE
QGDVVVHSGRVVHGAAPVTEGKRLILVAFLNVRPPACAP

Codon-optimized NHI 255 sequence:

ATGCCAGTAGTCATTCCGACACCGGAATTACTGGCACAATTTAATCGTGATGGATTTT
TGGTTTTACCGGATGTTCTTTCTCCGGCTGAGGTGACTACTCTTCGCAACGGCCTG
GAACGGGTCTTTAACCAGTTTAGTCCAGAAGCCGATATATACCATATGCAGGACATT

GGCGTCCAAAAATGTTCTGAACATGGCGAGGAATTCGAACAACCTCATTGACCATCCA
GGAATCGCCGATTTCTGCTGAGGCCGTTCTCGGGAAAGATTGCCACATGATCGCAGA
AACTGGTCTCCGCACGTCACCGGGAAAGACTATAACCTTCTGGCATTTAGACGACA
CTGTACGGTTTCTTTAGCAGATGGTCAGAACTCGATCCGGCGATTGTTATGCCAA
CATTTGTAATAAATATGAATTACTATCTTTGTGATGTAGATGAGGAACTAGGACCTACA
CAGTTTATACCAGGATCACACCGCGCAGGTCGATCGATGCGCCCGGAAGATAATGA
TGCGTCGGGGAAACCCCACTTGGGAAGGGCGGTCGATGGTGTCTTCGACTGGAAA
GGCAGGCACTCTCGTTCTGTGGAATGACCAAGTTTGGCACCGCGGTGGACCAAAT
GTCAGCAACGGGCGTATTCGCTGGGTTATTCAAACACCGTTTCGCACAGAGGTGGG
TTAGCCTGAGATACTGGCCACATGTTAATTATCATATGCCAGAAGAAGTCATCGCACG
GGCGAATCCCCGACGTAAACGTCTCTTAGGTTTCCATCCGATAGGGGCATATGGTTA
A

NHI 255 protein sequence:

MPVVIPTPELLAQFNRDGFLVLPDVLSPA EVTTLRNGLERVFNQFSPEADIYHMQDIWR
PKMFEHGEEFEQLIDHPGIADFAEAVLGKDCHMIAETGLRTSPGKTITFWHLDDTVRFP
LADGQKLDPAIVMPTFVINMNYLDCVDEELGPTQFIPGSHRAGRSMRPEDNDASGNP
TWEGRSMVSSTGKAGTLVLWNDQVWHRGGPNVSNGRIRWVIQTPFAQRWVSLRYW
PHVNYHMPEEVIARANPRRKRL LGFHPIGAYG

Codon-optimized NHI 256 sequence:

ATGCGTTACTTTAAAAATGAGCAGGATTTTACTTTCTGAGTAGTTTCAAAGATAATTA
TAAGGTGATTACAGAGGAACTGATCAACTTTTTGAACAATCCCAATGTGGACTTTCA
AAAATTTGTTT CAGACAAGTTCTGCGCAGAATTTCGATTAACAAAGTTGATTTTTGGAAA
ATCATCGCTTTATATATTCATCTGAAAACCCCTCTGGAAATATTCCAGGAGTACAGCG
ACTTTTATCAGGTGAATATCGAGCAGGTTAAGCAAGCCTATGACTATATTTACAGCCA
GTTTCCGCAGACGTGGAAGATCGTTTCGCGAACTCACAGCGTCGCAGGACAATGGG
ATCATAAATGTCTTTTTTTCATACTTTGAGCCCGGCGCAAACTCAACTTACACGTCA
ACGATGATCCTTACATGTACCGTGCTCATTTAGGACTGATAGTCCCGGAAGGCAACA
TTGGCTTTAAAGTCTGTGACGACTTAGTAAATGGCAGGAAGGCGAGGTGCTTGTG
TTTACGCCTACCAACCCCCACACAGCCTGGAACCTGACAAAACACCCGAGAGTAAT
TATGATTATAGATTTTTTTAAACCCGATGCTGATAGGGCCGAAATGAAACAGTTGGAA
CGGCAACAGTTCGAAAAAATGATGCTGATCAATCCATGGTCATTTGGGATGTCTGGT
GGCTACTCCGATCTGGATCCGGAAACAATAAAAAAATATGCCGTCTTAGATATCTAA

NHI 256 protein sequence:

MRYFKNEQDFTFLSSFKDNYKVITEELINFLNNPNVDFQKFVQTSSAQNSINKVDFWKII
ALYIHLKTPLEIFQEYSDFYQVNIEQVKQAYDYIYSQFPQTWKIVRELTA SQDNGIINVFF
SYFEPGAKLNLHVND DPYMYRAHLGLIVPEGNIGFKVCDDLKWKQEGEVLVFTPTNPH
TAWNLTKHPRVIMIIDFFKPDADRAEMKQLERQQFEKMMLINPWSFGMSGGYSDDLPE
TIKKYAVLDI

Codon-optimized NHI 257 sequence:

ATGCCTCCTACTCAAAAATTCGAGGAACGTATTGTACGAGTCGAAAAACCATCAGCC
CATTTTGCCCTGTTGCGTAATGAGAAGGGTGATTTTCTGGGGGTATCAGAGGGGGA
GACGGCGGTATTTGATCATGCTGATGATAAAGCTATATGGAAAGAGGAAGGTGGCAC
CTATCGGCACGTGGTGAGTGATTTGACTCTCGATGTCTCGGCCGCTAATGGTGAGC
ATCTCGCCCTGAACGGTAAAAGTCTGGGCGAAGACGGTTCTGAATCCTCAGTACCG
GGTCGTTTTTCAGCCTGGGCATGGCCCAGCGCATTTGCCGTCCGAATACTTACAGCA
GATCCGGGAGAAATGGTTGGGTATGCCTTCCTTCCATTCTTTCTCCTCACGCCATTGA
GGAActACAACGCGTAAGCTGCACGGGAAAATGGAACCATGAGGAACTGGACCGT
TCGTTGCCTACCCTCACTCAATCGGTTGAGGTTTCACGGGCAGCCACAGAGCCCG
TATCCCTCTGGGTGATGCGCGAGTACATGCAATGCCGAGAGATTCGGCTTGACAT
CGACCGGGTTTTGCAGTCGTAGCTCCGGATGATGGTGAACGTCAGGTTGGCGGAT
GGCATAGCGATTACCCCTACCTGTGGGGGATTGCTCGAAATAGTAGTGATGGCAAC
CGTATCGTGCCACATAATGCCTTAAATCTGGTACTCGGAGTTCAACGTAACCTGTGC
GTGACCGAGTTTAAAAGTGAAAATGGTGCCACGTGCTTCAAGCTGGGCTCACACAC
ATTTGGACAGGGTCCGCCACCGGAGTGGGGTTTCGGGCAATGCGTTTCGTGAGGA
GGGTGCCAGGGAAGCGAAGGGTTTGCCGTACACGGGTTCTGAAGCGGACGTTGT
GGAAGCCCCGGCAGGGAGTTATGTTATATATGATGCCCGCACCTGGCATCGCGCGG
GTGTAAATCGCACCGATAAGAAACGGGCTGCCATGCTGCAGAGCGTTGTGCCCATG
TACATTATGCCGTTTATGGAGACTTCACGCCCGTATAAAGAGTTTTTGGCCTCGCCA
CTAGCATCTCAACTTACCGAAAGGGAACATATCGAGCTAGAGTCACTGCTGGTCTCT
CGTATTGATGGCCCGCAGGGCAGATTGGCCATTACCATGGACGAGGAGTTGTGCG
GCTAA

NHI 257 protein sequence:

MPPTQKFEERIVRVEKPSAHFALLRNEKGDFLGVSEGETAVFDHADDKAIWKEEGGT
YRHVSDLTLDVSAANGEHLALNGKSLGEDGSESSVPGRFQPGHGPALPSEYLQQIR
ENGWVCLPSILSPHAIEELQRVSCTGKWNHEELDRSLPTLTQSVEVSRAATEPVSLWV
MREYMQCREIRLAHRPGFAVVAPDDGERQVGGWHSYDYPYLWGIARNSSDGNRIVPH
NALNLVLGVQRNLCVTEFKSENGATCFKLGSHTFGQGPPPEWWSGNAFREEGAREAK
GLPYTGSEADVVEAPAGSYVIYDARTWHRAGVNRTDKKRAAMLQSVVPMYIMPFMET
SRPYKEFLASPLASQLTEREHIELESLLVSRIDGPQGRLAITMDEELSR

Codon-optimized NHI 258 sequence:

ATGCCGCATTACATTGATACTACCGCGAAAACCGGTGACTGGCGGGATGCTCTTTAC
GAGGATGGCTTTGTTGTTGTCAAGGGCGTGCTGAGTCAGGATAAGGCCTCTTCATA
TGTTGACCGTATGTTCCAGTGGCTGGAAAGTTTTCCATTTGGTTTTAAACGGGACGA
TCCTTCGACGTGGAATGCTAACCATCTCCCAGCTCATATGAAAGGTGGAATGTTCCA
CGGCTATGCCGTTTACGCATGAAAAAGTCATGTGGGATGCACGCTGCGAGCCTAAGC
TTATTGAGGCGTTTTCTAAATTATGGGGTACTGATAAACTACTGGTTTCCTTCGATGG
AATGAATCTGACAATACCTGCCACTGATCGTCCTGCGTCTGAACCCTGGCCCCATG
TCGATCAGAGTCCACTGCGTAAAGGAATGCAGTGCGTACAGGGCATCCTTAATTTTC
GCACCCAACGGCCCTAAAGACGGTGGTTTGATCGTTGTGAAAGGTAGTTCCAAACT
GGAAGAACTTTTTCTTTGAGGCCACAGAGATGTGCAGGGGCGTGAAACTTGGGGA

CCCGCAGATTGGTTTGGCTTCCAGCAGGACGAAGTTGGATGGTTTCTGGACAGGG
GTTGTGAGGTCTTAAAGGTATGTGCGGATCCGGGCGATCTTATTTTATGGGACAGTC
GCACCGTACATTGGAACGTTATGCCGGAATCAGATGTTACACGAGCTGCGATGTATA
TTTGTTATACACCCGCGAGCTTTGCGTCAGCGGAGGATCTGGAAATCAAATCAGCA
CTCTTTAAACAGCGTTGCGGGACTGTCACCATACACCCCCGCTTTCCTAA

NHI 258 protein sequence:

MPHYIDTTAKTGDWRDALYEDGFVVVKGVLSQDKASSYVDRMFQWLESFPFGFKRDD
PSTWNANHLPAHMKGGMFHGYAVQHEKVMWDARCEPKLIEAFSKLWGTDKLLVSFD
GMNLTIPATDRPASEPWPVHDQSPLRKGMQCVQGILNFAPNGPKDGGLIVVKGSSKLE
ELFFEHRDVQGRETWGPADWFGFQQDEVGWFLDRGCEVLKVCADPGDLILWDSRT
VHWNVMPESDVTRAAMYICYTPASFASAEDLEIKSALFKQRCGTVTIHPRFP

Codon-optimized NHI 259 sequence:

ATGACAAATGTTGGTCGCGTGACGGCACTGCCAGTAGTTGACTTACGGGCGGACC
CTGCAGCGCTTAGAGAGCTGTAAAGAGAAGCGGCTCACCGTGTAGGCTTTTTTTTAT
CTTACTGGGCATGGTGTGCCGGGTGAACTGGTGGAGAAAGTGCTGGGAGCAGCA
CGGTCTCTGTTTGGTTTGCCTCAGGCCGATAAAGATGCCGTTGCTATGGTACGTTCT
CCGCATTTTCGCGGCTATACGCGACTGGGTGGAGAGATTACCAGAGGGCGCCACTG
ATTGGCGCGAGCAGATTGATATTGGACCGGAACGTCCCCCGGTCTGGTGGGCCGGG
AAAACCTGGATATCTTTGGCTCCAGGGTCCGAACCAAGTGGCCTCCAGCATTGCCGG
AACTGCCGGGTATTATCGCTGAATGGGAAGCGGCGTTATCTGGTGTGCGGAGAGAA
CTGCTGCGTCACTGGGCGGCCAGTTTAGGCTCTCCGCCAGACGTCTTCGACCCCG
CGTTTGCAGAAACCCCCGCGACATTGATTAAAGTTGTAAGATATCCAGCAAGAGCC
GATAGCCCGCAGGGCGTAGGTGCGCATCGTGATTCCGGAGTGTTAACCTTATTACT
GGCAGAGCCGGGTTCTCGTGGCCTGCAGGTTCTGCTCTCCACGTGCCGGGCACGA
TGGATGGATAGATGCACCGCCTGTTGATGGGGCTTTCATAGTAAATATAGGCGAGCT
TCTTGAAGTCGCAACCAGGGGATACCTTCGGGCAACCGAACCGCGTGAACCTC
GGTGGCGCAGAGAGAATCAGCGTCCCGTTTTTCTTCAATCCGCGGTTGGATGCGC
AGATTCCGGTACTGTCGCTCCCGGCGGACCTGGCAGCGCGTGCCGGTAATGGCTG
GACGCCGGCAAGAGACCCATCAGACCCGATTTTCGCGGTGTATGGACGTAATGCAT
GGAAAAGCAGATTACGTGCACATCCGGACGTAGCTGCTGCGCACGGTTACTCTTAA

NHI 259 protein sequence:

MTNVGRVTALPVVDLRADPAALRELLREAAHRVGFFYLTGHGVPGELVEKVLGAARSL
FGLPQADKDAVAMVRSPHFRGYTRLGGEITRGATDWREQIDIGPERPPVGGPGKPGY
LWLQGPNQWPPALPELPGIIAEWEAALSGVARELLRHWAAASLGSPPDVFDPAFAETPA
TLIKVVRYPARADSPQGVGAHRDSGVLTLLEAPGSRGLQVRSPRAGHDGWIDAPPVD
GAFIVNIGELLE VATRGYLRATEHRVNLGGAERISVPFFFNPRLDAQIPVLSLPADLAARA
NGWTPARDPSDPIFAVYGRNAWKSRLRAHPDVAAAHGYS

Codon-optimized NHI 260 sequence:

ATGAATTTGTCTATAATGATCATAATTGGCCTCATCGTTTACAGCATTGCCGCGATGA
CCTATGTCTATCGCTGGCGTGGGAAAGCACGCTACGACAGCTTATCCCAATACTTAC
GCAAATCTTGGCCAATATTTGCCCCATTCAATTGCGTGCTATATATGACGACCCGGTC
CTTTGCCAAAAAACCGATCCTTGATGCGGATTTTCTGGAGAATATCGAAGTTTTGCG
CGCAAACCTGGACAATTATTCGCGACGAAGCAATAGCACTAGAATCCTCAGGTGTATT
TGAAGTGATAAAAACCCCGGGTGCGGACGGGTATTATGATGTAGGATTCCGCGACCT
TCTATAAGCGCGGTTGGAGCAAGTTTTATCTTAAATGGTATGGGACAACCTCATGTCTC
TGCCCAGCGCCTTTGTCCCAAGACGCTGGCATTACTGAACCAGGTTCCCGCTATCC
GTGGAGCCATGTTTTCCCTGCTGCCGGCGGGCTCAGAACTAAGTCTGCACGCAGA
TCCAATTGGCAGCAGCTTTAGGTACCACCTTGGGCTGCTCACGCCAAATGCTGAGA
ATTGTCAAATTAACATAGACGGCCAGACGAGAACATGGTTTGATGGCAAAGACTTTG
TGTTGACGAGACGTATCCGCATTTTGCGTACAATACTGCAAATTCGGCCCCGTCTGA
TTCTTATGTGTGACGTGGATCGCCCAATGTCTCTGTTTGGACGAATTTTCAATTCTG
CCTATAGGATCCTAGTTAAGGGTACTGTTGTTCCCTAATATGCCAGAAGATAAACGTGG
AGTATATAGTGCGATTTTTAAATTCTTTGCTCCTTTTCGTCAGTACTCAATACAATTTA
GGGAAAAACATTTTAAACATATAAGATACTGAAATTTATATTAAATTTGACGCTGCTTA
GCCTAATTTTTATGCTTCTGTACGGGGTCGTTTATTTGTTTGAGATGCTTTTTTTAATG
AATTAG

NHI 260 protein sequence:

MNLSIMIIIGLIVYSIAAMTYVYRWRGKARYDSLQYLKSWPIFAPFNCVLYMTTRSF
AKPILDADFLNIEVLRANWTIIRDEAIALESSGVFEVIKTPGADGYDVGFRTFYKRGWS
KFYLKWYGTTTHVSAQRLCPKTLALLNQVPAIRGAMFSLLPAGSEL SLHADPIGSSFRYH
LGLLPNAENCQINIDGQTRTWFDGKDFVFEDETYPHFAYNTANSARLILMCDVDRPMSL
FGRIFNSAYRILVKGTVPNMPEDKRGVYSAIFKFFAPFRQYSIQFREKHFKEYKILKFI
LNLTL LSLIFMLLYGVVYLFEMFLMN

Codon-optimized NHI 261 sequence:

ATGGAAGGCCAGTACCCGGGAGGTAGCGCTCCTCGTCGGCGTCTGCTGAATCAAG
AGGAATTGGCTATTACCACTCGGTTGGGTAGTGCTGTGCGCCAGATGAATCGTAGT
GGCAACTTCGCATGGGGGGGTGTTTTAAGTTGCAACCTTCGAATTTATTATGAACGG
TTGGGAACTGATGAGGCTAAAGGTCAGCTTAACTGACAACACTGCCTTTTCGACGA
AGAAGGTGCGAGGGGAAATATATCTGGCAGGTACTCCGTCACCGTTTGGGCGAGGC
AAACAGACCGTATATGATGAAGAGTACCGCCAGGCTAGAGAAATCAAAGTTCGCGCAT
TTTGCGCTGTCTCCAGACCCTTTCCTGCAGTCCGGTCTGGCAGGACTGTTATCGCG
CAAACCTGGATTATGACTCAGCTCTGATTTTCCGCTCTGAACAAATTAAACGCCTATGGT
AAAGGCGGTTTTCTTTAAAGAACATCAGGATACTAGCCAGGGTGTTGGCCATATTGGC
ACGCTTATTCTGTGTTTACCCTCACCATTAAAGGTGGCGATCTCCTTGTCGCCCAT
GGAGGACAGACCACAACCTTCGACTGGTCAGATCAAGTATGTGATGGAGAAATAGC
ATGGGGTTTCCTGTACTCAGATTGTAAGCACGAGGTACTGCCTGTGGAAGATGGGT
TTCGTATTACCCTTCAGTATGATGTATTCGTCAGTGATTGTAGCAGCGATTTCAGACTC
CGATAGTGATAGCGATTTCAGACTGCGCCTATATGTATGATACGCGTTTGAAAACGGTA
AGCTCAGCATTTTCATGAAGTGATCCATGGGCCATTTCTTCCGGAAGGCGGAGTTCT

GGCCTTCGGTCTGCAGTATGAGTATCCTATCGAAGAAAGGTATAAAAACACTACCTT
AGGTAATTTGGAGTTTAGGTTGAAAGATATTGACGCCGTCTTTATGAAATGCTTGAAG
AGCACCGGGCTGAAATGGGAATATTTTCGGTGTATTTGACACTTGGGAGCTGTTCTGA
AGACCGCCAAAGCAGGAGTTCGGATTGTTGGGATGGGTCGAGTTCGCCTGAATGG
GCCGAAGACCTTGCGAAAAATGCAAATGCTGAAACTGAACACTCTAGCGATGGAGC
CAGCACGGGTGAAGATGACACACCAACGGATTTCGGCTCAGAGTAACCAGCAGAGA
CGCAAGTCTGACCCTACCTATCGGCGCGATTATGGGTGTCTGAACAGCATCCATGG
CGTCGATGGACAGTTCCTTGAAAGCGGGTCCTTAGACGAGCTGGATTTAGAACGAA
AGAGCGAAATCGTTTGGATTACTGAACCTTATTATTATAATGTAAAAAATGATTACCAT
ACTTATGGTAATGAATACCAGAAAGAAACGATTATGCAGCGGTTGCCGTGAAGGTA
TTCTTGCCGGCGGTTGGTGACGCTATCCGCCAACCTCGTCCTACTACCGAACCCT
CAATAAACGAAAACGTACTGATTAA

NHI 261 protein sequence:

MEGQYPGGSAPRRRLNQEELAITSRLGSAVAQMNRSGNFAWGGVLSCLRIYYERL
GTDEAKGQLKLTTLPFDEEGAREIYLAGTSPSPFGRGKQTVYDEEYRQAREIKVPHFALS
PDPFLQSGLAGLLSRKLDYDSALIFRLNKLNAYGKGGFFKEHQDTSQGVGHIGTLILCL
PSPFKGGDLLVRHGGQTTTFDWSQVCDGEIAWGLYSDCKHEVLPVEDGFRITLQY
DVFVSDCSSDSDSDSDSDSDCAYMYDTRLKTVSSAFHEVIHGPFLPEGGVLAFLGLQYE
YPIEERYKNNTLGNLEFRLKDIDAVFMKCLKSTGLKWEYFGVFDTWELFEDRQSRSSD
CWDGSSSPEWAEDLAKNANAETEHSDDGASTGEDDTPTDSAQSNQRRKSDPTYR
RDLWVSNSIHGVDGQFLESGSLDELDLERKSEIVWITEPYYYNVKNDYHTYGNEYQKE
TIYAAVAVKVFLPAVGDAIRQPRPTTEPLNKRKRTD

Codon-optimized NHI 262 sequence:

ATGACATCGGACTCAGCATTGCAAGAGGGTATGATGAAAACGGTGGTTGAGAGCTT
TGAAACCGTTGCATTACGTACACACCTGGAAGCGAACAACGGTATCAAAGGCCTGG
AACTATTACAACCACATGAAGTGGACCGGGCTGTAAACTCTTCCAGAGGGATGGC
TTTGTAGTAGTAACCAACGTTCTTGACGAAGAACAGACAAGATTCTGGCTAATGGC
TGTTCCGAAGTCGCTGCTCAGATCCTGGCGCTGGACCGCGAGCGCTCTGGAAATC
GTGGTTCACATCGTTACAGTTTCGGAGGCAGTTCGCTCACTCGTTCTCAATTACATA
GACCTGAGTGGCAAATGCTGTAGAGATTGCTGTAGTGGACGAACTAGTCACGGCT
ATTTTTGGCTCTGGTGACTATTCCCTGCGCGCAGCATCAGGGGACTTTTGTCTTCC
GGGAGCAATTGGGTATCAACCACTGCATAGCGATGTGGGCGATTGGACGTCTGCAT
CTAAATCCCGCTTCAGTTCTTTTACGATCCTCGTGGTCAGCTGACCATTCGTGACC
TGCCATGTCCGTATGTTTGTGTTAACTTCCTGCCACAAGACGTGACTCGTCTTAATG
GTCCACGCGCCAAATCCCGGAACCCAGCATTGCGGTGTCCCAATACCAACACTT
GAGGACGAACCGGAATGGATGAGGCTTCAACCGTTTGCCCCGCACCGGCAGGC
GCCATTATGATCCGCGACGTTCTGGGCCTGGCATGGTGGTACGCCGAATATAAGCGA
AAAAATGCGGGCCATTCCAACTTAGAATTCTACGCACCATGGTTTCGCGAGCCTAT
AGTCCCTGGCATATCATACTCTGACCATAAAAAATTGTCTAAACGTGCCAGTTTCTG
TCGCGTTTCTGTGTGCGCGATTTCATCAGAACCGCTGAAGACCGAGGCCACCCTATG
GGCGCCCTGA

NHI 262 protein sequence:

MTSDSALQEGMMKTVVESFETVALRTHLEANNGIKGLELLQPHEVDRAVKLFQRDGFV
VVTNVLDEEQTRFLANGCSEVAAQILALDRERSGNRGRSHRYSFGGSSLTRSRLHRPE
WQMLLEIAVVDELVTAFGSGDYSLRAASGDFCLPGAIGYQPLHSDVGDWTSASKSRF
SSFHDPRGQLTIRDLPCPYVCVNFLPQDVTRLNGPTRQIPGTQHSRVPIPTLEDEPEW
MRLSTVCPAPAGAIMIRDVRAWHGGTPNISEKMRAIPNLEFYAPWFFREPIVPGISYSDH
KKLSKRAQFLSRFCVADSSEPLKTEATLWAP

Codon-optimized NHI 263 sequence:

ATGAATCTGTCTGAAGAACAGAAAAAATATTTCAAGAAACGGGCATACTACATTTAA
AAAAAGCTCTGCGTCCGAATGACGTGAGCATTGTACAACAAGCGATACTGTCTGAG
CTTGAACGGTTAAAGCTGAAAGTTGGCAGCAAGTTAAGCTCCTCCAAGATAAATGAT
CTGCCATTATTTTCAGCAGACAGGTCGGCTCGGTCAGATGGTTAAAGTGGAGAGCCA
GTTAACCACCTCTTTTTCGTCATGATGTAATTGTAGCCGCAGTTCGGAGCTTAGTCTC
CAACAACCTCTCCCGCCCTGTCAATTCACCCGCAGTTATTATTGAGCTTCCCTCACAA
AGCGGAATGGTCCTTAGCGAAGTTAAATTGGCATCTTGATATCACCGTTCCGAAGCA
AAATGTCCTGGTCGGCGTGCAGGCGTTTGTGTTAATTGACGATGTACAGACAAGAG
GGGGCGCTACCCTGGCAATAGCTGGCTCCCACCAGCTGCACTATCTGCCGCAGGC
TCAGGGTGGTAACGCACATAAATTATTGAGGGACGATCCACTTTTCACTCAGTTATAT
TCTGGGGACTCTGTTGACGCGGAAAACTGGCCAAGCCACATAATATCCATGGCGT
TGACGTTCTGGTCATTGAAATGGCAGGTAAGGCGGGCGATGTGTTCTTTATGGATAT
GCGGGTCTTACATGCACCGAGTGTGAATGCTACTAAAAAATACGGATGATGGCCA
CTAATAGGTTTATATAA

NHI 263 protein sequence:

MNLSEEQKKIFQETGILHLKKALRPNDVSIVQQAILSELERLKLKVGSKLSSSKINDLPLF
QQTGRLGQMVKVESQLTTLFRHDVIVA AVRSLVSNNSPALSIHPQLLLSFPHKAEWSLA
KLNWHLDITVPKQNVLVGVQAFVLIDDVQTRGGATLAIAGSHQLHYLPQAQGGNAHKL
LRDDPLFTQLYSGDSVDAEKLAKPHNIHGVDVLVIEMAGKAGDVFFMDMRVLHAPSVN
ATKKIRMMATNRFI

Codon-optimized NHI 264 sequence:

ATGGCTGTGTCTCCCGAAAGCATGCCGGAAAAACCCCTTTGATTTCCGCGCCCCCCC
TCCGAGTCCTATTGCGAGCGGTAGACGTAGCTGCGTGACGAATGATGACGTATTAA
GCGAATTTTATAGAGCATTACATACGAGTTCCGGATTTGATTCTGCCGGATAAAGTATT
TCCCGTCAGAAATTTATTGAAAATCCGCCGAAAATCGATTTCCAACCTGCTCTCATC
CATGGAATCAGATACTCTGCCTAAAATTCTGGACTCAATAGCAACAATCGGTTGCTTT
CAACTCGTAAACTACGGAATCCCAGGCGAAAGCATTCTGTCAGCCCTGGCTGCTGC
GGCCGGTATCTTCCAGCTGCCTCCAGAGAAACGTGCAGCAGTTACACGTTACACCG
GAAAACTGTACGGGTTTGAAGAGATACATGAAGAAGAAGAAGGAGAAATGTCCGA
AGAATTTGTTTGGTGTGCGCGGAGAAGGATTAAACTGGAGATGGAAGGGATCTGGC
CGGTTGGCTATTCAAACCTCAGTGAAAAGATGGAAAACCTTCTGTCCGATATAGAAA

AAGTTGCAGAAAAGATTTTGTGGTTATCACCGAGAGTTATCCGACGAAACCGGGC
TACGAAAATGAGATGATGCAGGGACAAGATGTAGTGGGGAGTGCATGCTACTTATAT
AAGCATTACAAAACGTGAGCGCCGATAAATGGTCGAGCTCATTAAAGATATGACGTT
ATTCGAATGTTAATTCGCGGTATTGACTACTCACATGCTTTGTGTCTGCACATTTGTG
ACGGTAGCTCAGAGTTTCATGTGTATTCTAAGAAAGGCTGGGTCTCCTTTTCGACCG
GATAAAGATGCGCTGGTGATCACGATCGGAGACCAAACACAGGCATTGTCTGGTGG
CCAGTTTAAACATGTAATCGGCAGGCCGATCTATAAAGGAGAAAAGAAGGAATATATC
TCAATGGCATTCCCTGTATACTCCTCCGTCAATCACAAGTCGGCCGGTGGATCCAGAA
AAGGGTAAAACTATTTTCGCTGAGCCAACAGGCAATTGCCGCAATTGTACTTACGCTT
GTGTATCACATTTTGGTATATGTATATAACAAATTTTAA

NHI 264 protein sequence:

MAVSPESMPEKPFDFRAPPPSPIASGRRSCVTNDDVLSEFLEHSLRVPDLILPDKVFPR
QKFIENPPKIDFQLLSSMESDTLPKILDSIATIGCFQLVNYGIPGESILSALAAAAGIFQLPP
EKRAAVTRSPKLYGFEEIHEEEEEGEMSEEFVWCRGEGLKLEMEGIWPGVYSNFSEK
MENLLSDIEKVAEKILLVITESYPTKPGYENEMMQGQDVVGSACYLYKHSQNVSADKW
SSSLRYDVIRMLIRGIDYSHALCLHICDGSSEFHVYSKKGWVSFRPDKDALTITIGDQQTQ
ALSGGQFKHVIGRPIYKGEKKEYISMAFLYTPPSITSRPVDPEKGKTISLSQQAIAAIVLTL
VYHILVYVYNKF

Codon-optimized NHI 265 sequence:

ATGCCCAAAGGACGTCCGAATACGATGAATAATTATGGTGTCTTCTCCATGAACTC
GGCCTGGATGAACCATTAATGACGCCTCTGCGCGAACGTTTCCTGCAACCACTGAT
GGCGCTGTTGTATCCAGACTGTGGGGGTGGTCGCTTGGATTTCGCACAGAGCATTT
GTAGTCAAGTATGCACCTGGCCAAGACTTGGAGCTGGGCTGCCACTACGACAATGC
CGAACTGACATTAAATGTGGCACTGGGTAAAGTATTTACCGGGGGCGCCCTATATTT
TGGCGGGCTGTTCCAAGCACCGACTGCATTAACCGAGCCTCTTGAAGTAGAGCAC
GTTGTAGGGCAGGGCGTATTGCATCGGGGGGGACAATTACATGGGGGCACGCCCGT
TAGGGACCGGCGAGCGGTGGAACCTCGTAGTGTGGTTGCGTGCGTCTGCCGTTAG
GAATTCATTGTGCCCTATGTGCTGTCGCGAACCTGATCTAGTTGATGACGAAGGATT
TGGTGATGGCTTCACTCGTGAAGAACCGGCCACAGTGGACGTGTGTGCTCTTACC
TAA

NHI 265 protein sequence:

MPKGRPNTMNNGVLLHELGLDEPLMTPLRERFLQPLMALLYPDCGGGRLD SHRAFV
VKYAPGQDLELGCHYDNAELTLNVALGKVFTGGALYFGGLFQAPTALTEPLEVEHVVG
QGVLHRGGQLHGARPLGTGERWNLVWLRASAVRNSLCPMCCREPDLDDEGFGD
GFTREEPATVDVCAALT

Codon-optimized NHI 266 sequence:

ATGGTAGAGTTAGAGCAGGAAGTGGAGAGACGCCAGAGATTGGGACAGGAATCCG
CGGCTCGCAAAGCTCTCATCGCCTCATCTTACCACCCGGCGCGCCCGGAGGTCTA
TGATTCATTGCAAGACGCTGCTCTTGCTCCCGAATTCCTGGCAGTTACGGAATATAG

TGTTTCTCCGGATGCCGATCTCAAAGGACTCCTTCAGCGCCTCGAGACTGTGTCCG
AGGAAAAACGTATTTATCGTGTACCGGTTTTTACCGCTCCATTTTGTGAGGCACTGC
TGGAAGAGTTGGAGCATTTTGAACAGTCAGATATGCCTAAAGGCCGTCCAAATACCA
TGAACAATTATGGCGTCTTACTACACGAGCTGGGTCTGGACGAACCCTTGATGACA
CCACTGCGTGAACGGTTTCTGCAGCCTTTAATGGCTCTCTTATACCCGGACTGTGG
CGGAGGTCGTCTGGATAGCCATCGCGCATTTGTAGTGAAGTATGCCCCAGGCCAG
GATCTGGAGCTTGGGTGCCACTACGATAACGCGGAACTTACCCTGAACGTAGCTCT
GGGTAAAGTTTTTACAGGTGGGGCACTGTATTTTGGCGGTTTGTTCAGGCTCCCA
CCGCTCTTACCGAGCCTCTGGAAGTCGAACATGTCGTAGGTCAAGGCGTGTTACAT
CGTGGGGGTCAGCTGCATGGTGCCCGACCGCTTGGGACAGGTGAAAGATGGAAC
CTGGTGGTTTGGCTGAGAGCCAGTGCGGTAAGAACTCACTGTGCCCGATGTGTT
GCCGAGAACCAGATCTTGTGCGACGATGAGGGTTTTGGAGATGGCTTTACTAGAGAA
GAACCAGCTACGGTTGATGTCTGTGCCCTTACATGA

NHI 266 protein sequence:

MVELEQEVERRQRLGQESAARKALIASYHPARPEVYDSLQDAALAPEFLAVTEYSVS
PDADLKGLLQRLETVSEEKRIYRVPVFTAPFCQALLEEHFEQSDMPKGRPNTMNNY
GVLLHELGLDEPLMTPLRERFLQPLMALLYPDCGGGRLD SHRAFVVKYAPGQDLELGC
HYDNAELTLNVALGKVFTGGALYFGGLFQAPTALTEPLEVEHVVGQGV LHRGGQLHGA
RPLGTGERWNLVWLRASAVRNSLCPMCCREPDLDDEGFGDGF TREEPATVDVCAL
T

Codon-optimized NHI 267 sequence:

ATGTCCCAGAGCACGCCATATAGGCAACAGGGGCTGTGTTATGATCGATACAGATCA
ACCCACCGCGCTAAGCAGATGTTGTCCGATGCCAAAGTGCGTGATGCCGTAGAGC
AATATCGTGAAGAAGGTTATGCCATCGTGCGCCAGTTTGTGCGATGGTGACGAAATGA
TACGTTTGCCTAAGGAGACAGATGCTGTATACGAAGAAGGCCTGAAACACCATGCC
ACGTATCGTCATGGTAATTTGAGCTTTCAGATATTGCCTGAAAGCGACTTCGGTAAG
CGGTATGTCCTGCAAGCATATTGGTTTTCTTGGGTTAATTCATACTTCGAACAATTCC
GTCGCAACCCGGACTATCTGCGATTGTTAGAAGGTCTGATCGGACGTGATATACGTC
AGATTGCGCAGCAACTTCACTGGAAACCGCCGGGGGCAAATCTTACGGGCTATCG
CTACCATCAAGATCTGAGGTTTCGCAATCAAGCGGCATTTGATAACGTGGCGGATG
CAACGGTTACTACAGGGTTGGCCGTTGACCGCGCGACCTTAGAAAATGGTTGTCTG
CAGGTGGTTCCGGGCAGTCATAAACTGGGGTATCTTGGCTTGAGTGATGAGGGTAC
CGGGGAACTGATGAAAGGGCTCACAGCGGAAGATGAATTACGTAAAGTTGGGATC
GATCCGGCTACTATCGTCCCGTTGGAACCTGAACCGGGTGACTTGGCTATGTGGGG
TTTGCTGACTGTACATGGATCTGCACCGAACAAAAGCCAACATGATCGAGCATTG
CGTTGTCTTCCTATGTACGCGCCGATACAACCTCAGCGGGGAGAATGGGCTTTTGA
GACGGAGTTTCGGTTCCACTGGGTGATGCGCCAGTCCTTTGTAAGTATGAAAACT
GTTTGAAGAACCAGGCCCCATGTACGACACAACCGCGTGGTGGAAGTGA

NHI 267 protein sequence:

MSQSTPYRQQGLCYDRYRSTHRAKQMLSDAKVRDAVEQYREEGYAIVRQFVDGDEMI
RLRKETDAVYEEGLKHHATYRHGNLSFQILPESDFGKRYVLQAYWFSWVNSYFEQFR
RNP DYLRLLLEGLIGRDIRQIAQQLHWKPPGANLTGYRYHQDLRFRNQAAFNDVADATV
TTGLAVDRATLENGCLQVVP GSHKLG YLGLSDEGTGELMKGLTAEDEL R KVGIDPATIV
PLELEPGDLAMWGLLTVHGSAPNKSQHDRAFALSSYVRADTTQRGEWAFRDGVS VPL
GDAPVLCKYEKLFEEPGPMYDTTAWWK

Codon-optimized NHI 268 sequence:

ATGGATTTGATTGCACGCTATAGTAATGCTGGGTATGGAGCTGTTGCCGATGGGGTC
ATGGCCTTCTTTGATAGACGCCCAGATTTACAACGCCCTGGCGTGGCGTTTGGTCC
AGCAGATGCCGCGGAACCAGCCAAGGTGTGCGACTGACATTAGCCTCGTGGCGATC
GATAGATCGGACCCGGAGGCATTGCGCCCTGGCAGAAAGTGATCGTGCGGGGCGTTT
CGGCCGCATTAGACAGATACCTCCAAGAGCGTCCACTGTTCCGACAGGTCTGCCC
GGATCAGGAATTGTTCTGCTTACCGATTTTCAACCTCCAGAGATACGCCCTGGTGA
AGGATTCCGGCAGTGGCATTGTGATTGGACAATCGGGGATGAAGCCACTGAACCT
GTCCATCGCGTTTTAGCTTGGATTCTTTACTGCAATAGCGTACCTGAAGCCGGTACC
GAGTTCCACTGGCAGCAACATCATGAAGACGCGGAACGCGGTAAGCTGGTCATATT
TCCGGCTGGCCCGTCTCACATCCATCGCGGTCGTGTTAACCATACTCATTCCAAAA
CCATTGCAACGGGTTGGATAAATGCTGGCTCGCGTCAAAGTTTTTTTGAACGTCTC
GCAGGCTTAAGTGTGGAGGCAGCGCCTGGCTGGTACTGA

NHI 268 protein sequence:

MDLIARYSNAGYGAVADGVMAFFDRRPDLQRPGVAFGPADAAEPAKVSTDISLVAIDRS
DPEAFALAEVIVRGVSAALDRYLQERPLFRQVCPDQELFVLPIFNLQRYAPGEGFRQW
HCDWTIGDEATEPVHRVLAWILYCNVPEAGTEFWQHHEDAERGKLVIFPAGPSHI
HRGRVNHTHSKTIATGWINAGSRQSFLERLAGLSVEAAPGWY

Codon-optimized NHI 269 sequence:

ATGAAATACTATCGCCAACAGTCAAATGCATTCCCGGCAAGTTACCTGAATGACCTG
TTTGGAGAAATTAAGGCGTGTCCATATTTCTGTAACATAACCTGAATCGTGATTTTG
TTGCCACTAAAGGTTTTTCCGTAGTCTTTTACGACAGTCGGGGCTCATGGAAGTTGAG
GAAAAGTTCCCGTTCTTCAAGCGCTACCTGGACGTTGCCCTTCAGTCAAACCTGCAA
TGCATTTTATCTGAATCCGCTGCTGCTGCAAAGTGGATCAAGAGTCGACCCGCATAT
AGACCGCAGTCTTCGTAGTTACTGTAAACTATTGAACCGCCGCTGTTTGTTAGCGT
GCTTTATGTACGTATCCCAGAAAACATGGAAGGTGGCGAACTTATTTTACGTTGTCAA
AACGTCAGGTAGGCCAAATCAAACCGGAAATAAATAATCTCGTCTATTTTCAAGGT
GATCTGACTCACTCAGTAAATGCGGTGAAAACACGGGTAATCGGCTTAGCCTGGT
TTGCGAACAGTACTCGCTGAGCGATTGGAAGTGAAGAGATCCCGAATTTCTAG
TAGAATCGCGCATCGTACAGCCTGCCAAAAAAAAGATGCGTTAA

NHI 269 protein sequence:

MKYYRQQSNAFPASYLNDLFGEIKACPYFVTNNLNRDFVATKGFSVVFQQSGLMEVEE
KFPFFKRYLDVALQSNCAFYLNPLLLQSGSRVDPHIDRSLRSYCKTIEPPLFVSVLYVR

IPENMEGGELILRCQKRQVGQIKPEINNLYVFQGDLTHSVNAVKTGNRLSLVCEQYSL
SDSELEEIPNFLVESRIVQPAKKKMR

Codon-optimized NHI 270 sequence:

ATGCATTTACATAGTGATCGCATCGCAGCAGCATATGATCAGCTAGACCGTCGTCAG
AAACATGCGTTTTTCGTTTCCCGAACACACCGATGGCTTCCTGCCGTTTGGATTAGA
GTATAGTCGGACTCCTGAACGTCCGGACCTCTGCGATCGCTTTTGTTACTGGGTTG
CGCGTAGAGATGCCACACCGGATATGCCCTCACAAAAGCGCTTTCTATCGAGAA
TTAGCTGCATATGAGGCTTGTATAAATGCAATTGCTCAGGACCTTCTGGATGCGGTG
TGTGAAAATCTGGGAGGAACGGCACAGCCGCCGGTACGTCACTCTAGCTATCTGCA
GTTCTGTGCCTATGAACCGCATCACTGCTCACAAGATCGTGCATATCTGCAGGATCC
CCACGAAGATGGACACCTGCTTAGTTTTATTCTGCTCCTGCCGGCGCCCGGCCTGGTC
CTGCTGCCGGATAGCTCACCTGTTAGTGCGTTGCCACGTCCAGATGAAATGATAGT
GCTTGCCGGCTCATTATTGGAAGCGCTGACTGACGGAGAAGTACCGGCGATGCAA
CACGCCGTAGAACGGCCGAGAGCACGCGTGAGACGTACATCACTTATGTACTTTGT
GAATCCAGATCTTAGCGCGGGTTACGCTAGTACAATTGTTCATAGACGGCCTCTGGA
TCTACGCGCATTAGCAGAACAGCGTCACGTAGCTTTTGGAATTCGACCTTAGGAC
GTCCGTGTGCCGCGTAA

NHI 270 protein sequence:

MHLHSDRIAAYDQLDRRQKHAFSFPEHTDGFLPFGLEYSRTPERPDLCDRFCYWVA
RRDAHGHGYALTKSAFYRELAAYEACINAIAQDLLDAVCENLGGTAQPPVRHSSYLQFCA
YEPHHCSDRAYLQDPHEDGHLLSFIRPAAPGLVLLPDSSPVLSALPRPDEMIVLAGSL
EALTDGEVPAMQHAVERPRARVRRSLMYFVNPDLASGYASTIVHRRPLDLRALAEQR
HVAFGNSTLGRPCAA

Codon-optimized NHI 271 sequence:

ATGAATCCTTTGCCTGGCGTTCCCTTAGTAGAATCTCCACTATTCCCTAAGCTGAAG
GACTCATTGGGCCTGACAGCGGAAGAAGAACGAATTGCAACATCATTACATGAAAAT
GGTTATGCCGTGCTTGATTTCCAGATGCGGATCTGCATGCTCGCATCGAACGCAT
CAAACATAATCTTGGCCCTCGGTATGGTATTGACTTTAACGATCCTCAGTCCGATAAG
ACCGTTGGGGAGCGCAGAATCCAGGATGCATGGACCTTTGATGAAGACGTGCGTG
CAATAGCTGCAAACGCTGCTGTCATGGATCTGCTCTCCAAGCTTTATGGTCGCAGA
GTGTTCCCATTTTCACTTTAACTTCCAGTTGGTACCCAGCAAGATGCACATTCA
GATTCTGTACATTTTAGCTCTCTGCCGGAACGATTATGTGTGGGGTTTGGCTCGCC
ATGGAAGACATCGGCGCCGATGCGGGTCCACTGTTCTATTACCCGGGGTCCCACC
GCTGGCCCATTATGACTAATGCGATGATTGGGCGTCGTGGCTTCGGGAGCGATCTG
CAGTCAGCACAGGATCCGTACGGTCCGGCCTGGGATGCCATGCGAGACGCCTGC
GACGCGCGCCAGGATATTTTTTTAGCGAGAAAAGGCCAGGCTCTGATTTGGTGTGC
TAATCTGCTGCATGGCGGGACGCCGCAAGCCAATCCGCACCTGACAAGATGGTCG
CAAGTTACTCACTATTATTTTGGACGACTGTATTTACTACACGCCCGCTTTTTTCGGATG
AAGCACTCGGTCAGCTGAGATTACGCGACTTAGTTGGGATCGATGATGGCCAGCCG

CGGTAAACCGCTATCTGGGGGAAGCGCTGCCAAAAACACCAGTAACACCGCGTG
CCAGCTTCCGTCGTAGGCTGATCAAACGTATACGAATTTGA

NHI 271 protein sequence:

MNPLPGVPLVESPLFPKLKDSLGLTAEERIATSLHENGYAVLDFPDADLHARIERIKHNL
GPRYGIDFNDPQSDKTVGERRIQDAWTFDEDVRAIAANAAMVMDLLSKLYGRRVFPFQT
LNFPVGTQQDAHSDSVHFSSLPERFMCGVWLAMEDIGADAGPLFYYPGSHRWPIMTN
AMIGRRGFGSDLQSAQDPYGPAWDAMRDACDARQDIFLARKGQALIWCANLLHGGTP
QANPHLTRWSQVTHYYFDDCIYYTPAFSDEALGQLRLRDLVGIDDGQPRLNRYLGEAL
PKTPVTPRASFRRLIKRIRI

Codon-optimized NHI 272 sequence:

ATGCAGCAGCAGGCTTCATCTGCACCAGCGGCTTCTTCTCGTCCAGATAATCCCTC
ACCACCACCAGCACCTCCGGCCAGCTCGGCGTCAGCAGTTAAACGCAGTCCGGCA
GCCACACCTACCGCCCCGCCATCACTCGCCCCGCTTAGCTCCGCGCCTCATCGAC
GGGACGCACCCGGTGGCCCGGCTCCCCACCTTTACTGGCTGCCGCCCATCCTC
CAGGCGCTGAAGCAGCTGTTACTAGCAGCATGGCTCGCGTTTCGCCTTTCCGACATT
GCCCCTTATGACGGCGCCCCAGCGGGTCCTTATTTACGGGCGGTCTGAAGCACTGT
CAGGTTCTCTCACCCGTCATAACGCCGCGGTAATCGAATTGGGCCCGGAAGATGCA
GCGTTGATGCGTTGCGGGCTCGAGGCAGCGAACTTTATTTGCGGACTCGTAGCC
AAGCTCCAGCCGCAGGCAAAGGCTCACCGCGAGGGGTGTACTTATATCGTGCCGG
CCGTCCAATTGAAGATGGCGACTCAAGTCCTCCTTGTATGGGTGAGATCTTCAAATG
CATGGGTAAAGTTGCCCGTGCCGCATTGTGCGCCATCGCACGCCACTTGCGGGCTC
CGATCTGATGCGTTCAACCATTTACTTGATGATATTCGTTACCTGCGAATGAGGTTT
CAAGCTCGGTATTACTGGCCTCGTATAGTCCCAATACTCTCCAGAATGGCAAATAA
CCATAAGTGGTGGGAACTCTCAGTTAATGCAGAAGTTGAGAAAGGACTGCTGACG
CTGATCAGCAGTGACAACCCGGGTGTCCAAGTGTTTGACCCGAACGGTTCGTTGGT
ATTTAGCAGATGGGGGCTCTTCTTTCCGAGATCTGCTTCTTGTGACTGGCAAAGCAT
TATCCACATTACAGCCGGTCTTAGACCAGCCGCACTGCATCGCGCTGCACCCGAT
TGTTTTGCAGGTAGTTTTGGAGGCGGACGAACGTCTCTTTCGCTTTTCGCTTAATGCC
GCAAAGCAATGCTGTGCTGGATTGTTTCGCCGATCGCTGCAGCCGGACACGTTATTC
CCCAGTCATACGTTAGAGTTTCTGTTAGTCAGTTCATGGATGACTTGAGCGCTGAGG
AAGATGCACTGTGCCCCAATCCGGAAAATGTCTGTGTTCCGGGTAACAATAGCAAC
AAGGAGCCAACCTTAAGGAGTGTTCTGTGCGATCCAATTAGTGGTGCGTTTTTTGGA
AGACGCCGTGGTCGTGAGCTGTGGCCACTCCTTTGGAGGTTTCATGTTAAAAAGG
GTAATTGAAACGTCTCGGTGCACATTATGTTCCGCGGAGATCAAAGGTAATACGTTT
ATACCAAATCATGCCCTTCGGGCCGCGAGCCGCCGCTGTAAAATTGGAGGATGATCG
TCGTCTGTTCCATAACGCACAACCTTCGTAAACGTCGTAAAGAAATGGGGGATCAGG
CCGATCCGATGCGGCGTTTACACCGTGAAAACGGTGAGTCTGGTGCAGACAATGG
GCTCCATAAAGGTGTTTCAGTACCCATTTATGGTTAACGAAAAAGTGTTAATCAAGGG
GAACAAACGTACTCCGGAAAAATTTGTGGGTAAAGAAGCAATAATTACCTCCCAATG
TCTGAATGGCTGGTATCTGTTAAAAATAATAGAAAGCGGTGAAAATGTACGTCTGCAA

TATCGAAGCCTGGAGAAAATCCCAAATTCGAATTCGATTGATGATCGTTGCCCATCA
CAAATACAGAACGGCTCATCCTAA

NHI 272 protein sequence:

MQQQASSAPAASSRPDNPSPPPAPPASSASAVKRSPAATPTAPPSLAPLSSAPHRRDA
PGGPAPPPLLAHAHPPGAEEAVTSSMARVRLSDIAPYDGAPAGPYLRAVEALSGSLTR
HNAAVIELGPEDAALMRCGLEAAKLYLRTRSQAPAAGKGSPPRGVYLYRAGRPIEDGDS
SPPCMGEIFKCMGKVARAALCAIARHLRLRSDAFNHLLDDIPLPANEVSSSVLLASYS
NTLQNGKITISGGKLSVNAEVEKGLLTLISSDNPGVQVFDPNGRWYLADGGSSFGLLL
VTGKALSHITAGLRPAALHRAAPDCFAGSFGGGRTSLAFRLMPQSNVLDSPIAAAGH
VIPQSYVRVSVSQFMDDLAEEDALCPNPENVCVPGNNSNKEPTLRVLSDPISGAFL
EDAVVVSCHSFGGFMLKRVIETSRCTLCSAEIKGNTFIPNHALRAAAAANKLEDDRRL
FHNAQLRKRRKEMGDQADPMRRSHRENGESGADNGLHKGVQYPFMVNEKVLKGNK
RTPEKFVGKEAITSQCLNGWYLLKIIESGENVRLQYRSLEKIPNSNSIDDRCPSSQIQNG
SS

Codon-optimized NHI 273 sequence:

ATGCCGGCCAAAAGAGATCTTGCGAGGTACGTGCAGTGGTTTGATAACGCACTGGA
TGCTTCGCTCTGTCAGCGCATGATCGACTCTTTTCAGCAACTGAGCCGCTTACAGA
CTCGTAACGAACGGGGCTCGATAAAAGCCCTGACCTCTTCTGCCTGGACCGAACT
GAACGTGAGCAAGGTTGCAGATGCAAGTTTTGAAGGGCTCTTTCGCGAACAGATTC
AGCGACACCTGGATTTATATAATGAGCGCACAGGCCTTACTCTGCCGGTGCCAGCA
CGTGGAAGACTGGAAAATTTGCGAATCAAGCGGTATCTCGTGGAAGCCGCGGATCA
GTTTCAACCGCACTTTGACGCTCTGGATTATACGTGTAATCGATACATGGTGTTCTTG
TGGTATTTGAATGACGTGAGCGAAGGTGGAGAGACGGAATTCTGTGACCTTGATATA
CGTGTGAGCGCCTGTGCAGGTAGACTTCTGATGTTTCCACCATACTGGATGTTTCA
GCATGCTGGTCTGCCGCCGAGATCGAATGATAAATATATAATATCGACATATCTTCTAT
TTAG

NHI 273 protein sequence:

MPAKRDLARYVQWFDNALDASLCQRMIDSFQQLSRLQTRNERGSIKALTSSAWTELVN
SKVADASFEGLFREQIQRHLDLYNERTGLTLPVPARGRLENLRIKRYLVEAADQFQPHF
DALDYTCNRYMVFLWYLNDVSEGGETEFCDLDIRVSACAGRLLMFPPYWMFQHAGLP
PRSNDKYIISTYLLF

Codon-optimized NHI 274 sequence:

ATGCCGGAATCTACAATGCCGCAAATCACCATGATAGAGCTCACCCCGGAAGAACT
GACTTCAAATCGATTGGCTCACACAATTTACAGAAGAGCCTAGAGGCACTCCATCG
AGACGGCATAGTGGTGTTAAAAAATGCAGTCGATCCGGATCACCTGGACCGCTTGA
ATGCACGTATGGTACCGGAGGCCAAACAGCTGTACGCGCGGACCGAGACCCACCG
TAATTTTGGGCCGAATACGGGTAAATATCCAACAGGAGCCAGTTTGTGAGCCAGAGTA
TATCTTTGAAGACGTTATCGCAAACCCATTTGCGACGTGGTGATCGAGGGCATTAT
AGGCCCCCACCACCAGCTGCGGTTTTATAGTGCAAACACGGCGTTTTAAAGCGACC

GCGCGTCAGCCCGTACATATTGACATTGACTTTGACATGCCTCGCATGCCGTTTCGC
ATTCTGCGTAAACATAAATCTGGTGGATACCAGTCCGGAAAACGGAGCTACAGAAGT
CTGGCTCGGTTTCGCATATTGATACGGATCAGTCGGTACTCGATCACTCAGTGAAACA
TAAGCAAGTGAAAGCTGATCTGCTGGAAGCTCGTCGTAAGATTTGCCCCGGTATCC
AACCTGGCTTGCCTAAAGGTTCCCTGGTGATTCTGTGATTTCCGGCTTTGGCACGCT
GGGATGCCGAATCAGACCGATGATCCGAGAGTAATGCTCGTGACAATTCAGTTTGC
GAATTGGTATAGATCTGAGCAAAAACCTGTTACTGCCTAAATCCTTACAAGGCAAGGT
CAATTTTGGGCGCTTGGTTCCGTGTGTTGACTGGGTAGATGATGGCTATGACTATCT
GAAAGGGGCCCATACACATGACTTTTCCCTGTTACCTTAA

NHI 274 protein sequence:

MPESTMPQITMIELTPEELTSKISGSHNLQKSLEALHRDGIVVLKNAVDPDHLDRNLNARM
VPEAKQLYARTETHRNFGPNTGNIQQEPVCEPEYIFEDVIANPFATSVIEGIIGPHPQLRF
YSANTAFKATARQPVHIDIDFDMPRMPFAFCVNINLVDTSPENGATEVWLGSHIDTDQS
VLDHSVKKHKQVKADLLEARRKISPGIQPGLPKGSLVIRDFRLWHAGMPNQTDPRVML
VTIQFANWYRSEQKLLLPKSLQGKVNFGRLVPCVDWVDDGYDYLKGAHTHDFSLLP

Codon-optimized NHI 275 sequence:

ATGCGTCTTGAACGAGAACTGAGCGACGCCCAACAGCGTCTAGCCCAAGCTACGT
ACAATCCTGAGGATTTTACCGCTAATCTTGTGCAGTCGCGCAGTTACGCTGTCAACC
CGAGCTCCGGAACCTCAGCTAAAGTGGTCGATCAGTGTGTCGATTCAGTGCAGCG
CTATGGTTTTTTCGTCGTTGATAACGCCATACCGTCAAATCAAGTGAGTGTTCATCCG
GCAGGAGGTTATTCAGGCACAAACAACCATTTTCGCAGAATTTAAAAAAAATTCGTGA
GCGTGTTGACAACATTGGGCTGAATCCCAGTAAACTGTTGACAGGTACCGATGCAG
AACTGCGTCCGGTCCGCCGTGTGCGGCATTTGCCCAAACCTCCTAATGACATAGTG
TGGATGCCGCAATATGCTCAATATTTGGCACACCCGGTAATTACAGCACTGGCGCG
GCAAGTCCTGGATGACCATCTGCGCATTGCCCAGCTGCATCTGCGCATTATAGAATC
AAAGCAGCCAGATGGTACACCGGGCGGGTTCGGTAAAGTGCAATATCGCAGCCGT
GATAATCGTGGTTGGCATAAGATTGGCCACATGACTTATCGGCTTATGGCGGCGAT
AAACCGGAACACAATGCCGGTTGTATCCGTCAACCGTTTCCTGACGTCACTATGTG
CCTGGTCATGATATGGTACCTGACCGATGTGACGAAAATAGCGGCGGTACGTGGG
TGGTTCCTGGCAGTCATCGCGATAAGAGGAATCCGCGCGGACCAAGTGACAACATT
AACGTAGTCGCTCCAATTCCAGGTGAAATGCAGGTTACAGCGACCGCTGGTTCTGT
GTACATACAGGACAGCCGGAGCTGGCATGCATCGCCAATGCATAACCCGGGTGGG
CAAGACCGTGTTGCCGTTATCAACCGATGGTGTCTTGGTGGCTGTCAGTTGATGA
TTATGCACCTGAAAATATTTTCAACACCATCTGCCAGCCTCTTTTCGAGAGCCGAATA
CGAATCACTGCCACCGAACTGCAACCATTTCATGAAACATCTCTGCCCGGAGGTCT
GGGACACGATTCAGCAGCCAGTCCTGGATCGCGCGAAAGCAGCGGCCTTGCGGA
CGAAGTGGGGTTTTGATCAGCTGGAAAACCTATCCGGGAATCTTAGCCAGGCCAAC
GCCCATATTCGAGTTCGGTCTCTTCCGGATAGTCATTGA

NHI 275 protein sequence:

MRLERELSDAQQLAQTYNPEDFTANLVQSRSYAVNPSSGTPAKVVDQCVDLSLQRY
GFCVVDNAIPSNQVSVIRQEVIAQTTSQNLKKIRERVDNIGLNPSKLLTGDAELRPV
RRVGHLPKPPNDIVWMPQYLAHPVITALARQVLDLHLRIAQLHLRIIESKQPDGTP
GGFGKVQYRSRDNRGWHTDWPDL SAYGGDKPEHNAGCIRQFPDVTMCLVMIWYL
TDVDENSGGTWVVPGSHRDKRNPRGPSDNINVVAIPGEMQVTATAGSVYIQDSRSW
HASPMHNPGGQDRVAVINRWCPWWLSVDDYAPENIFNTICQPLSRAEYESLPTELQPF
MKHLCPEVWDTIQQPVLDRAKAAALRTKWGFDQLENLSGNLSQANAHIRVPSLPDSH

Codon-optimized NHI 276 sequence:

ATGAGATTGATTGCGTCCTTTGAGGACCCCGGCTACGGTGCCTTAGCAGATGCGGC
CATGGCATT TTTT GATCGTCGCACTGATCTTCAGCGGAGGGGGGTTGCATTCTCCT
TTGGCGGTGAACCCGGAGATGGCGCAGAAGCGGATCCTGGGAAAATCTCGACTGA
TATTCGTTAGTTTGGATTGATCGGTCAGACCCGGAGGCGCAGGGCCTTGCTGATG
TCATTATGCGTGGCGTGAGTGCCGGTTTAAAACGTTACCTGGCCGAACGTCCCCTG
TTCCTTTTCATGTTGTCCAGAAAGGTCCTTTTTGTAAATCCAATTTTCAATCTACAGC
GTTATGCCCCCTGGCGAAGGCTTTTATAGTTGGCACTGTGATTGGAACACAAGTGATG
AAGCTACTGAACCTATTCGACGTGTCCTGGCATGGATACTGTACCTGAATACTGTAC
CTGACGGCGGCACTGAGTTTCATTGGCAGGATCACCATGAAGAGGCTGTAAAGGT
AACTGGCGATTTTCTGCTGGCCTTAGTCATCTGCACCGTGGCAGAGTTAGCCA
AACCCATACTAAAACAATTGCGACTGGCTGGATTAATGCAGGCACGTTAGATGCCTA
TGTCACAAGACTGGCAGCGGGCTAA

NHI 276 protein sequence:

MRLIASFEDPGYGALADAAMAFFDRRTDLQRRGVAFSFGGEPGDGAADPGKISTDIS
LVWIDRS DPEAQGLADVIMRGVSAGLKRYLAERPLFLSCCPERSL FVNPIFNLQRYAPG
EGFYSWHCDWNTSDEATEPIRRVLAWILYLNTVDPGGTEFWQDHHEEAVKGKLAIFP
AGLSHLHRGRVSQTHTKTIATGWINAGTLDAYVTRLAAG

Codon-optimized NHI 277 sequence:

ATGTCTCAATTTATCGAAGTTATTGATAATGCGCTACCGGAAGAACTCTGCGAGAGT
CTAATCCGCCAGATTGACACCTCACCTAATCGTCAACCTGGCCGGACAGGTGGTGG
CGTTGATACATCTAAAAAGGTCTCTGAGGATGTTTCAATCTGTACGCATGATGAATTC
GCATCGCTTTTGCCTAAGGTGTTAGAATGCACCACATCTCATCTCGTTGAATATTTGC
CTAAATACTATTTGCACTGATAGGCCCAATTGGTCTGACACTCAAACATCCGAAAA
CTGGTGAACCTGTAAAGCTGACCCAGGATAATTCGATGAAGTTGCTCGTCCGAATC
TGCAGTCTCTCGTTCAGTATCTTTCCGTATGGGTGATATCAACGCACAAAAATATCC
CGCATCCAAAGGTGGTTATCCTTACTGGCATAGTGAAGTGTATCCGCAGACTGGAC
ACAATGAAGCTCTTCATCGGATTCTGCTGTTTATGTATTATTTAAACGATGTTGAGGA
AGGAGGAGAGACTGACTTCTATTATCAAGATCTGAGCATTAGACCTAAGAGAGGAAC
TATGGTTATCGCACCGCCTATTTACGCATACCCACCGTGGCAATGTCCCTGTTAG
TAATGATAAATATATTCTTACATCGTGGGTGTTGTTAATCGTGCGGAGAATCTGTATC
GGGGCTGA

NHI 277 protein sequence:

MSQFIEVIDNALPEELCESLIRQIDTSPNRQPGRTGGGVDTSSKKVSEDVSICTHDEFASL
LPKVLECTTSHLVEYFAKYFALIGPIGLTLKHPKTGEPVKLTQDNFDEVARNLQSLVQ
YLFRMGDINAQKYPASKGGYPYWHSEVYPQTGHNEALHRILLFMYYLNDVEEGGETD
FYYQDLSIRPKRGTMVIAPAYFTHTHRGVNPVSNDKYILTSWVLFNRAENLYRG

Codon-optimized NHI 278 sequence:

ATGTCAGCGCCTACTGCGCCGGTAACCGGAGCGTTGCCGGATTACCGCATTGGG
AAGAAACCCCGGCGGATTTGCCGGCCGCCATTCCGGAGGTGAAAGCAGCACTGC
GCGCTCGAATAACTGCGAGTGGAAGAACAGTGGAGGAAGTTTTTTCGGTTGTCTGA
AAGACGCGTTCGTACTGCCGTTGATGAGATCACAAACGGCCCGTGAACGCGGCGAG
AGTGTATGGCCCGTTGTGGATTACGCAGATATAGCCGCTGGTACTGTGCCGGCGGG
CCAACCTGGCCCTATTACGCAGGCGGGGCTGCCTGGTTGTTAGAGGCCACTTTGATC
GAGATCAGGCTCTGCGTTGGGATCGGGAAATCGTTGATTACGTCGATGGCAACCGG
TTTTTTGAAAATTACCGTGGACCAGGAGACGACTTTTTTGGTTCAGTCGGTAGTAGA
CCGGAGATCTATCCAATCTATTGGAGCCCAGCGCAGATGCAGGCGAGACAATCCGA
CAGGATGGCCCGTGTGCAGGCATTTCTGAATCGTCAGTGGAAACACGAGAGCGAA
GGCGTTCGGTGGTTTGACCCCGAACGTGATAGCCTGTATCCTGACCGTATTAGGAG
ACGTCCTGAGGGTGCTGATTCTGCGGGCTTGGGTGCACACTTGGATCCGGGCACA
CTGGATCTTTGGATGACTGAGAGTTATCAACGCGCGTTCCGCCATCTTTTTGATGGG
ACCGTGGAGCAGTATGACCCGTGGGATGCGGCCCATCGAACGGCAGGGCCGCAA
TATCCTGGCAGTACCATGTGCAGTGCCTTCCGGACCTTTCAGGGTTGGACCGCGCT
GTCCGACATGGACCATGACCAGGGTGTGCTCCATACGGTGCCGATACCTGAAGCA
ATGGCATACTGATGTTACGCCCACTGCTGGCGGATGTCCCGGATGACGATATGTG
TGGTGTCACCGTAAATCAGGTCTTTCCGGCGAATGAACGTTGGCACCCCTTTACTAAT
GAGGGCGTTGTCTGGGATCCCTGATGTCCGCGCTGGCGACTCAGTGTGGTGGCAT
TGTGATATGATTCAGTACGCCCCTGTACGGGATCAAAAAGGTTGGGGTAATGTT
ATGTATATCCCGGCTGCACCGTGGTGCCCGCGTAATGAACGGTATGCTGCAACGGT
TCGCGAGGCGCTGCGAACCGGGAGCTCACCTGATGATTTTCCTGCGGAACATTAC
GAACGGAGTTGGCCAGATCGCTTCCGCCCTGAACAATTGAATGATACCGGCCCGG
CGGATTGGGTTTAGATTAA

NHI 278 protein sequence:

MSAPTAPVTGALPDLPHWEETPADLPAAIREVKAALRRARITASGRTVEEVFAVVERRVR
TAVDEITTARERGESVWPVVDYADIAAGTVPAGQLALLRRRGCLVVRGHFDRDQALRW
DREIVDYVDGNRFFENYRGPDDFFGSVGSRPEIYPIYWSPAQMQRQSDRMARVQA
FLNRQWKHESEGVRWFDPERDSLYPDRIRRRPEGADSAGLGAHLDPGTLDLWMTES
YQRAFRHLFDGTVEQYDPWDAAHRTAGPQYPGSTMCSAFRTFQGWTALSDMDHDQ
GVLHTVPIPEAMAYLMLRPLLADVPDDDMCGVTVNQVFPANERWHPLLMLRALSIPDV
RAGDSVWWHCDMIHSVAPVRDQKGWGNVMIYIPAPWCPRNERYAATVREALRTGSS
PDDFPAEHYERSWPDRFRPEQLNDTGRRGLGLD

Codon-optimized NHI 279 sequence:

ATGGCCGGTAACGGGCTGCCGACTCTGGGACGTGTCAAACCTCACTGACCTGGTCTG
CTAAGGAGGGGTTACCTTCCGAATCATATAAAGTCTCAGTCAGCACGCTGTGCCAG
TCACTAGCTCAGTATTCTGCGGCAATTGTGCAGTTACCGTCGGGCGACGGTGCAC
GCTGCGTAGCTGCCTTGACAGTGCACGTTTGTATTTTCATCATCGTCCTTCATATCC
CAGCGAGGACATGATCCATACAAACGAATCGAGGGATTGGTGTAAAACGTCCGGAT
ATTATGCCGATCCCCAATTATGGCAAGAGAGTATGATTTCCGTCCGGGTTTGACGC
CCGCGGAGTTAGAAAATGAAATTCACCTTTTCGCCTGCTGGCCTCGTTGATATCTACG
CCCTTTTAGGAAAGGCGGCAAGAGAAATATTGGATGCTATTTCAATCAACCTATCACT
CAGGTCCAGCCCGTTTACGGAAATACTGGATAATGTACCGCTCCGTGGTTCGTGAAA
TCTCGTCCTCGGTATTGTCCGTATGTTGTCAAGCGCGACCGACGTTCCATGGCGCC
CAGCACCACAACTTAACGAGTCAAGAAGATGGTAGCCTGATTATGTTTAGCGAGCAT
GAGCACCCCGCGGACAAAAGCCTGATCAGCATTGTCAAATCAGATAAATCAGGCTT
ACATATTAGGGATTTTCAGGGTCATTGGGTACTGGTGGATGGCGATCTGGGCCCGC
AAGAAGCAGTGATTTATCCAGGGCTGGCTCTTTACCAGGCGACTGCAGGCTATATTA
ATCCAGCCTTGCATCGTATCGAAATAACAAACCCGCAATCTAATATTCACGGCCGTT
GCTCCGTGACGTTTAACTTATGCCTAAGAGCATGACCCATCTTAGTTGTTCTGAAAT
GCGCGCGGCGGGCCATGGGGTTGAAGCGCAGTTTCAGCTGCCGGTTCCAGTAGA
TGACTTTATGCAGCGTCCACATTGACAGATAATCCGATGAATCGTCAGAGCGTCCC
GTCCTTTAATTTCCCTAATAGTCATGACGGTCCCATGAAACCGCTGATAAAGCGCCG
AAAGAACAATTCTAAATGTAAACCGCTTCCGCCTTCTAAACGGCTGCGACTGGAGG
CCCAGCGCGTTTTTAAAAGAACGCGTTCAGGATATTGCAGATAAAAAGGGTATAAAGC
TGCGTTTCTGCTCACTTAAAGAGTGCGAAGCTCATATTCATTCTCTGGATTCTCCGT
GTGCGAATATTCGTATGGAAATTGGTTGGCCACCGGGTGTGCCGTTTCGTGCATCCG
CATGATTTGCCAAACAAGGCAAAGATTGGGTTTTTGGAAAGCGTATGAGCCGGGTTG
GACCATTACCCACGACATGGAGCTTTCTCTGATTGACCCGGGGCAATCAACAGAAC
ATTCCGGGCATTATAGTCAGGAAATTTAA

NHI 279 protein sequence:

MAGNGLPTLGRVKLTDLVAKEGLPSESYKVSVSTLCQSLAQYSAAIVQLPSGDGALLRS
CLDSARLYFHHRPSYPSEDMIHTNESRDWCKTSGYYADPQLWQESYDFRPGLTPAEL
ENEIHFSPAGLVDIYALLGKAAREILDAISFNLSLRSSPFTEILDNVPLRGREISSSVLSVC
CQARPTFHGAQHNLTSQEDGSLIMFSEHEHPADKSLISIVKSDKSGLHIRDFQGHWWL
VDGDLGPQEAVIYPGLALYQATAGYINPALHRIETNPQSNIHGRCSVTFKLMPKSMTHL
SCSEMRAAGHGVEAQFQLPVPVDDFMQRPHSTDNPMNRQSVPSFNFPNSHDGPMK
PLIKRRKNNSKCKPLPPSKRLRLEAQRVLKERVQDIADKKGIKLRFCSLKECEAHIHSLD
SPCANIRMEIGWPPGVFPVHPHDLPNKAKIGFLEAYEPGWTITHDMELSLIDPGQSTEH
SGHYSQEI

Codon-optimized NHI 280 sequence:

ATGGATGCAAAATTGAAAGGTGTGCAACAGATACTGTCTTTTGCTAAGTTACCGTTAA
GCTGTGATTTTGAAGCAATTAATACCGAAATAAATAACCTCGATGACTCGCAGTGGT
GTATGCATGTCAATCAGGCGTGTTATAATGGTGGCTGGGATGTGCTGCCCTTTATG
CACAGACGGCTCACTTGCAGAGTCATCCTATACTCCAATGCTTCAGCATTGAACATA

CAAACGTGACTTTCTCTCCACTGCCTATAATGGAACGACTGCCTGTTCTTGCTCAGT
TCCTTGCTCAGTTTGTGTGCCCTCTCAAAGCGTTAGACTTATGAGATTACACCCGC
AGTCTGAGATTTTGCCACATAATGATCAGCAGGTTGCTCTGGAGTACGGCGAAGCC
CGCATTGATGTCCCTCTTACGGGCATAGACGAGGTAGACTTTGTCATAAACGGCAG
CACAGTTCCCATGATGCGCGGGGAGGTTTGGTATATGAATGCGGACTTAGAACACT
ATGTTTCTAATCGTGGGGCAGAGCCGCGTATTAATTTAGTCATCGATTGCAAAGTGG
AGGATTGGTTAAAAAAGATCATTAAATCTAGCGAGCAGAAATTCTAA

NHI 280 protein sequence:

MDAKLKGVEQILSFAKLPLSCDFEAINTEINNLLDSQWCMHVNQACYNGAWDVLPLYA
QTAHLQSHPIQCFSIEHTNVTFSPIMERLPVLAQFLAQFVCPLKSVRLMRLHPQSEI
LPHNDQQVALEYGEARIHVPLTGIDEVDFVINGSTVPMRGEVWYMNADLEHYVSNR
GAEPRINLVIDCKVEDWLKKIISSEQKF

Codon-optimized NHI 281 sequence:

ATGCCTATTGCCGTTGATACAGCACCGGTAGAACAAACCAGACAGTAGTTTTAAGAAA
CGCTTCACGGAGCGTACCACACCGCCTCCAGAATTGCCTCCGTTTTTCTATGCCGA
CCGGTTTGATAAAGCGCATTTTAATGATTGGCGGGATGAGCTTGCAACCAAAGGCTA
TACGGTGGTAAAAGCTATACCTACAGAAAAGGCGCTGGAATATCGGGAGAGGGCCT
TTCAGTGGATGGAAAGCTTTCCTCTGGGCTTTGATCGGAACGATGTCAAACGTGG
AAGAACGAACACTTGCCAGTTCATATTAAAGGCGGTATGTTTCATGGCTATGGATTCT
ATGACATCTCCCAGTTGTGGGATATCCGCTGCGAGGATGGTGTCATTGATGCCTTC
GCCAAAGTGTGGGGCACAGACGAGTTAATAACATCATTTGACGGCGGATCTATCAT
GCTCCCGAATCGTGTTGATGTGATGGACAGCGGTAAATGGGAACACATGGACCAGT
CACACTACCGACGCGGATTTTACTGTTGTCAAGGCTTGGTTAACTTAAACAACAATG
GTCCTGATGATGGCGGTCTGATGGTACTGGAAGGAAGCAGTACGCTTGTTGAAGAA
TACTTCGACACTCATGGCCGAAATAGCTATAAAAGCTGGGGGCCATTGATTGGTTT
GGATTTACCGAAGAGCAGCAGCAATGGTTCCTTGACAGAGGCTGTAAATGGGTAA
GGTTTGTGCCGAACCCGGGGATTTGATTCTGTGGGATTCTCGTACCATGCACTATAA
CGTACGCCCCGAAAGGTGATAGAGACAGGGTGTGCACCTATATTTGTATGGCGCCGG
CTCACTTACTTACAGAGGAAGATAGGCAGCTCCGCGTGGAGTGCTTTGAGCAGAGT
AAGGGTACGACCCATGTTCCGTTTGCTGCTATCTACGCGAGGGATTTGAACCAGT
GAAAAGAAGTGACGGGTCCCCATGCCACATGATACTGGCAAGCCAAAAAATCCGC
CGGTACTGAATGACCGTATGGCCAAGCTGGTCGGTATTAAACCGTATTAA

NHI 281 protein sequence:

MPIAVDTAPVEQPDSSFKKRFTERTTPPELPPFFYADRFDKAHFNDWRDELATKGYT
VVKAIPTEKALEYRERAFQWMESFPLGFDRNDVKTWKNEHLPVHIKGGMFHGYGFYDI
SQLWDIRCEDGVIDAFKVVWGTDELITSFDGGSIMLPNRVDVMDSGKWEHMDQSHYR
RGFYCCQGLVNLNNNGPDDGGLMVLEGSSTLVEEYFDTHGRNSYKSWGPFDFWFGFT
EEQQQWFFDRGCKWVKVCAEPGDLILWDSRTMHYNVRPKGDRDRVCTYICMAPAHL
LTEEDRQLRVECFEQSKGTTHVPFAAIYARDFEPVKRSDGSPCPHDTGKPKNPPVLND
RMAKLVGIPY

Codon-optimized NHI 282 sequence:

ATGCGCAGTCTGACTGAATCCGAGAAAACAAGCTTTCAAGAGAATGGCTTTCTGAA
ACTGACTGACCTGCTTACGAAAGAAGAAGTTGATTGCTGATTAGATGGACCTCAG
AAGTTAAGAACTTACCGAACGTGGTGGGTGAGCACATGCCATACGAAGAGATTGAC
GCTACAGGTAAAAGAGTTCTGTGCCGAACAGAGAACTATTGTAATTATCATCCGGGT
TTTAACAGTATTCTGCGTGGCGAAAACGCCCTGTCCGTGCTGCAGCAACTGTCAGG
CGAAAAAATGCATCTGTTTAAGGAGAAAATCAATTATAAACAACCGCACGCGGGGGG
CTTTGATGCACATTTTATGATGCGCCGGCATAACAATCATATAAAAGCCACTAAACATCTC
ACTATCTTAATGGCGGTTGAACCTGCTACGCTCGAAAACGGATGTCTTGAAGTGGTT
CCGGGGAGTCAACAAGGAGCCTATCCCCCTGGGTGAGGATCGCTGCATTACCAAAG
AATGGTGCAGAAATGCACGATTGGATACCTGTTCCACTGGATACGGGCGAGCTCCTG
ATATTTGGTAGTTACCTTGCACATCGCAGTGGAGCTAATCATTATCATTAGGTGCGG
CGGCAATATACGCAACCTATAATTGCGATTGAGATGGTGGGGATTACATGATGAGT
ATTATGTTTCATCGCCGGAAATTGTGGCCGCCTACACACGAACGCCTGGTAGGTGAA
AAGTACGAAGAAGGTGCAGTGCTTTACGGGTTCGGTTCGCCTATGCTGACAATTCA
AGAGAAGGCCTGA

NHI 282 protein sequence:

MRSLTESEKTSFQENGFLKLTDLTKEEVDSLIRWTSEVKNLPNVVGEHMPYEEIDATG
KRVLCRTENYCNYHPGFNSILRGENALSVLQQLSGEKMHLFKEKINYKQPHAGGFDAH
FDAPAYNHIKATKHLTILMAVEPATLENGCLEVVPGSHKEPIPLGEDRCITKEWCEMHD
WIPVPLDTGELLIFGSYLAHRSGANHSSLGRAAIYATYNCDSDGGDSHDEYYVHRRKL
WPPTherLVGEKYEEGAVLYGFGSPMLTIQEKA

Codon-optimized NHI 283 sequence:

ATGACACTTAATTATGTTCTGATCCATAATGCAGACGGCTATCTAGTAAGCTGTGATG
GTCAAGCACTTCGCACTGCCGCTCATGGGGATGATGCCTGCTACTGGCAGACCAC
TGATGATGGATATCGTCACGCCCTGACAGGCCGTCTGCTCACCGGTGTGGAAACG
GAAACGGGAACCGACTTACAGGATCGCAATGGCAATAAAGTGTGCGGGCGGACCGT
TTCGTCTGACGGATGCACCGCCGCGCCTGGCTTCCGAGATACTCGCCACTCTTAAT
GATCAGGGCTTTGCAATTATCGAGAACTGATGTCTGATCGGGAAATTTCCAGCTT
AAAGAAGAGACTGCAGTTGCACGTGCGAAAGATCATGCTGATGAAACCCCAAAGA
TGGAAACTTCTGGATAACAGACTCACTATTTGGTCTGTAGATGTCGCCCCGGGCTGT
CACGCACCCGGTAGCATTATGGGTGATGCAGCAATATATGAGTTCTGATGAGATCCA
TTTCTGTCATCAACCGATAGTGAACACTCTGAAGCCCGCTGACAACTGAAAGGTC
AGTTTCCGGAAGGAGGATGGCATAGTGAATATCCGTATCACGGAAATGTGTTCCCC
AATAATGATTGGCCTGAGCAGCCGGTGTGGCGTTCAATTCAATATTTGCATCGAT
GAATTTGCGCGAGATAATGCAGCTACACAGTACGTACCGGACAGTTATAAACTAAGA
AAAATTCCACCTCAAGAAATAAATACCGGAGGAACACGTATGGGTGAGGCCATACAT
AAGGATGTGAAACAATGGATCGCTCCTGCCGGCTCAGCTGTAATCTATGATTCACGA
ATGTGGCATAGAGCTTGTACGAACTGAATGTGAGTGGTCTGGATCGGATTGCAGT
TCTTAATGCTGTTAGCCCGGCTTATGTCCAACCCATGATGAATAAATCTAACTTAGGA

CGTCAGTATCCGAAGTCGCCGGTGGCAGCGATGTTGACTGAAAGGGAGAATATCG
ACATCGACCGGTTATGTTGCCGCCCAATGCTGCCGCTACCCCAGGGAATGCCAGCT
ATGCATGGCCGCACGCCCCGAGTAG

NHI 283 protein sequence:

MTLNYVLIHNADGYLVSCDGQALRTAAHGDDACYWQTDDGYRHALTGRLLTG VETET
GTDLQDRNGNKVSGGPFRLTDAPPRLASEILATLNDQGFAIEKLMSDREISQLKEETAV
ARAKDHADETPKDG NFWITDSLIWSVDVARAVTHPVALWVMQQYMSSDEIHFCHQPIV
NTLKPADKLKGQFPEGGWHS DYPYHGNVFPNNDWPEQPVFGVQFNICIDEFRADNAA
TQYVPDSYKLRKIPPQEINTGGTRMGEAIHKDVKQWIAPAGSAVIYDSRMWHRACHEL
NVSGLDRIAVLNAVSPAYVQPM MNKSNLGRQYPKSPVAAMLTERENIDIDRLCCRPMLP
LPQGMPAMHGRTP E

Codon-optimized NHI 284 sequence:

ATGGTGTCATCAACGCCATATCTCGACGCTCTTCGTAGAGACGGATTCGTTAAAATT
CCCCATCTGCTTCCGT CACACGTACTGTTGGCCCTGCGCGGCTGCTGTAAATACAC
TACCGAAAGGGCCAGGAACGGAAATGGCCCTATGTTAGGACAGTACCCAAACAAT
ATCCGCCCTGGCAAGAATGGACGCCAGGTGATAATATTTGGGGGGTGCAGCACTTG
CTCCACCCGGACATGAACGTTAGAGATACATTTGCTGAAGTCTATTT CAGCGACGAA
GTTCTGGATGTTGTTAAAGAACTCGTAGGGCTTAAGGGCGATCCTACCGGGGATGA
CAA ACTGTTATGGA ACTGTTTAACCTCCTCGTCTCACC GGCGGATAGGGTTGATTT
CGAACTTTGTTGGCACC GGGATGATATTAGACCAGACGTAACCCCGGAAGAGGAG
GGCCGGCAACTCAAAGAGAAATCACCAGAAGGACAGCAGTTGCATGCTCAGTATAA
TATTGCACTTTTTTGAAGATACCTCATTAGTTGTCTGTC CCGGGCAGCCACCGCCGGG
TGCGAACAGAACTGAACGTCAGGCCGCACCATACGAACCTAATCTTCCTGGGCAA
GTACTGGT CGAACTCCACCCCGGTGATGCAGTGTTCTATGATAGTAATATCCTGCAC
AGAGGCGTGTATAAAGGGATAGATACATCATCCGAACTTGGTCGCATGACGCTGCA
CGGATCAGTTGGATTAGCAGGACACGGA ACTGAACGTGCGAGACAGGTGCTGCAG
CATGCGGTTGGTGAATGGGTGGATCGGGCACCGTTTAGCATAGAAGGCCCGAAAG
GTGAACGCGCAGAGGCCATGAGAAAACGACTGGTTGACATGGGATCAGGGAAGGA
TCTGGGTTATAGTCTTGTTGGTTAG

NHI 284 protein sequence:

MVSSTPYLDALRRDGFVKIPHLLPSHVLLALRGCKYTTERARNGKWPYVRTVPKQYP
PWQEWTPGDNIWGVQHLLHPDMNVRDTFAEVYFSDEVLDVVKELVGLKGDPTGDDK
LVMELFNLLVSPADRVD FELCWHRDDIRPDVTPEEEGRQLKEKSPEGQQLHAQYNIAL
FEDTSLVVVPGSHRRVRTETERQAAPYEPNLPGQVLVELHPGDAVFYDSNILHRGVYK
GIDTSSELGRMTLHG SVGLAGHGTERRARQVLQHAVGEWVDRAPFSIEGPKGERAEAM
RKRLVDMGSGKDLGYSLVG

Codon-optimized NHI 285 sequence:

ATGGCAGCAATGACACTGTCCAAAGCTTTGTCTCGTTCCAAAAGCCAACTGCTAAC
ACGCACGGTGCCCATTCGATGCATGTCCACATCAACGAGTACTTCGACACTGCCAA

TCACAATCAAACCCACAACCTAAAGAACTTTTCGGCTGGCTTCTTGGGTGAGAGAAATT
TAGAAAAGGCGATGAGAGGCTTACATGAAGATGGTTTGGTTGTTGTGAGTGACGTC
ATCCGCGATGATCATCTGGATCACTTAAACAATAAAATGGTGCAGGATGCACGCACC
CTCCAGGCCAAAGGGAAAGATATGCCTTATAATTACAACGTAGGAAACATTTCAGCAG
GATCCTCCACCTGTAAAAGAACATTTTGAATCTAGTATATTCCTGAACCCGATTGCCA
ATCAAATTACTACCGGAATGCTTGGGCCACGCCCTAAATGGACCTTTTGTTCAGGCA
ACAGTGCCATGCCACCAGAGGCTGGGGCGCAGCCCCAGCGACAACCCGTCCATG
CGGACAGTGATTTTGGCGATCCGAGTCATCCCTTCGCCCTGGTCGTGAATGTCCCG
CTGATTCGTTTTACTCCCGAGAACGGTTCCACTGAGACCTGGCTGGGTACTCACAC
GGGTGACTTGAGCGGCCTGCAGGTTCAACAGGGTGCAAAAGGTACCCGAGCATCC
GGCCGTATATGTGAAGATCTGCTTGAACAGCGTCGGCAAGTGCCTGGACCGAGCC
AACCGGTAATTGAAAAAGGTAGTATCGTGATCCGGGATTAAAGATTGTGGCATGCTG
GAATGCCTAACATGACGGATGAAGTGAGAGTGATGCTGGCAATGATCCATTTGCA
CCCTGGTATCGCAACCCGATGAAATTAGAATTATCTGAAGATTTAATGCACAAGATTA
GATCACAAAATGATCTTCAGATCCCAGTTGATTGGGTGTCTCGAGATGAAGCCCTCA
AGAGATATCTGAATAGGGGCTTTGGCAATTCATATGACTTTGGGCAGGCGGAATAA

NHI 285 protein sequence:

MAAMTLKALSRKSQLLTRTVPIRCMSTSTSTSLPITIKPTTKELSAGFLGERNLEKA
MRGLHEDGLVVVSDVIPHDHLDHLNKMVQDARTLQAKGKDMYPYNYNVGNIQQDPPP
VKEHFESSIFLNPIANQITTGMLGPRPKWTFCSGNSAMPPEAGAQPQRQPVHADSDFA
HPSHPFALVVNVPLIRFTPENGSTETWLGTHTGDLGLQVQQGAKGTRASGRICEDLL
EQRRQVRGPSQPVIEKGSIVIRDLRLWHAGMPNMTDEV RVMLAMIHFA PWYRNPMKL
ELSEDLMHKIRSQNDLQIPVDWVSRDEALKRYLNRGFGNSYDFGQAE

Codon-optimized NHI 286 sequence:

ATGCCCCGGGATGGGAATGATGGGGTTAGGCGCTGGCGCACCTAGACAGGCCCGC
AGCGAGGGCGATATTAGTTCTGTATTTGCTAGCCTGTCTGGTGAAGAAGCGAAACC
GTTGCCTCCTCGCTTTATCGACCTAAAACGTCAAATTATTGGCGACGAAGCCAACCA
ACGTGCTTTGACTGACTCATGGGTGAGGCTCTGTGATCGTCTGGGCCAGGCCGGC
GAGGAAATTGAACGTAAAAACAGGACTGCATTCCACAGATTGCCTACGAAGAACT
GACATCACCCTACCGAGCACAAGTACCCTGTCTGCCCTGAAACGCGCGGGCTCT
TTCGTCGTCAGAGGCGTGGTGGATGAGGAGACCGCCACTGGATGGCTGAAAGGCT
GTGAAAAGTATATTGGGGACAATCCACAAGTTCGGGGGTTCCCAAAAGATGATAAG
CAAGTTTTTGAACTTTATTGGAGTAAACTCAATTAGCTGCACGGTCTCATCCACGG
AGTCTGGCTGTGCAGCGGAGCCTCCTGACCCTCTTTACACATCCGCCGGATTTTCC
GATCTCATTAACGACTCCCTTAACGTATGCGGATAGGCTGCGTATAAGACATCCGGG
GGATGCCCAATTTGCTCTTGGTCCGCATATGGATGGCGGGTCTATCGAGCGCTGGG
AGGATCCCATGTATCGGGCTGTTTACAAAGACATCCTGAAAGGTAAGTGGGAAGCG
TTTGATGCGTATACGATCGGCGAGCGTGGTGTAGCTAAACAAAATCTGTACGACGG
CCCGGGTAGCTGTGGCGTTTTTATAGACATTCCAGGGCTGGACCTCTATGAGTGAAA
CGGGCCCAGGAGAGGGGACGCTGCGGGTCTATCCTTTTATAAGAGAACTTACGGC
CTATACGATATTACGTCCGTTATTTCTGTGAAAAGAGTCCCGAGCTAGCCTGACTTAT

GAACAGTATCTGGATCCGTCGAATTGGGTTCTGGACCCGACCACCAGTGCCTTTCC
TGGCTCGCCTCTGGCACGGAGCCAAGAATTCAATGATGGTACCCATCCGCATCTGG
CTTTGAATCGTAGCATGGTTAGCATGCCGACTGTAAACCTGGCGATCAGGCGTGG
TGGCATTGCGAAAGCGTGCACAACGGTACGGGTCCTAGTGCGGTTCTGTACATACC
GGCCGTGCCACTTACGCCTTCAAACATTGAATATATTAAGGATCAACGGAGCACGTT
TTTTGAAGGGCGTCCAGGCCCTGATTTCCCTGGAGGTGAGGGTGAGGCCCATTTTC
GTCGGTAAAGGGGTAGAGGGTGATATACTGAGTAAAGAGGGTCGCCGCGCAATGG
GTTTGGAGCCATTTGAGATCACAGCCGATCTCTCCTCTGGTGAGAAGTCTATACGTC
AGAAAGCGTGA

NHI 286 protein sequence:

MPGMGMMGLGAGAPRQARSEGDISSVFASLSGEEAKPLPPRFIDLRQIIGDEANQRA
LTDSWVRLCDRLGQAGEEIERKKQDCIPQIAYEELTSPLPSTSTLSALKRAGSFVVRGV
VDEETATGWLKGCEKYIGDNPQVRGFPKDDKQVFELYWSKTQLAARSHPRSLAVQRS
LLTLFTHPPDFPISLTTPLTYADRLRIRHPGDAQFALGPHMDGGSIERWEDPMYRAVYK
DILKGNWEAFDAYTIGERGVAKQNLVDGPGSCGVFRAFQGWTSMSSETGPGEGLRVY
PFIRELTAYTILRPLFREKESRASLTIEQYLDPSNWVLDPTTSAFPGSPLARSQEFNDGT
HPhLALNRSMVSMPTVKPGDQAWWHCESVHNGTGPSAVLYIPAVPLTPSNIEYIKDQR
STFFEGRPGPDFPGGEGEAHFVGKGVEGDILSKEGRRAMGLEPFEITADLSSGEKSIR
QKA

Codon-optimized NHI 287 sequence:

ATGTTAAAACTGGATACCCTTCGCGCTACCCGCATTGAGCGTGATCCCTTCGACTAT
GTGATTGTGCGGAACCTTTGTTGAGCGTGAAAAATTGGATCAGGTTCTTTCCGATTAT
CCGGAGGTACCGGGACCCGGGTCTCATCCGCCAGGTGGCCTGAAGATTTTCAGGTC
ACTTTAAAAAACTGATGGACGAACTGCTGGATGCTCCTTTTCGTCAGCTGGTTGAAG
AAAAATTTGACGTTGATCTGACGGGGCCGTCCGACAATGTATACGGTTCGCGGATTCT
GTCGTGCGCGGGACGGAAAAATCCATACCGATAGTAAGACGAAGATTATCACTGTC
CTGCTTTATATGAACGATGAATCGTGGGAGAGTTCCACTGGGCGTCTGCGCATACT
GAGAAATGGTACCGATCTAGAAAACTTTGCGGCTGAGGTGAGCCTTCTGGCGGAA
CTTTGCTAGTTTTCAAGCGTTCAGATAACTCGTGGCACGGGCACCATCCGTTTGAA
GGGAAACGCCGAGCGGTTTCAGCTGAACTGGGTAAACCGATCAGTCAGTCGTGGACA
GAGAACAGGGCCGACATGGATTCTCATCAGCAATTAAACGCCTGATGGGTCTCGGC
GCTCATTA

NHI 287 protein sequence:

MLKLDTLRATRIERDPFDYVIVRNFVEREKLDQVLSDYPEVPGPGSHPPGGLKISGHFK
KLMDLLEDAPFRQLVEEKFDVDLTGRPTMYTVRGRFCRARDGKIHTDSKTKIITVLLYMN
DESWESSTGRLRILRNGTDLENFAAEVEPSGGTLLVFKRSDNSWHGHHPFEGKRRAV
QLNWVTDQSVVDREQGRHGFSSAIKRLMGLGAH

Codon-optimized NHI 288 sequence:

ATGACCACTCGTATTCTGGGTGTTGTTTCAGTTAGATCAGCGCAGATTAAGTATGATGAC
CTTGCTGTTCTGGCAAAAAGCAACTTTTCAAGCGAATATAGCGACTTTGCCTGTGGT
AGATGGGAGTTTTGTATGTTGCGGAACCAAGTCTGGCAAGCAGGAAGAACAGCGAG
TTGTGGTGCACGAGACCCCTGCCTTAGCCACACCACTGGGACAGAGCCTCCCTTA
CCTGAACGAGCTTCTAGATAATCATTTTGACAGAGATTCTATACGATATGCACGCATA
ATACGAATATCCGAGAATGCTTGTATCATACCTCACAGAGACTACTTGGAAGTGGAA
GGTAAATTCATTCGCGTGCAATTTAGTTTTGGATACGAATGAAAAATGCTCGAACACTG
AAGAAAACAATATTTTTCACATGGGCCCGGGGAGAAATTTGGTTTCTGGACGCTAGCC
TTCCACATTCCGCAGGTTGCTTCTCGCCGACCCCCCGTCTTCATCTGGTCGTAGAT
ATCGAGGGGACCCGGTCTCTCGAAGAAGTAGCCATTAATGTGGAGCAACCATCAGC
ACGAAACGCGACGGTGGATACCCGCAAGGAATGGACGGATGAGACCCTCGAATCT
GTTCTTGGGTTTTTCAGAAATTATTAGCGAGGCAAATTATCGTGAAATTGTGGCTATTT
TGGCTAAGTTACACTTTTTTTCACAAGGTACATTGTGTTGATATGTATGGCTGGCTTAA
GGAAATATGTCGGCGTCGCGGTGAACCGGCTCTTATCGAAAAAGCTAACTCACTGG
AACGCTTCTATCTCATTGATCGTGCCGCGGGAGAAAGTCATGACTTATTAA

NHI 288 protein sequence:

MTTRILGVVQLDQRRLTDDLAVLAKSNFSSEYSDFACGRWEFCMLRNQSGKQEEQRV
VVHETPALATPLGQSLPYLNELLDNHFDRDSIRYARIIRISENACIIPHRDYLELEGKFIRV
HLVLDTNEKCSNTEENNIFHMGERGEIWFLDASLPHSAGCFSPTPRLHLVVDIEGTRSLE
EVAINVEQPSARNATVDTRKEWTDETLESVLGFSEIISEANYREIVAILAKLHFFHKVHCV
DMYGWLKEICRRRGEPALIEKANSLERFYLLIDRAAGEVMTY

Codon-optimized NHI 289 sequence:

ATGGCATCCTGGTCACACCCACAATTTGAAAAAGGAGCGACTACTAGAATTCTGGG
AGTAGTACAGCTGGACCAGCGGCGTCTAACAGATGACTTAGCGGTGCTGGCGAAAT
CTAATTTTTCTCAGAATATTCAGATTTTGCTTGCGGTCTGTTGGGAATTTGTATGTTA
CGCAACCAAAGCGGTAAGCAAGAAGAGCAGCGTGTCTGTTGATTGAGACACCGG
CTCTCGCGACACCTCTTGGTCAGTCTTTGCCGTATCTGAATGAATTATTGGACAACC
ATTTTGACCGTGATTGATCCGTTATGCCCCGTATAATACGGATCTCGGAAAATGCATG
TATCATCCCTCATCGTGATTATCTGGAAGTGGAGGGAAAGTTTATTCGGGTCCACCT
TGTTCTGGATACTAACGAAAAATGTTCCAATACTGAAGAAAATAACATCTTTCATATGG
GTCGTGGTGAGATTTGGTTCCTGGATGCGAGTCTGCCACATTCCGCCGGTTGTTTC
TCACCGACCCCGCGACTGCACCTCGTTGTTGACATTGAAGGTACCCGGAGCCTTG
AAGAAGTAGCTATTAACGTTGAGCAACCATCTGCTCGTAATGCTACGGTGGACACTA
GAAAAGAATGGACGGACGAAACACTTGAAAGTGTACTTGGCTTTAGCGAAATAATCA
GCGAAGCTAATTACCGTGAAATCGTAGCTATACTGGCTAAACTGCATTTCTTTCACAA
AGTGCATTGTGTGGACATGTACGGATGGCTGAAAGAGATTTGTCGCCGGCGGGGT
GAACCCGCGCTGATTGAAAAAGCTAACAGTCTCGAACGCTTTTATCTTATTGACCGG
GCAGCAGGCGAGGTTATGACATACTAA

NHI 289 protein sequence:

MASWSHPQFEKGATTRILGVVQLDQRRRLTDDLAVLAKSNFSSEYSDFACGRWEFCML
RNQSGKQEEQRVVVHETPALATPLGQSLPYLNELLDNHFD RDSIRYARIIRISENACIIPH
RDYLELEGKFIRVHLVLDTNEKCSNTEENNIFHMG RGEIWFLDASLPHSAGCFSPTPRL
HLVVDIEGTRSLEEVAINVEQPSARNATVDTRKEWTD ETL SVLGFSEIISEANYREIVAI
LAKLHFFHKVHCVD MYGWLKEICRRRGEPALIEKANSLERFY LIDRAAGEVMTY

Codon-optimized NHI 290 sequence:

ATGCCCTGACACATGACCAGCGTGATCATTTTTTTAGAACATGGCTGGGTAAAGTT
CCGAATGCCATTAGCAAAGCAATTATAGAGGAATGGACGAAGAATATCTGGGTCCGC
CTTGTTACGACGAGAACGATAAATCAACATGGCTGGAGGAATATCTGAAACTGCC
GCGTCACCGTGAAATACCGGTTGAAGAACTGGCCCCTGGTGCTTGGGAGGCTATG
TGTGAAATTGTGGGCGGAGAAGATAAAATAGACCCAGTACGTGAGAGATATCACGG
TGATCAATTTATTATAAACTTCGGTTCGGACTATTGGGAAACAGCTACGCCTCCGCC
GCAGGA ACTTCGCGGATGGCACCATGATAATGATTGGTACCGTCAGTTTTTAGACTC
ATCCGGTAATGCACTTACTATTGTCCACTGCTTTACCGATATACCGCCGCGCGGAGG
TGGGACCTGGTTGGCTGAAGATGGCATTGCAAGCATCGTGAAATACTTGTATGATCA
TCCTGAAGGCCTGGATCCACCGCTGGAAAAAGTGCTGCATACGCATACCAAAGACT
GTAAAAAATTTGTGCAGGTCGAAGCCAAAGCTGGTGACACACTTATTCTTCATGGCT
TACTGCCACACACCAATGGAGTGAACCATCTGCATTATGCCCGCGTTATCACCAATC
CCCACGTTAATATGGTAGAACCTTTCAATCTTAATCGCTCAGATGGTAACTACACACT
GTGTGAGCAGGTCATCTTACGGGCTCTGGGGCGTGAATCAGTGCCGGAATATAAGC
CGACACGAGAGCGAAAACGGTACCATCCTCGCACTGCGCCGTTTAAACGTGTACG
GGTTGAACCAGAATTA AAAAG AATGCTTGAATATGCAAAAGCACATGGGCTGCCGCA
GGACTCGGTTGACTCCGTGTACCTCCGCGGTGAAGAAGAAATTCGTCTGCATGAAC
AACGTAATGGCTATGACCAACCGCATGGCCCCGGACCGATCGCGTACTCAAATAAA
GACTATTTTTT CACAAGAGAGGAAGGAATAACCACACAGGACTAA

NHI 290 protein sequence:

MPLTHDQRDHFLEHGWWKVPNAISKAIIEEWTKNIWVRLGYDENDKSTWLEEY LKLPR
HREIPVEELAPGAWEAMCEIVGGEDKIDPVRERYHGDQFIINFGSDYWETATPPPQELR
GWHHDNDWYRQFLDSSGNALTIVHCFTDIPPRGGGTWLAEDG IASIVKYLYDHPEGLD
PPLEKVLHHTKDKCKFVQVEAKAGDTLILHGLLPHTNGVNLHLYARVITNPHVNMVEP
FNLNRSDGNYTLCEQVILRALGRESVPEYKPTRERKRYHPRTAPFKRVRVEPELKRML
EYAKAHGLPQDSVDSVYLRGEEEEIRLHEQRNGYDQPHGPGPIAYS NKDYFFFTREEGIT
TQD

Codon-optimized NHI 291 sequence:

ATGACTACTACCCTGCCCGTGATTCGCATTAATCCATCCCTTGACCCTGCGCCCTTT
GCAGCGGCGTTTTAGCGTGATGGGGTGGTT CAGATTCCGATCTTCCTGGAGCCGG
CAGACGCAGAGCGTGTTGCCGGAGTTTTGGCTGGTCTAACGTGGAATGTCGTGCG
TCCGGACGAGACTTCGGAAACCCTGGTGATAAGCCCACAAGTTATACAAAAGTTTG
GTGAAGCTCAGGTTTCGACAGTTTTTACAGGGCGCATTGAAACGTGCGAGTCGTGG
ATTTAGCTTTATACACTTATCTTACGCGCTTCAGGATGAATATGCAAGAGATCCGACC

GCACCGATTACCAAGCGACCGCTTTCCTGCAGAGCCGCACTTTTCTGGATTTCGG
ACAGGCGGTGATAGGCTCTGACCAGGTAGATGGGGTCCGCGTTTCAGGCGAGTAAC
TATCGCCCGGGTGATTTTCTTACGTTGCATGACGATTCGCATAAACGAGATGATCGC
CTGGCCGCATTTACGTTGGGGTTTACGCGAGATTGGAGACCAGATTGGGGGGGAC
AGCTTCTGTTTCATGACGTTGAAGGCCAAATTGAGAGGGGCTTCATGCCTGGTTTC
AATGTTCTCACTCTTTTCAGAGTTCCTCGAGCACATTCAGTAGCTCCCGTGGCTGCA
TATGCCGCAACTAAAAGACTGAGTCTGACCGGATGGTTGGTTCGCGACGCCAATCC
TTCAGCGTAA

NHI 291 protein sequence:

MTTTLPVIRINPSLDPAPFAAAFQRDGVVQIPIFLEPADAERVAGVLAGLTWNVVPDET
SETLVISPVQVIQKFGEAQVRQFLQGALKRASRGFSFIHLSYALQDEYARDPTAPIHQATA
FLQSRFTLDFGQAVIGSDQVDGVRVQASNYRPGDFLT LHDDSHKRDDR LA AFTLG FTR
DWRPDWGGQLLFHDVEGQIERGFMPGFNVLT LFRVPRAHSVAPVAAYAATKRLSLTG
WLVRDANPSA

Codon-optimized NHI 292 sequence:

ATGCCCCGGAATCGATCTCCAGACAGCAGGATTGGCTGTCAATGATGGCCCCCTGTT
ACCGGGCTCATTTGATTTCTTGACACAATCCTCACCGAGCGAACCTCTCGATGTGT
TACGAGCGCGCTATGAAGAGGACGGTATGTTACTCTTAAAAGGATTAATCCCGCGTG
AAGATGTGCTTCGGGGCCCGCACAAAGTACTTCGAAATGATGGCACCTTCAGGCGTT
CTGCAGCAAGACACGCAGCCAGTACAGGGTATATTTAATTCAGACGGTAGTCCTGA
GGACTTCCCTGGCATCGGTGCCGGGGCTACTGGAAACGATGGGCGTCCCGGTGG
AGAATCTGCACAGGCATTTGTTGACCTCGCGATACAGGCTCATTATGAAGATTGGTA
CACGCAAGATCTGGCGGGCCATCCAGCCCTGATTGATTTCTGTCGCGAAGCTGACG
GGCTGGAATGAAAACACATTAGAAGTGAAGATCCCTTCTGCGTAACAACGTTCCA
GGAACAAAACCAATTGGTGTCCACTATGATCAAATCTTTTTGCGCTATGGCGATCCTA
CTTCAGTCACGGCGTGGGTGCCCATCGGAGATGTTTCTCTCACTGGAGGAGGACT
GATTTATCTGGAGGATGGGGATGCAGTAGGTACGCAGATTGAGCAGGATTTCACTC
GTAAAGCACTGGAATCCGGCCTTACAGAGGAACAAGCGCGTAATGCCTTCAATCAG
AATATGATGTCTACCGGTCTCCTGAGTGAATATCCGGCAGAATTTGCACGTAAGTATA
ATCGTCGCTGGCTCGTTAGTGCGTACGAAGCAGGAGACGTAGTGCTACATAAACCT
CACGCTATTCATGCGAGCACCGTTAATAATGACCCAGATAATGTTATCCGACTGGCA
ACAGATCTGCGCTTTGTAGATAAAAGTAAACCGTATGATACACGGTGGACAAAATATT
ATGAGTTTAATGATGGTGTGTGA

NHI 292 protein sequence:

MPGIDLQTAGLAVNDGPLLPGSFDFLTQSSPSEPLDVLRLARYEEDGMLLLKGLIPREDV
LRARTKYFEMMAPSGVLQQDTQPVQGIFNSDGSPEDFPGIGAGATGNDGRPGGESA
QAFVDLAIQAHYEDWYTQDLAGHPALIDFVAKLTGWNENTLELKRSLLRNNVPGTKPIG
VHYDQIFLRYGDPTSVTAWVPIGDVSLTGGGLIYLEDGDAVGTQIEQDFTRKALESGLTE
EQARNAFNQNMSTGLLSEYPAEFARKYNRRWLVSAYEAGDVVLHKPHAIHASTVNN
DPDNVIRLATDLRFVDKSKPYDTRWTKYYEFNDGV

Codon-optimized NHI 293 sequence:

ATGGCGGTGGACTGTATCGCACGCATTCCGAGCATGCCGCCGCATCCGCCTAAAG
AGGAACGTCAGTCAGAAAAGAACTTCTGGTATTTGATGCCGCATTAATTAGACACC
AGCCAACTATCCCGCCTCAGTTTATCTGGCCGGACGAAGAAAAACCCTGCAGTAAT
GTTCCAGAACTGGGAGTTCCCCACATTGACTTAGGCGGGTTTCTGTCAGGGGACC
CAGCGTCAACCACAGAAGCTTCCCGGCTGATTGGCGAAGCCTGCCAACGCCATGG
ATTTTTCTCGTGGTAAACCACGGAGTGGATTATAAACTGATAGCAGATGCACATCG
TTACACCAAAGATTTCTTTGAACTGCCGCTTTCAACAAAACAGCGTGCTCTGAGGAA
GGCCGGTGAGCACTGTGGATATGCATCCAGTTTTACGGGGCGGTTTTCAAGTAAAC
TTCCTTGGAAGAAACCCTGAGTTTTCGCTATTCGGCTGACCCGAATTCCTCAAACG
CCGTGCGGGACTATCTGTGCGATAAAATGGGTGAGGATTTTAAACAGTTTGGTCGG
GCATATCAAGGTTACTGCGAAGCGATGTCGACACTGTCTCTTGGTATTATGGAAGT
TTCAGCGATGTCTCTGGGTGTCTCCCGAGCTCACTTTAAGGAGTTCTTCGAGGAGAA
TGATTCCATCATGCGTCTGAACTATTATCCACCCTGTCAGAAACCTGAGCTAACATTA
GGCACGGGGCCACACTGCGATCCGACCTCCTTGACCATTCTGCACCAAGATCAGG
TGGGAGGACTGGAAGTCTTCGTTGACGATGAGTGGCGATCAATAAGCCCGAATTTT
AACGCTTTTGTATTAAACATAGGCGACACGTTTATGGCATTATCAAATGGGCGCTATA
AATCCTGTCTGCACAGGGCCGTGGTTAATAGCAAGACCCCCCGGAAAAGCCTTGC
GTTCTTTCTGTGTCCACGCAATGACAAAGTCGTAAGTCCGCCTAGCGAGCTTGTGG
ACACTATGTGTCCGCGTCTGTATCCGGAATTCACGTGGCCTATGCTTCTCGAGTTCA
CGCAAAAACATTATAGAGCGGACATGAATACTTTAGAGGCCTTCTCAAATTGGCTTC
AGCAGAAGAATAGTTGA

NHI 293 protein sequence:

MAVDCIARIPSMPPHPPKEERQSEKKLLVFDAALIRHQPTIPPQFIWPDEEKPCSNVPEL
GVPHIDLGGFLSGDPASTTEASRLIGEACQRHGFLLVNVHGVVDYKLIADAHRYTKDFFE
LPLSTKQRALRKAGEHCGYASSFTGRFSSKLPWKETLSFRYSADPNSSNAVRDYLC DK
MGEDFKQFGRAYQGYCEAMSTLSLGIMELLAMSLGVSRAHFKEFFEENDSIMRLNYY P
PCQKPELTLGTGPHCDPTSLTILHQDQVGGLEVFVDDEWRSISP NFNAFVINIGDTFMA
LSNGRYKSCLHRAVVNSKTPRKSLAFFLCPRNDKVVSPPSELVDTMCPRLYPDFTWPM
LLEFTQKH YRADMNTLEAFSNWLQQKNS

Codon-optimized NHI 294 sequence:

ATGACCACGCCAAACGCAAGTCCGGCGAGTACAGGGTTGCCTATAATAGACGTAGC
TGCCCTTCGCGCGCCTGATGATGCGGATGGACGTACTCGAGTAGCCCAACAGATTC
GCGCCGCGTGTCGAGAACACGGTTTTTTTTTATGTGAATGGCCACGGTGTTTCGCCG
GAACTGATCAGCCGCCTGGAGCGCCTGTCCCACGATTTCTTCAATCTGGATGAGAC
GACTAAACTGCAGTGGCGCATGGCCCTTGGTGGACGTGCATGGCGTGGCTATTTTC
CCTCTCGGCGGTGAACTTACATCTGGCCGCCCGGATTGGAAAGAGGGTCTGTATCT
GGGCACTGAATTAGCCGCCGACCACCCGCTGGTCCAGGCCGGTACACCAGTTCAT
GGCGCCAACCTTTTTCTGATGTGCCCGGCTTAAGAGCTACCATTCTGGAGTATATG
GCGGCTACGACCCAGTTAGGGCACACAGCTGATGGAGGGTATCGCCTTGAGTTTGG

ATCTTCCGGCGTCTTACTTTTCATGATCGCTACACCGCCGATCCATTGATTCTCTTTTCG
GATTTTTTAATTACCCCAAGTCAAGCAGTTCCCGAGGGTCTGGATGTACAGTGGGGGG
TGGGTGAACACACGGATTATGGCCTGTTGACCATTCTGTTACAAGATCACATAGGTG
GTTTAGAAGTGCGCACTCCGGGCGGTTGGATTGATGCACCGCCCGTTGCGGGTGC
TTTCGTTTGTAAATTGGGGATATGCTGGACCGTATGACTGGTGGGCTGTACAAATC
GACACCGCATCGCGTTAAACGTAACACGAGCGGGCATGACCGCTTAAGTTTTCTC
TGTTTTTTGATCCGAACTTTTTTGCCCGCGTGCAGCGCATCGAAGGTTTAGCTGATG
CCCCGGCGCAGGATGATAGCGCTGAGCGCTGGGATAGAGCGAACGTCCATGCGTT
TAATGGTATTTACGGTGACTATCTTCTCGACAAAGTATCGAAAGTGTTCCTGAATTA
CGCCGTGAAGTTTTGTAA

NHI 294 protein sequence:

MTTPNASPASTGLPIIDVAALRAPDDADGRTRVAQQIRAACREHGFFYVNGHGVSP
SRLERLSHDFFNLDDETTKLQWRMALGGRAWRGYFPLGGELTSGRPDWKEGLYLGTEL
AADHPLVQAGTPVHGANLFPDVPGLRATILEYMAATTQLGHQLMEGIALSLDLPASYFH
DRYTADPLILFRIFNYP SQAVPEGLDVQWGVGEHTDYGLLTILLQDHIGGLEVRTPGGW
DAPPVAGAFVCNIGDMLDRMTGGLYKSTPHRVKRNTSGHDRLSFPLFFDPNFFARVQ
RIEGLADAPAQDDSAERWDRANVHAFNGIYGDYLLDKVSKVFPELRREVL

Codon-optimized NHI 295 sequence:

ATGTTGTCTCCACAAGAAGAGAAAAATATGGTTATCACTAAGACCGGCGAGGTTTCAG
GCAATTACAATGCCCCGATTACGATCGCAAAAGTGAATTGAAAGCATTGATGAGTCA
AAAGCAGGTGTTAAGGGTCTGGTTGATAACGGACTGGCCAAAATTCCGCAAATTTTT
GTTTCATGAACAGAACAAATTTTGAAGAAAATCTGGGCTACGGGAACACTCAGTTCTC
CATACCCGTGATTGATTTTTCAGGGCATAGATGAAGATGCGACACTGCGCTCAGAAAT
AATTTTGAAGGTAGGCGACGCTTGTGAAAAATGGGGATTTTTTTTCAGGTTGTCAACCA
TGGTATTCCTGAATCTGTTATGAACGAAACCATCGACGGCGTCCGCCGCTTTTACG
AACAGGATACCGACGTCAAAAAACAGTTTTTATAGCAGAGATGTAACCTCGGAAGTTTA
TTTATAATAGCAATTTTATGCTGTTTTCAGGCGCCGGCCGCAAATTGGAGAGATACGG
TATACTTTGTCATGGCTCCTCATCCCCGGATCCTCAGGAAGTGGCCCTGGTGTGT
CGTGACATACTCTTCGAATATAGTAAATATGTCATGAAACTGGGTCTGACCTTATTCG
AACTGCTGAGTGAAGCCCTGGGTCTGGACCCCAATCACCTGAAGGACCTGAATTG
TGCGGAAGGCCTGTTCTTTGTCGGTCACTACTACCCGGCATGCCCGAACCAGGGT
AGTACGTTTCGGGACCAGCAACCACAGTGACTCAAGCTTTTTTAACGGTTTTTGTACAA
GACCAAATGGGTGGCCTGCAAGTCCTGCACGAAAATCAATGGGTGGAAGTTCCACC
ACTGCCAGGAGCCCTGGTAGTGAACATTGCCGACCTGCTACAGCTGATCACCAAC
GATAAATTTAAATCCGTCAACCACCGAGTTCTTGCAAAAAAGGAAGGACCTAGAATA
TCTGTAGCAGGCTTCTTTTGAACACATTTTACAGAAAGCAAATACAAGTCGAGTATAT
GGTCCACTTAAAGAGCTGCTGTCTCAGGAGAATCCTCCGATTTATCGCGAAACAAC
GATCAAAGACTTTATTACGCACTATTATAAAAAGGGGCTGGACGGTACGTCTGCAATA
AGCCACTTCAAACCTGTGTAAATAA

NHI 295 protein sequence:

MLSPQEEKNMVITKTGEVQAITMPDYDRKSELKAFDESKAGVKGLVDNGLAKIPQIFVH
EQNNFEENLGYGNTQFSIPVIDFQGIDEDATLRSEIISKVGDACEKWGFFQVVNHGIPE
SVMNETIDGVRRFHEQD TDVKKQFYSRDVTRKFIYNSNFDLFQAPAA NWRDTVYFVM
APHPPDPQELPLVCRDILFEYSKYVMKLGLTLFELLSEALGLDPNHLKDLNCAEGLFFV
GHYYPACPEPGSTFGTSNHSDSSFLT VLLQDQMGG LQVLHENQWVEVPPLPGALVVN
IADLLQLITNDKFKSVNHRVLAKKEGPRISVAGFFRTHFTEANTS RVYGPLKELLSQENP
PIYRETTIKDFITHYYKKGLDGTSAISHFKLCK

Codon-optimized NHI 296 sequence:

ATGCATCTTTATGAACCGCCGAAAGCACCACAAAGCATTCCGCTTATCGATTTGTCTG
CGGGCTGGTGATGAAGCGGGCGAGAGGGCAGTGGCGTGGGACATTCATAGGGCA
TGCCGTGAAACGGGTTTTTTTTTATATTACCGGACATGGTGTTAGTGC GGCGCTTGTC
GCGCAGCATTTTCAGTTTGCTAAGGCCTTCTTCGATTTGCCGCTGGAGCGTAAGAT
GGCCATCCATATGAAGCAAAGCCCCACA ACTGCGGGATACGAACCTATTGGTGGTC
AGGTACTGGACTCTCAGGATGATAAAGCAGAGGCTGCTCCACCGGATCTGAAGGAA
TCTTTTTACTGCGGTATGGAGTTGCCGGATGATCATCCCTGGGCGATAAAACGGATT
CGTAATTTTCGGTCACAATCAATGGCCTGATGAATTACCAGAATTTCTG GCCCACATG
GTGAGTTATTGGGCCCAGATGCGTGCCCTGGGAGACCGCCTGTTGGCGTTATTAGC
TCTGAGCTTGTATCTGCCGGCTGATTGGTTCGCTTCTAGTTTTGATATGCCGTCAGG
AACCGTTCGCCTGATTAAATATCCTCCTCAGCCTGCCCAAGCACTGTTTAATCAGAT
CGGCGCAGGCGCCCATACAGACTGGGGCGGGCGTGACGATTCTCGCACAAGACGC
GACAGGAGGCCTTGAAGTGAGAAATGCCGCAGGCGCATGGATCGAAGCGCCACC
AGTAGAAGGGAGCTTCGTGATAAACCTCGGTGACCTAATGGCGCGATGGACGAATG
GTCTGTACAACAGCAATTTTCACCGTGTTAAGAATAACCGTAGCGGTCAAGATCGGT
ACTCTGCGCCTTTTTTCTACACTGCCCCGCCCAGATGCGCTCATCGATGCCGTCCT
GGTAGCATAACAGAAGCACATCCCCGTCGCTTCGAGGCCTGTACTGCATACGACCA
CATGGCCGAAATGTTCCGACGTAGCTATGGTTATGCCCCGAAGGCTGTTTCTTAA

NHI 296 protein sequence:

MHLYEPPKAPQSIPLIDLSRAGDEAGERAVAWDIHRACRETGFFYITGHGVSAALVAQH
FQFAKAFFDLPLERKMAIHMKQSPTTAGYEPIGGQVLDSQDDKAEAAPPDLKESFYCG
MELPDDHPWAIKRIRNFGHNQWPDELPEFRAH MVSYWAQMRALGDRLLALLALSLYL
PADWFASSFDMPSGTVRLIKYPPQPAQALFNQIGAGAHTDWGGVTILAQDATGGLEVR
NAAGAWIEAPPVEGSFVINLGDLMARWTNGLYNSNFHRVKNNRSGQDRYSAPFFYTA
RPDALIDAVPGSITEAHPRRFEACTAYDHMAEMFRRSYGYAPKAVS

Codon-optimized NHI 297 sequence:

ATGACGACAGCTTTTTCAACCCTGCCAATTGTTGACGTCGGCGTGCTGTCTGAAGT
TCAGCCCAAGGCCCAGGACGTCCTGGTACTTACCCAGAAGCTTTATGATGTTTTCA
CAACTGTGGGTTTTGCATATCTTGTGAACGCGCCGCTGACATTTACCCATGCTGACA
TCTTTGGATTGGCGTCAGATTTTTTTTCGCTTAGAAGAAACGGAGAAACTGCGGCTTG
CTACAAAAACGTCAGTGCCTTCCAACAGCAACACATACCGTGGCTATTTTCCTTTCC
AGCCAGGTTGTGATAGTTTGAAAGAGGGTTTTGAGATTGGGCCGGCC CAGACGCC

AGGACGTTCTGCATTCGGCAAAACACAGCGCTATGATCTCACTGAGCCGAATGTAT
GGCCGGCCGGAGCAAGTTTTTCATGATGGGCGGGTCAAATTAGAACGACTACATGCT
GAATTACAAAACTCGCCTCAACTCTGCTGCTGATGTTGGGCATTACACTGGGTAAG
CCGGCCGATTATTTTCGCTCCATATCTGCTGGAATCCCTGTCAACGTTAAGACTGCTG
CATTATCCGCCGCAAGAATCTACGGAGACTGAAGTTGCTGCTATTAAATTATGTTGTA
CACCGCACACAGATAGTGGAATTCTGACTTTGCTCCATCAAGATCAGACAGGCGGT
TTAGAGGTGTTGAATGCCGAGGGCCGATGGATTGCAGCACCTTATGTGCCTGGGTC
AATAGTCGTCAATATTGGCGATCTCATGGCCAGAGTGAGTGGCGGGCGCTTCGTTG
CTACTATGCACCGCGTCCGTACAAGCCCGGGTAAGGGCACTAGAAAAGATGGCTTA
GGTCGTTTCTCGGTTCCGTTCTTTTTTTGAACCAGGAGAGGCGTGCCTGATACGCAG
TATAGATGGGGGAGAAGGCGTTGTCTACGGGGAGTATGTGCGCCGGAAGATGGGC
ACATGGTTAGAATATCAGAGTAGTCCGACCCAAGAGCCGGATGCTACAATTGCCGT
CAGTGCTGGTATCGTAAAAGTGGCGTCCTGA

NHI 297 protein sequence:

MTTAFSTLPIVDVGVLSEVQPKAQDVLVLTQKLYDVFTTVGFAYLVNAPLTFTHADIFGLA
SDFFRLEETEKRLRLATKTSVPSNSNTYRGYFPFQPGCDLKEGFEIGPAQTPGRSAFG
KTQRYDLTEPNVWPAGASFHDGRVKLERLHAELQKLASTLLLMLGITLGKPADYFAPYL
LESLSTLRLHYPPQESTETEVAAIKLCCTPHTDSGILTLLHQDQTGGLEVLNAEGRWIA
APYVPGSIVVNIGDLMARVSGGRFVATMHRVRTSPGKGTRKDGLGRFSVPFFFEPEGEA
CLIRSIDGGEGVVYGEYVRRKMGTWLEYQSSPTQEPDATIAVSAGIVKVAS

Codon-optimized NHI 298 (XenC) sequence:

ATGGGCAGTTTGACCGACAATGCCGCGATTCCCACCGTGGATATCTCGGCGTTCTT
AGATCCTAATGCCTCGCAGGAGGCACGTCAGGACGTTGTGAATGCGATGTCGAATG
CCTGCCACGTATATGGTTTTTTCAATCTGGCGGGTTCATGGCATTCCACAAGAGACCT
TGCGCGAAGCATTCGAACTTAATAAGATGTTTTTCGCCTTGCCAGAGGAATCAAAAA
AAGAAGTGTTGATTAGTAAGTCAATCGGACAATCATTCCGTGGTTACGAGCCGCC
GGCATCCAGACACATCACAAGGGCCTTCTTCCCGATATTAAAGAGACGTTTCATGGTC
GGGCGTGAAGTACCGCTTGACGACCCTGATTGTGGCACATTCTCAACGGGTCCCA
ACCTTTGGCCCTCATCTTTACCGAAAGAGAAATTTACGACCGCATCATGGCTTACC
AGGGTAGCATGTTAGAACTTGTAAGAATATTCTTGCTATTTTGGCACAAGGGCTGC
CAAAGGAATGGGGATGCTCACCGACCGTTTTCAACTCTTTATTGGATAAGCCGAGTA
TTCCAATGCGTTTTCTTACACTACGCCCCCGTCCCCTCACAACCTTGAAGATGTACGCC
AGTTTGGGGTAGCTGACCACACTGACTTTGGTTGTGTAAGTATTTTGTGTCAGGAG
CCCGGAACCTTCGGGCTTAGAGGTCTACTATCCCCCGTCCGACTCGTGGATTCTGT
CCCAGTTATCGACGATGGATTCGTGATCAACATGGGTGATATGATGCAACGTTACAC
CGGGGGATATTACCGCTCAGCTCGCCATCGCGTCCTTACAAACCGCGAGAAACATC
GTCACAGTGTGGCGTTTTTTCTGAATGGGAACCTTGGGATTAAAGGCGAAGGCTTTA
GATGGCAGCGAAACGGAGACAGTAGTTGGAGATTGGATTCGCGGGCGTCTGATTG
ACACTATGGGACAGACGGGGAAGTTATTGCAGCGTGAGAGTCCGAAACCGGTAGT
ACTGCCG

NHI 298 (XenC) protein sequence:

MGSLTDNAAIPTVDISAFDPNASQEARQDVVNAMSNACHVYGFFNLAGHGIPQETLR
EAFELNKMFFALPEESKKEVLISKSIGQSFRGYEPPGIQTHHKGLLPDIKETFMVGREVP
LDDPDCGTFSTGPNLWPSSLPKEKFQDRIMAYQGSMLVLKNILAILAQGLPKEWGCS
PTVFNSLLDKPSIPMRFLHYAPVPSQLEDVRQFGVADHTDFGCVSILLQEPGTSGLEVY
YPPSDSWIPVPVIDDGFVINMGDMMQRYTGGYYRSARHRVLTNREKHRHSVAFFLNG
NLGLKAKALDGSETETVVGDWIRGRLIDTMGQTGKLLQRESPKPVVLP

Codon-optimized NHI 299 (SwnH2 X. hyp.) sequence:

ATGGAACAGACCGGTAAGTACAAAGAGTCTCCGGTCCCACGGCTGCTGCCGCATTT
TGACGCGAGCTATCAGCCGTCCCGCGAAATTACCAAAATCCCCGCCACGTCCAGCT
TGGAAGAAATTCTGACCCTCCTGGATCGTGATGGTGCTGTAATCCTGACCGATTTCA
TCAGTCTTGAAACGCTGGATAAAATTGATGAAGAACTGCAACCTTATACGCATCCCA
TCGTAGAAAATGATTCCTATGACAATTTTATTGGCAAAAAACGCTGGTGTTACCCGG
GTTGGTCGGCAAGAGCGATACGGTTGCGAATATTCTGGACACGAACGAAACCATCG
AAAACTTCTGAAAGTGATCTTAGAAGAACGTCACCCTGCAGTTTTTGAAGAACATA
CCGAAGAGTTAGTTGTTGAACCGTTGCTGAGCATCGCAATGGGTTTTTATGTGGGC
CATGACAGTCCTCGTCAGGCTCTTCATCGCGATGATATGATCTTCAGTTCGAAACAT
CGTGTGGACCTGAAGGTGCATGAAAATGATGGCTTCTCTTGCTTCATTGCCGGTTC
TCGTGTCACCCGGGAAAACGGCGGTACCATGGTTATTTTGGGTAGTCATAAATGGG
AACATGATCGGCGTGGCCGTCTGGATGAAGTTTCGTTCCCTGGAAATGGAGCGCGG
ATCTGCAATGATTTTTCTGGCTAGTGTCGCGCATGCCGCCGGGTATAACACTATTCC
GGGGGAAGTGCGGAAAGTAATCAATTTTGCCTTTGTTCGGGGCATCCTGCGTCAAG
AGGAGAACCAAAGTCTGTGCAACTCTCGCTCAAAAGTTCTGAAAATGTCACCGAAA
CTGCAAACGCTGCTCGGATTTAAAAAACC GGCGGGCACGTGGCTCGGTCTGGTGG
AGAATGATGATCCGGCGAAAGATCTGGCCGCCGTTTATGAGCGCGTACTGGCCTAA

NHI 299 (SwnH2 X. hyp.) protein sequence:

MEQTGKYKESPVPRLLPHFDASYQPSREITKIPATSSLEEILTLLDRDGAVILTD FISLETL
DKIDEELQPYTHPIVENDSYDNFIGKKTLVLPGLVGKSDTVANILDTNETIEKLLKVILEER
HPAVFEEHTEELVVEPLLSIAMGFYVGHDSPRQALHRDDMIFSSKHRVDLKVHENDGF
SCFIAGSRVTRENGGTMVILGSHKWEHRRRGRLEVSFLEMERGSAMIFLASVAHAAG
YNTIPGEVRKVINFAFVRGILRQEENQSLCNSRSKVLKMSPKLQTLLGFKKPAGTWLGL
VENDDPAKDLAAVYERVLA

Codon-optimized NHI 300 (SwnH2 T. ben.) sequence:

ATGGATAAAAAATATGCTGCAGCGCGTTTTGCTTCCTCCAATTGATGCCTCGTATCAG
CCGGCACGCAGCGTTACGAAAATTCGGGCAACTTCCAGTCTTGAAGAGATTCTGGA
AGTTCTGGAGCGCGATGGTGGTGTTATTTTAACGGATTTTCGTACCGAAGGAACTAT
GGATAAAATTGACGAAGAATTGGAACCGTATACGAAAACCATCCCGGACAGCGACA
GCTACGACGATTTTATCGGCAAAAAAACCTGGTGATTGCTGGACTCATCAGCAAAA
GCGATACTCTGGCAAATATCTTAGACACCAACGAGACGATTGACAAACTGCTGAAAA

TTATCCTGGAGGAGCGGTATCCGGCGGTATTTGAGGGTCATACGGAAGAGTTGGTA
ATCGACCCGTTGTTGAGTATTAGCATGGCCTTTACGTGGGTCAGGGCAGTCCACG
CCAGGCTTTACATCGTGATGATATGGTTTTTAGCAGTAAACACCACCCGAATATGAAA
ATCAACGAAGTAGATGGTTTTAGTTGCTTCATCGCGGGCAGCAATGTCACACGCGA
AAATGGCGGCACCATGGTTATCCTGGGCAGCCATAAGTGGGAACATGATCGTCGTG
GCCGCCCCGGACGAAGTCTCGTTTTTAGAAATGGAGCGCGGTAGCGCTTTTATCTTC
TTATCGACCATGGCGCATGGTGCGGGGTACAACACCATCCCGGGAGAAAATCCGTAA
GATCATGAATCTGGTCTTCTGTCGCGGGACCCTGCGCCAGGAAGAAAATCAGTTCC
TGTGTAACCCCCGCTCCAAAGTCCTTAAGATGTCCCCAAAAATGCAGACCTTACTTG
GCTTTAAAAAGCCCGCCGGTACCTGGTTGGGCATGGTGGACAACGATGATCCTGC
GAAGGATCTGCCGGCCATTTACGAAAAAATTATGCAGTGA

NHI 300 (SwnH2 T. ben.) protein sequence:

MDKKYAAARLLPPIDASYQPARSVTKIPATSSLEEILEVLERDGGVILTDVFPKETMDKID
EELEPYTKTIPDSYDDFIGKKTLLVIAGLISKSDTLANILDTNETIDKLLKIILEERYPAVFE
GHTEELVIDPLLSISMAFHVGQGSQRQALHRDDMVFSKHHPNMKINEVDGFSFCFIAG
SNVTRENGGTMVILGSHKWEHRRRGRPDVFSFLEMERGSAFIFLSTMAHGAGYNTIP
GEIRKIMNLVFCRGTLRQEENQFLCNPRSKVLKMSPKMQTLLGFKKPAGTWLGMVDN
DDPAKDLPAYEKIMQ

Codon-optimized NHI 301 (SwnH2 A. oxy.) sequence:

ATGGAGCATATGGAAGCTGTTACTAATGCGTCAGCCCCGCGCCTGCTGCCGGCGCAT
CGATGCCTCATATCAGCCATCGCGTAGCGTCACGAAAATTCCGGCGAACTCCAGTC
TGGATGATATCCTTGAGATCCTGGAGCGTGATGGCGGTGTCTGCTGACTGATTTT
GTATCGTTTGAAACACTGGACAAAATCGATATGGAAGTGGAGCCGTATACTAAGCCC
CCCGTGAATTCTGACTCATATGACGACTTCATTGGAAAGAAAACCCCTGGTCATTCCG
GGCCTGGTGGGAAAAAGCGATACAATTGCGAACATCCTGGATACCAACGAACTCT
GGAGAAACTGTAAAGGTCATTCTTGAAGAAAAATATCCGGCTGTGTTCGAAAATCA
TACCGAGGAACTGGTTGTGGAGCCACTCTTATCTATTGCGATGGCGTTTAACGTCG
GCGAAGGCTCTCCGCGTCAGGCGTTGCATCGGGATGATATGATTTTCAGTAGCAGC
CACCACGCTGATATGAAAATCAACGAAGTGGACGGTTTCTCATGCTTCTTAGCGGG
CACCCGTATTAATCGTGAAAACGGCGGGACGATGATTATTCTGGGCAGTCACAAATG
GGAACATGAACGCCGGGGACGTCCGGACGAAGTTTCCTTTCTGGAGATGGAACGC
GGCTCGGCCTTCATCTTCCTGAGCAACTTAGCCCATGGCGCCGGTTATAATACGATT
CCGGGTGAGATCCGCAAAATCATCAATCTGGTTTTCTGCCGTGGTACATTGCGCCA
GGAAGAAAATCAATTCTTGTGTAACCCTCGTTCAAAAGTTCTGAAGATGAGTCCGAA
GTTGCAAACTGCTCGGCTTCAAAAAACCGGCGCGCAATTGGCTGGGCATGGTC
GAAAACGAGGATCCGACGAAAGATCTTGCTGCGGTGTATGAAAAGATGTTGGCGTA
A

NHI 301 (SwnH2 A. oxy.) protein sequence:

MEHMEAVTNASAPRLLPAIDASYQPSRSVTKIPANSSLDILEILERDGGVVLTDVFSFE
TLDKIDMELEPYTKPPVNSDSYDDFIGKKTLLVIPGLVGKSDTIANILDTNETLEKLLKVILE

EKYPAVFENHTEELVVEPLLSIAMAFNVGEGSPRQALHRDDMIFSSSHHADMKINEVDG
FSCFLAGTRINRENGGTMIILGSHKWEHERRGRPDEVSFLEMERGSAFIFLSNLAHGA
GYNTIPGEIRKIINLVFCRGTLRQEENQFLCNPRSKVLKMSPKLQTLLGFKKPARNWL
GMVENEDPTKDAAVYEKMLA

Codon-optimized NHI 302 (SwnH2 *M. rob.*) sequence:

ATGATTAACAGTGATGCCCAGTCCGCACAGAAACAGGTAGAAGTGGAGAAGCCGG
ACGAAAAATACTCAGCACCGCGTCTGCTGCCTCCGATCCCGGACAGCTATCAACCA
GCGAAGGCGATTACCAAATCCCTGCGACGTCCTCTTTAGAGGACATTCTTGCGAT
CTTAGAGCGTGATGGGGGGGTTATCTTAACAGACTTTGTCAGCCTGCAGGAACTGG
ATAAAATCGATGAAGAGTTAGAACCCTTACACGAAATCCTCTATTGCCGATGATGATTC
GTATAATAACTTTATTGGCAAAAAAACCCCTGGTGATCCCGGGGCTGGTCCGCAAATC
GGACACAATCGCGAACATCCTGGATACGAACGAAACCATTGACAAACTGCTGAAAG
TGATTCTGGAAGAACGCTATCCAGCGGTCTTTGAACAACACACGGAAGAACTGGTG
GTGGATCCGCTGTTGTCTATCTGCATGGGTTTTTCATGTGGGGCATGGCAGCCCTCG
CCAGGCCCTGCACCGTGATGATATGATCTTTAGCAGCAAACACCGTCCTGATATGAA
AATTAACGAGGTGGATGGCTTTTCTGTTTCTTGGCTGGCACCCCGGATTACGCGCG
AAAACGGGGGTACGATGGTGATCCTGGGAAGCCACAAATGGGAACATGATCGCCG
CGGGCGCCCCGACGAAGTAAGTTTCTGGAAATGGAACGCGGCTCTGCGTTCATC
TTTCTTTCAACCTTGCGCGACGGCGCGGGTTATAATACCATTCTGGGGAAGTGCG
TAAATTACCAATCTCGTCTTTTGTGCGCGCACATTGCGCACCGAGGAGAACCAGTT
TTTGTGCGTGCTCGCAGTAAAGTGCTGAAGATGTCGCCGAAAATGCAAACGCTCC
TGGGTTTTTAAAAGCCGGCAGGGAGCTGGCTGGGCATGGTTGAAAACGAGGATCC
GGCAAAAGATTTAGAAGCGATTATGAGAAGATGCTTAAATAA

NHI 302 (SwnH2 *M. rob.*) protein sequence:

MINSDAQSAQKQVEVEKPDEKYSAPRLLPPIPDYQPAKAITKIPATSSLEDILAILERD
GVILTDFVSLQELDKIDEELEPYTKSSIADDDSYNNFIGKKTLPGLVGKSDTIANILDTN
ETIDKLLKVILEERYPAVFEQHTEELVVDPLLSICMGFHVGHGSPRQALHRDDMIFSSKH
RPDMKINEVDGFSCFLAGTRITRENGGTMVILGSHKWEHRRGRPDEVSFLEMERGS
AFIFLSTLAHAGYNTIPGEVRKITNLVFCRGTLRTEENQFLCVPRSKVLKMSPKMQTLL
GFKKPAGSWLGMVENEDPAKDLEAIYEKMLK

Codon-optimized NHI 303 (SwnH1 *E. spin.*) sequence:

ATGGGCCTGAGTATGTTACTGCCGCCGGAACCAATCGATCCGGCCTATCAGCCGTC
TACCTCTATCGCTAAAATCCCGGCTAACGCCCAATCGAAGATATTCTGGAGATTATC
GAACGCGACGGGGGTGTGATCCTTACGGAGTTTACGTCCGCTGAAGAACTGGCAG
CCATTGACCGCGATGTTGACGCGCACCGCAAGCAGACACGCGCCGAAAAAGGAG
CTCTCCCGCAGATCCCGAAAGAGACACTCAGTGTTGCAGGATTAGTTGGCAAAAGT
CCGACCGTGGCCCGCATGTGCGAATACCCCGTACTGGAAAACTGCGCACCGCTA
TTCTGCAGGAAAAATTCGATGTGATTCGTGAAGACTACGTGGACCGCAATATTATTG
AGCCGTTGCTGTGATTTGCTGACCTTCTACATTGGCCCGGGTGCGCCGCGCCA
GCGCCTCCACCGCGACGACAACACCCATGGCACGCGTCATGCGGGGGAAGGAAG

CTTCGACCTCAAGCGCGCTGGTCAATTTGCGTGCCTTGTGGCGGGCTCGAAAAC
ACGCGTGAGAATGGAGCGACCATGTTTCATTCCAGGTAGCCACAAATGGGATGACAC
CCGGGTCCCACGCATCGATGAAGTGTGCTTCGCGGAAATGGAACCGGGCAGCGC
CCTTATCTTCCTGGCTAGCTGTTATCATGGTGGCGGTCATAACAGCACGAAAGATGA
AGTACGCCGCGTCCATGGTCTCTTTTTTGTGCGCGGGACGATGCGTACCGAGGAA
AACCAGTTCCTGGCAGTACCGCGTAGCAAAGTCCTGACCATGAGCGATAAAATGCT
GAGTCTGCTGGGTTATAAGAAACCCACATCTGCCCTGGGCATTGTTGAAAACGAAG
ACCCAGCCAGCAACCTGCGTACGTTCTGGACATGGCCTCGCAATAA

NHI 303 (SwnH1 *E. spin.*) protein sequence:

MGLSMLLPPEPIDPAYQPSTSIKIPANAPIEDILEIIERDGGVILTEFTSAEELAAIDRDVD
AHRKQTRAEEKGALPQIPKETLSVAGLVGKSPTVARMCEYPVLEKLRTAILQEKFDVIRE
YVDRNIIPELLSISLTFYIGPGAPRQRLHRDDNTHGTRHAGEGSFDLKRAGQFACLVAG
SKTTRENGATMFIPGSHKWDDTRVPRIDEVCFEMEPGSALIFLASCYHGGGHNSTKD
EVRRVHGLFFVRGTMRTENQFLAVPRSKVLTMMSDKMLSLLGYKKPTSALGIVENEDP
ASNLRTFLDMASQ

Codon-optimized NHI 304 (SwnH2 *R. nec.*) sequence:

ATGGAACAGTCATCAAGCCTGCGCCTGCTTCCACCTATTGATGCGTCCTATCAGCC
GGCACGTGAAGTCACGAAGATTCCGGCCACGAGCTCTCTGGAAGAAATCCTGGCG
GTTCTCGAACGCGATGGAGGGGTGGTTCTGACGGATTTTGTAAAGCCTGCATACCAT
GGATAAAATCGATGAAGAACTCGAACCTTACGCCAATCCGATCGCCGACAACGATTC
GTATGACAACTTTATTGGCAAAAAGACGGTGGTGATTCCGGGTCTGGTGGGAAAAA
GCGATACGATCGCAAACATTATTGATACCAACGAGACCATTGAAAACTCCTTAAAGT
TTTACTTGAAGAACGTTATCCGGCCGTTTTTCGAACAACATACAGAGGAACTCGTCGT
GGATCCCCTGTAAAGCATTGCCTTAGGGTTTTATGTTGGCCATGGCAGTCCCCGCC
AGGCCCTCCATAAAGATGATATGATCTTTTCTAGTAAACACCGCCCGGATATGAAAAT
CAACGAGGTGGATGGCTTCAGCTGCTTTCTCGCCGGCACGAACATTACCCGCGAG
AACGGGGGGCACATTGGTCATCTTAGGCTCTCACAAATGGGAACACGAACGTCGTG
GCCGTGCGGACGAGGTTTCTTTTTTGGAAATGGAGCGTGGTTCGGCGTTTATTTTT
CTGGGCAACTTAGCTCATGGCTCAGGTTATAACACCATCCCCGGGGAGGTTTCGGAA
AATCATTAATTTGGTGTCTGTGCGGGGACACTGCGCCAGGAGGAAAACCAAGTTTT
TGTGCAACCCGCGTAGCAAAGTGCTGAAAATGAGCCCGAAGCTGCAAACCCTGCT
GGGCTTCAAAAAACCGGCCTCCACGTGGCTGGGTATGGTTGAAAACGAAGACCCG
GCCAAAGACCTTGCGGGTGTGTACGAAAAAGTGTTTCGCCTAA

NHI 304 (SwnH2 *R. nec.*) protein sequence:

MEQSSSLRLLPPIDASYQPAREVTKIPATSSLEEILAVLERDGGVVLTDVSLHTMDKIDE
ELEPYANPIADNDSYDNFIGKKTVVIPGLVGKSDTIANIIDTNETIEKLLKVLLEERYPAVFE
QHTEELVVDPLLSIALGFYVGHGSPRQALHKDDMIFSSKHRPDMKINEVDGFSCFLAGT
NITRENGGTLVILGSHKWEHERRGRADEVSFLEMERGSFIFLGNLAHSGSYNTIPGEV
RKIINLVFCRGTLRQEENQFLCNPRSKVLKMSPKLQTLTGFKKPASTWLGMVENEDPA
KDLAGVYEKVFA

Codon-optimized NHI 305 (SwnH1 X. hyp.) sequence:

ATGCAGGCTTTCCCGCCACCTATTGACCCCTCCTATGTGCCGTCTGTGTCTCTGGC
CGAAATTCGGCAACAGCGCCAACCGGGCGATATTATCGCCATCCTGGAACGCGACG
GGGCTCTCATTCTGACCGATCTTGTCTCTTCCCAAGATATCGCTGCGGTAAATGAGG
AATTGGAACCGTATATTCAGAAGGCCAAAGCGGAGACCCATGCCGCCTACTCGTTG
ATTCCAGGCCAAACCGTTGTAGTTCCTGGTGTCTGTGGGAAAGTCGCCGACCATGG
CGCGTATTGCCGAATTCGAAGCAATTGATCAGTTACGCACCTTAGTCCTGCAGAAAC
GTTGCACCGCGACGTGGGAAGATCGCATTGAAGAGTTCACGATCGGTCCTCTCCT
GAACAGCAGCCTGACGTACAACATTAGTTACGGTGGCCCACGTCAACGGCTGCAC
CGCGACGACATGATTCATGGTATCTATCACAGTGGCGATTATAGCCTTTCAAATGAGA
CCATGCTTGGTTTTATGATCGCGGGTTCTAAGACAACACGTGAGAACGGCGCAACG
ATGGCCGTACCGGGCAGTCATAAATGGAACCACACCCGTGTGCCCCAGACCGATG
AAGTTTGCTTTGCGGAAATGGAATTGGGTTCGCGCTGGTGTGTTTTGGGCACGGTT
TATCACGGGGCGGGTCATAAGTGTGCCGGACCAAGGTGCGTAAACTGTTCCGGCCT
GTTTTTTATTCCGGGCACTCTGCGCCCCGAAGAAAACCAAGTTTCTTGCCATCCCCC
GCTCGAAAGTGCTGGGCATGTCCGACAAAATGTTGTCCTTGTTAGGCTACAAAAAA
CCTGAGACCTGGTTGGGTATTGTTAATAACGGCGACCCGGCAGAAAATCTCCAGGA
AGTGTTCATCTGGTGAACCTGTAA

NHI 305 (SwnH1 X. hyp.) protein sequence:

MQAFPPPIDPSYVPSVSLAEIPATAPTGDIIAILERD GALILTDLVSSQDIAAVNEELEPYIQ
KAKAETHAAYSLIPGQTVVVPGVVGKSP TMARIAEFEAIDQLRTLVLQKRCTATWEDRIE
EFTIGPLLNSSLTYNISYGGPRQRLHRDDMIHGIYHSGDYSLSNETMLGFMIAGSKTTR
ENGATMAVPGSHKWNHTRVPQTDEVCF AEMELGSALVFLGTVYHGAGHNSVPDQVR
KLFGLFFIPGTLRPEENQFLAIPRSKVLGMSDKMLSLLGYKKPETWLGIVNNGDPAENL
QEVFHLVNL

Codon-optimized NHI 306 (SwnH1 A. oxy.) sequence:

ATGTCCCTCTTTCCGCCGCCCATGATCCGACTTACGTTCCGAGTACGAGCATTGC
GCGTGTGCGCCGCACTGTTCTGTAGAAGAAATGATCTCTATCATTGAGCGCGACG
GTGGCCTTATTCTGAAGTCCCTGGTGGCGGGCAAAGATGTTGCCTCCATCAACAAC
GAACTGGAACCGTATGTCGAAAAAGCCCGCGCCGAAAGCCACGCTGCGTATGATC
TCGTTCCGAAACAAACAATCATGGTCCCTGGCACCGTGGGCAAAGCCCGACAAT
GGCGAAAATCGCGGAATTAGAAGTCATCGATAAACTGCGCACCCCTCGTTCTGCAGA
AAAAATGTACAGCGACATGGGAAGATAAGACTGAAGAATTTACAATTGGGCCGCTGT
TGAATAGTAGCCTCACCTATCATATTTCCCATGGCGCCCCTCGTCAGCGTTTACATC
GCGATGATATGATTCATGGTATCTACCATT CAGGTGAATACAGCCTGTCAATGAAAC
CATGTTAGGTTTTATGATCGCGGGATCACGTACGACCCGCGAAAACGGGGCTACTAT
GGCAATTCGGGTTCTCATAAATGGAACCACTCGCGCATCCCGCGTGCAAACGAAG
TGTGCTTCGCGGAAATGGAACCGGGCGATGCGTTTGTGTTCTGCGGCACTGTATAT
CATGGCGCTGGCCATAACGCGGCGGTGGATCAGGTT CGTAAACTGTATGGTTTTATT
CTTTATCTCGGGAACCCTGCGGCCTGAAGAAAACCAATTTCTGGCTGTCCCACGCA

GTAAAGTCCTGGGCATGAGTGAAAAAATGTTAAGCCTCCTGGGCTATAAAACGCCG
GGCACATGGCTGGGCATTGTAAACAATGGTGATCCCGCTGACGACTTAGTAGAAGT
GCTGCGGTATGCGAACGAATAA

NHI 306 (SwnH1 *A. oxy.*) protein sequence:

MSLFPPPIDPTYVPSTSIARVAATVPVEEMISIIERDGGILKSLVAGKDVASINNELEPYV
EKARAESHAAYDLVPKQTIMVPGTVGKSPTMAKIAELEVIDKLRTLVLQKKCTATWEDKT
EEFTIGPLLNSSLTYPHSHGAPRQRLHRDDMIHGIYHSGEYSLSNETMLGFMIAGSRTTR
ENGATMAIPGSHKWNHSRIPRANEVCFAEMEPGDAFVFLGTVYHGAGHNAAVDQVRK
LYGLFFISGTLRPEENQFLAVPRSKVLGMSEKMLSLLGYKTPGTWLGIVNNGDPADDLV
EVLRYANE

Codon-optimized NHI 307 (SwnH1 *M. rob.*) sequence:

ATGGGGGCCTTTCCACCACCGATCGATCCAAGCTACATTCCATCGGTTTCTCTGAC
CCGCTTGCCGGCGACGGCGCCAACCGCCGACATCATCGCAACGCTGGAACGTGA
CGGAGCTTTGATCCTTGTCGATCTGGTCAGCCCGCAAGATGTTGCGGGCGATCAACG
CCGAAATTGAGCCTTACATCCAGAAAGCTCGTGCAGAGTCTCACGAGGCCTACGAT
CTGATTCCTAAACAAACGATCATGGTGCCTGGTGTGTAGGCAAATCCCCGACTATG
GCGCGGATGGCTGAGCTTGATGTAATTGACACACTGCGTACCCGTGTTTTGCAGCG
TAAATGCACCGCGACTTGGGAGGATCGGACCGAAGATTTCTCCATCGATCCTCTGC
TGAATCCAGTCTTACATATCATATTAGCTACGGGGGCCCCCGGCAACGCCTCCAC
CGTGACGATATGATCCATGGTATTTATCATCGTGGCGGCGAATATCGCCTGTCAGAT
GAAACCATGCTGGGCTTTATGATTGCGGGCAGTAAACCACTCGTGAAAACGGTGC
GACCATGGCAATTCGGGGCTCTCATAAGTGGGACCATGCGCGCGTGCCCCGCGTG
GATGAGGTCTGCTTCGCGGAGATGGAACCGGGGTGCGCTCTCGTGTTTCTGGGCA
CAGTTTACCACGGTGCGGGCCACAACCTCGGTACCGGATCAGGTCCGTAAAATTTAT
GGTTTGTTCCTTCCAGGTACCCTTCGGCCGGAAGAGAATCAGTTCCTGGCAAT
CCCGCGCAGCAAAGTTCTGGGCATGTGCGGATAAAATGCTCAGTCTGTAGGCTACA
AGAAGCCGGGTACTTGTTGGGAATTGTGAACAACGGCGATCCGGCCGAGAATCT
GGCAGAAGTGCTGGGAATGGCGAATAGCTGA

NHI 307 (SwnH1 *M. rob.*) protein sequence:

MGAFPPPIDPSYIPSVSLTRLPATAPTADIIATLERD GALILVDLVSPQDVAAINAEIEPYIQ
KARAESHEAYDLIPKQTIMVPGVVGKSPTMARMAELDVIDTLRTRVLQRKCTATWEDRT
EDFSIDPLLNSSLTYPHSHGAPRQRLHRDDMIHGIYHRGGEYRLSDETMLGFMIAGSKT
TRENGATMAIPGSHKWDHARVPRVDEVCFEMEPGSALVFLGTVYHGAGHNSVPDQV
RKIYGLFFIPGTLRPEENQFLAIPRSKVLGMSDKMLSLLGYKKPGTWLGIVNNGDPAEN
LAEVLGMANS

Codon-optimized NHI 307 (SwnH1 *T. ben.*) sequence:

ATGCCGGAGTTCCCGCCGCCTATTGATCCTAGCTACGTGCCATCAGTGTCAGTACTGAC
GCGTATCCCAGCGAACGCGCCGATCGAAGATATCTTGGCCGTGCTGGAACGTGAT
GGCGGTCTTATCTTAACGGACATTATCTTCCCAGGATGTGGCCGCCATTAACGAC

GAACTGGATCCGTATGTGCAAAAGGCACGTGCCGAATCACACGCGGCATACGACCT
GATCCCGAAACAACTATCATGGTCCCCGGGATCGTGGGCAAATCTCCGACTATGG
CCAAAATCGCAGAATACGAAGTTATTGATAAACTGCGCACTATGGTTCTGCAGAAAA
AATGCACTGCGACCTGGGAGGATCGTACCGAAGAGTTCACCATTTGGACCTCTGCTG
AATTCGTCCCTGACGTATAATGTTTCTTATGGTGGCCCGCGCCAGCGCCTGCATCGT
GATGATATGATTCACGGTATCTATCATCACGATGGTGAGTATTCTCTGTGCAACGAGA
CAATGCTGGGTTTTATGTTTGCTGGCTGCAAGACCACCCGCGAAAACGGCGCGAC
CATGGCTATCCCGGGCTCGCACAAATGGAATCATACCCGTGTTCCGCGTACAGACG
AGGTGTGTTTCGCGGAAATGGAACCGGGTTCGGCCTTCGTGTTTCTGGGAACTGT
GTACCACGGGGCAGGCCATAATTCGGTGCCGGATCAGGTTGCAAGGTTTACGGT
CTTTTTTTTATCAGCGGGACCTTACGTCCTGAAGAAAATCAATTTCTGGCTATTCCCC
GTTCCAAAGTGCTGGGAATGTCTGATAAAATGCTGTGCTGCTGGGATATAAAAAAC
CGGAAACCTGGTTGGGCATCGTTAATAACGGTGACCCGGCAGAGAACCTGAAGGA
GGTTCTCGATATGGCAAACCTCGTAA

NHI 308 (SwnH1 T. ben.) protein sequence:

MPEFPPPIDPSYVPSVSLTRIPANAPIEDILAVLERDGGILTDIISSQDVAAINDELDPYVQ
KARAESHAAYDLIPKQTIMVPGIVGKSPTMAKIAEYEVIDKLRTMVLQKKCTATWEDRTE
EFTIGPLLNSSLTYNVSYGGPRQRLHRDDMIHGIYHHDGEYSLSNETMLGFMFAGCKT
TRENGATMAIPGSHKWNHTRVPRTDEVCFMEMPGSAFVFLGTVYHGAGHNSVPDQ
VRKVYGLFFISGTLRPEENQFLAIPRSKVLGMSDKMLSLLGYKKPETWLGIVNNGDPAE
NLKEVLDMANS

Codon-optimized NHI 309 sequence:

ACGATGGCCACCACAACCTAGCAGCTCGTTTTACATCCCCACCGTTGATATCTCTCCG
TTTCTGAAAGATCCTTCAAGCCCAGCCGCGCAGCAAGTCATCGAGGATGTACGGGC
AGCGTGATGAGCACGGGATTCTTCCAGATCACGGGCCATGGTATCCCTAAAGAGT
TACAACAATCAGTTTTCGAGGCTGCCAAGAGATTCTTCGCCTTGCCATTCGAGGAAA
AGAAGAACTCGACGCAAAGAAGAACGTAGGCCATCGTGGCTACGATGTCTTAGGT
AGCCAGTCATACGAGGATGACGTGTTACCGGATCTGAAAGAGGGCTTCTTTGTGGG
ACAGGATATACCACCTGACGACCCTCGGGTACAGGCGCGTCGGTTCTTCATGGGTC
CAAATGTTTGGCCACCCACGAGTCTTCTCCCGCCCGAGGAGTTTCGGGAACCCGT
AGAAGAATACTACGCGGCGATGTACAAATTATCACTACCGTGCTTGATCTCATTGC
TCGGACACTGCCGTACGGACCTCATGTGTTTCGACGAGTTCAAGTCCAACAACCCTG
CCGCACCGATGCGCCTGCTTCACTACCCGCCGGCCCGCTCGACCGACAAGCGGC
AATTAGGGGCTTCAGCACACACCGACTTTGGAGCAATTACATTGCTGCTTCAGGAC
GAAAATCCCGGATTGCAAGTGCTGGATCAAAGACGGGCGAATGGGTGGACGTTTC
CACCAAACCCTGACGCTTACGTTGTAAACGTTGGGGATATGTTGAGCAAGTGACACA
GGCGGACACTACAAGAGTTCAGTGACACAGAGTGATCAATAAGAACCCTACAGATCG
CTACAGTGTTGTTTTCTTCTTTGATGGGAACCTTGACTGTCCACTGTCTCCGCTGGA
CGGATCTGAGCCGGGCGCTGACAGTTGAGGAACACATGATCGAGCGCATGACAACG
AGCTACGGTAAGAAGAAGTAA

NHI 309 protein sequence:

TMATTTSSSFYIPTVDISPFLKDPSSPAAQQVIEDVRAACMSTGFFQITGHGIPKELQQS
VFEEAKRFFALPFEEKKKLDAKKNVGHARGYDVLGSQSYEDDVLPDLKEGFFVGGDIPP
DDPRVQARRFFMGPVWPPTSLLPPEEFREPVEEYAAAMYKLSLTVLDLIARTLPYGP
HVFDEFKSNNPAAPMRLHYPPARSTDKRQLGASAHTDFGAILLLQDENPGLQVLDQ
KTGEWVDVPPNPDAYVVNVGDMLSKWTGGHYKSSVHRVINKNPTDRYSVVFVFDGN
LDCPLSPLDGSEPLTVEEHMIERMTTSYGKKK

Codon-optimized NHI 310 sequence:

ACAACGGCGGCCCGAAACCATACCTACGGTGGATATCTCCCCCTGGCTGTGCGCCAAA
TGCCAGCGAGGAAGCTAAGGACCAGGTAGTGGAAGCTGTATCTCATGCGTGCTCA
ACATACGGCTTTTTTAACCTGGTAGGCCATGGTATTCCTGTCTGAAGAGCAGCAAAAAG
ATCCTGGATTGTGCCAAAGCTTTTTTTGACTTGCCTCTGGAAGAAAAAATGGAAGTC
AGTATCGACAAGTCCATGGGTAAGTCGTTTCAGAGGGTATGAACCCTCTCGTATTCAA
ACTCACCAAGAAGGGCTGTTACCAGACACCAAAGAGTGTTTTATTATTGGAGCGGA
AGTTCCTGCGGACGACCCTGACGCCGGTACCTTTTCTACCGGGCCTAACCTGTGG
CCGAAGTCCCTGCCGGACGAAGAATTCGAACCCCAATAATGGAGTATAGAGCCCG
TATGCTGGAGTTAGTTAAAGTTTTGTTACGCATTTTAGCAAGAGGATTACCGAAGGAA
TGGAATTGCCCGCCTGACGTCTTTGACGAGTTCTTGATAAACCCATCGATCCCAATG
CGCCTTTTACACTACGCTCCCCAGACTTCTACTGACCCACGCCAATTTGGCGTAGG
AGATCACACCGACTTCGGCTGCATAACGATTCTCCTTCAGCAACCGGGAAGTAAGG
GGCTTGAAGTCTGGTACCCGCCAACAGAGACGTGGATTCCCGTGCCGGTTGTGGA
AAACGCATTCGTGATTAACATGGGCGACATGATGCAGAAATGGACCGGTGGTTACTA
CCGGAGCGCAAGACACCGAGTCATAACATCGGGTGAGAAACATAGATATTCCGTCC
CGTTCTTTCTCAATGGTAACCTGAAATTGAAAATCAAACCGCTGGACGGATCAGGTG
AGGAAACAACAGTGGGCGAACACATTAGACAACGATTGGCAAAGACGTTAGGAGA
GAATGGTAAGGCGCTGAAGTGA

NHI 310 protein sequence:

TTAAETIPTVDISPWLSPNASEEAKDQVVEAVSHACSTYGFFNLVGHGIPVEEQQKILDC
AKAFFDLPLEEKMEVSIDKSMGKSFRGYEPSRIQTHQEGLLPDTKECFIIGAEPADDP
DAGTFSTGPNLWPKSLPDEEFRTPIMEYRARMLELVKVLLRILARGLPKEWNCPPDVF
DEFLINPSIPMRLHYAPQTSTDPRQFGVGDHTDFGCITILLQQPGTKGLEWYPPTET
WIPVPVVENAFVINMGDMMQKWTGGYYRSARHRVITSGEKHRYSVPPFLNGNLKLKIK
PLDGSGEETTVGEHIRQLAKTLGENGKALK

Codon-optimized NHI 311 sequence:

ATGACAACAACCTGCACCGGAGGCCATCCCGACGGTTGATATTTCTGCATGGCTGTC
ACCAAATGCATCCGAAGAGGCCAAAACAGCAGGTGGTGGGAAGCCATGCGCCACGCT
TGTAACACATATGGTTTTTTTTATCTGGTTGGACATGGCGTTTCGCCTGAAGAGCAA
CAAAAAGCTCTGGATTGCACCAAATTGTTCTTTGCCCTTCCAATGGAGGAGCGCAT
GGAAGTTTGGATAGGAAAATCCATGGGGAAGTCTTTTAGAGGTTATGAGCCCCCGG

GTATCCAAACTCACCATGAAGGCTTGTTGCCCGACACCAAAGAAACCTTTATGGTTG
GCGCTGAGGTCCCTGCTGATGATCCTGATGCGGGGACATTTAGCACGGGCCCCAA
TCTGTGGCCAAAATCCCTGCCAGATGAAGAGTTTCGTACACCTGTTATGGAATATCA
GGCGAAAATGGTGGAATTGGTTAAAGTTCTGCTTAAAATCCTGGCGCGGGGTCTGC
CCAAAGAGTGGAATTGTCCGCCAGATGTGTTTGATGAACTGGCGGTGAACCCTTCC
ATACCTATGCGCCTCCTGCATTATGCACCGCAGCCAGTTAGAGATGATCGTCAGTTT
GGGGTGGCCGACCATAACCGACTTTGGCTGCATTACAATTTTGTCTGCAGGAGCCGG
GTACCAAAGGGCTGGAGGTTTGGTATCCGCCGACAGAAACGTGGATCCCGGTGCC
TGTAAGGAAGGTGCGTATGTAATTAACATGGGTGATATGATGCAAAAATGGACGGG
AGGGTATTATCGGAGTGACGACATCGTGTCTAACTAGCAGTGACAAACACCGGT
ACAGCGTGGCTTTTTTTCTGAATGGCAATCTCAAACCTGAAATGTAAAGCCTTAGACG
GGTCCGGTGCCGAAACTGTCGTGGGGGAACATATCCGTCAGCGTCTTATCGAGAC
TATGGGTGAAACAGGTAAAATGCTGAAATAA

NHI 311 protein sequence:

MTTTAPEAIPTVDISAWLSPNASEEAKQQVVEAMRHACTTYGFFYLVGHGVSPEEQQK
ALDCTKLFFALPMEERMEVWIGKSMGKSFRGYEPPGIQTHHEGLLPDTKETFMVGAEV
PADDPDAGTFSTGPNLWPKSLPDEEFRTPVMEYQAKMVELVKVLLKILARGLPKEWNC
PPDVFDELAVNPSIPMRLHYAPQPVRDDRQFGVADHTDFGCITILLQEPGKGLEVWY
PPTETWIPVPVKEGAYVINMGDMMQKWTGGYYRSARHRVITSSDKHRYSAFFLNGN
LKLKCKALDGSGETVVGHIRQRLIETMGETGKMLK

Codon-optimized NHI 312 sequence:

ATGGGCTCGACCACAAGTTCGGCGGCCATTCCCACCGTTGATATATCAGCGTTTTTA
TCTCCAAATGCTTCAGAAGAAGCCCGTCAGCAAGTAGTGGAGGCTATGCGTCACGC
GTGTACTACTTATGGCTTTTTTAATCTGGTAGGGCACGGAATTCCTCAGGAGGAATTA
CAAGAAGCATTGAGTGTTCTAAGCTGTTTTTCGCCCTTCCGGAAGAGAAACGGAT
GGAGGTCTGGATAGGTAAATCTGTTGGCCGGTCATTTAGAGGATATGAACCACCAG
GTATTCAAACCCATCACGAGGGTTTACTGCCAGACACTAAAGAACTTTTATGGTGG
GCCGGGAAGTCCCCGCTGATGACCCTGATTGTGGAAGTTTCTCTACTGGTCCGAAT
TTGTGGCCGAGCAGTTTACCAAAGGAAGAGTTTCAAGATCCCGTAATGGCATACCA
AGCAAGAATGCTGGAGTTGGTGAAGGTCATTCTTAAATTTTGGCCCAAGGGCTTC
CGAAGGAGTGGGGCTGCCCCCGGATGTTTTTGATTCACTGGCTGTGAACCCGTC
CATCCCAATGCGATTCCTTCATTATGGACCCGTTCAAGTTAAAGACCCGCGCCAGTT
TGGTGTTGCCGATCATACAGATTTTGGATGCGTTACGATTCTGCTGCAAGAACCTGG
TACGGAGGGCCTGGAGGTATGGTACCCGCCAACAGAGACATGGATTCCTGTTCTCTG
TTGTAGAGGATGGATTTGTCATTAATATGGGTGATATGATGCAAAAATACACTGGGGG
GTACTATCGCTCAGCCCGTCATCGAGTTATCACATCATCTGATAAACACCGTTACTCA
GTCGCATTTTTCTTAAATGGAAATTTAAAGTTAAAGGCAAAAGCCTTAGATGGCTCAG
GAGCAGAGACCGTTGTGGGAGAGCACATACGACAACGTTTAATCGAGACCATGGG
CGAAACTGGTAAGTTACTGAAATAA

NHI 312 protein sequence:

MGSTTSSAAIPTVDISAF LSPNASEEARQQVVEAMRHACTTYGFFNLVGHGIPQEELQE
AFEC SKLFFALPEEK RMEVWIGKSVGRSFRGYEPPGIQTHHEGLLPDTKETFMVGREV
PADDPDCGSFSTGPNLWPSSLPKEEFQDPVMAYQARMLELVKVILKILAQGLPKEWGC
PPDVFD SLAVNPSIPMRFLHYGPVQVKDPRQFGVADHTDFGCVTILLQEPGTEGLEVW
YPPTETWIPVPVVEDGFVINMGDMMQKYTGGYYRSARHRVITSSDKHRYSVAFFLNG
NLKLKAKALD GSGAETVVGEHIRQR LIETMGETGKLLK

Codon-optimized NHI 313 sequence:

ATGGG CACCAACAAGCGCAACCGCAGCTATTCCGACTGTAGATATCTCAGCATTTTTG
TCCCCGACGGCATCAGAAGCGGCTCGTCAGCAAGTAGTTGAAGCTATGTCACACG
CTTG TACGACCTACGGGTTCTTTAACTTGGTGGGTCATGGTATACCC CAGGAAGCA
CTTCAACAGGCCTTTGAATGTAACAAAATGTTTTTTGCTCTTCCTCAGGAAAAACGC
ATGGAGGTATGGATTGGTAAAAGCCTCGGGAGATCTTTTCGTGGGTACGAGCCCCC
TGGAATACAAACGCATCATGAAGGCCTGCTCCCGGATACGAAAGAGACTTTTATGGT
CGGCCGAGAAGTCCCGGAGGATGACCCAGATGCTGGCAGCTTCAGCACGGGTCC
CAATCTGTGGCCGTCATCGCTGCCGAAAGAGGAATTCAGGACCGTGTGATGGACT
ACCAGGCACGTATGGTAGAGTTAGTAAAAGTGATCCTGAAAATCTTGGCACAGGGA
CTTCCGAAAGAATGGGGATGCCCCCGGATGTATTGATTGATTGACCGTCGACCC
TTCGATTCCGATGCGTTTCCTTCACTACGGTCCAGTACCAGTCCGGGACCCGCGCC
AATTCGGCGTGGCCGATCACACGGATTTTGGTTGTATTAGCATCCTGTTGCAGGAAC
CAGGCACCAAGGGGCTGGAAGTTTGGTACCCGCCACCGAGACATGGGTTCGGG
TGCCTGTTGTGGAAGATGGTTTTGTGATAAATATGGGCGATATGATGCAGAAATACAC
TGGGGGCTATTACAGATCAGCACGCCATAGAGTTATTACGAATTCGATAAACATCG
ATATTCAGTTGCGTTCTTTCTGAATGGTAATTTAAAATTGAAATGTAAAGCACTGGAC
GGTTCTGGCGCAGAAACAGTGGTAGGTGAACATATCCGGCAGAGACTCATTGAAAC
TATGGGCGAAACGGGCAAGCTCCTGCAGTAA

NHI 313 protein sequence:

MGTT SATAA IPTVDISAF LSP TASEAARQQVVEAMSHACTTYGFFNLVGHGIPQEALQQ
AFEC NKMF FALPQEKRMEVWIGKSLGRSFRGYEPPGIQTHHEGLLPDTKETFMVGRE
VPEDDPDAGSFSTGPNLWPSSLPKEEFQDRVMDYQARMVELVKVILKILAQGLPKEW
GCPPDVFD SLTVDP SIPMRFLHYGPVPVRDPRQFGVADHTDFGCISILLQEPGTKGLEV
WYPPTETWVPVPVVEDGFVINMGDMMQKYTGGYYRSARHRVITNSDKHRYSVAFFLN
GNLKLKCKALD GSGAETVVGEHIRQR LIETMGETGKLLQ

Codon-optimized NHI 314 sequence:

ATGGG TAGCCAAACAAGTGACTCAGCTATACCGACAGTTGATATTTCCGGCGTTCCTG
AGTCCTACTGCCTCCGAAGCGGAGCGCAGACAGGTGGTGGAGGCAGTTCGGCAT
GCGTGTACCACGTATGGTTTTTTTAACTCTGGTCCGCCATGGTATTCCGCATGAACAG
CTTCAGCAAGCCTTTGAATCTTCTAAGTTGTTCTTTGCCCTGCCGGAAGAAAAGCGT
ATGGATGTGCACGTGGGCAAAGCTTTAGGCCGGAGCTTCCGTGGTTGGGAACCCC
CTCTTATACAGCAACATCAGGAAGGGCTGTTGCCGGACACAAAAGAGACATTCATT
GTAGGGCGCGAAGTGCCCGCGGATGATCCGGAAGCAGGGAGCTTCCTTACTGGG

CCGAATCTGTGGCCAGATCTGCCTAAAGAAGAGTTTCAGGATGTTGTCTTGGCGTA
CCAAGCTCGTATGGTCGAGCTGGCCAAAGTTATTGTCCGTATCTTGGTTCAAGGCC
TGCCCGAAGAATGGGGTTGTCCCCCAGACGCACTTGATGGACTCACAGTGGACCC
CGCAATTCGGATGCGCTTTCTTCATTATGGCCCCGTAAAGAGAAAGATCCGCGCCA
GTTTGGTGTGGCGGCACATACAGACTTCTCAGCGATTACTATTTTATTACAGCAGCC
AGGAACTGAGGGTTTGCAAGTGTGGTACCCACCTACAGAGGATTGGATCCCAGTAC
CCGTAGTTGAGGATGGTTTCGTAATTAACATTGGAGATTTAATGCAAAAATATACCGG
GGGCTATTATCGAAGCGCCCCGACATAGAGTTATAACTTTCTCTGAGAAAGATAAACA
CCGATATTCTATTGCGTTTTTTCTTGATGGTAACTTGCAGTTCAAGACCAAGGCTTTA
GACGGGTCAGGAGAAGAAACGGTGGTAGGTGAATATGTGCGTTCGTGTCTGATGG
GCACCTTAGGAACTCGCGGCCCTTTACTGTGA

NHI 314 protein sequence:

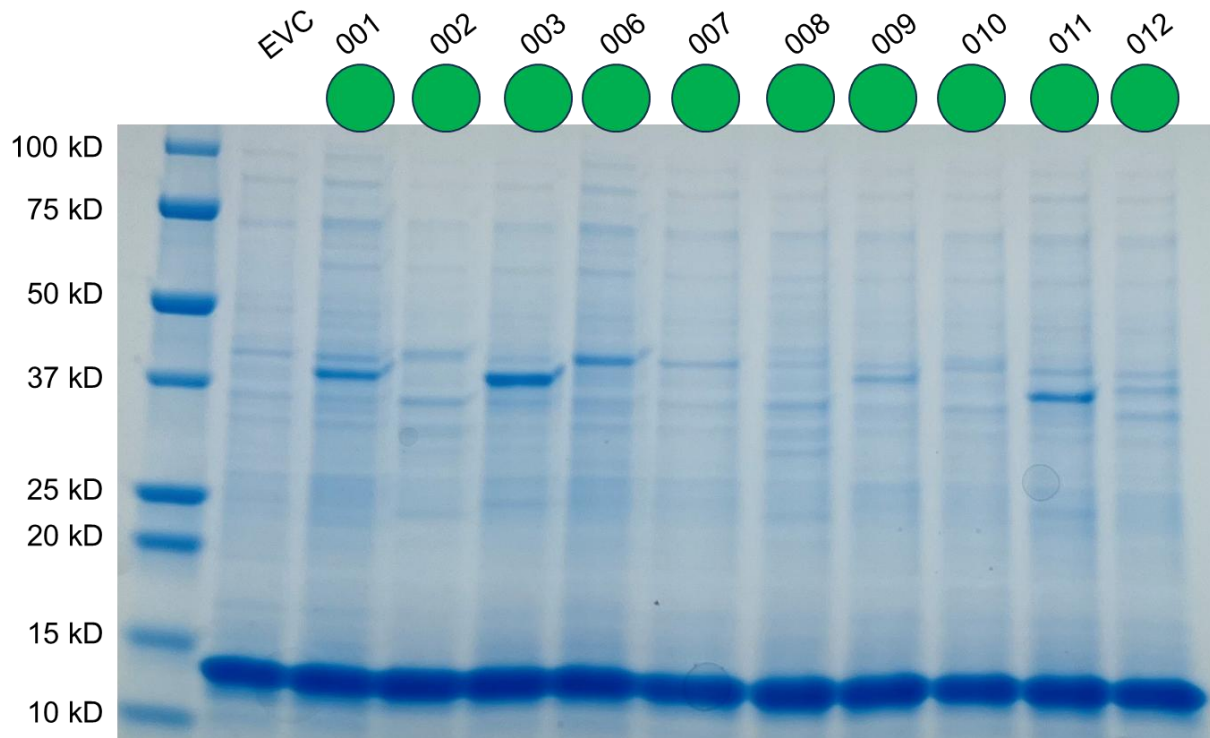
MGSQTSDSAIPTVDISAFLSPTASEAERRQVVEAVRHACTTYGFFNLVGHGIPHEQLQQ
AFESSKLFFALPEEKRMVDVHVGKALGRSFRGWEPPLIQHQEGLLPDTKETFIVGREV
PADDPEAGSFLTGPNLWPDLPKEEFQDVVLAYQARMVELAKVIVRILVQGLPEEWGCP
PDALDGLTVDPAIPMRFLHYGPVKEKDPQFGVAAHTDFSAITILLQQPGTEGLQVWYP
PTEDWIPVPVVEDGFVINIGDLMQKYTGGYYRSARHRVITFSEKDKHRYSIAFFLDGNL
QFKTKALDGSGEETVVGEYVRSCLMGTLGTRGPLL

7. Protein overexpression in 96-well plate format

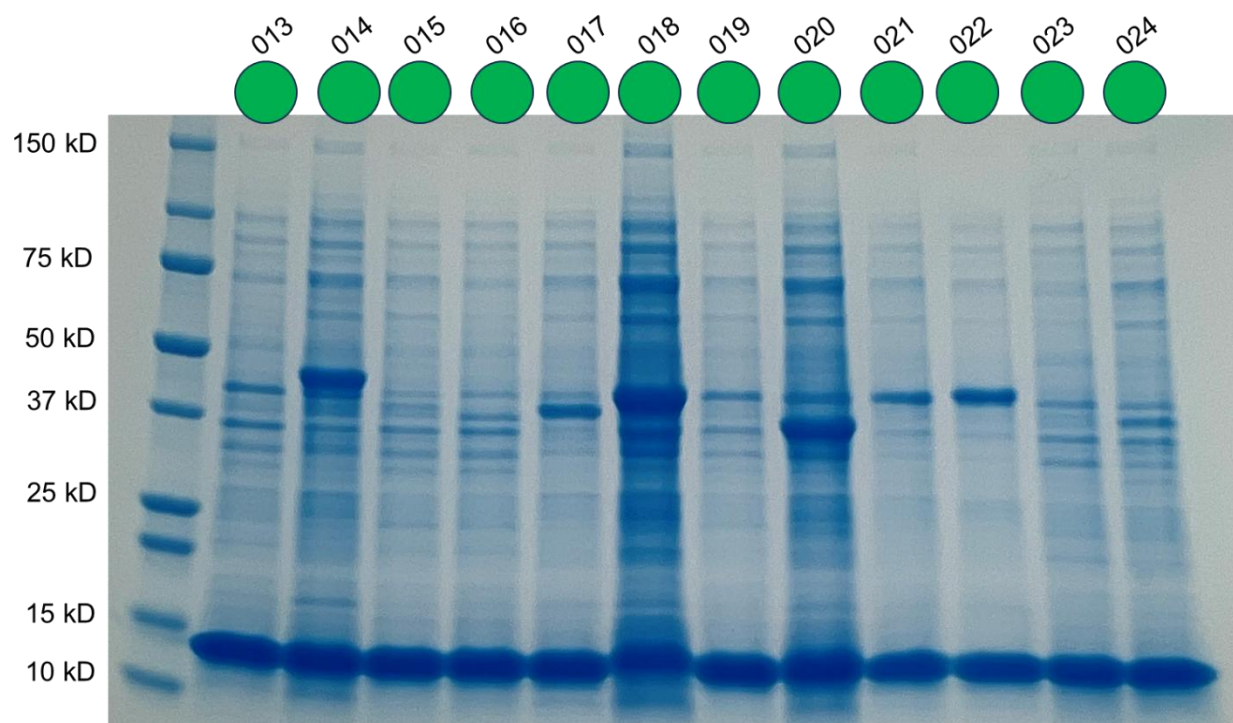
Chemically competent *E. coli* BL21(DE3) cells were transformed using standard heat-shock protocols to incorporate the plasmids for *NHI* 1-314. Glycerol stocks of these cells were grown and stored in 96-well plate format at -78 °C for further use. Overexpression of the full library (*NHI* 1-314) was achieved using 4% v/v glycerol Terrific Broth (TB) in 4 separate 2 mL 96-well plates. 500 µL portions of autoclaved media were inoculated with 50 µL of overnight culture prepared from the glycerol stocks of each *NHI* in Lysogeny Broth (LB) and 50 µg/mL kanamycin (Gold Biotechnology). One 500 µL overnight culture plate of each of the four sections of the full library (Plate 1 – *NHI* 1-96; Plate 2 – *NHI* 97-192; Plate 3 – *NHI* 193-288; Plate 4 – 289-314) was used to inoculate 10 growth plates for protein overexpression. Cultures were covered with breathable films and grown at 37 °C and 300 rpm until the optical density (at 600 nm) reached 0.8, approximately 4 h for most plates. The cultures were then cooled to 20 °C for 20 min and protein expression was induced by adding 50 µL of 5 mM isopropyl-β-D-1-thiogalactopyranoside (IPTG, Gold Biotechnology) to each well. Expression was continued at 20 °C overnight (approximately 18 h) at 300 rpm. The 96-well plates were then removed from the incubator and centrifuged at 1250 x g for 20 min. The majority of the supernatant media was then carefully poured off the plates and the plates were then placed upside down on paper towels and gently tapped to remove as much excess moisture as possible without dislodging the pelleted cell from the wells. Plates were then sealed with foil covers and stored at -78 °C for up to one year before use in whole cell reactions.

8. Gel electrophoresis of enzyme library

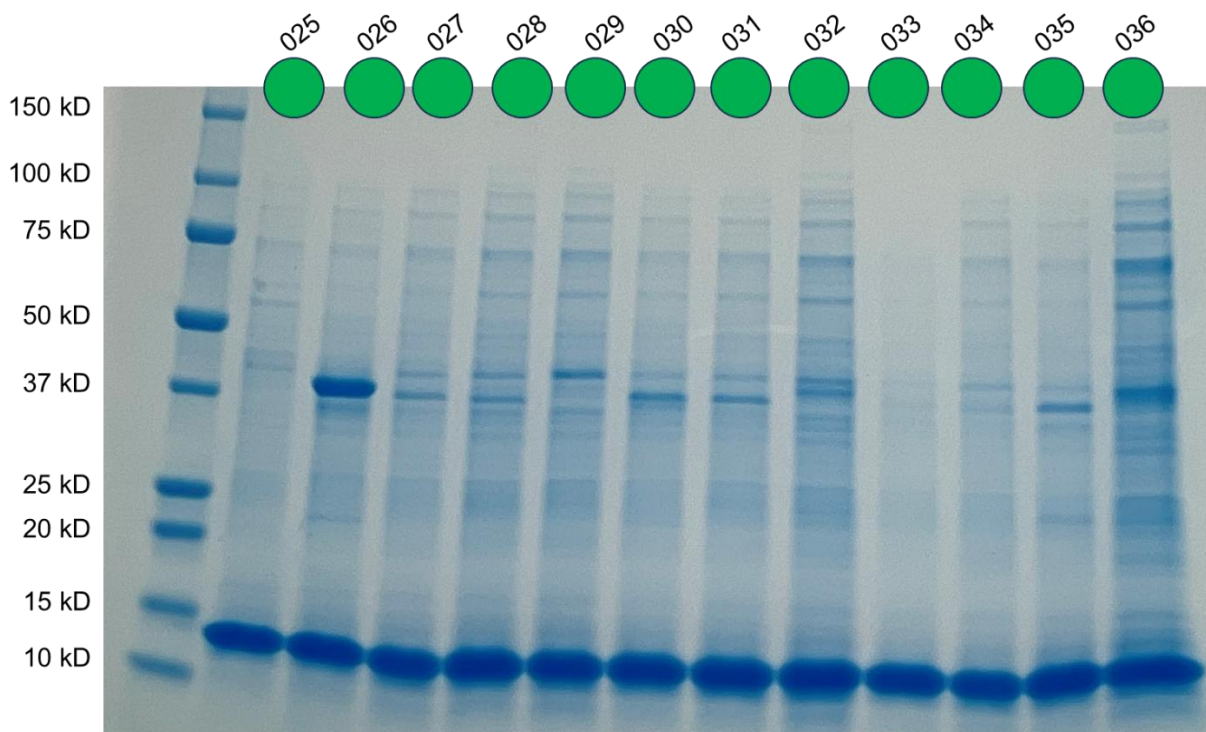
To analyze whether the enzymes selected from the family-wide NHI sequence similarity network were expressed in a soluble form, NHI 1-314 were grown and overexpressed using the glycerol stocks in 96-well plate format followed by lysis using freeze-thaw (4 cycles – 5 min in liquid N₂ and 15 min in warm water). The cell pellets were then resuspended in 200 μ L of buffer containing TES (pH 7.5, 50 mM), NaCl (300 mM), glycerol (10%), and lysozyme (50 mg/mL). The plates were shaken at 20 °C and 200 rpm for 2 h before centrifugation at 1250 x g for 20 min. For the SDS-PAGE gels 10 μ L of the clarified supernatant of each well was taken for analysis. A protein ladder standard was loaded in the first lane.



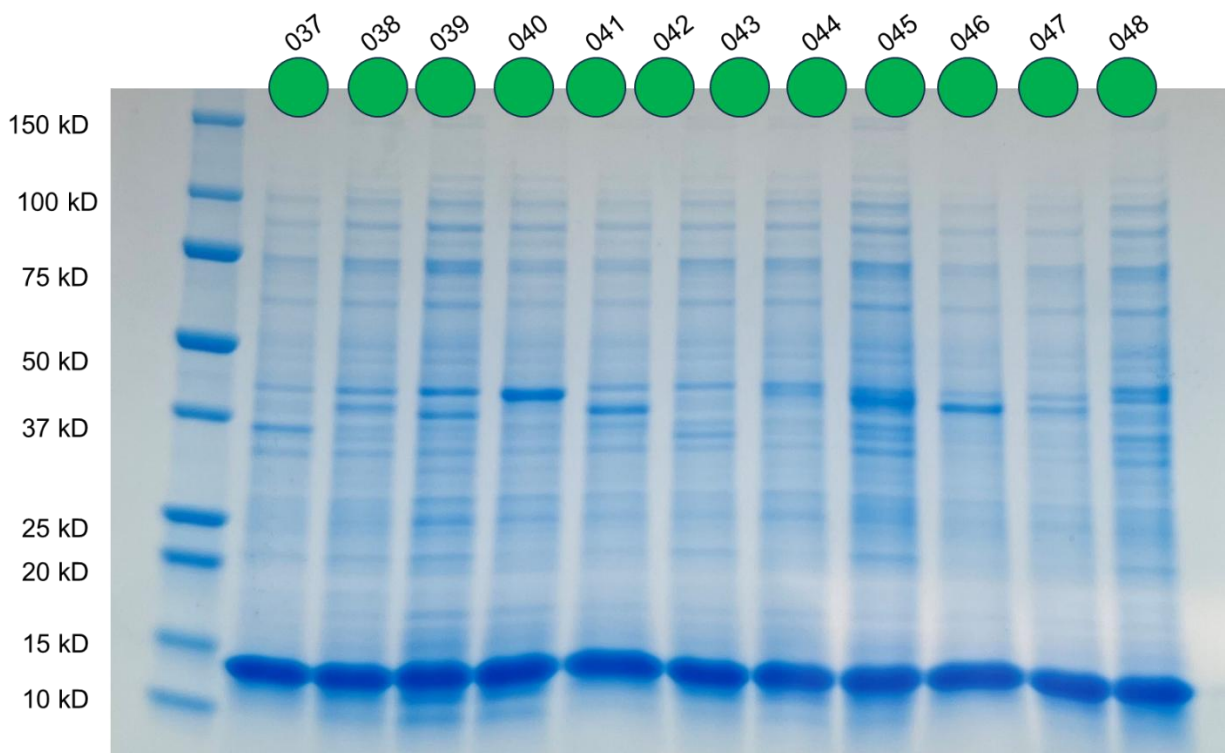
Supplemental Figure S6. SDS-PAGE gel #1 of NHI library clarified lysate (protein ladder standard in first lane labeled in KDa)



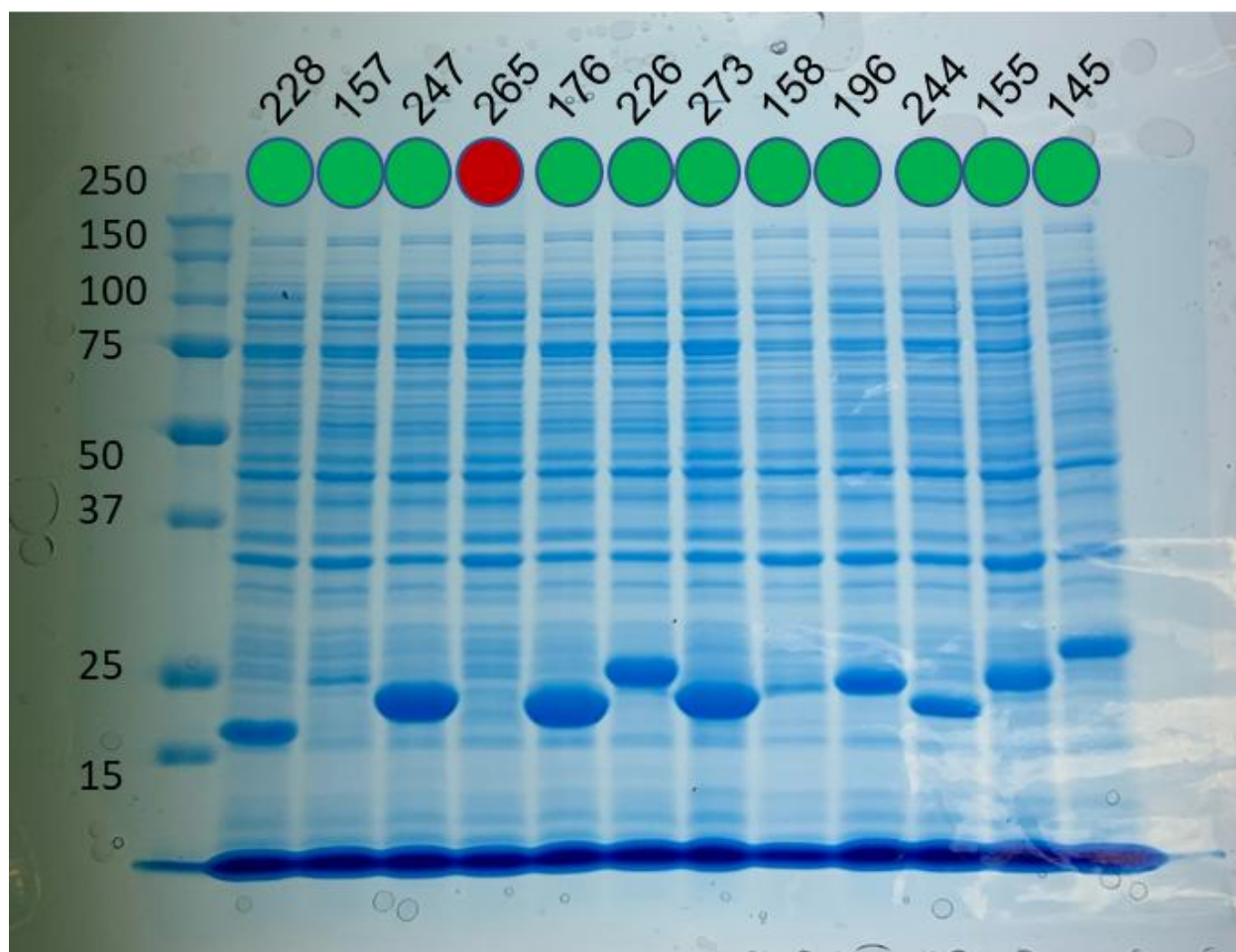
Supplemental Figure S7. SDS-PAGE gel #2 of NHI library clarified lysate (protein ladder standard in first lane labeled in KDa)



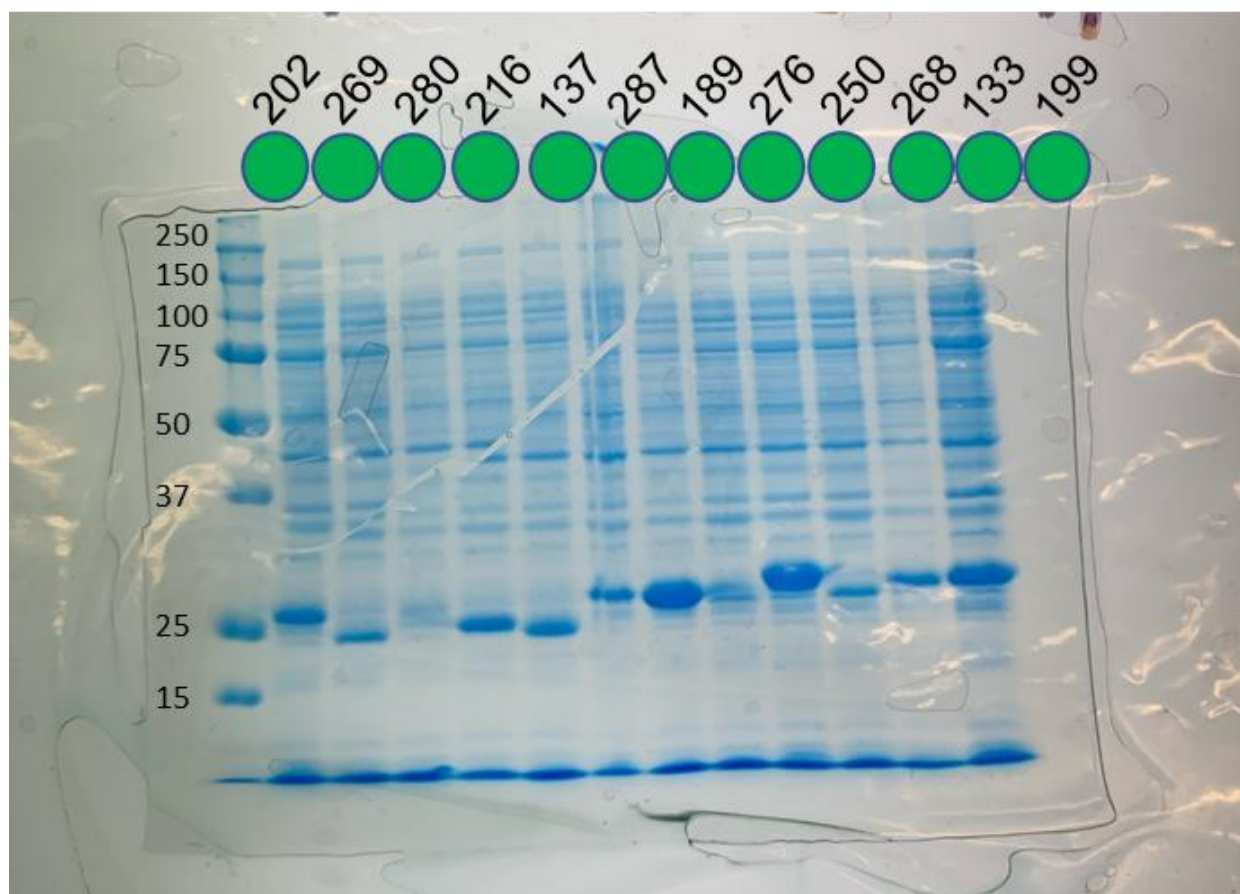
Supplemental Figure S8. SDS-PAGE gel #3 of NHI library clarified lysate (protein ladder standard in first lane labeled in KDa)



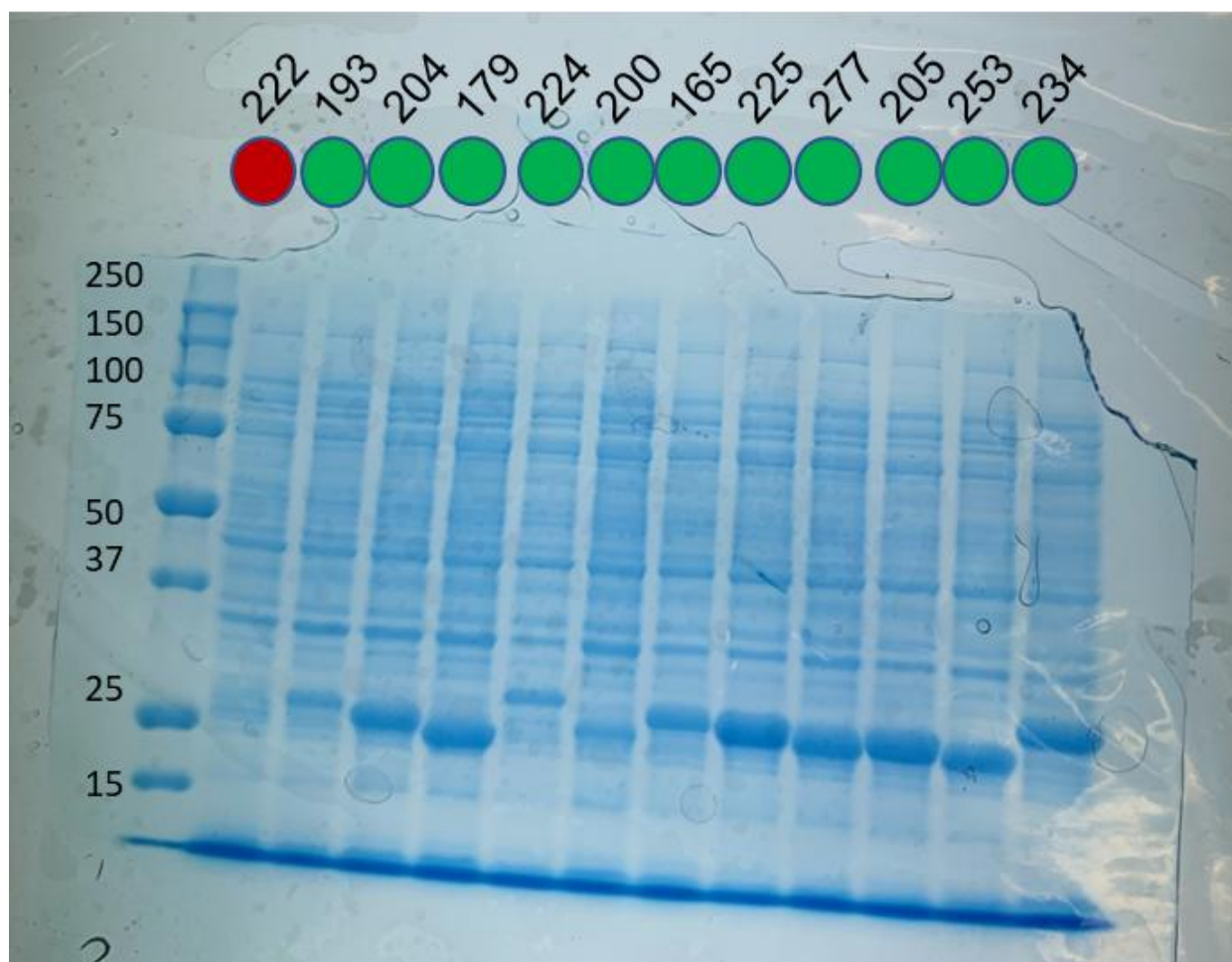
Supplemental Figure S9. SDS-PAGE gel #4 of NHI library clarified lysate (protein ladder standard in first lane labeled in KDa)



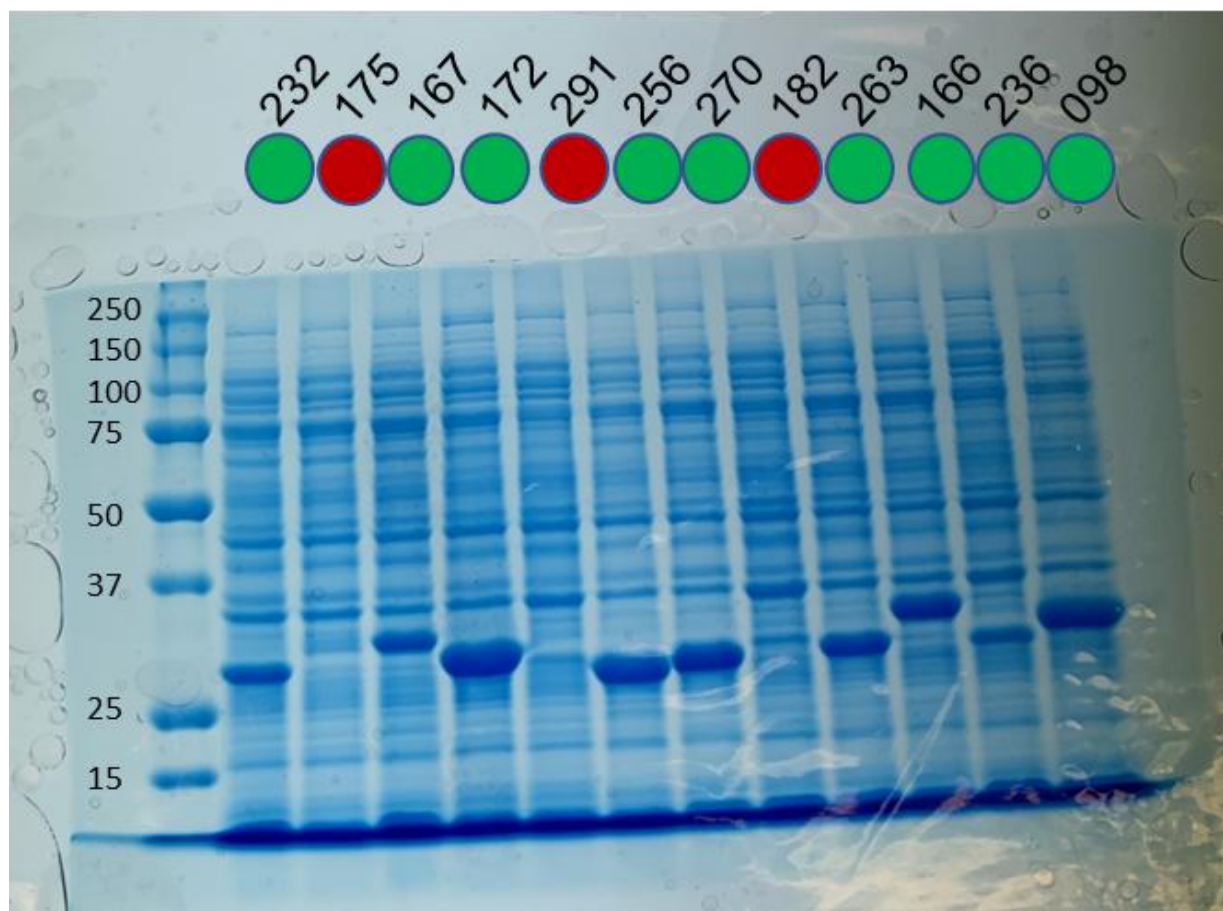
Supplemental Figure S10. SDS-PAGE gel #5 of NHI library clarified lysate (protein ladder standard in first lane labeled in kDa)



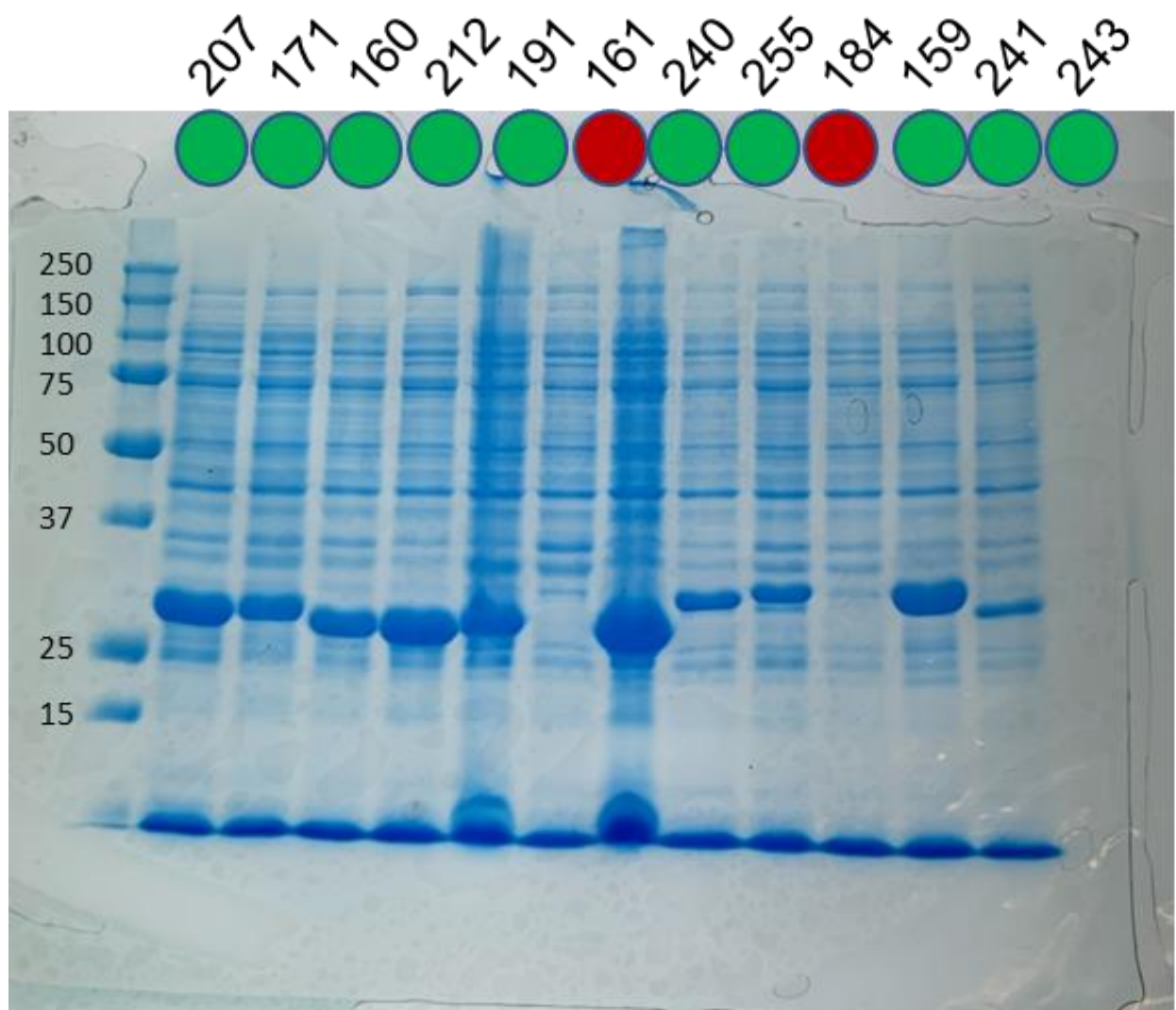
Supplemental Figure S11. SDS-PAGE gel #6 of NHI library clarified lysate (protein ladder standard in first lane labeled in kDa)



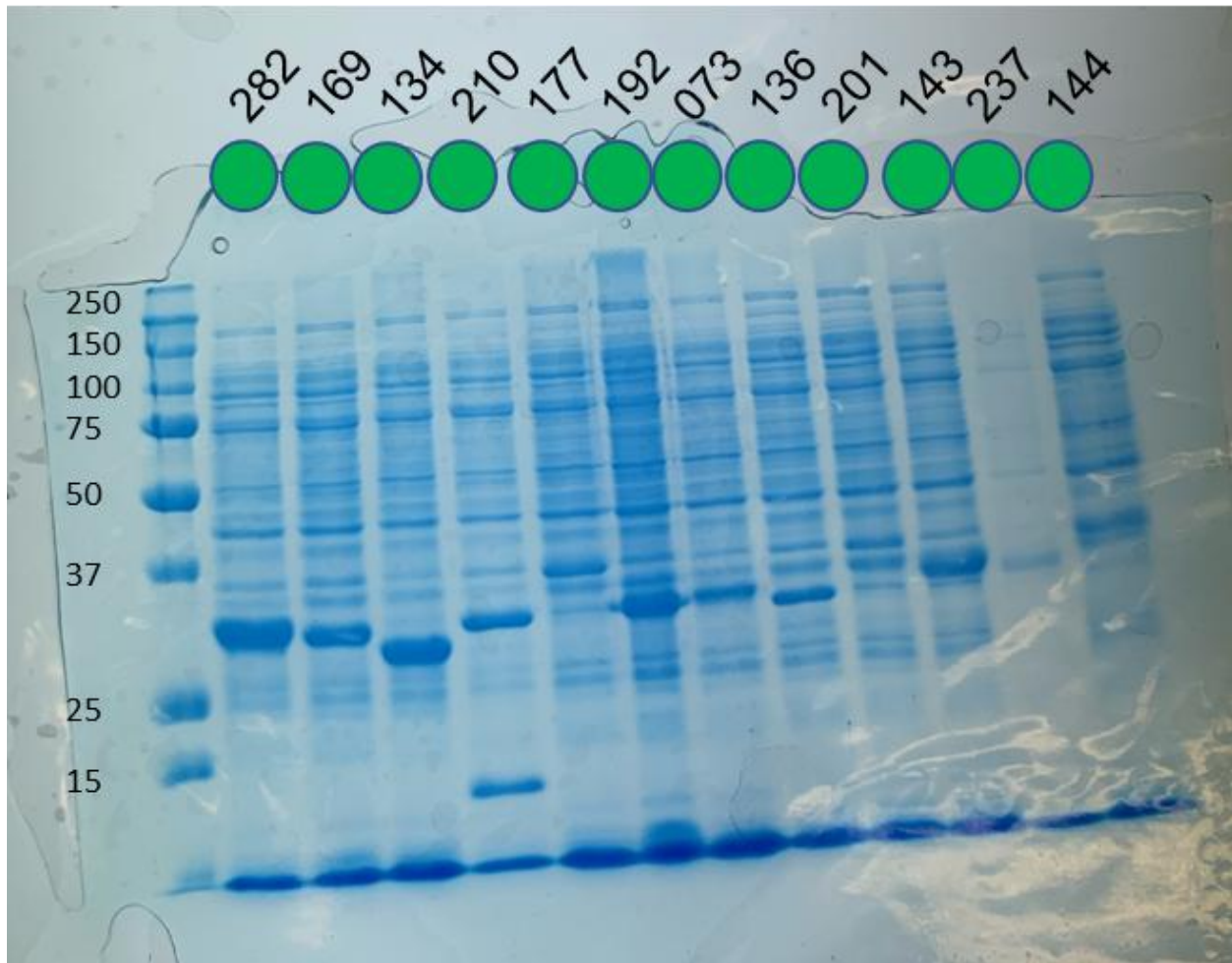
Supplemental Figure S12. SDS-PAGE gel #7 of NHI library clarified lysate (protein ladder standard in first lane labeled in kDa)



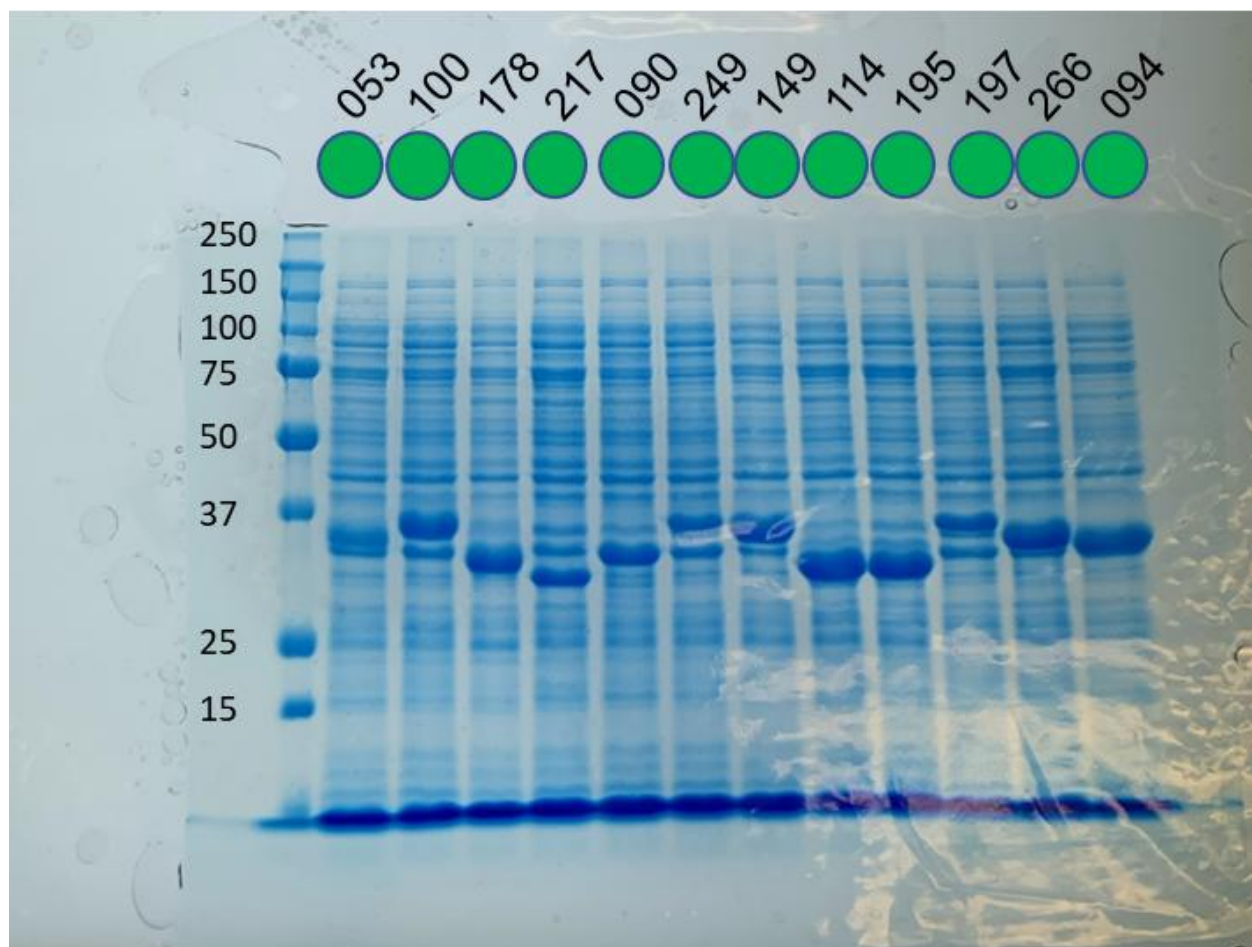
Supplemental Figure S13. SDS-PAGE gel #8 of NHI library clarified lysate (protein ladder standard in first lane labeled in kDa)



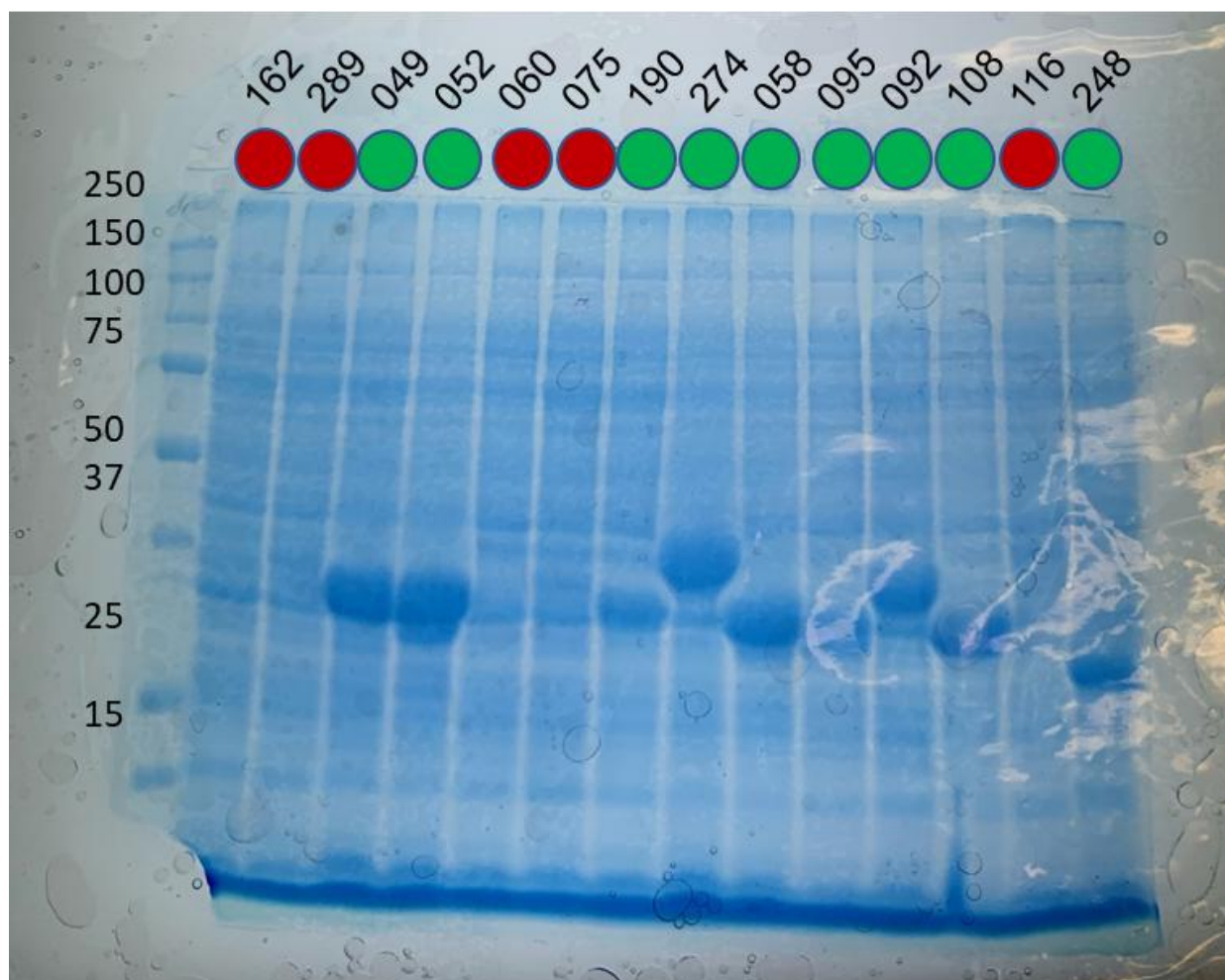
Supplemental Figure S14. SDS-PAGE gel #9 of NHI library clarified lysate (protein ladder standard in first lane labeled in kDa)



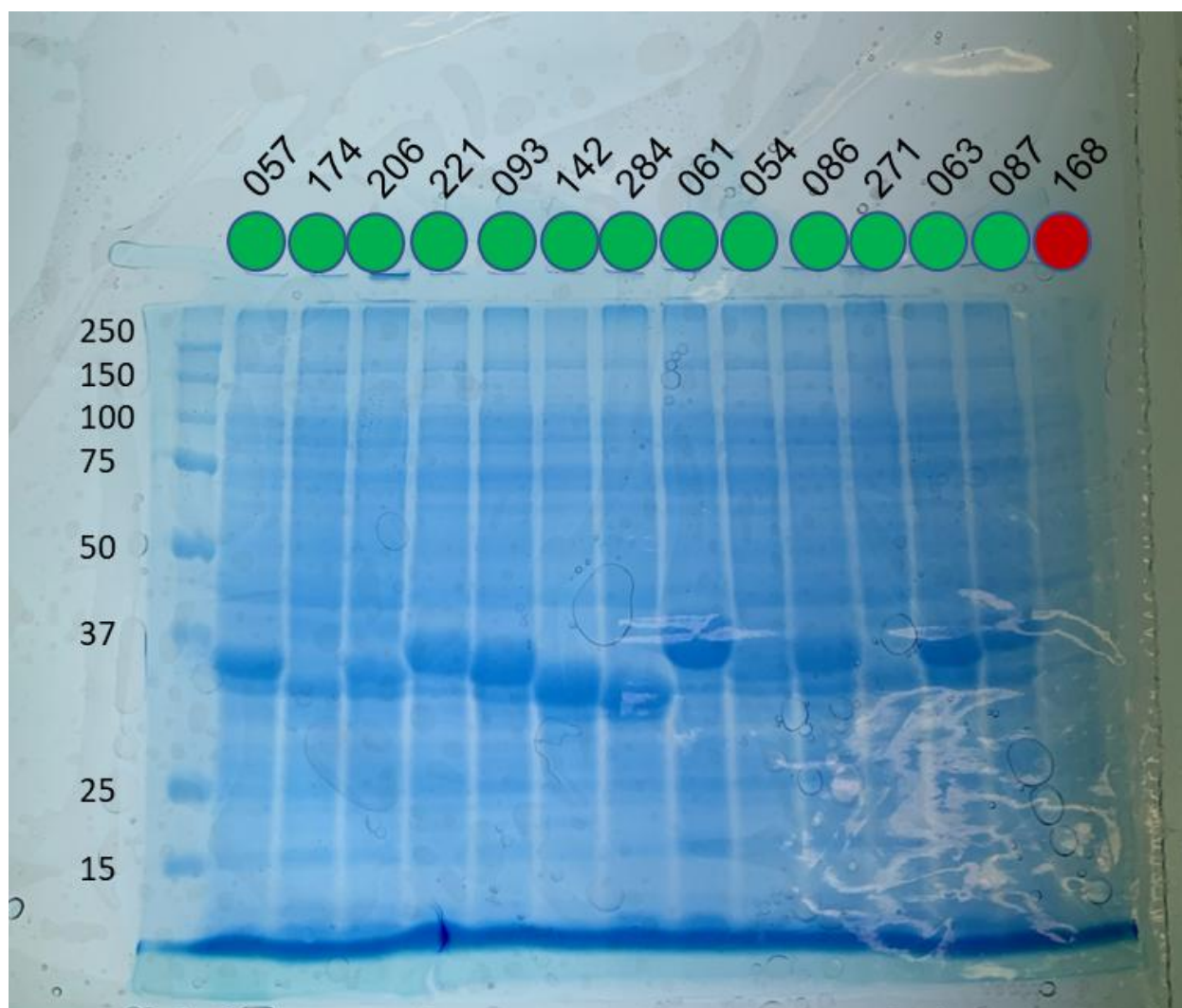
Supplemental Figure S15. SDS-PAGE gel #10 of NHI library clarified lysate (protein ladder standard in first lane labeled in kDa)



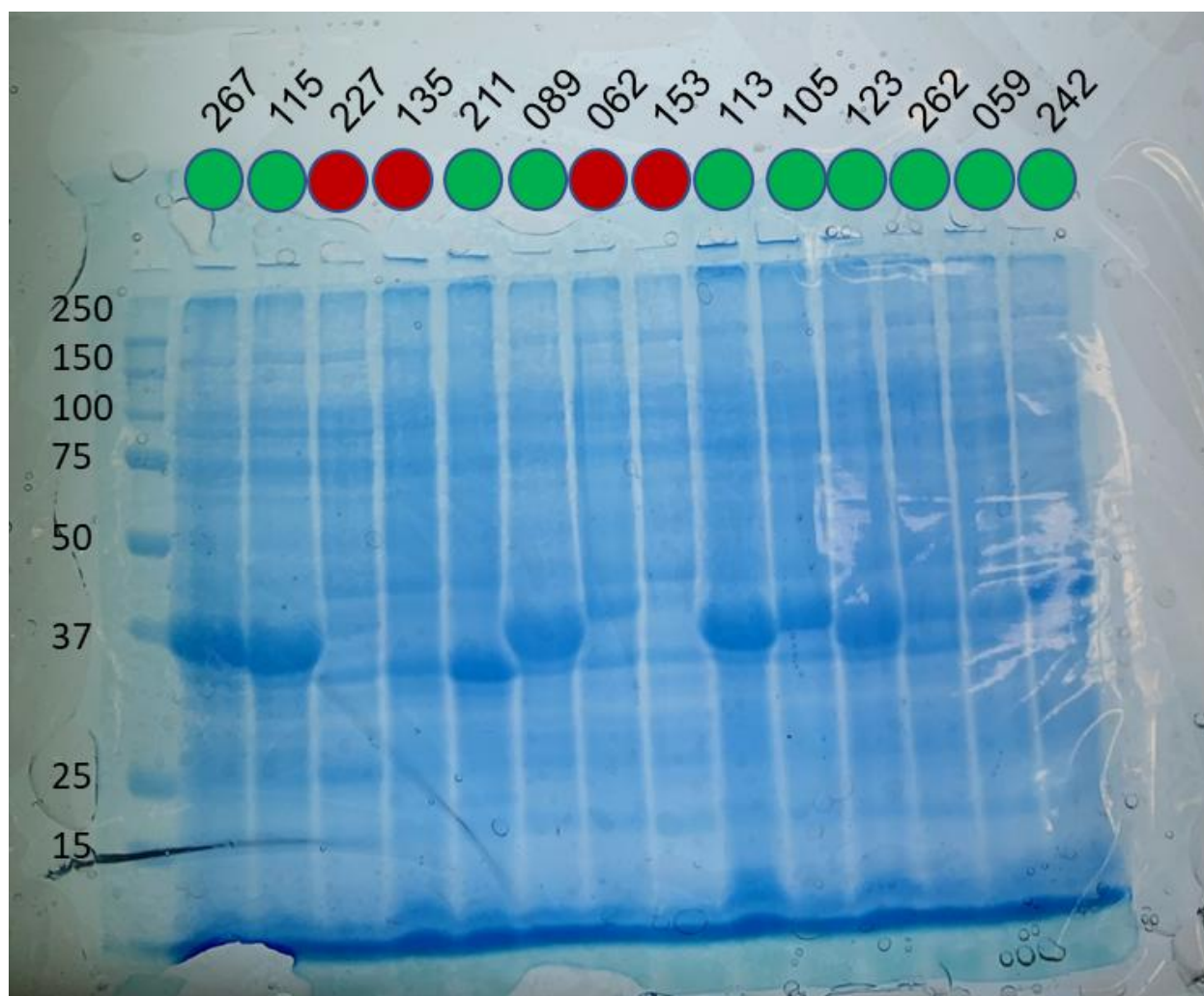
Supplemental Figure S16. SDS-PAGE gel #11 of NHI library clarified lysate (protein ladder standard in first lane labeled in kDa)



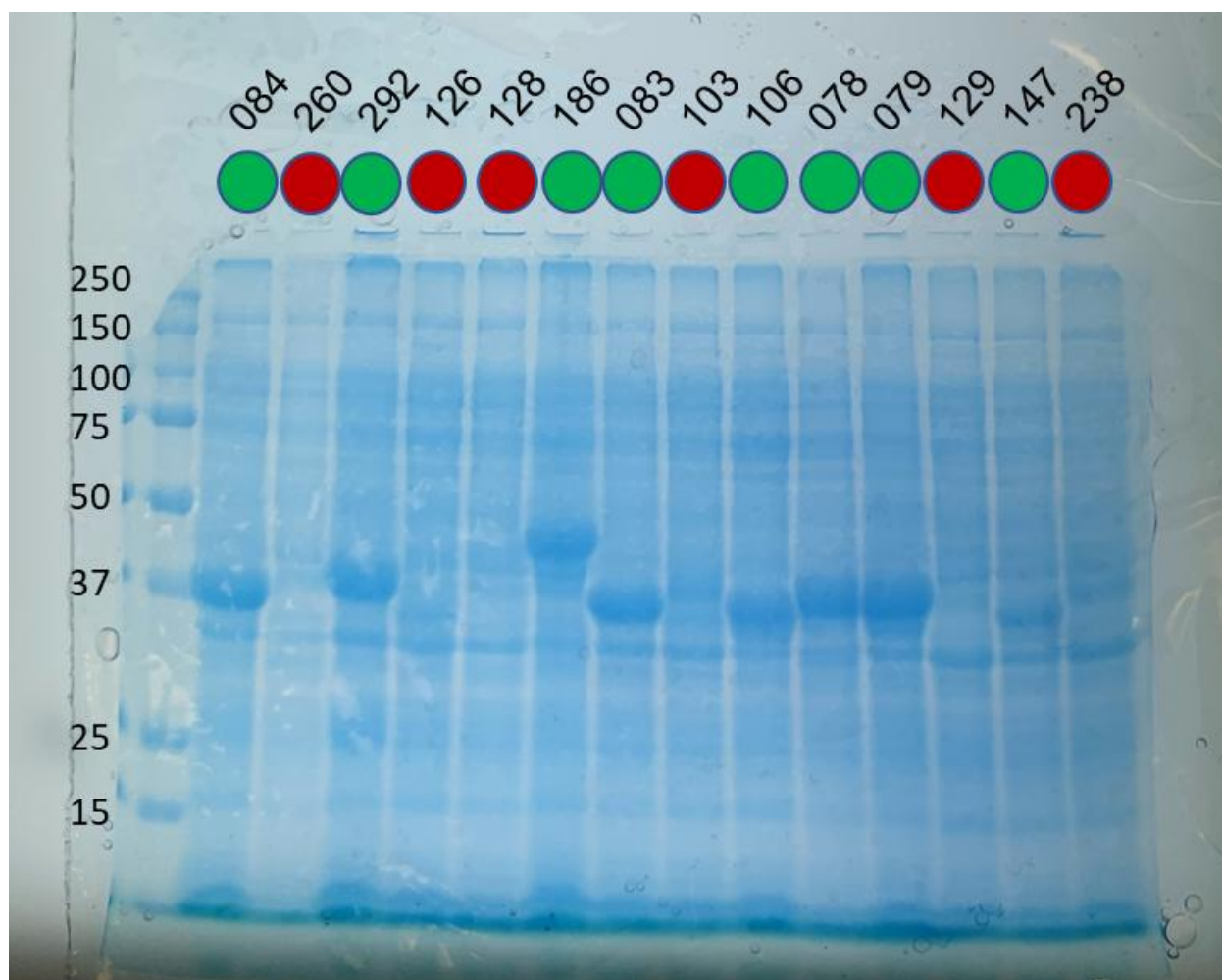
Supplemental Figure S17. SDS-PAGE gel #12 of NHI library clarified lysate (protein ladder standard in first lane labeled in kDa)



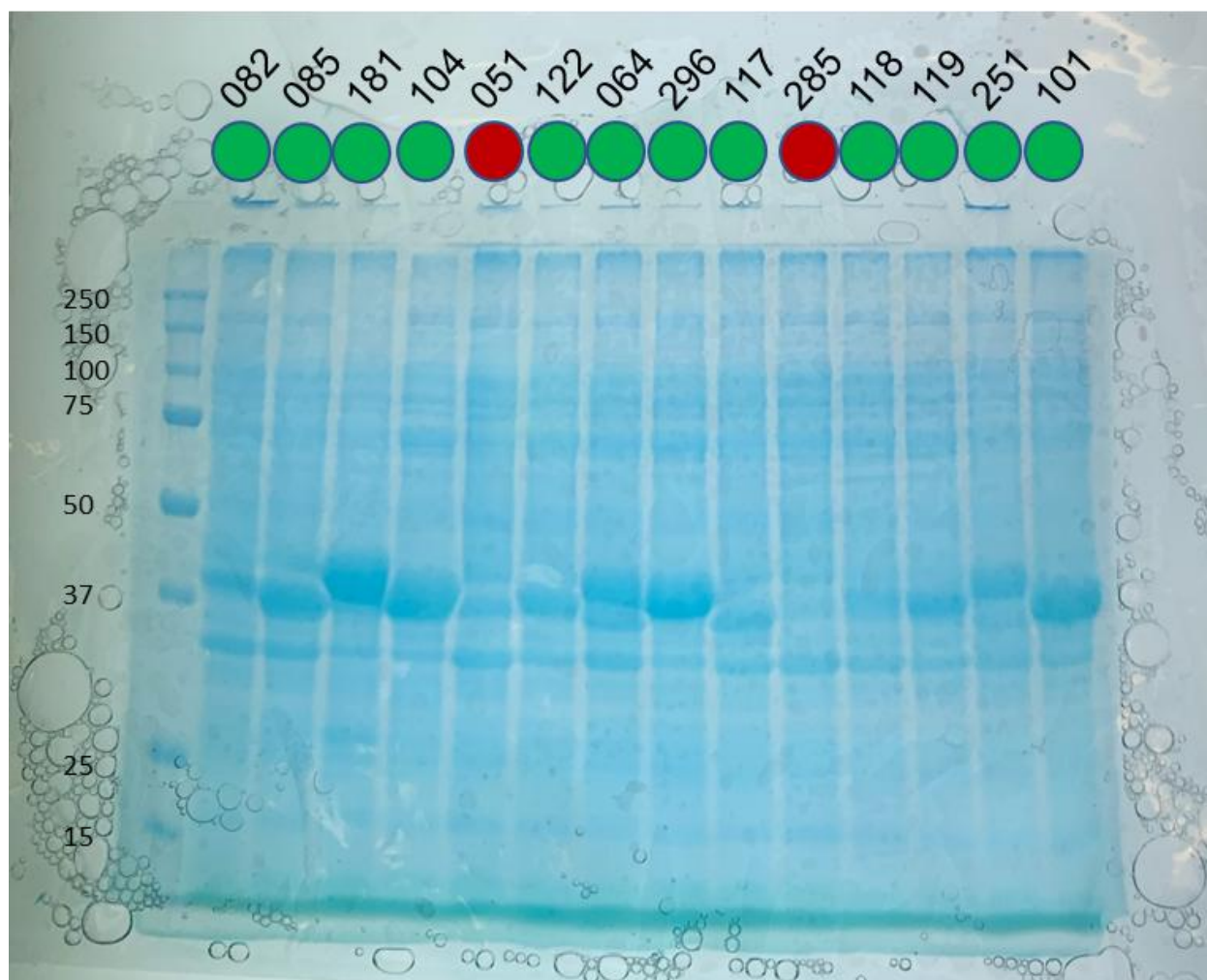
Supplemental Figure S18. SDS-PAGE gel #13 of NHI library clarified lysate (protein ladder standard in first lane labeled in kDa)



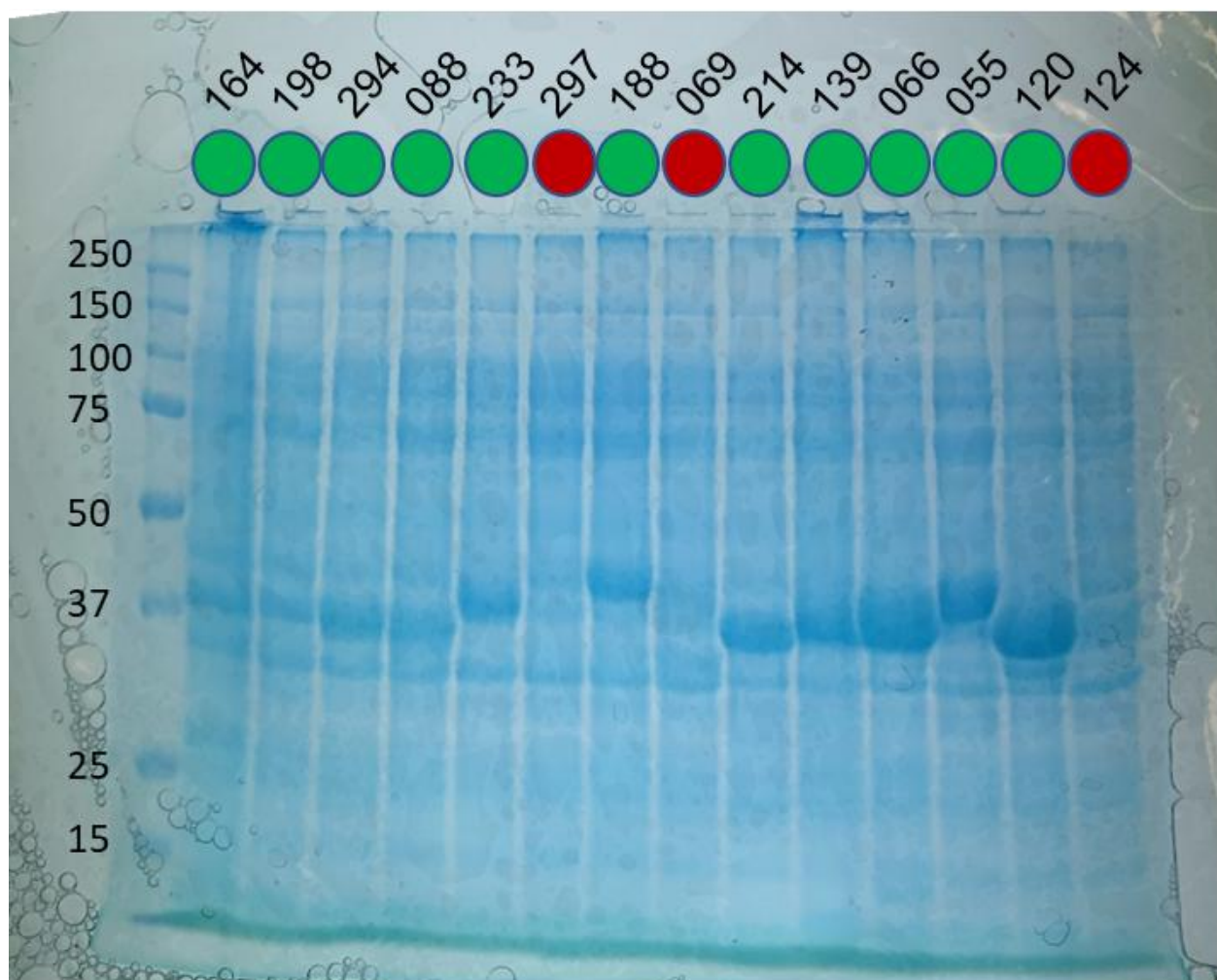
Supplemental Figure S19. SDS-PAGE gel #14 of NHI library clarified lysate (protein ladder standard in first lane labeled in kDa)



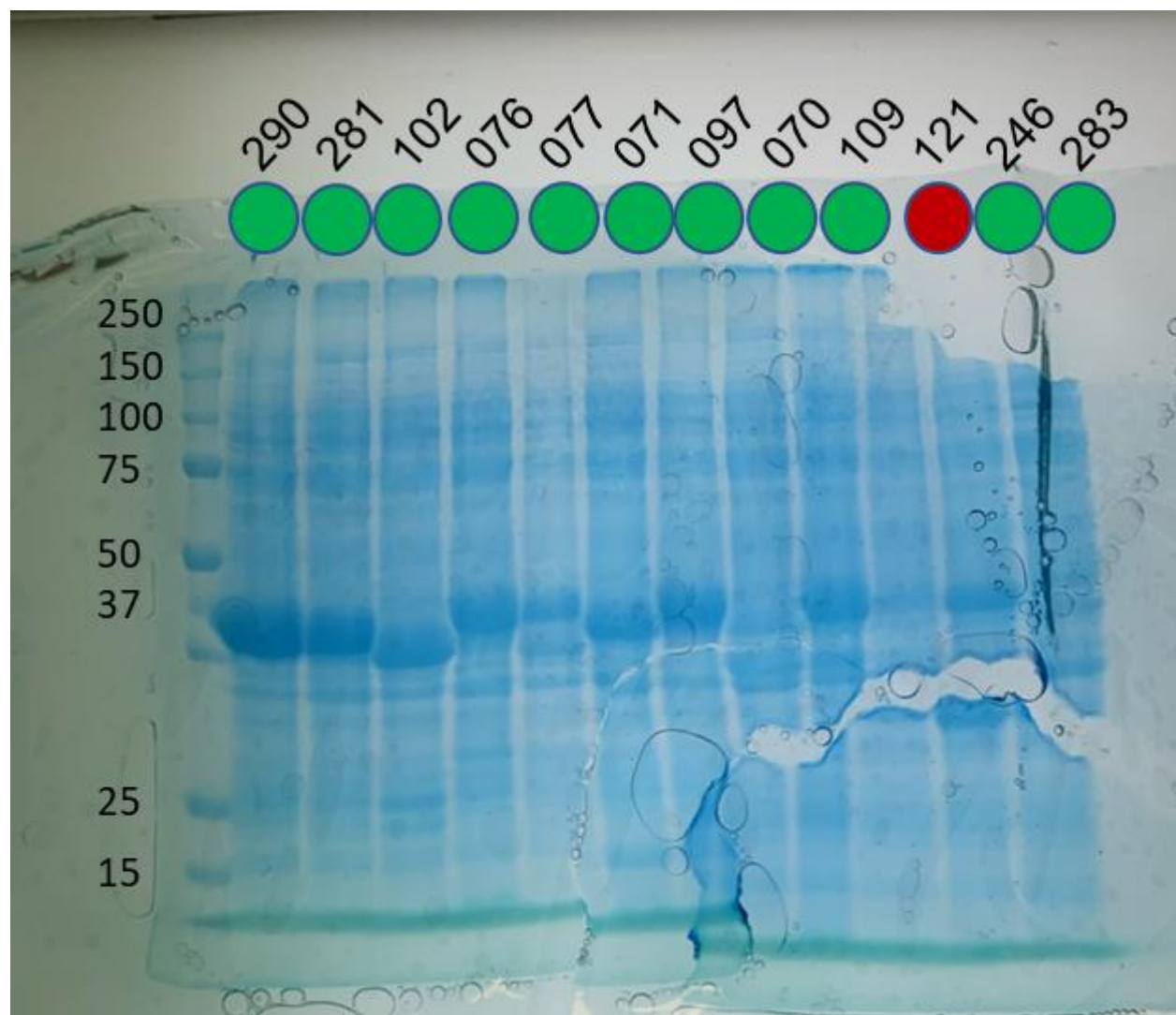
Supplemental Figure S20. SDS-PAGE gel #15 of NHI library clarified lysate (protein ladder standard in first lane labeled in kDa)



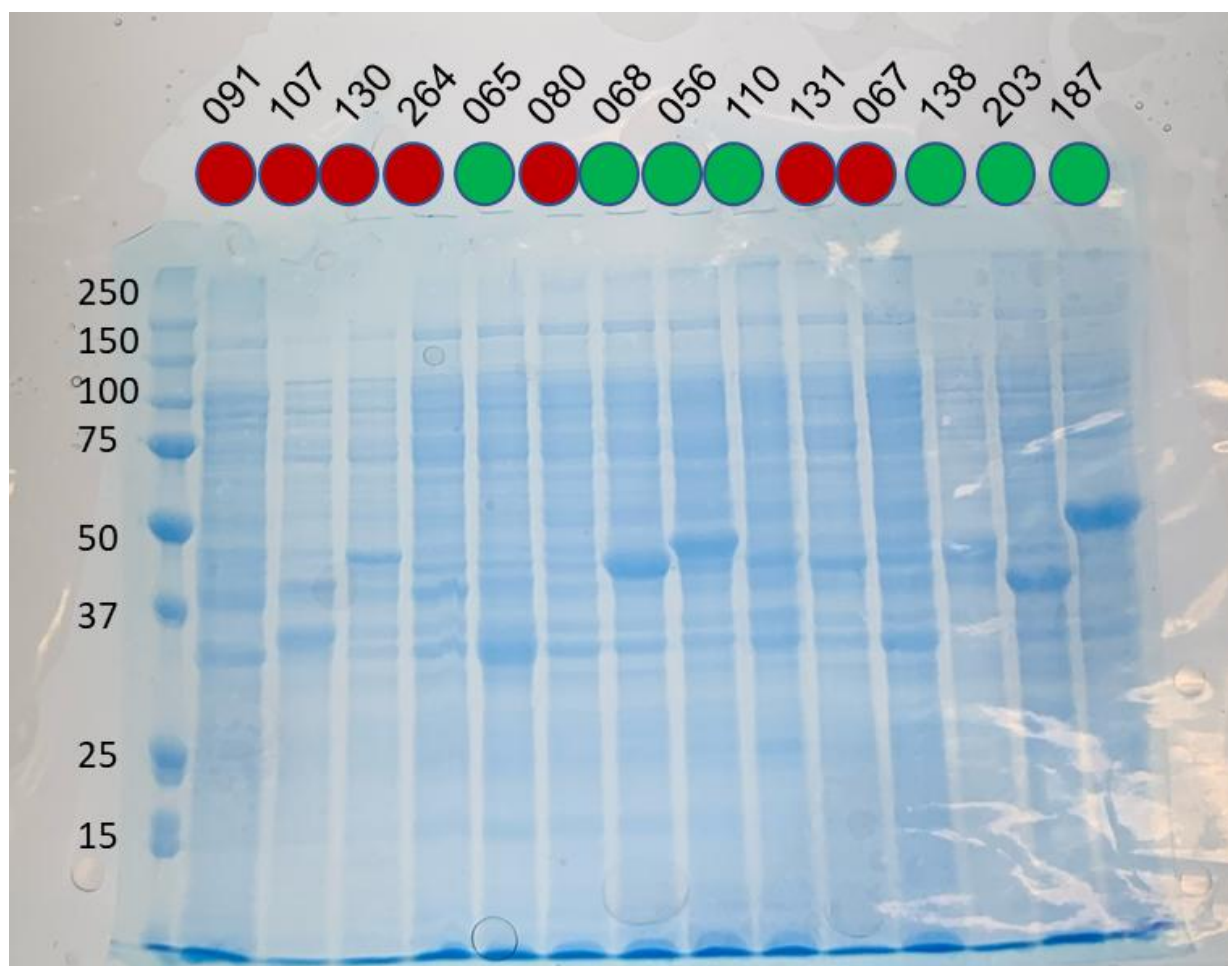
Supplemental Figure S21. SDS-PAGE gel #16 of NHI library clarified lysate (protein ladder standard in first lane labeled in kDa)



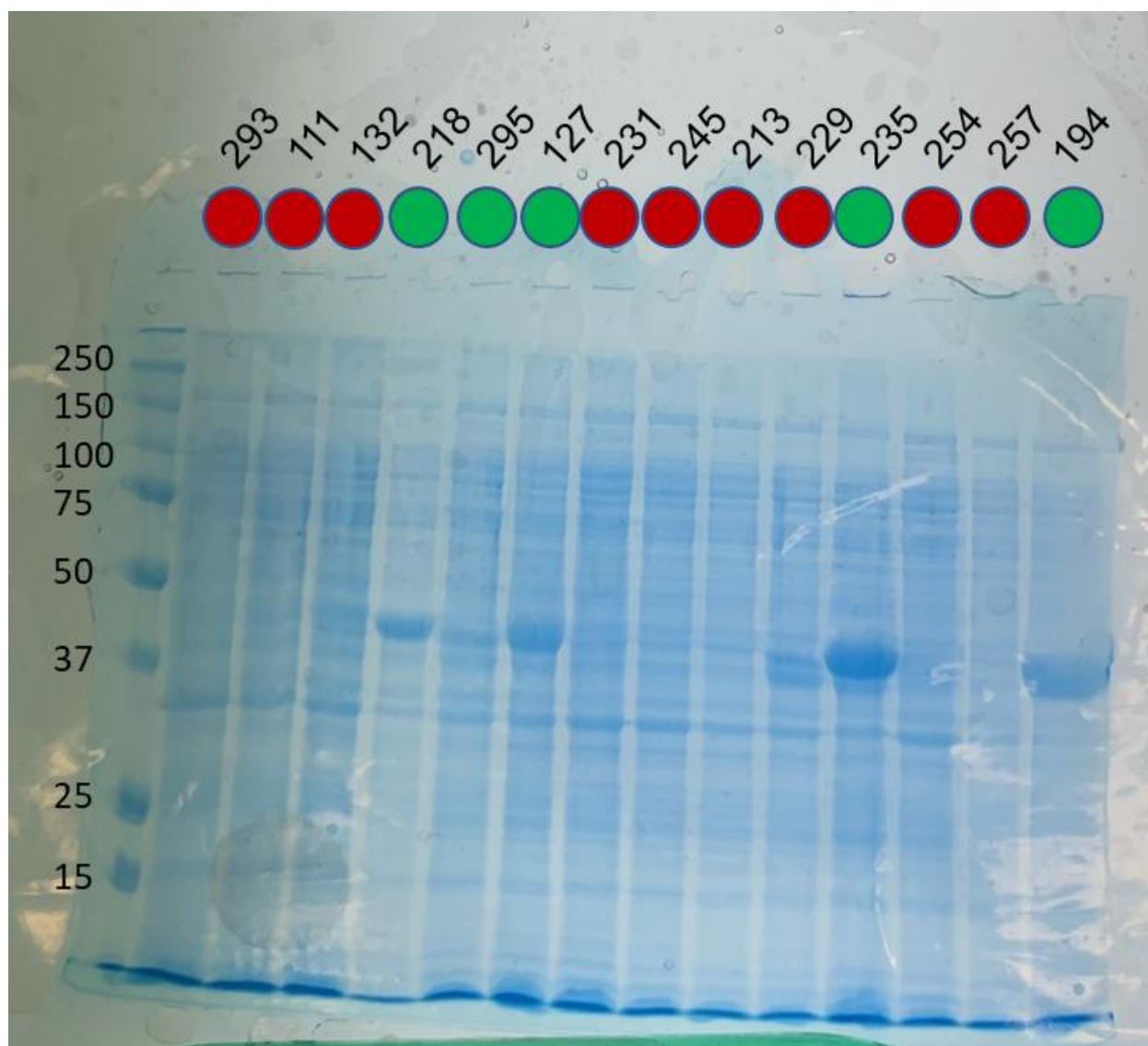
Supplemental Figure S22. SDS-PAGE gel #17 of NHI library clarified lysate (protein ladder standard in first lane labeled in kDa)



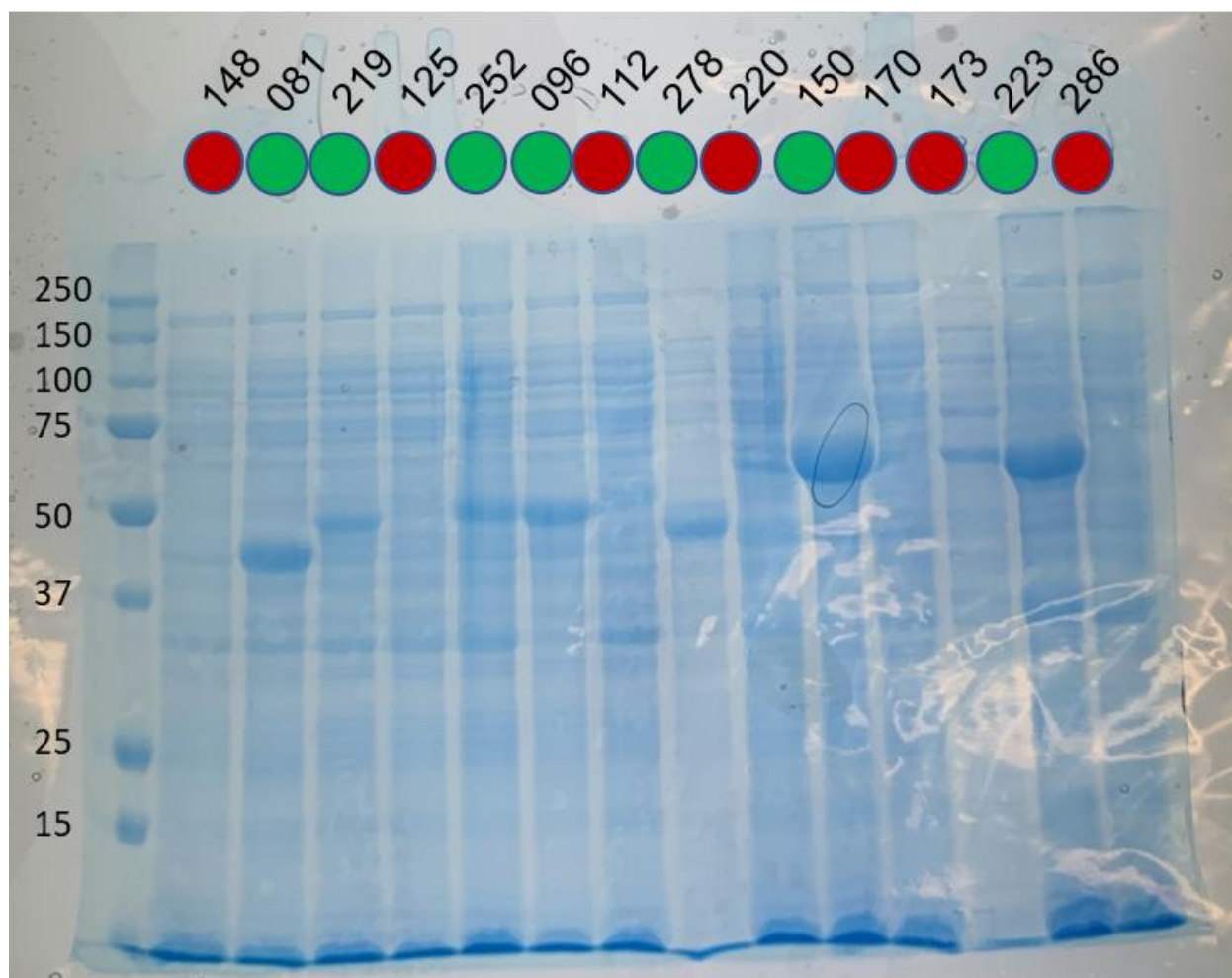
Supplemental Figure S23. SDS-PAGE gel #18 of NHI library clarified lysate (protein ladder standard in first lane labeled in kDa)



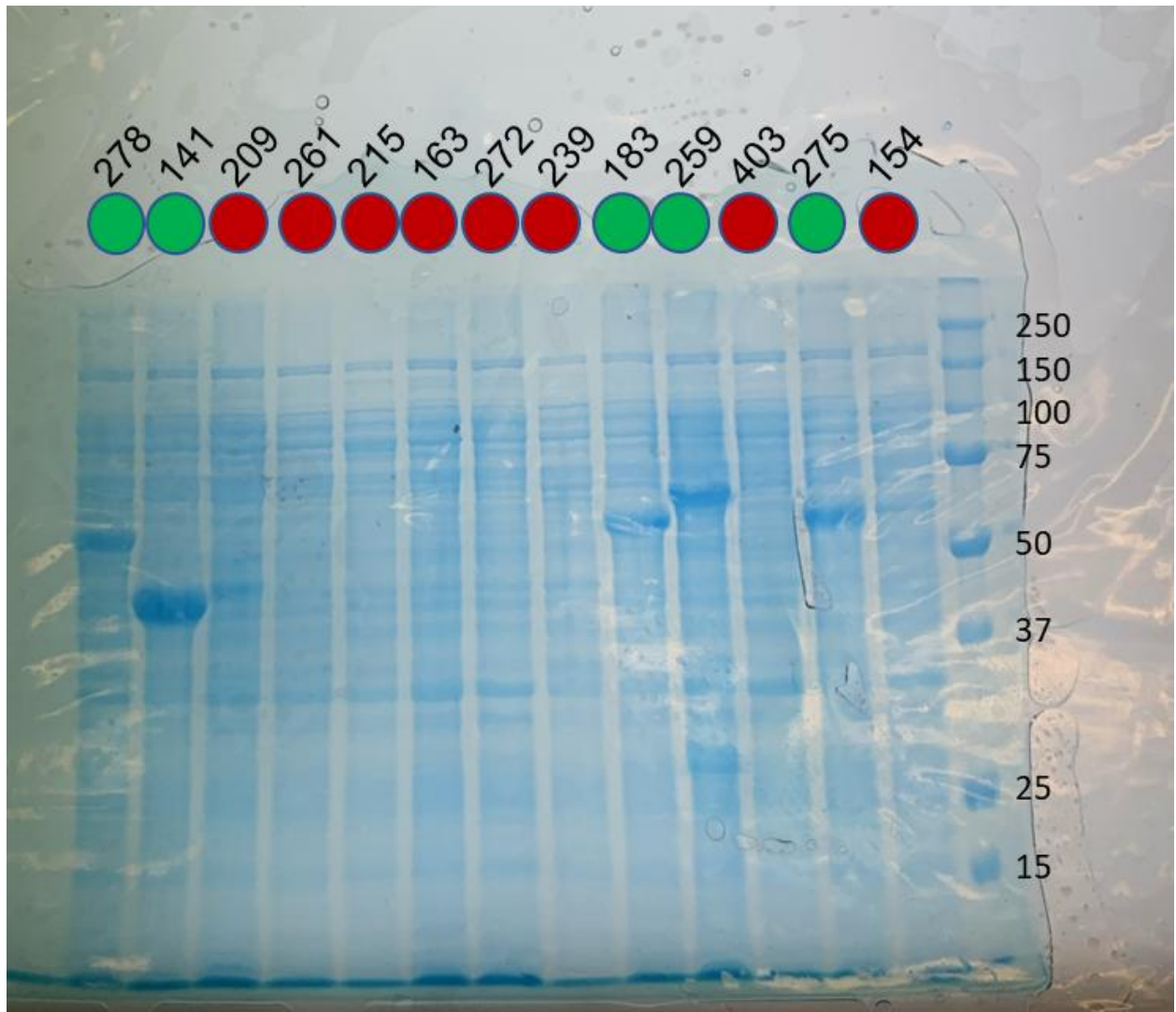
Supplemental Figure S24. SDS-PAGE gel #19 of NHI library clarified lysate (protein ladder standard in first lane labeled in kDa)



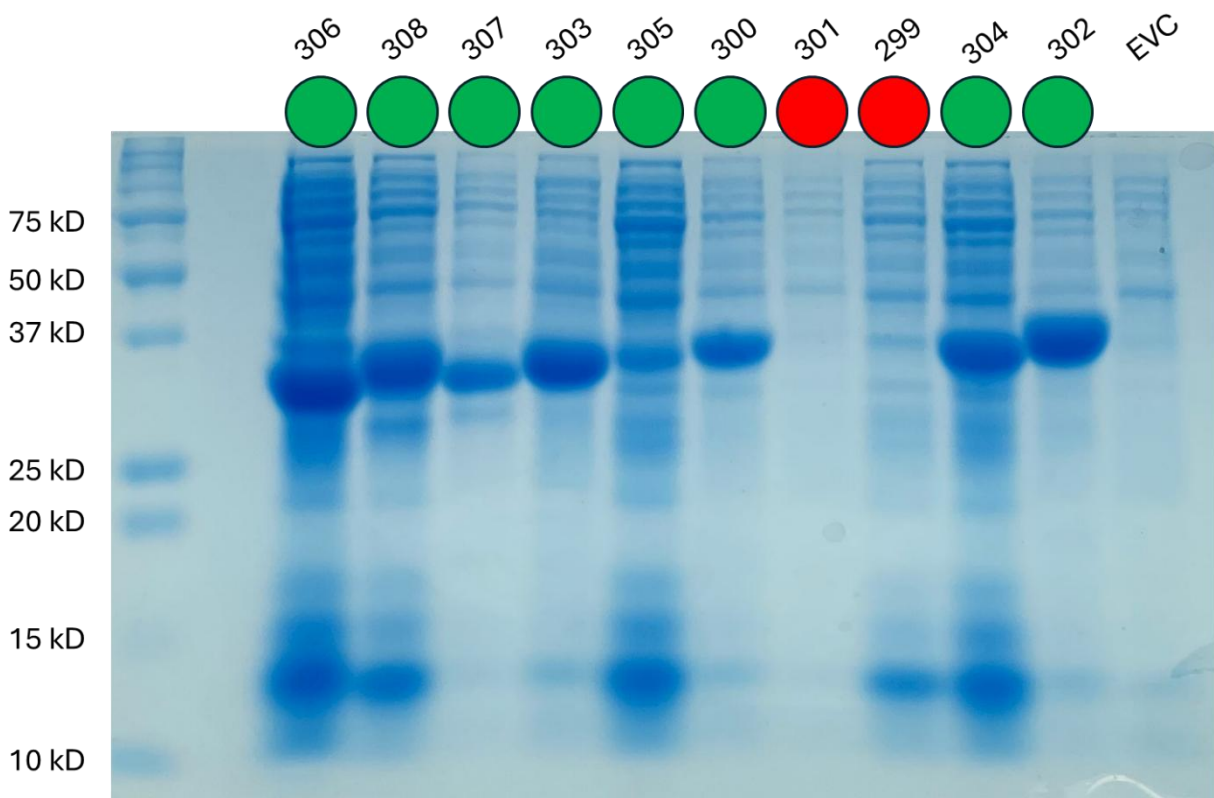
Supplemental Figure S25. SDS-PAGE gel #20 of NHI library clarified lysate (protein ladder standard in first lane labeled in kDa)



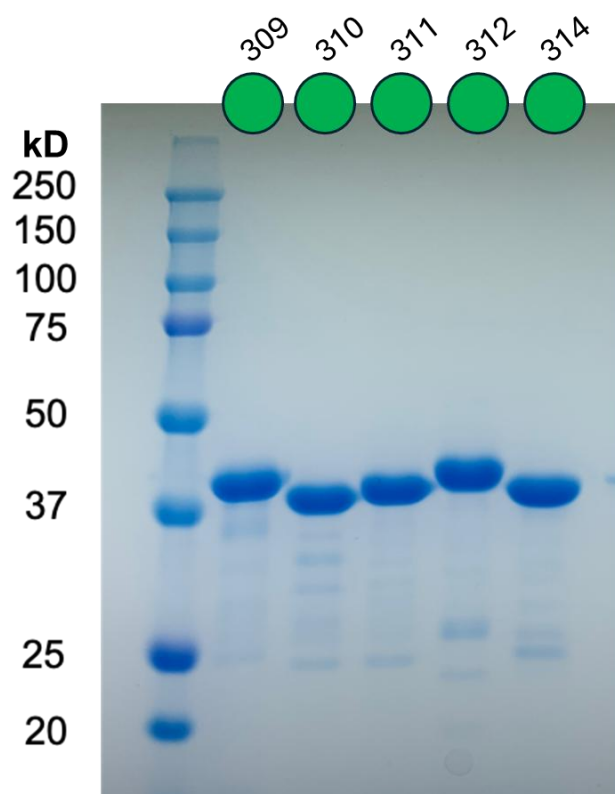
Supplemental Figure S26. SDS-PAGE gel #21 of NHI library clarified lysate (protein ladder standard in first lane labeled in kDa)



Supplemental Figure S27. SDS-PAGE gel #22 of NHI library clarified lysate (protein ladder standard in first lane labeled in kDa)



Supplemental Figure S28. SDS-PAGE gel #23 of NHI library clarified lysate (protein ladder standard in first lane labeled in KDa)



Supplemental Figure S29. SDS-PAGE gel #24 of NHI library clarified lysate (protein ladder standard in first lane labeled in KDa)

9. High-throughput reaction protocol

Stock solutions and library preparation:

Stock solutions of each substrate (50 mM) were prepared by dissolving the substrate in DMSO (analytical grade). Stock solutions of α -ketoglutaric acid (α -KG, 100 mM), ferrous sulfate heptahydrate (FeSO_4 , 10 mM) and L-ascorbic acid sodium salt (NaAsc, 100 mM) were freshly dissolved in milli-Q water before each use. 96-well plates containing cell pellets with the overexpressed NHI libraries were removed from storage at -78°C and allowed to thaw at room temperature for 15 to 30 min prior to reaction setup.

General procedure for 96-well plate NHI library reaction screens:

A master mix containing 5 mL of 1 M TES buffer pH 7.5, 40 mL of milli-Q water, 2 mL of α -KG stock solution, 1 mL of NaAsc stock solution, and 1 mL of FeSO_4 stock solution was prepared. 9.8 mL of master mix was added to 200 μL of stock solution of each substrate in DMSO. 25 μL of each substrate doped master mix was added to 4 x 2 mL 96-well plates, resulting in twenty 96-well plates (4 plates of each substrate).

Plates containing thawed cell pellets were prepared for distribution across the plates of substrate doped master mix. 100 μL of 50 mM TES buffer pH 7.5 was added to each well in the plate containing NHI_001-096 cell pellet and contents were resuspended. 20 μL of each well of cell suspension was distributed to five 96-well plates doped with 5 different substrates. This cell resuspension and distribution was repeated for plates containing NHI_097-192, NHI_193-288, and NHI_289-NHI_314. Experiments with each substrate also included an empty vector control. Each well in the twenty 96-well plate setup was spiked with 5 μL of toluene immediately before sealing with a breathable thin film. Plates were shaken at 30°C and 300 rpm (4 mM orbital plate shaker) for 4 h before being quenched by the addition of 1 vol of acetonitrile containing 3.5 mM pentamethyl benzene as an internal standard. Upon quenching, each plate containing the same enzymes was pooled and filtered through a 1.2 μm filter by centrifugation (1250 x g, 20 min). The resultant 4 plates of supernatant were then analyzed by LC-MS.

10. Parameters for reaction hit determination

All reactions were analyzed by LC-MS to identify product formation. All reactions were analyzed in positive mode, except where noted. Remaining starting material was identified by extracted ion chromatography (EIC) of the M+H mass. Substrates were compared to a substrate only sample to ensure proper peak identification. Retention time and peak intensity were noted. Then, hydroxylation, desaturation, hydroxylation/desaturation, dihydroxylation, chlorination, and rearrangement product masses were extracted in the corresponding ionization mode as the starting material. Product masses were extracted as shown in the table below:

	Neutral	Positive	Negative
desaturation	M-H ₂	M-1.00783	M-3.02349
Substrate	M	M+1.00783	M-1.00783
oxidation/desaturation	M+O-H ₂	M+14.991353	M+12.975693
hydroxylation	M+O	M+17.00273	M+14.98707
dihydroxylation	M+O ₂	M+33.00664	M+30.99098
chlorination	M+Cl	M+35.97673	M+33.96107

Supplemental Table S2. Extracted masses for LC-MS analysis

For each product, the existence of a new peak in the EIC was indicative of a potential product formation which required further confirmation as detailed:

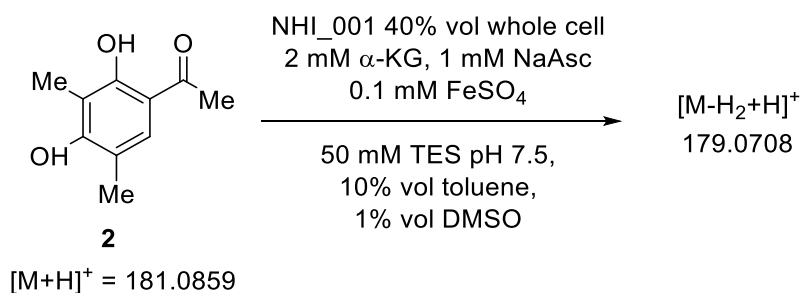
1. The product EIC intensity was required to be no less than one magnitude of intensity less than the starting material (e.g., if starting material EIC peak was 3.5×10^6 , product peak intensity must be at least 1.0×10^5).
2. The retention time of the product must be reasonable to that of the starting material. In a reverse-phase method, as was standard unless noted for a specific reaction, transformations to more polar products relative to the starting material, such as hydroxylation and dihydroxylation, were required to elute earlier than the starting material. Desaturation, oxidation/desaturation and chlorination products were not subjected to this requirement due to the diverse reaction pathways potentially responsible for these product formations. Rearrangement products

were identified by identical molecular weight as starting material, but the presence of a peak in the EIC at a different time.

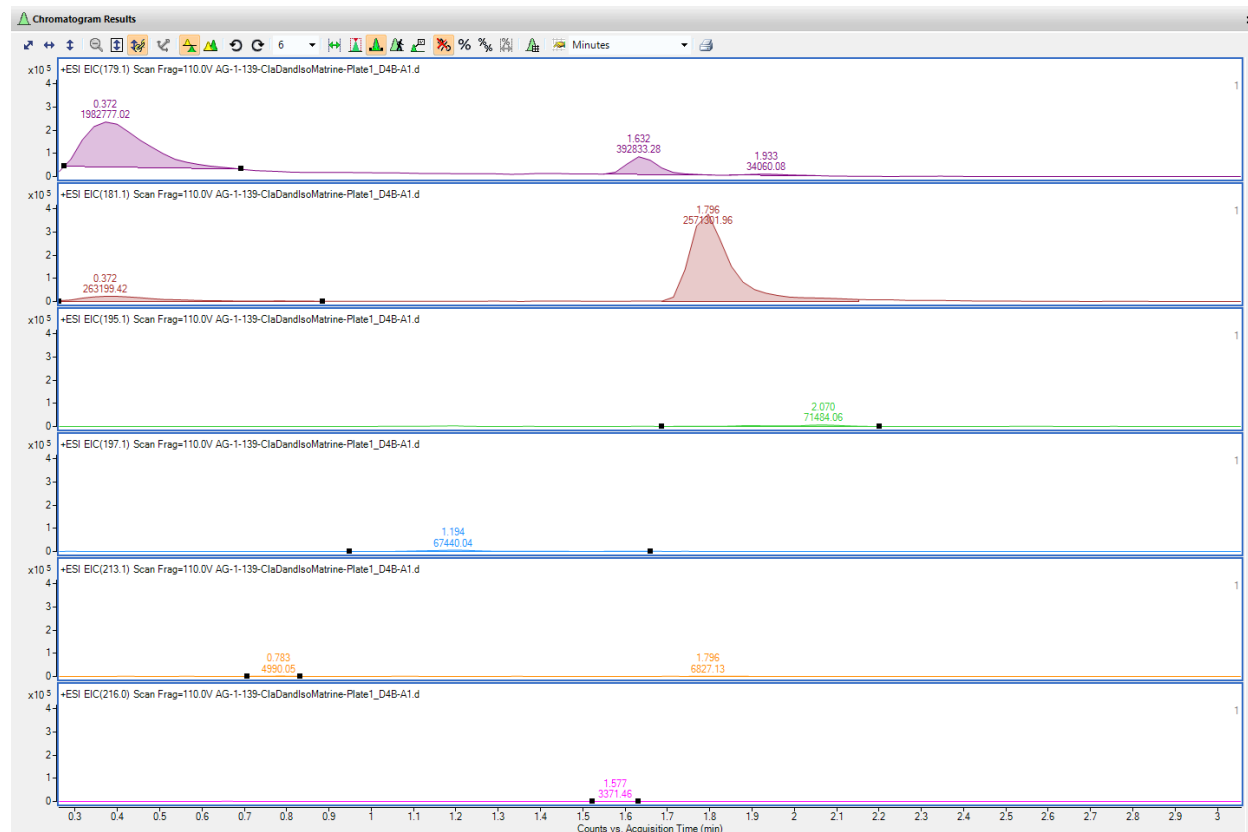
3. Chromatograms were inspected for anticipated isotopic patterns and peak abundance.
4. Reactions were compared to biocatalytic reactions with an empty vector control, to ensure that the observed product was enzyme derived.
5. Reactions were compared to no substrate controls, to ensure that the product was not an artifact of a different material produced from the enzyme with an unknown substrate available in the reaction contents.

11. Reactions discovered with high throughput platform

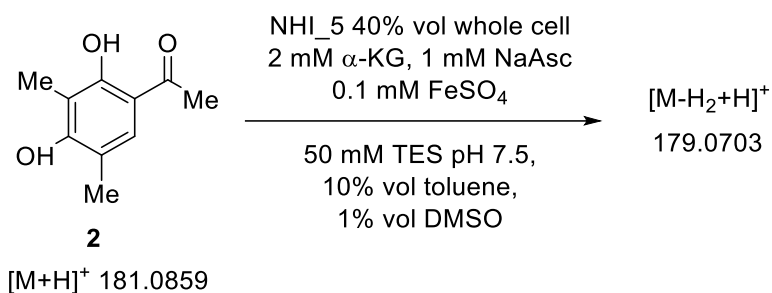
Discovered Reaction 1. Substrate_002 + NHI_001 = desaturation



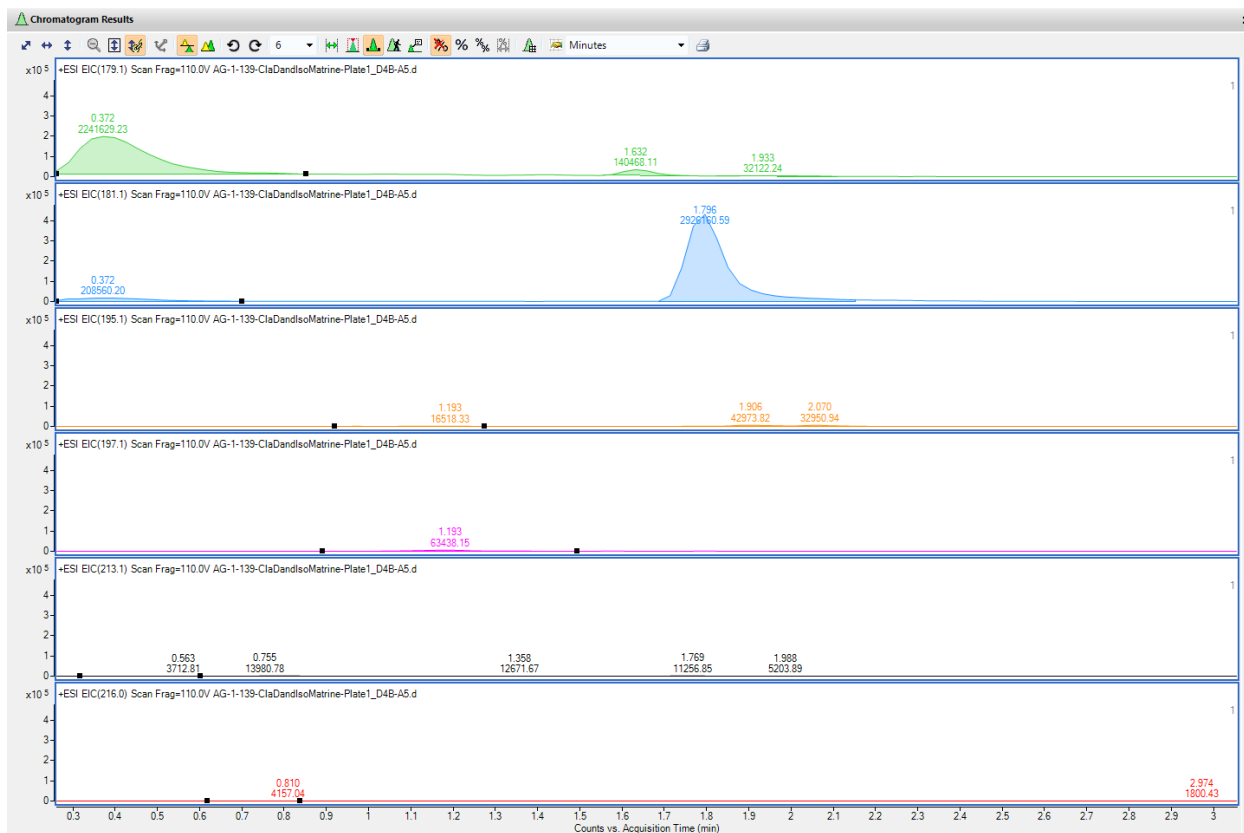
	Neutral	Positive	Negative
desaturation	178.0549	179.0628	177.0471
Substrate	180.0706	181.0784	179.0628
oxidation/desaturation	194.0499	195.0577	193.0421
hydroxylation	196.0655	197.0733	195.0577
dihydroxylation	212.0604	213.0682	211.0526
chlorination	215.0394	216.0472	214.0316



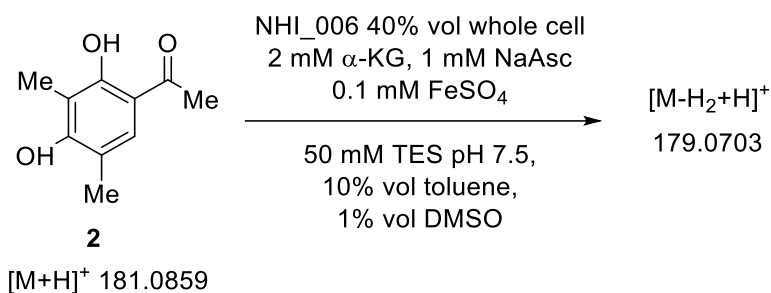
Discovered Reaction 2. Substrate_002 + NHI_005 = desaturation



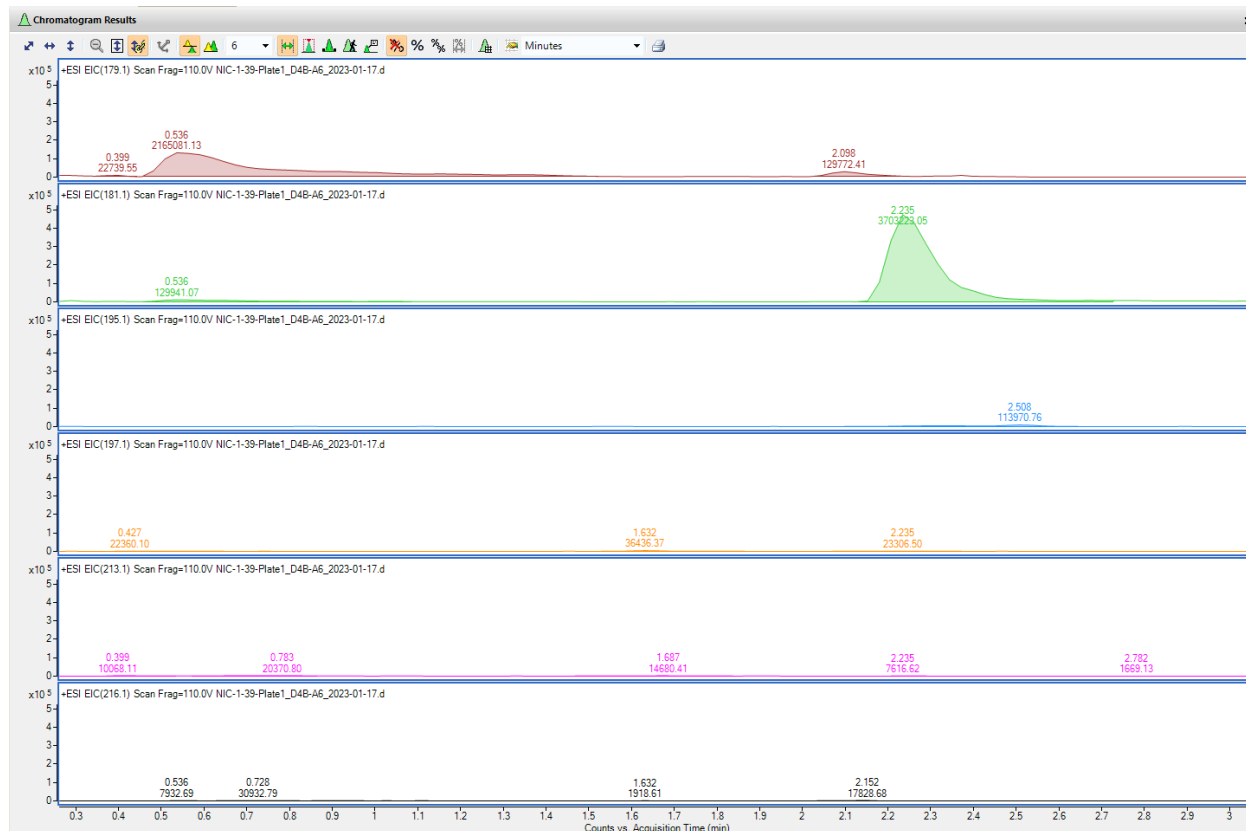
	Neutral	Positive	Negative
desaturation	178.0549	179.0628	177.0471
Substrate	180.0706	181.0784	179.0628
oxidation/desaturation	194.0499	195.0577	193.0421
hydroxylation	196.0655	197.0733	195.0577
dihydroxylation	212.0604	213.0682	211.0526
chlorination	215.0394	216.0472	214.0316



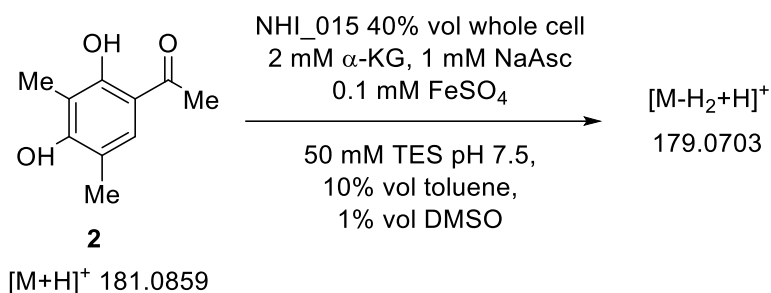
Discovered Reaction 3. Substrate_002 + NHI_006 = hydroxylation



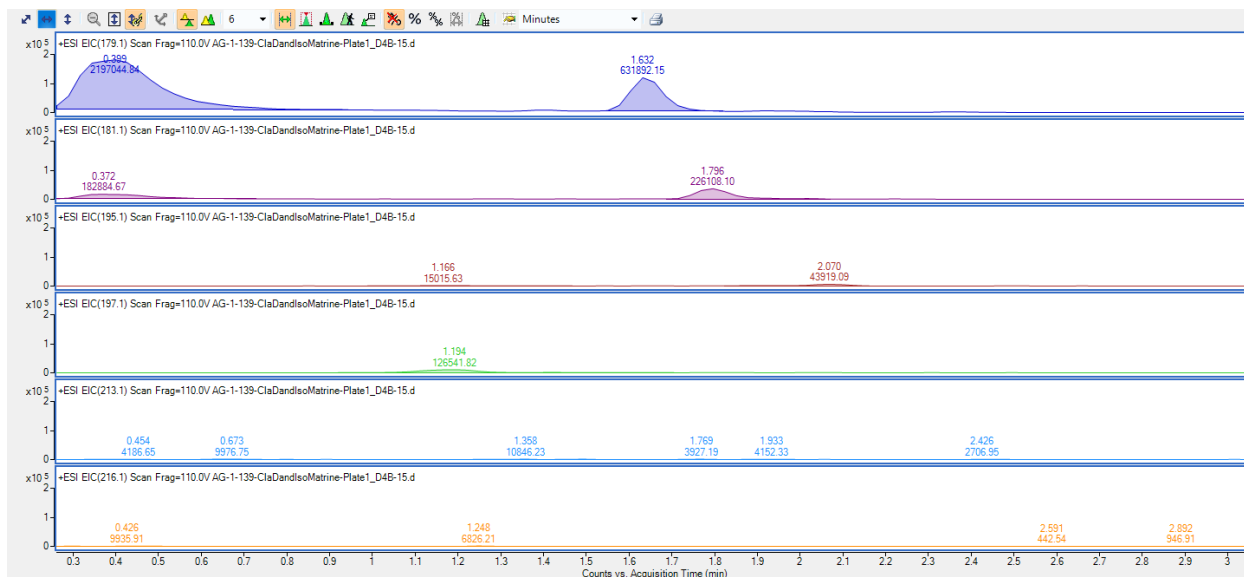
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Substrate	180.0706	181.0784	179.0628
oxidation/desaturation	194.0499	195.0577	193.0421
hydroxylation	196.0655	197.0733	195.0577
dihydroxylation	212.0604	213.0682	211.0526
chlorination	215.0394	216.0472	214.0316



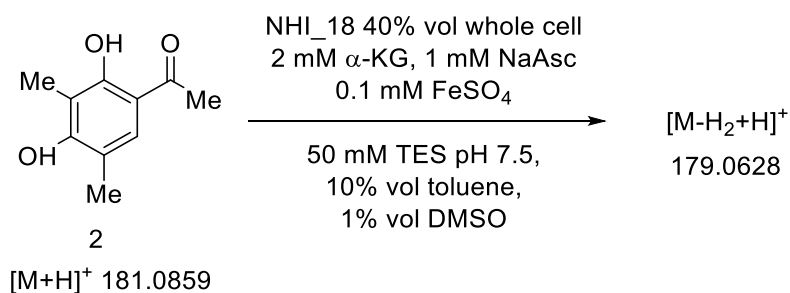
Discovered Reaction 4. Substrate_002 + NHI_015 = desaturation



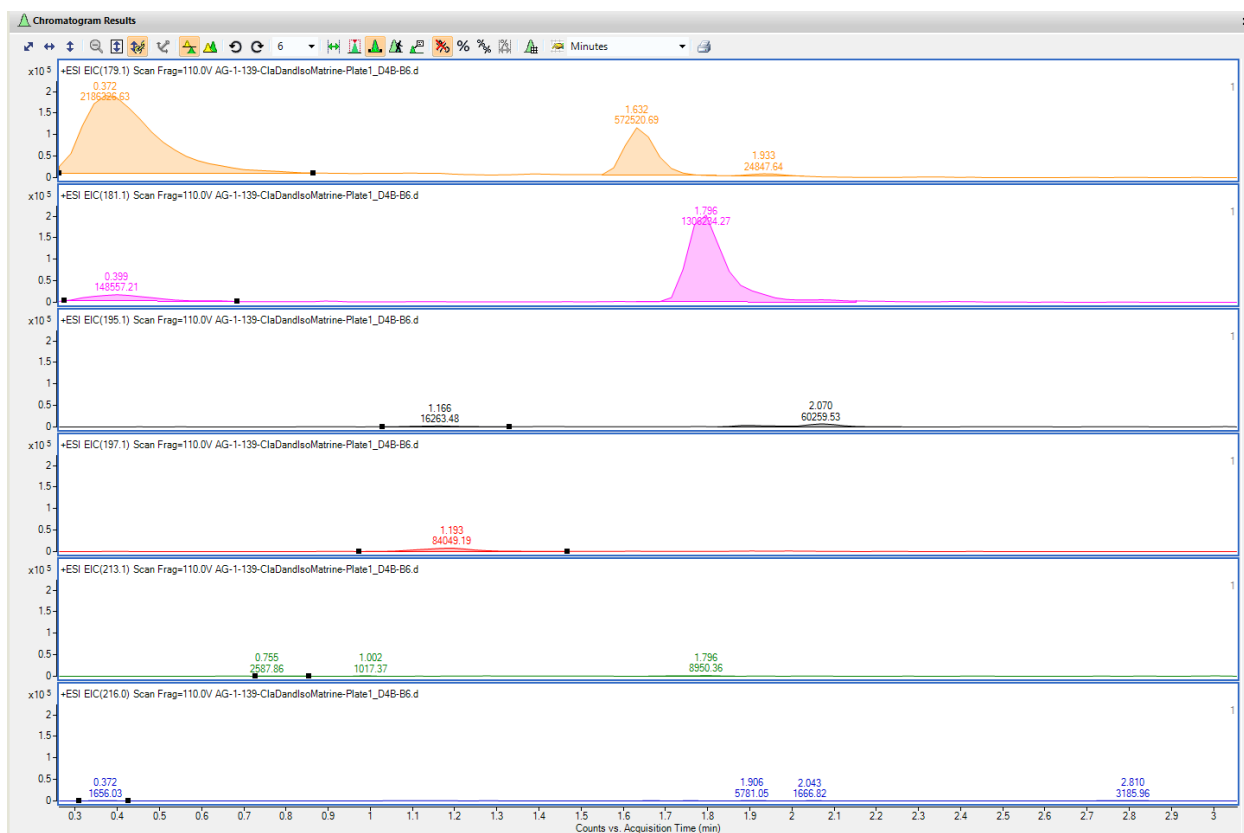
	Neutral	Positive	Negative
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Substrate	180.0706	181.0784	179.0628
oxidation/desaturation	194.0499	195.0577	193.0421
hydroxylation	196.0655	197.0733	195.0577
dihydroxylation	212.0604	213.0682	211.0526
chlorination	215.0394	216.0472	214.0316



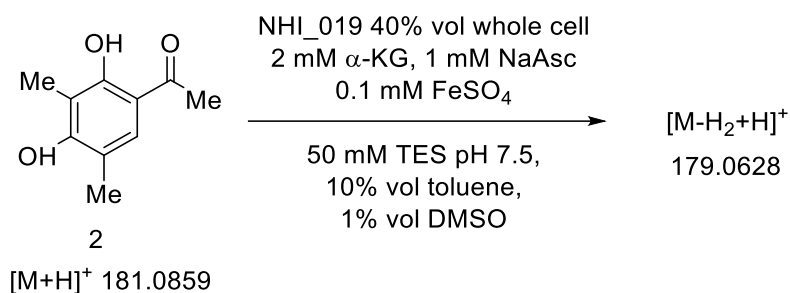
Discovered Reaction 5. Substrate_002 + NHI_018 = desaturation



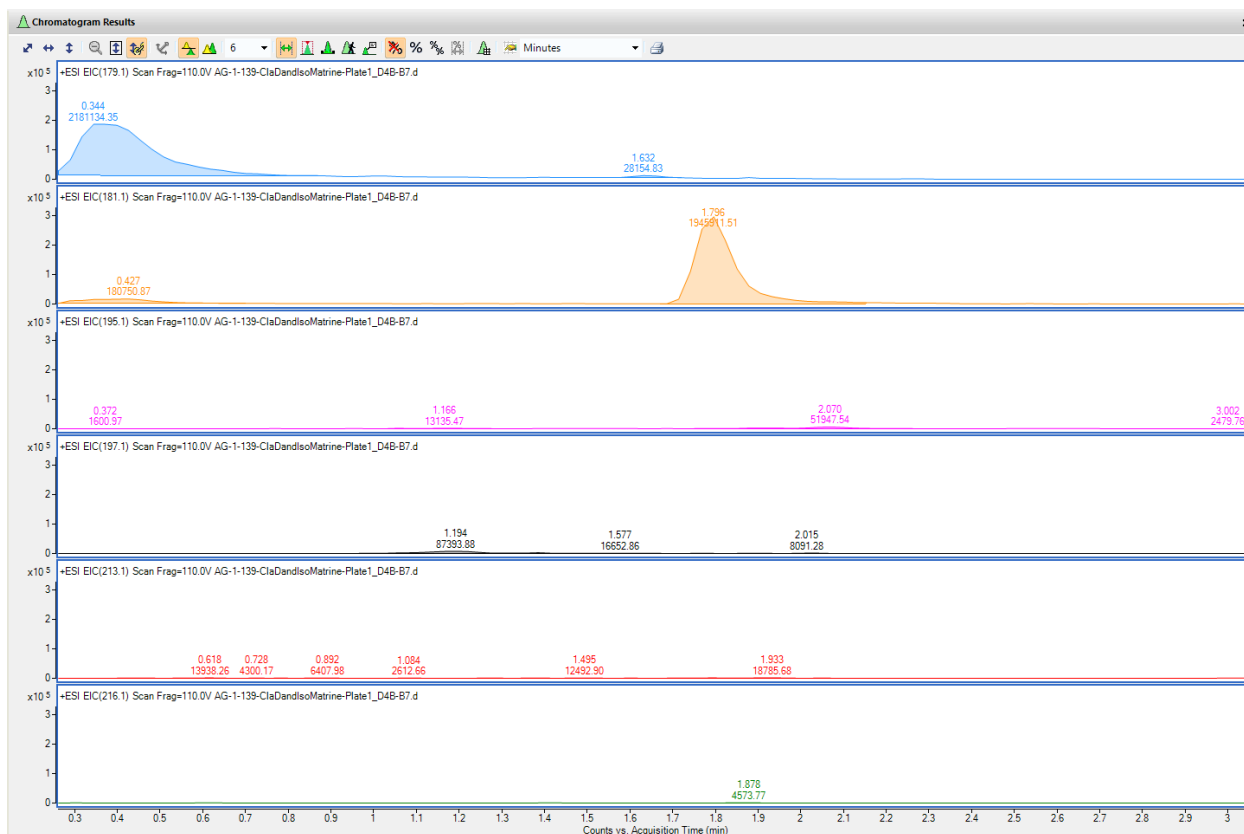
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Substrate	180.0706	181.0784	179.0628
oxidation/desaturation	194.0499	195.0577	193.0421
hydroxylation	196.0655	197.0733	195.0577
dihydroxylation	212.0604	213.0682	211.0526
chlorination	215.0394	216.0472	214.0316



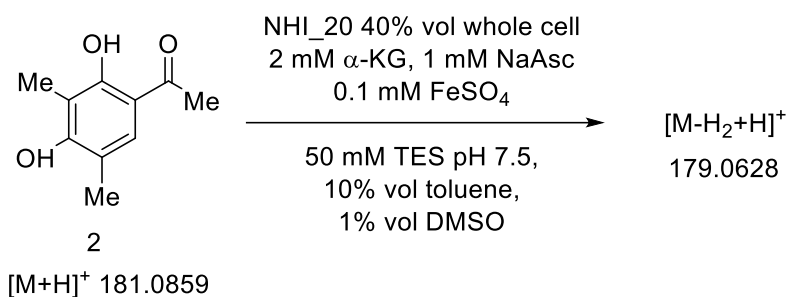
Discovered Reaction 6. Substrate_002 + NHI_019 = desaturation



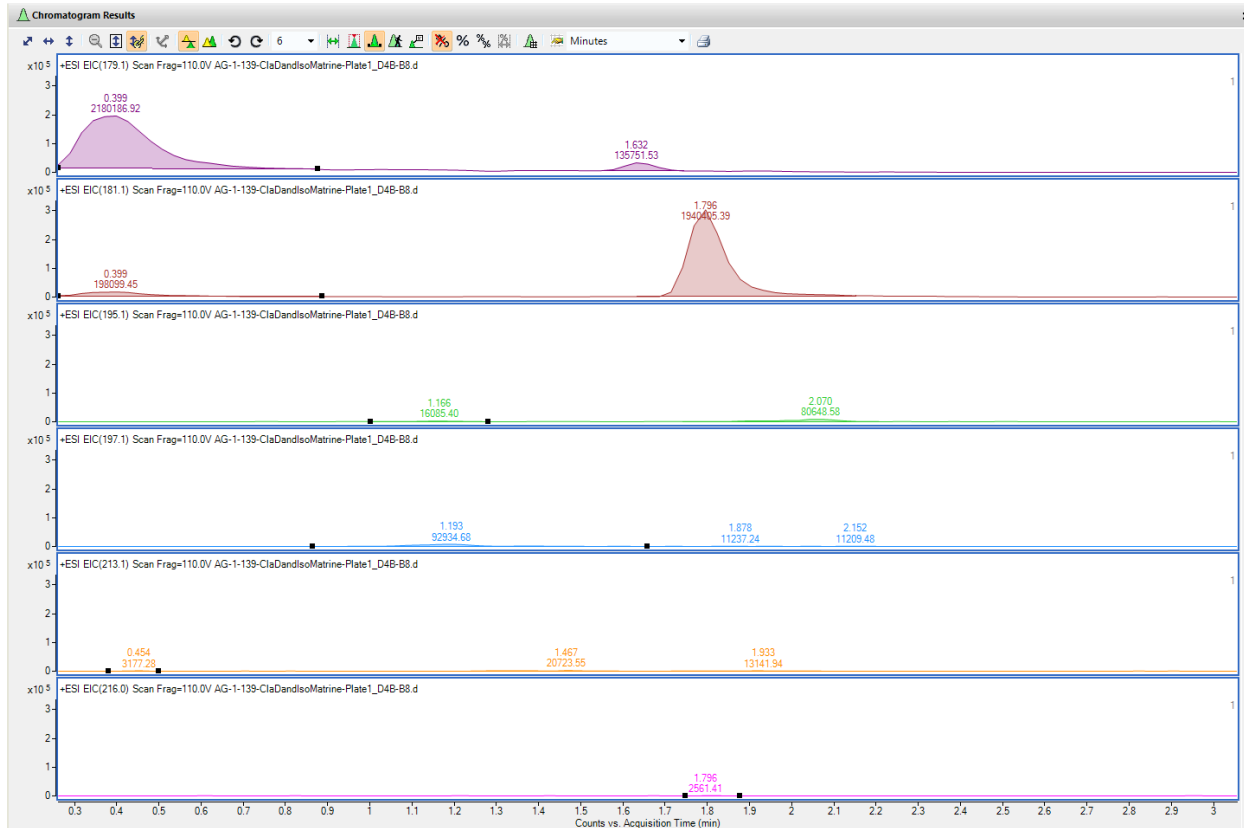
	Neutral	Positive	Negative
desaturation	178.0549	179.0628	177.0471
Substrate	180.0706	181.0784	179.0628
oxidation/desaturation	194.0499	195.0577	193.0421
hydroxylation	196.0655	197.0733	195.0577
dihydroxylation	212.0604	213.0682	211.0526
chlorination	215.0394	216.0472	214.0316



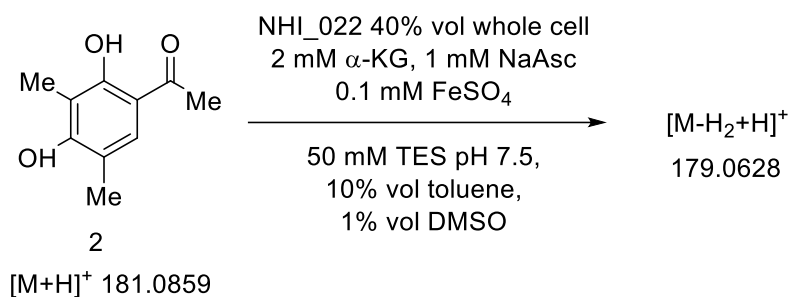
Discovered Reaction 7. Substrate_002 + NHI_020 = desaturation



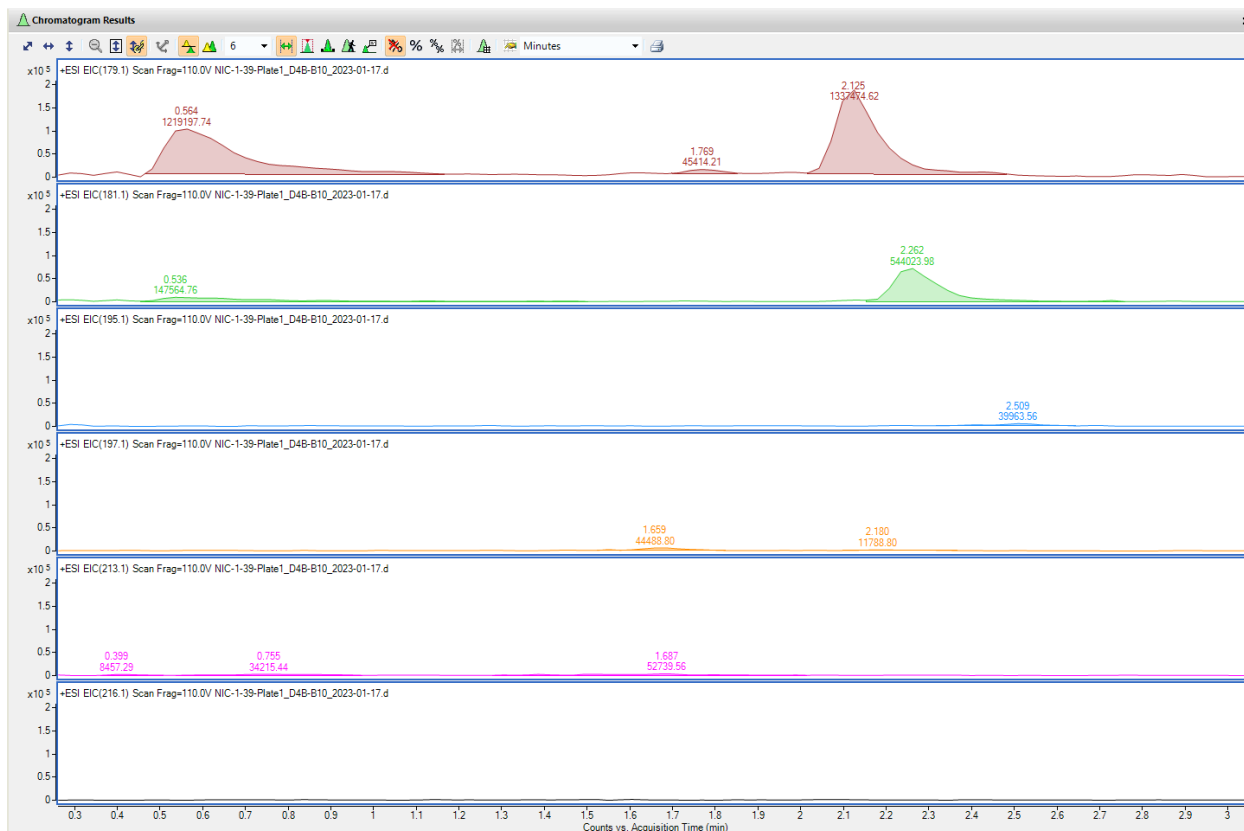
	Neutral	Positive	Negative
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Substrate	180.0706	181.0784	179.0628
oxidation/desaturation	194.0499	195.0577	193.0421
hydroxylation	196.0655	197.0733	195.0577
dihydroxylation	212.0604	213.0682	211.0526
chlorination	215.0394	216.0472	214.0316



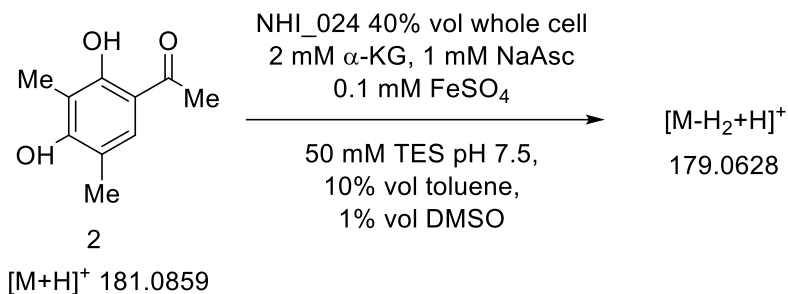
Discovered Reaction 8. Substrate_002 + NHI_022 = desaturation



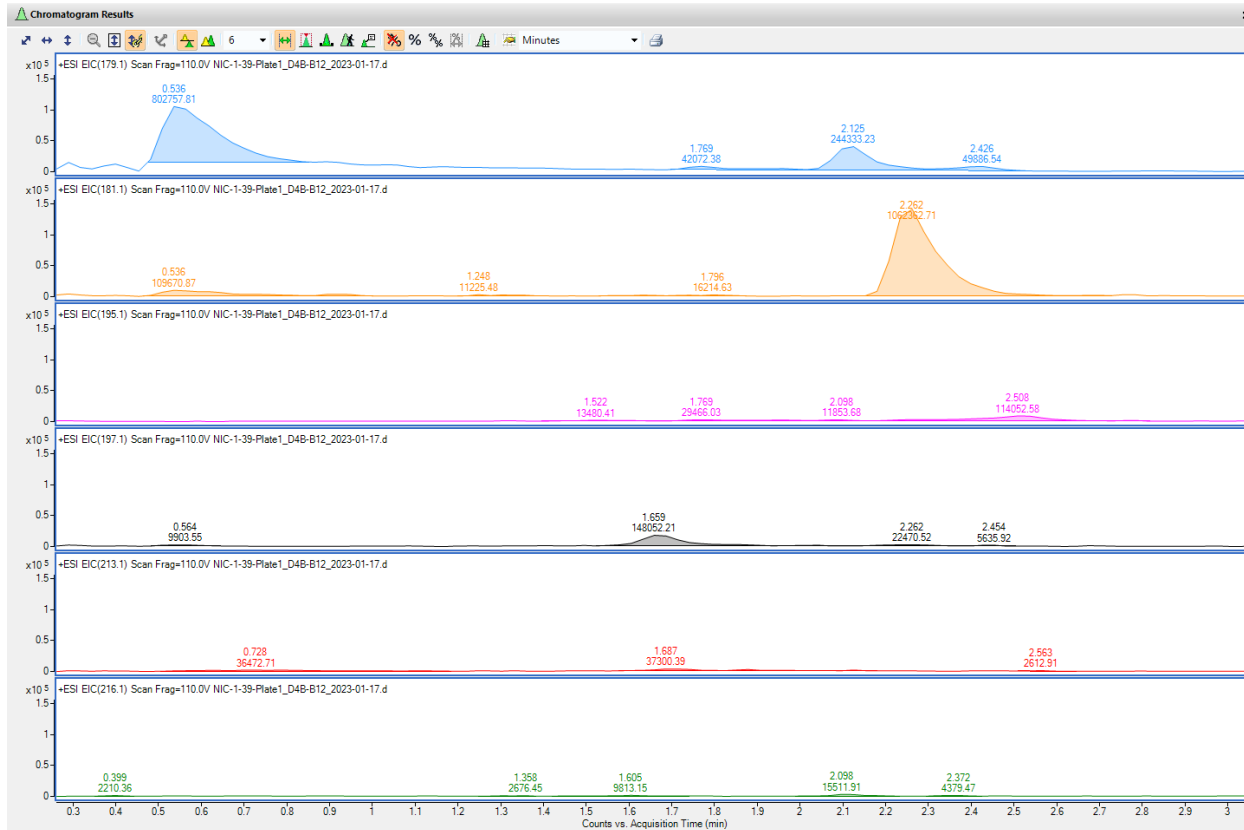
	Neutral	Positive	Negative
desaturation	178.0549	179.0628	177.0471
Substrate	180.0706	181.0784	179.0628
oxidation/desaturation	194.0499	195.0577	193.0421
hydroxylation	196.0655	197.0733	195.0577
dihydroxylation	212.0604	213.0682	211.0526
chlorination	215.0394	216.0472	214.0316



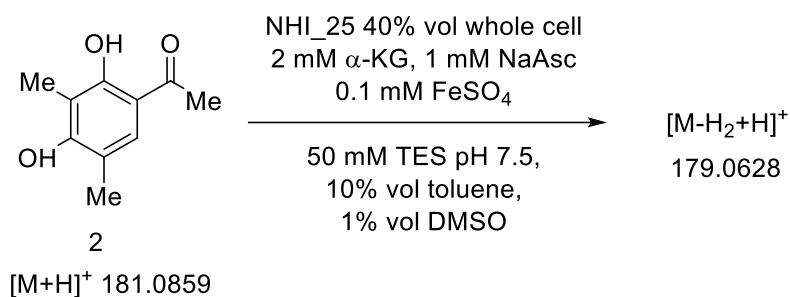
Discovered Reaction 9. Substrate_002 + NHI_024 = desaturation



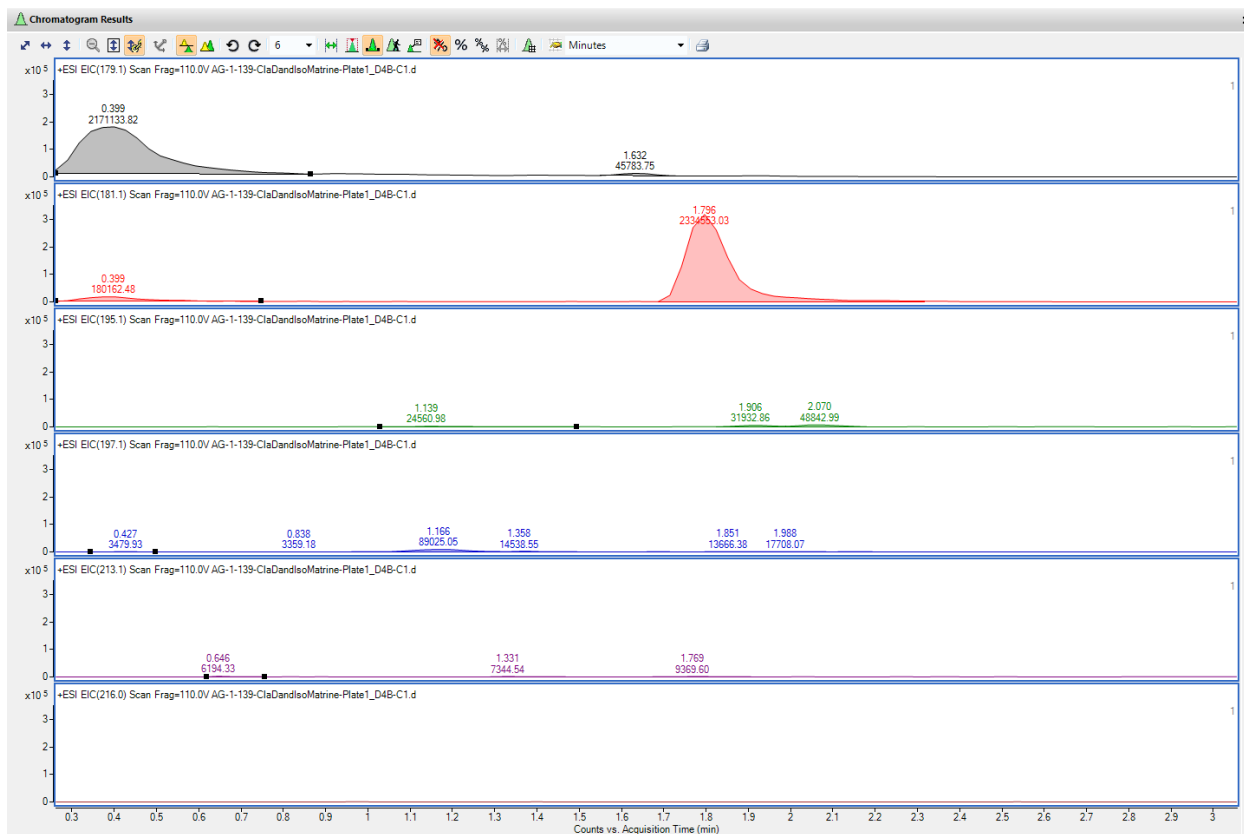
	Neutral	Positive	Negative
desaturation	178.0549	179.0628	177.0471
Substrate	180.0706	181.0784	179.0628
oxidation/desaturation	194.0499	195.0577	193.0421
hydroxylation	196.0655	197.0733	195.0577
dihydroxylation	212.0604	213.0682	211.0526
chlorination	215.0394	216.0472	214.0316



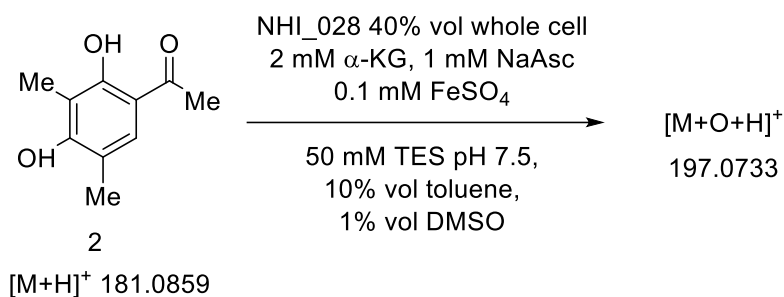
Discovered Reaction 10. Substrate_002 + NHI_025 = desaturation



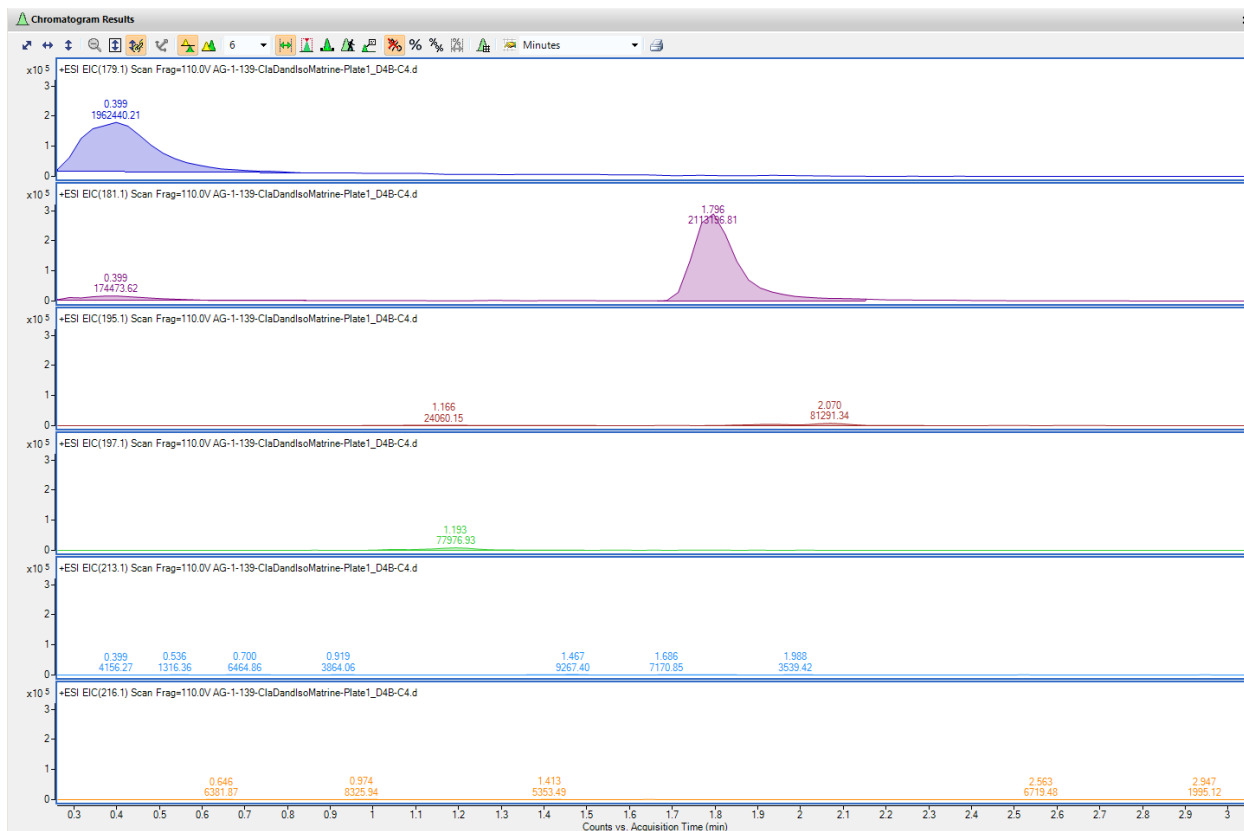
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Substrate	180.0706	181.0784	179.0628
oxidation/desaturation	194.0499	195.0577	193.0421
hydroxylation	196.0655	197.0733	195.0577
dihydroxylation	212.0604	213.0682	211.0526
chlorination	215.0394	216.0472	214.0316



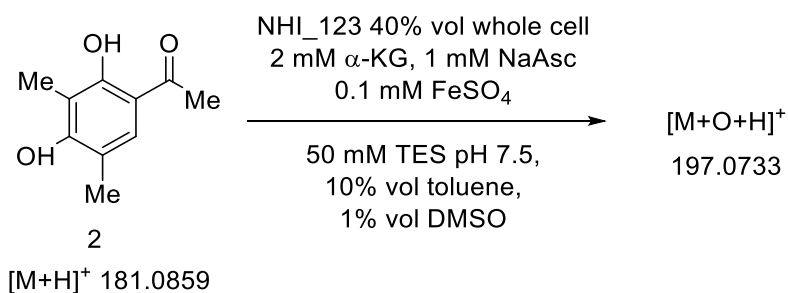
Discovered Reaction 11. Substrate_002 + NHI_028 = hydroxylation



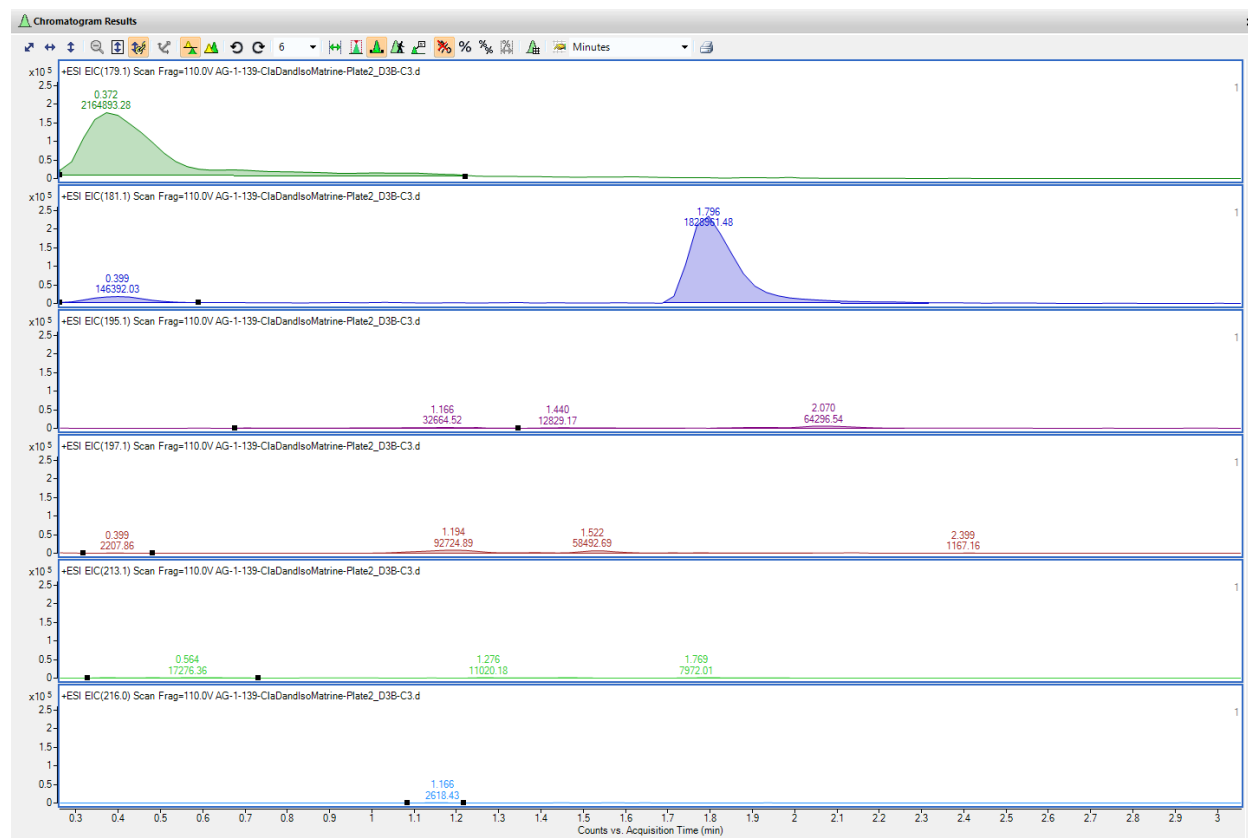
	Neutral	Positive	Negative
desaturation	178.0549	179.0628	177.0471
Substrate	180.0706	181.0784	179.0628
oxidation/desaturation	194.0499	195.0577	193.0421
hydroxylation	196.0655	197.0733	195.0577
dihydroxylation	212.0604	213.0682	211.0526
chlorination	215.0394	216.0472	214.0316



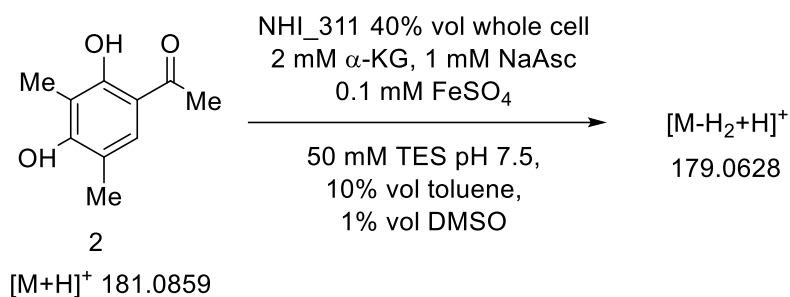
Discovered Reaction 12. Substrate_002 + NHI_123 = hydroxylation



	Neutral	Positive	Negative
desaturation	178.0549	179.0628	177.0471
Substrate	180.0706	181.0784	179.0628
oxidation/desaturation	194.0499	195.0577	193.0421
hydroxylation	196.0655	197.0733	195.0577
dihydroxylation	212.0604	213.0682	211.0526
chlorination	215.0394	216.0472	214.0316



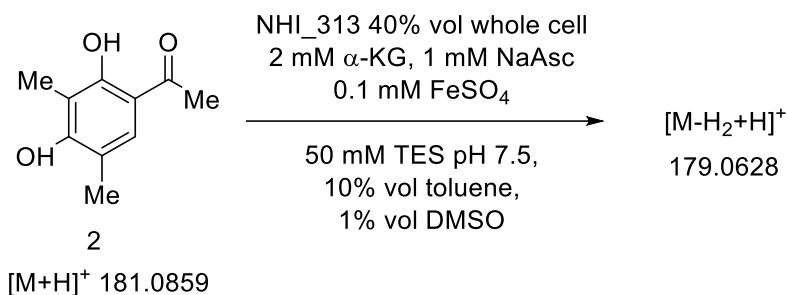
Discovered Reaction 13. Substrate_002 + NHI_311 = desaturation



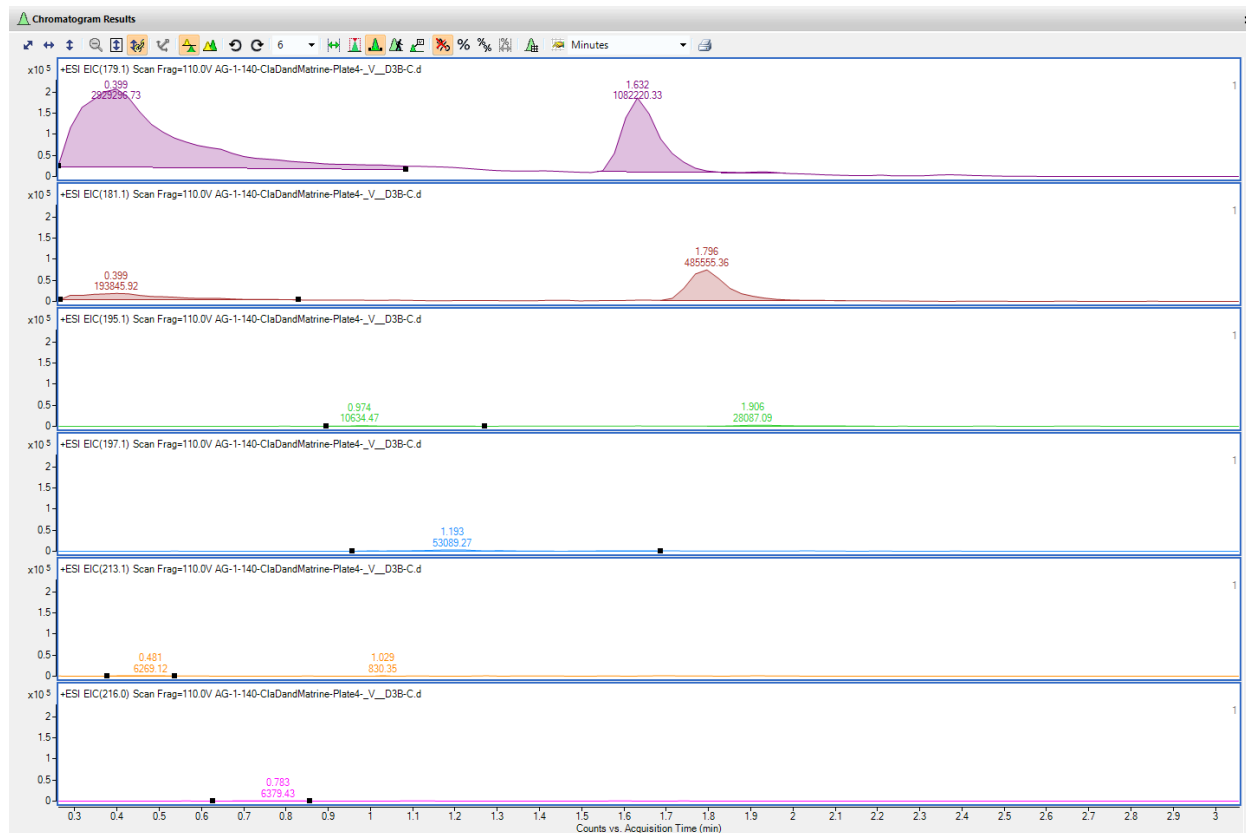
	Neutral	Positive	Negative
desaturation	178.0549	179.0628	177.0471
Substrate	180.0706	181.0784	179.0628
oxidation/desaturation	194.0499	195.0577	193.0421
hydroxylation	196.0655	197.0733	195.0577
dihydroxylation	212.0604	213.0682	211.0526
chlorination	215.0394	216.0472	214.0316



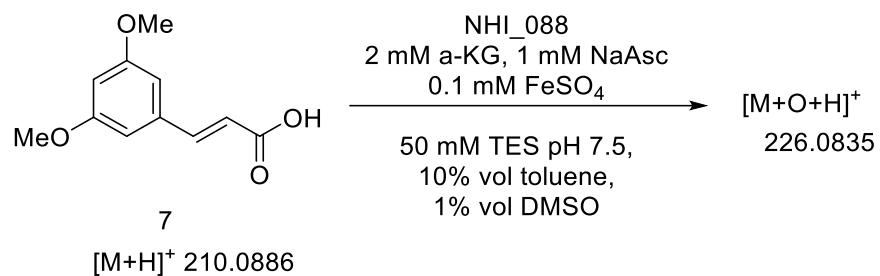
Discovered Reaction 14. Substrate_002 + NHI_313 = desaturation



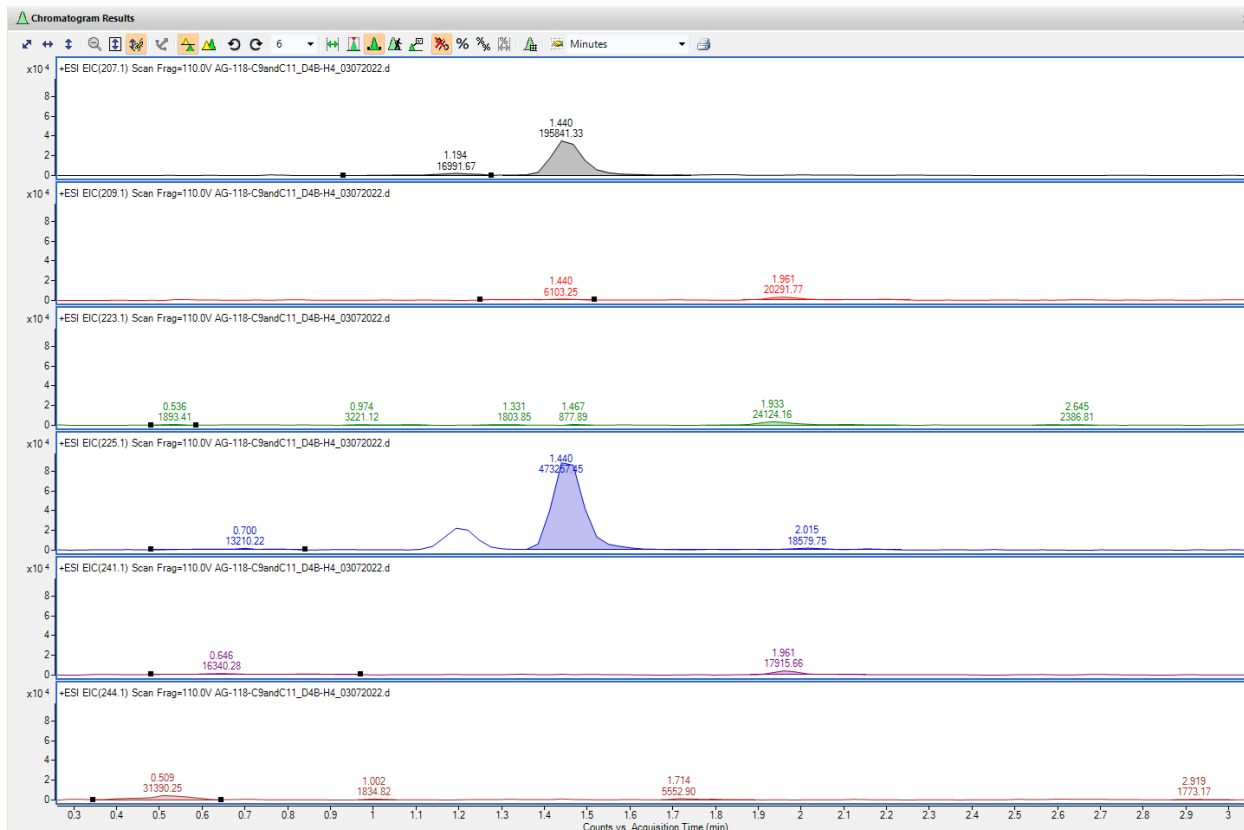
	Neutral	Positive	Negative
desaturation	178.0549	179.0628	177.0471
Substrate	180.0706	181.0784	179.0628
oxidation/desaturation	194.0499	195.0577	193.0421
hydroxylation	196.0655	197.0733	195.0577
dihydroxylation	212.0604	213.0682	211.0526
chlorination	215.0394	216.0472	214.0316



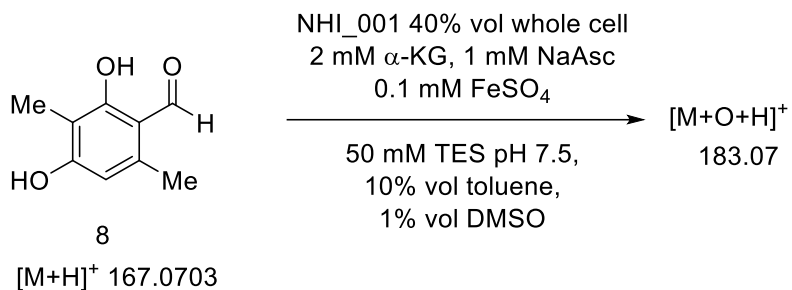
Discovered Reaction 15. Substrate_007 + NHI_088 = hydroxylation



	Neutral	Positive	Negative
desaturation	207.0651	208.073	206.0573
substrate	209.0808	210.0886	208.073
oxidation/desaturation	223.0601	224.0679	222.0523
hydroxylation	225.0757	226.0835	224.0679
dihydroxylation	241.0706	242.0784	240.0628
chlorination	244.0496	245.0574	243.0418



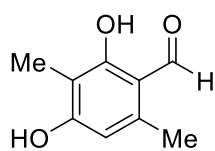
Discovered Reaction 16. Substrate_008 + NHI_001 = hydroxylation



	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



Discovered Reaction 17. Substrate_008 + NHI_002 = hydroxylation



8

$[M+H]^+$ 167.0703

NHI_002 40% vol whole cell

2 mM α -KG, 1 mM NaAsc

0.1 mM FeSO₄

50 mM TES pH 7.5,

10% vol toluene,

1% vol DMSO

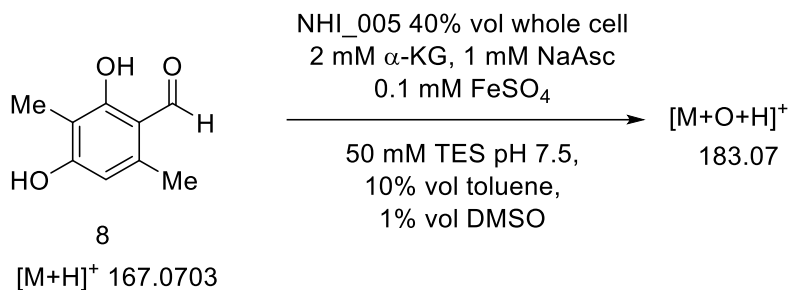
$[M+O+H]^+$

183.07

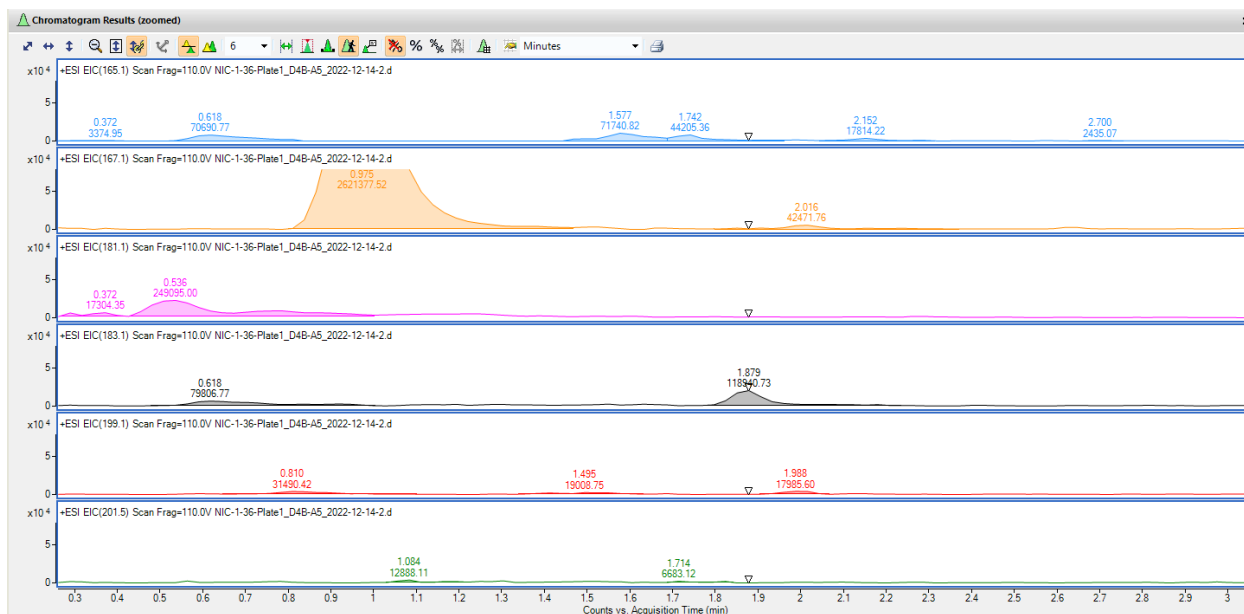
	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



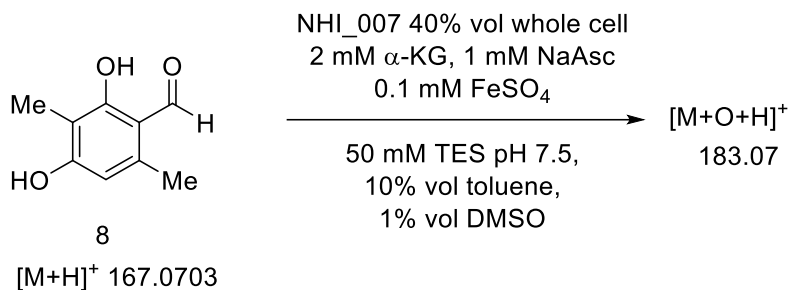
Discovered Reaction 18. Substrate_008 + NHI_005 = hydroxylation



	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



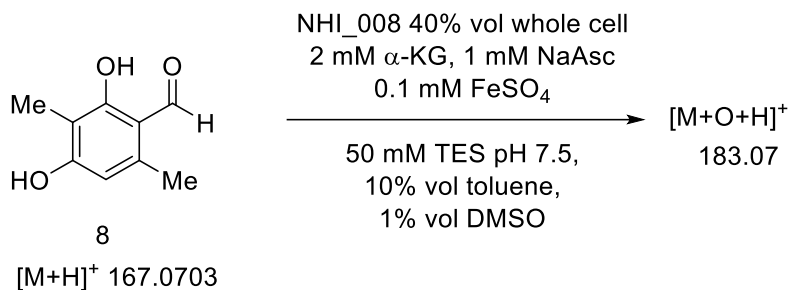
Discovered Reaction 19. Substrate_008 + NHI_007 = hydroxylation



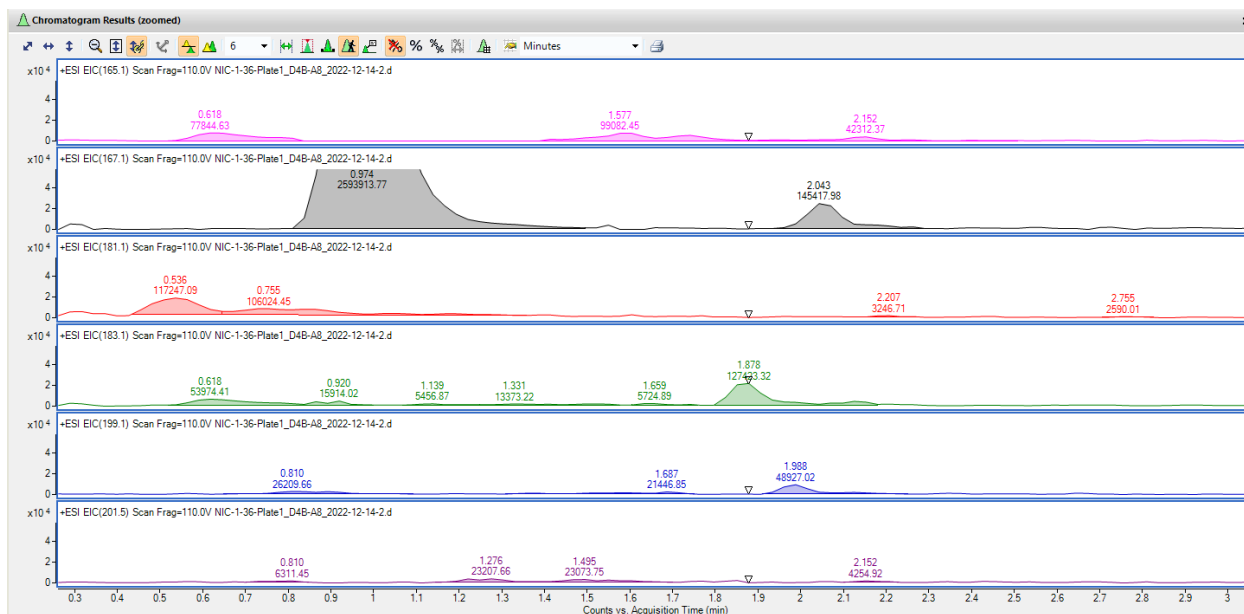
	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



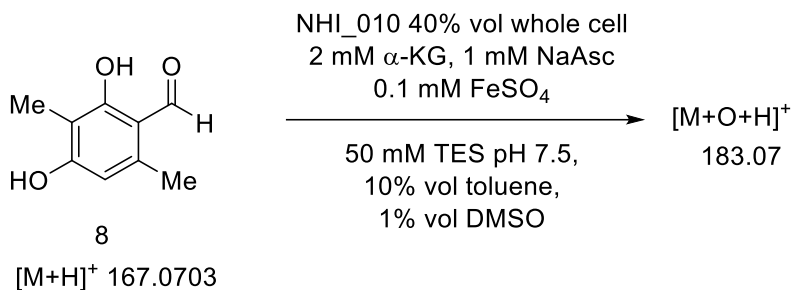
Discovered Reaction 20. Substrate_008 + NHI_008 = hydroxylation



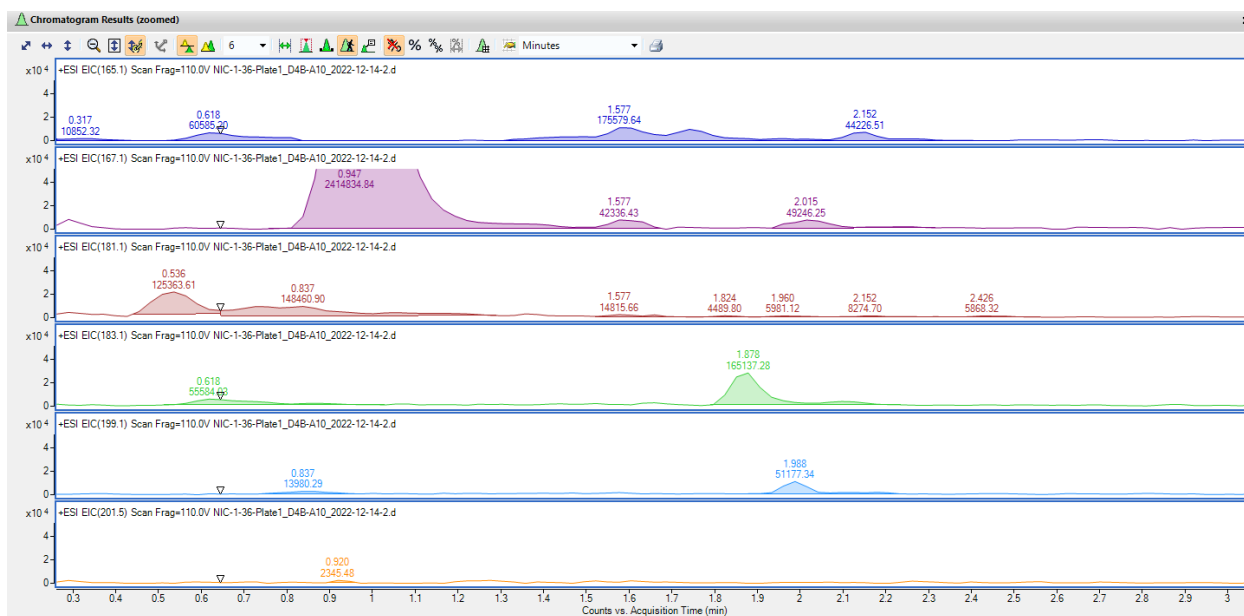
	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



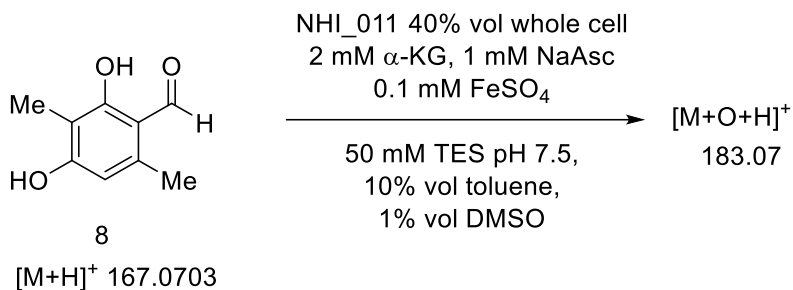
Discovered Reaction 21. Substrate_008 + NHI_010 = hydroxylation



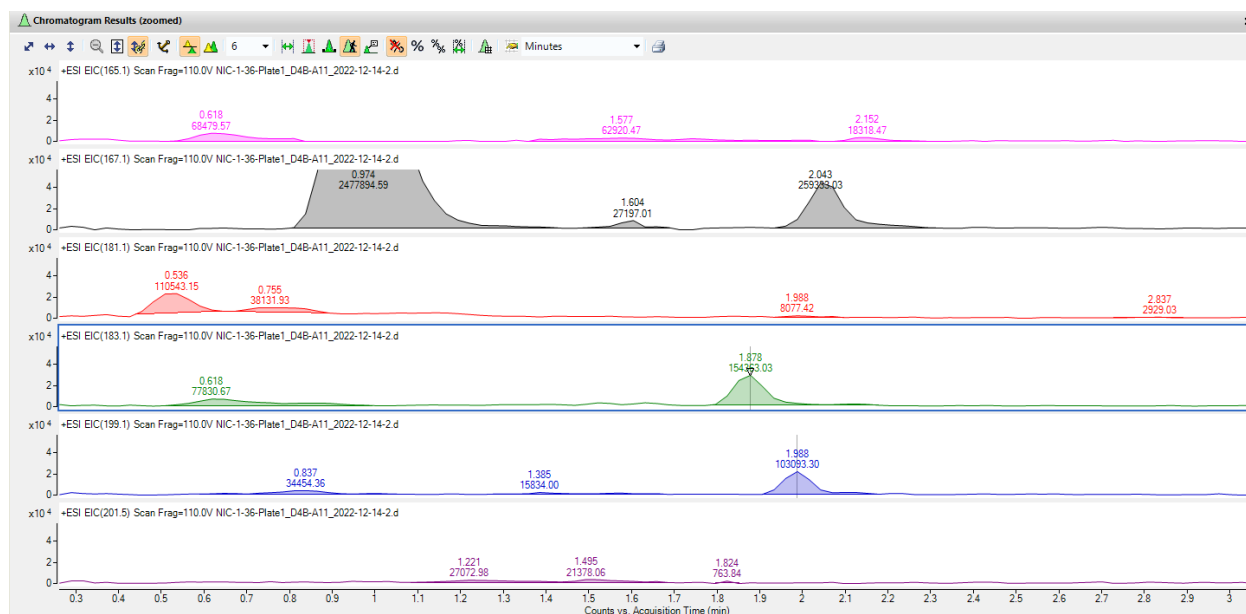
	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



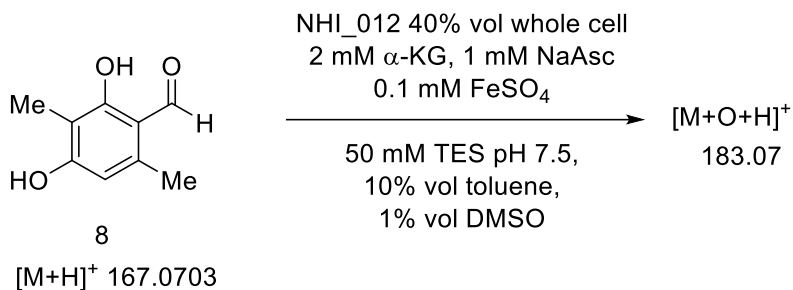
Discovered Reaction 22. Substrate_008 + NHI_011 = hydroxylation



	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



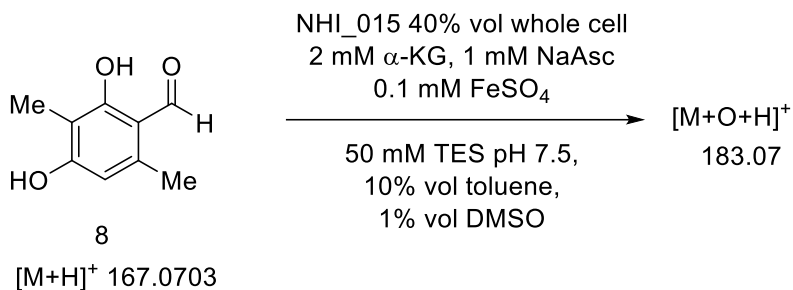
Discovered Reaction 23. Substrate_008 + NHI_012 = hydroxylation



	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



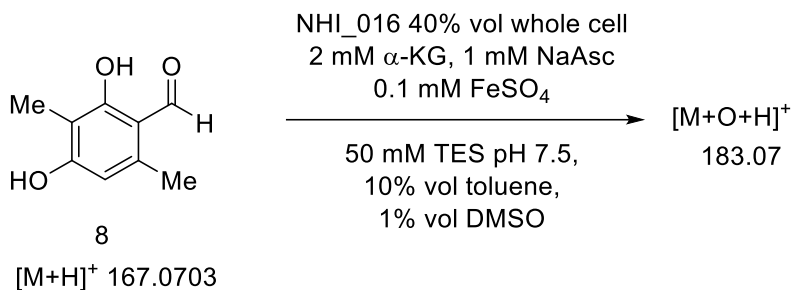
Discovered Reaction 24. Substrate_008 + NHI_015 = hydroxylation



	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



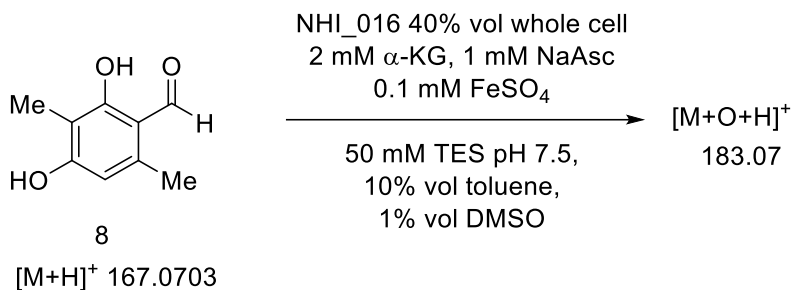
Discovered Reaction 25. Substrate_008 + NHI_016 = hydroxylation



	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



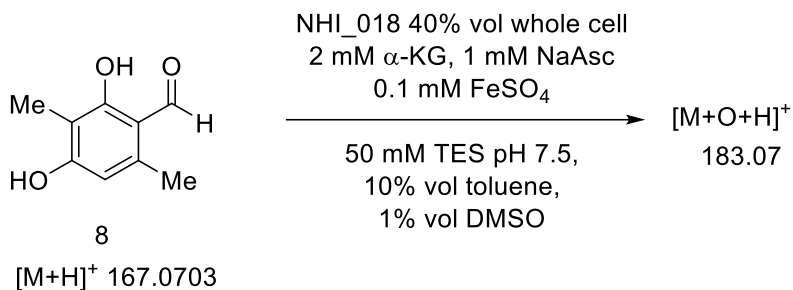
Discovered Reaction 26. Substrate_008 + NHI_017 = hydroxylation



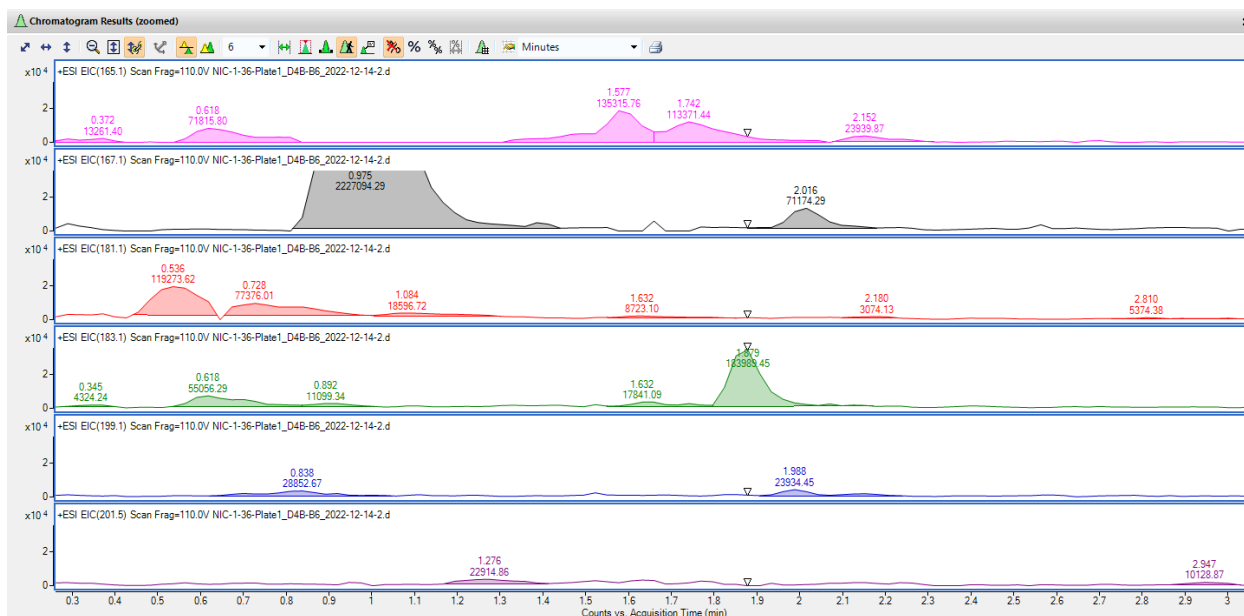
	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



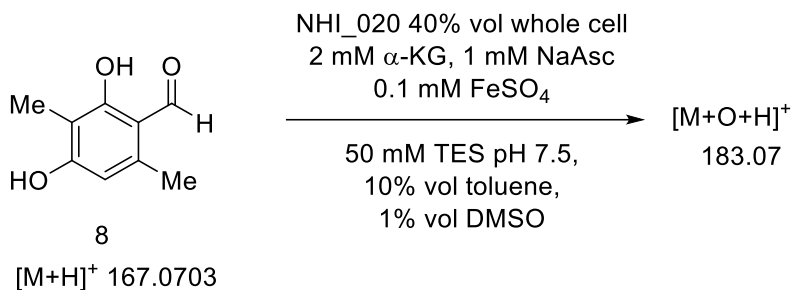
Discovered Reaction 27. Substrate_008 + NHI_018 = hydroxylation



	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



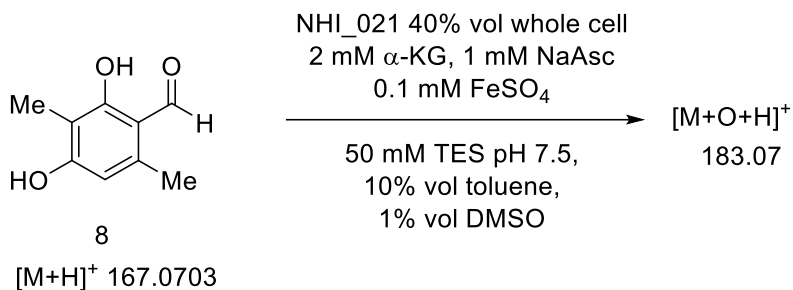
Discovered Reaction 28. Substrate_008 + NHI_020 = hydroxylation



	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



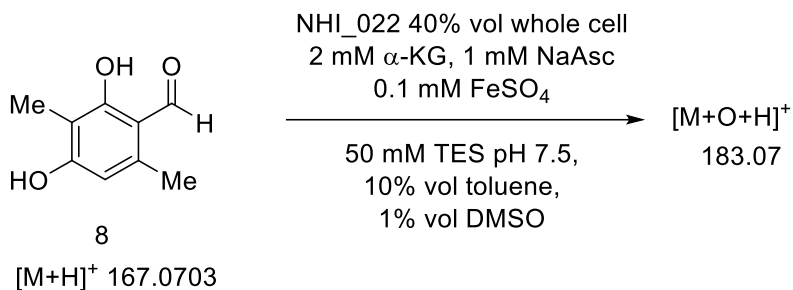
Discovered Reaction 29. Substrate_008 + NHI_021 = hydroxylation



	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



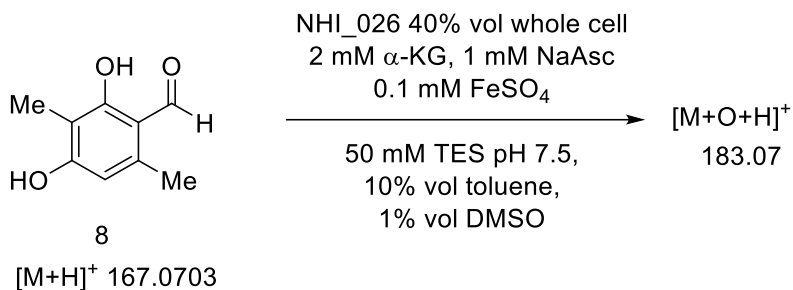
Discovered Reaction 30. Substrate_008 + NHI_022 = hydroxylation



	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



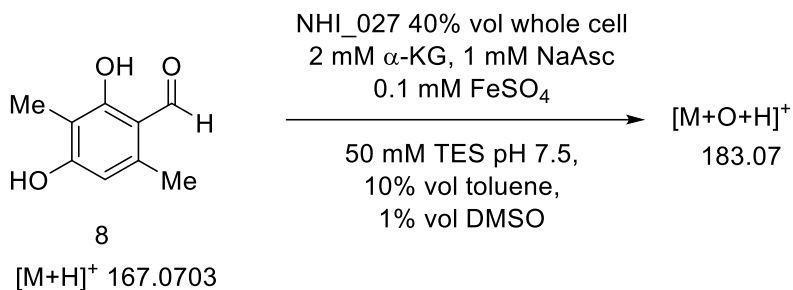
Discovered Reaction 31. Substrate_008 + NHI_026 = hydroxylation



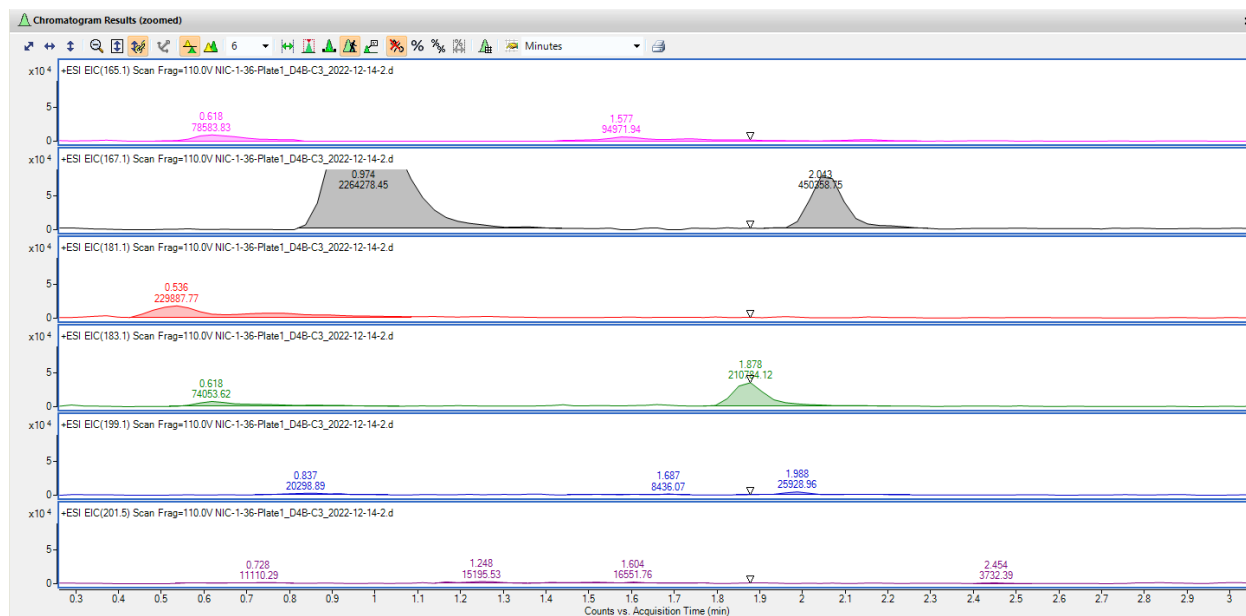
	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



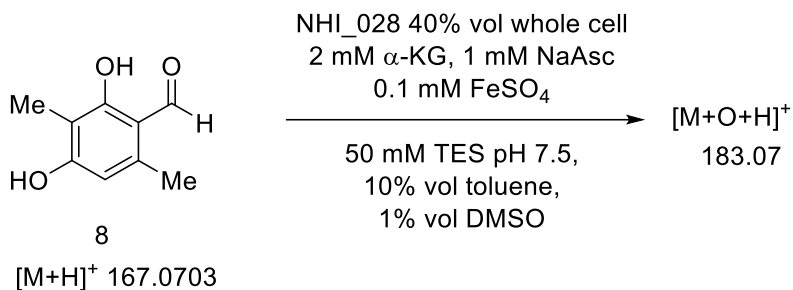
Discovered Reaction 32. Substrate_008 + NHI_027 = hydroxylation



	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



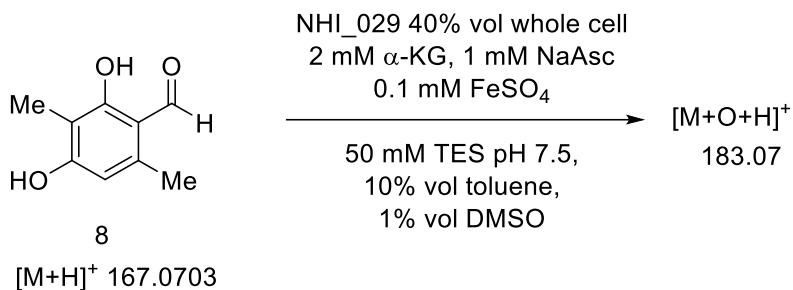
Discovered Reaction 33. Substrate_008 + NHI_028 = hydroxylation



	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



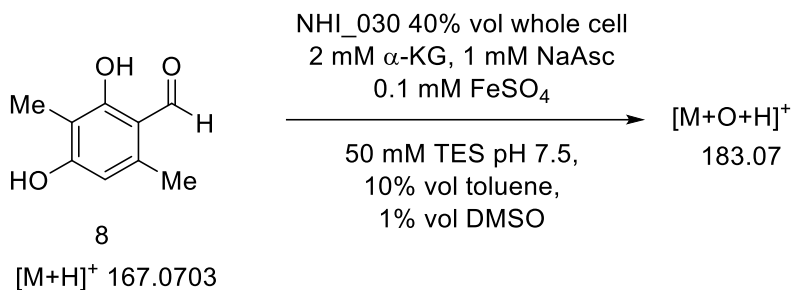
Discovered Reaction 34. Substrate_008 + NHI_029 = hydroxylation



	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



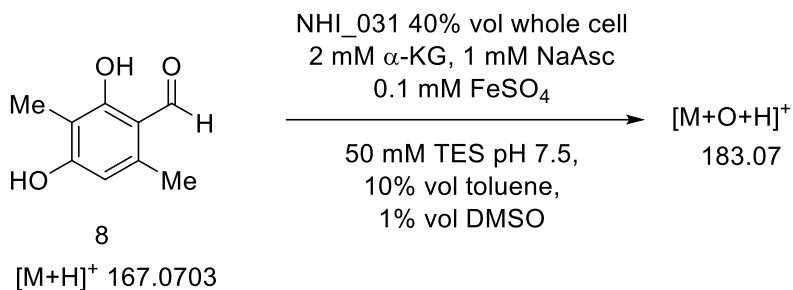
Discovered Reaction 35. Substrate_008 + NHI_030 = hydroxylation



	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



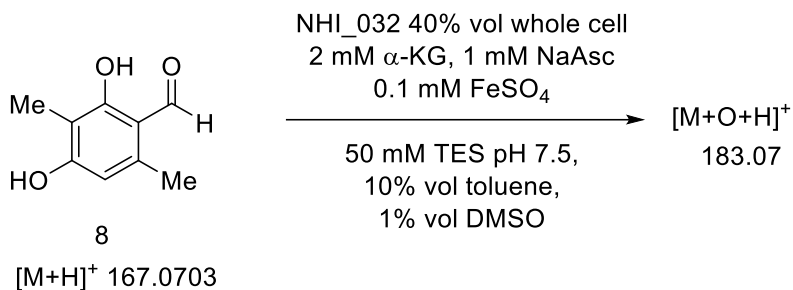
Discovered Reaction 36. Substrate_008 + NHI_031 = hydroxylation



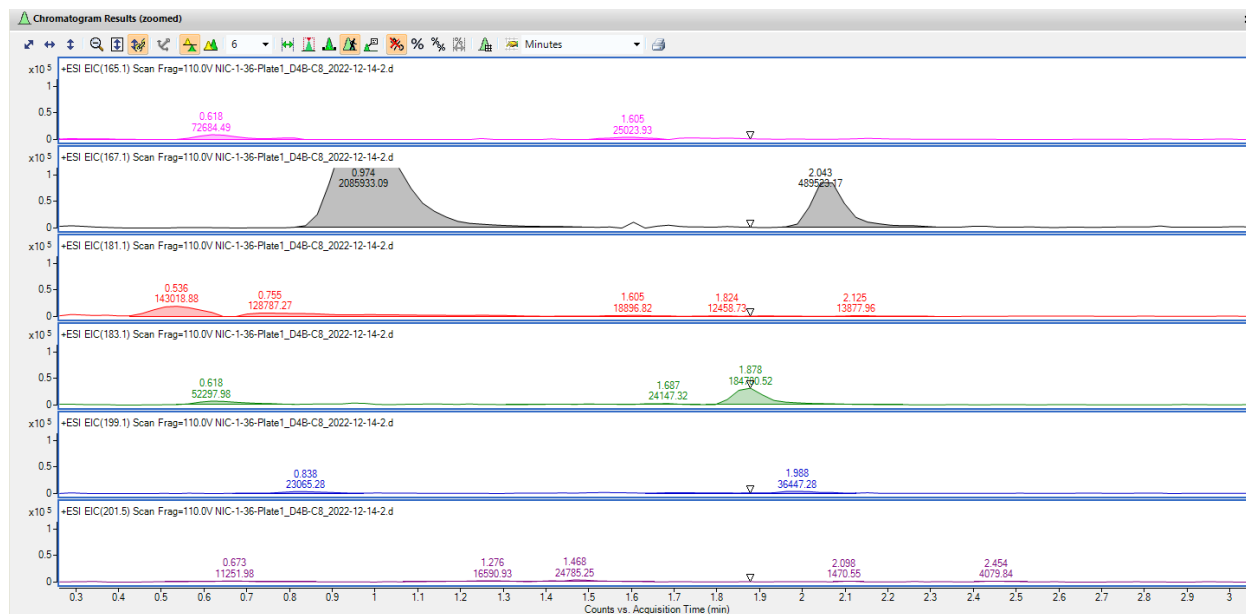
	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



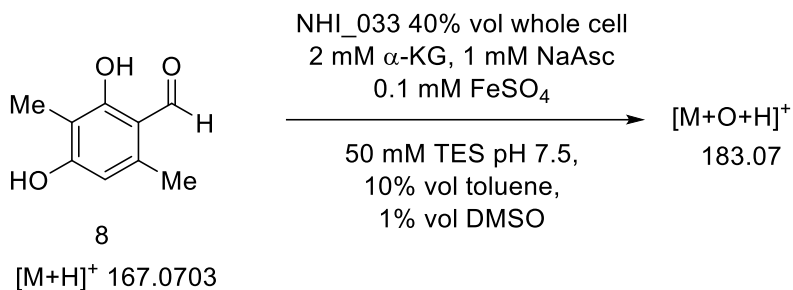
Discovered Reaction 37. Substrate_008 + NHI_032 = hydroxylation



	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



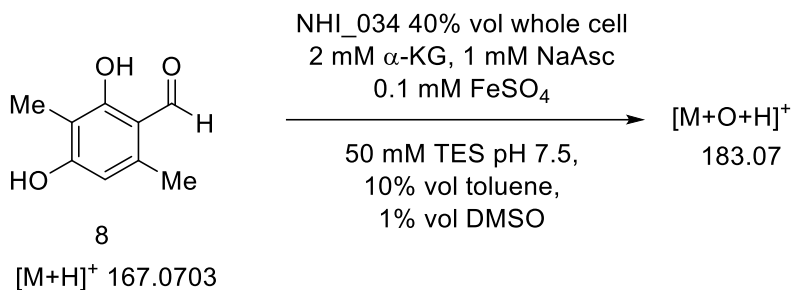
Discovered Reaction 38. Substrate_008 + NHI_033 = hydroxylation



	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



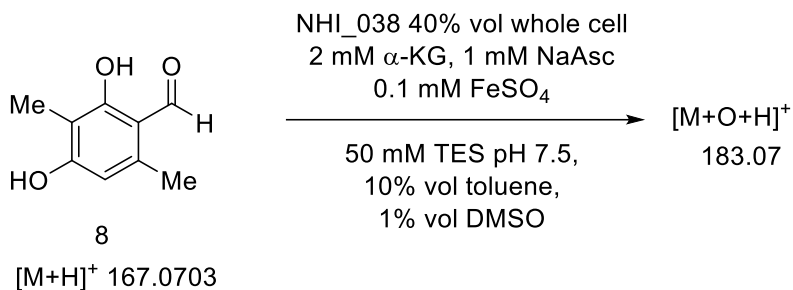
Discovered Reaction 39. Substrate_008 + NHI_034 = hydroxylation



	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



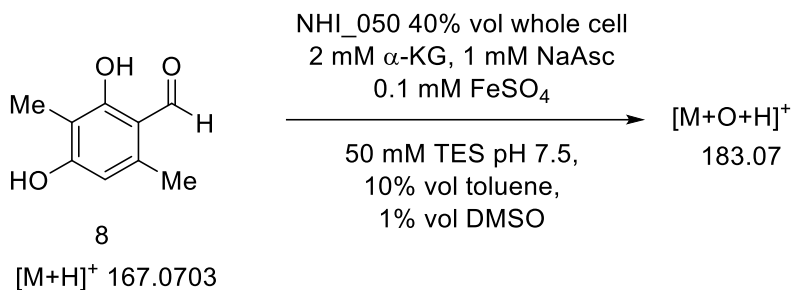
Discovered Reaction 40. Substrate_008 + NHI_038 = hydroxylation



	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



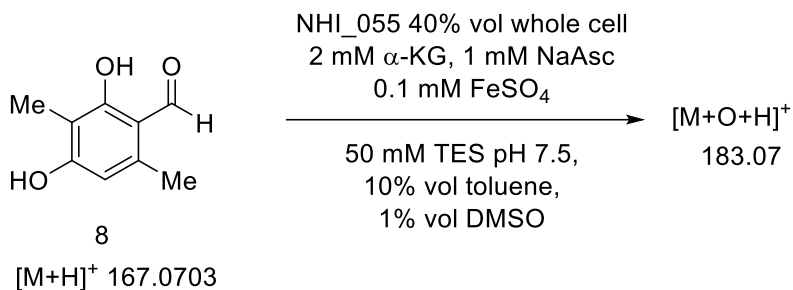
Discovered Reaction 41. Substrate_008 + NHI_050 = hydroxylation



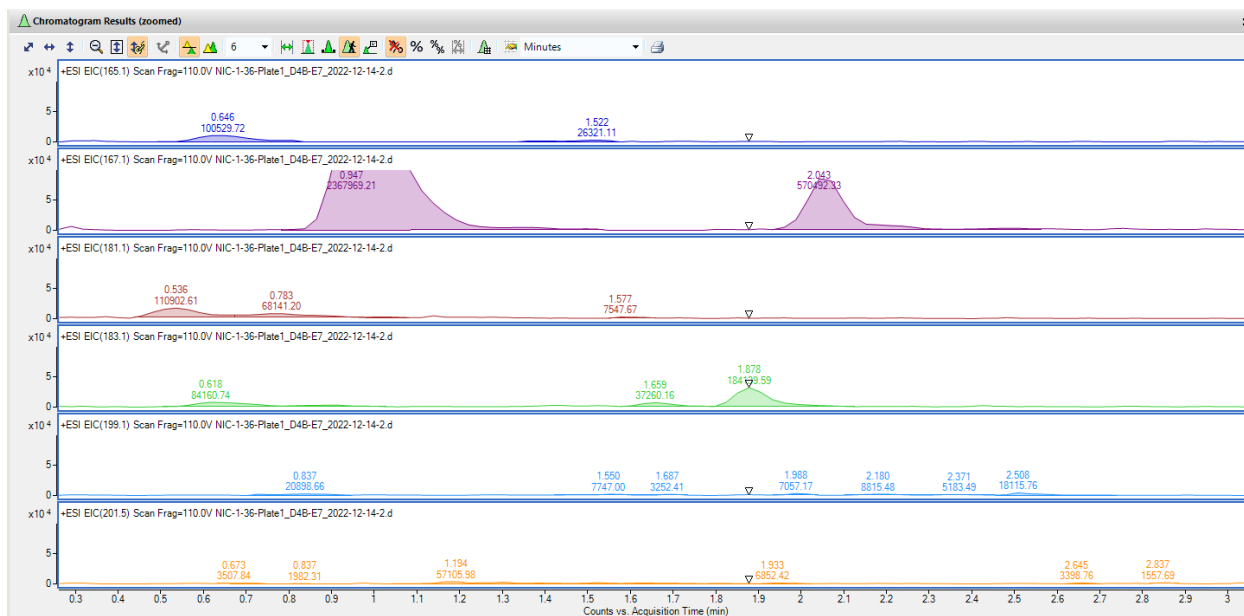
	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



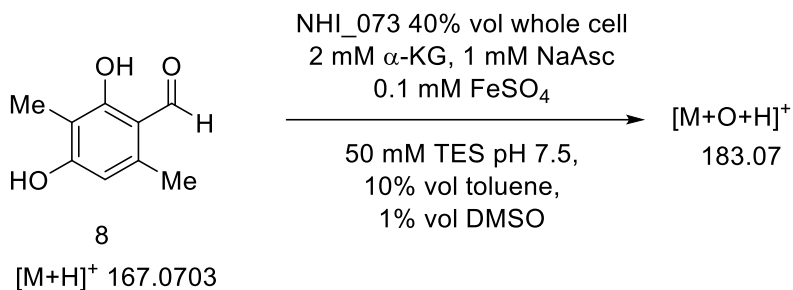
Discovered Reaction 42. Substrate_008 + NHI_055 = hydroxylation



	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



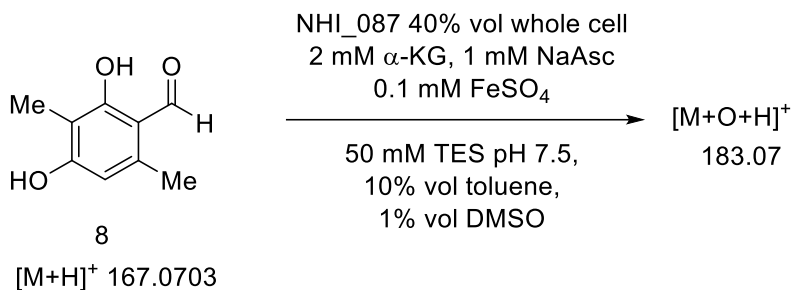
Discovered Reaction 43. Substrate_008 + NHI_073 = hydroxylation



	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



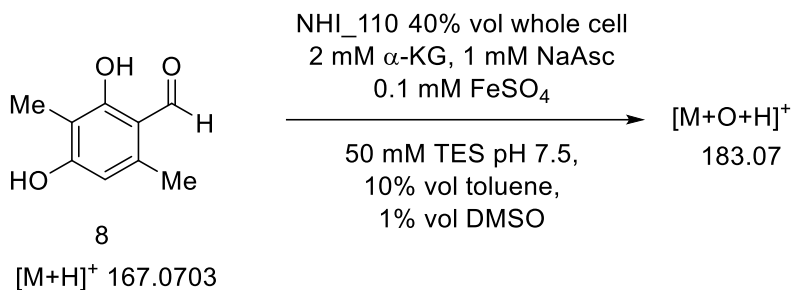
Discovered Reaction 44. Substrate_008 + NHI_087 = hydroxylation



	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



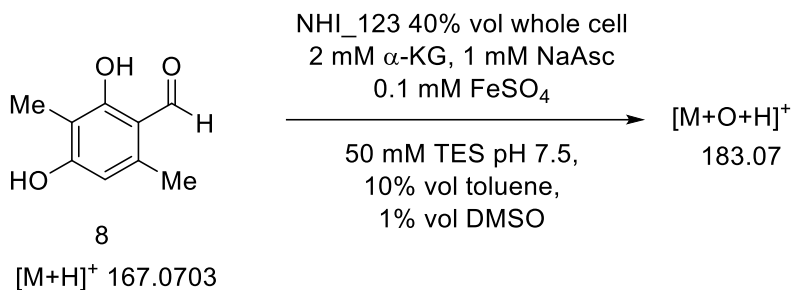
Discovered Reaction 45. Substrate_008 + NHI_110 = hydroxylation



	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



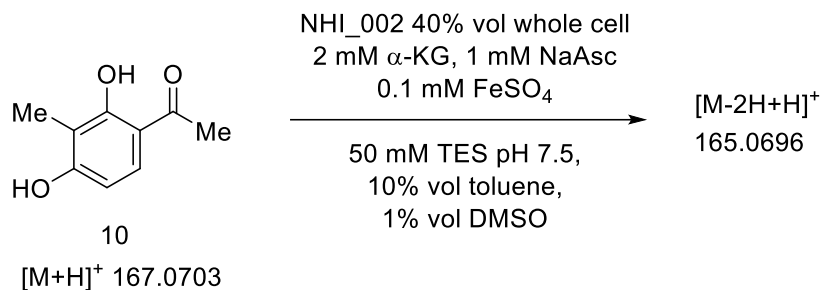
Discovered Reaction 46. Substrate_008 + NHI_123 = hydroxylation



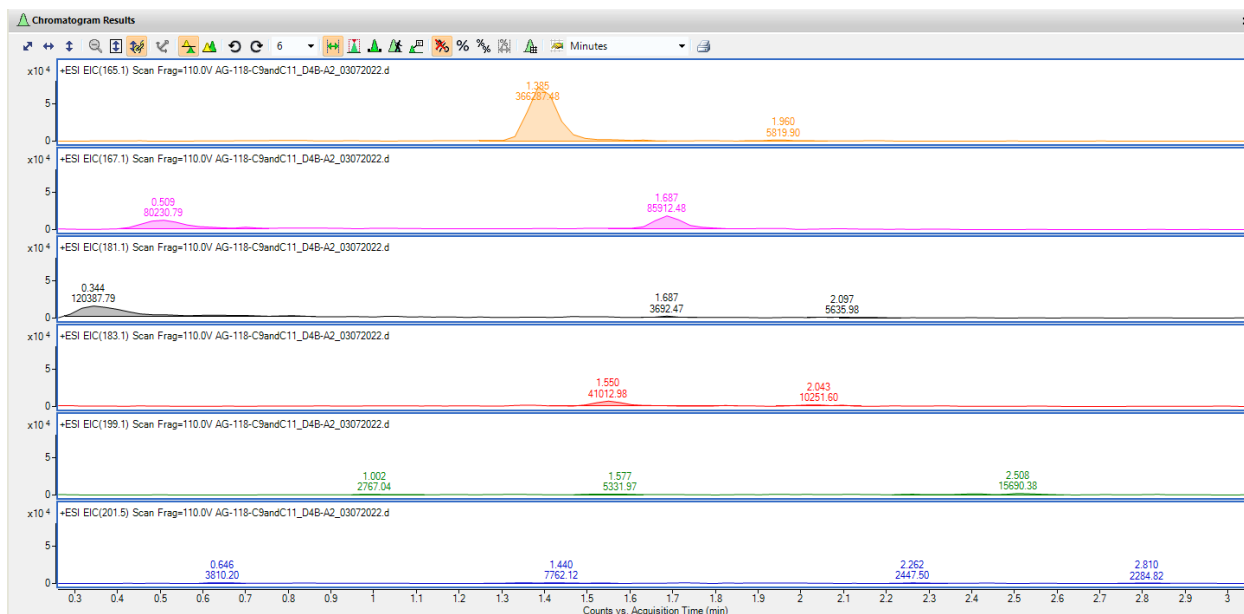
	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



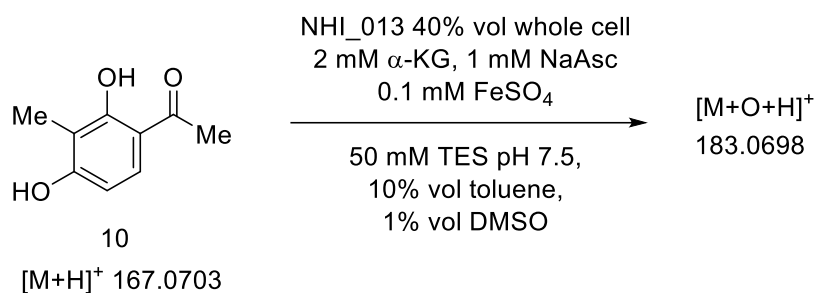
Discovered Reaction 47. Substrate_010 + NHI_002 = desaturation



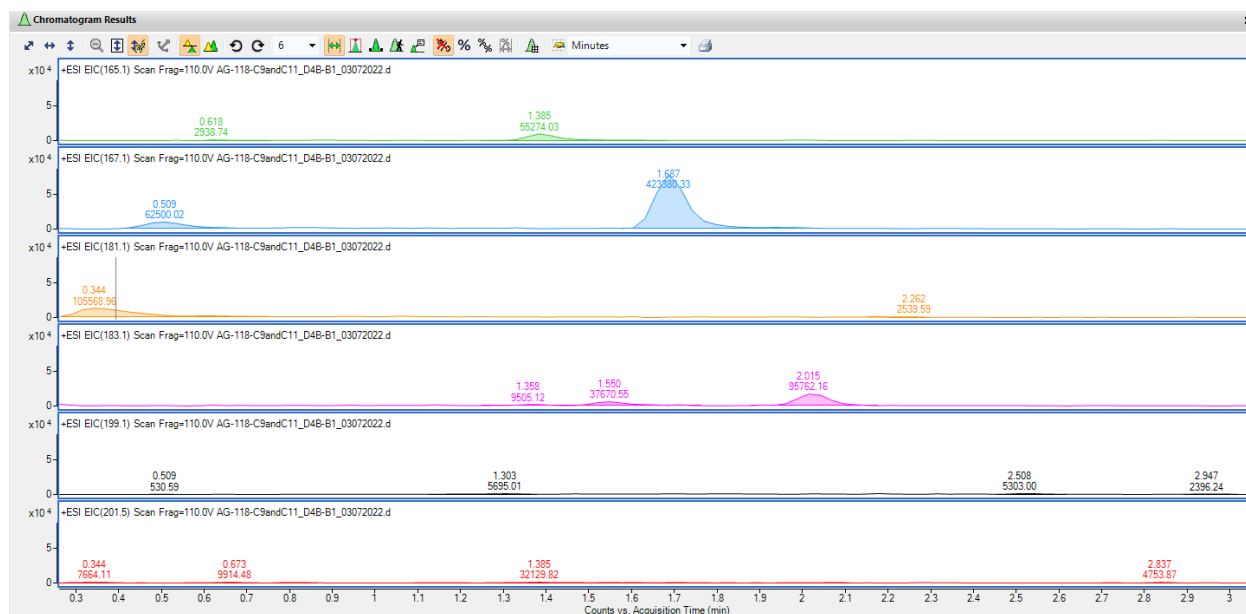
	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



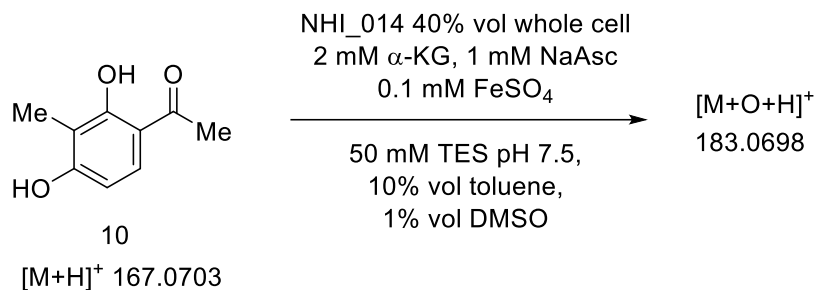
Discovered Reaction 48. Substrate_010 + NHI_013 = desaturation



	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



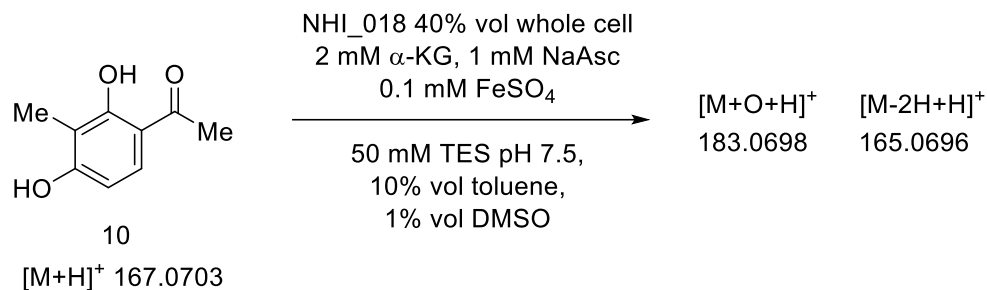
Discovered Reaction 49. Substrate_010 + NHI_014 = hydroxylation



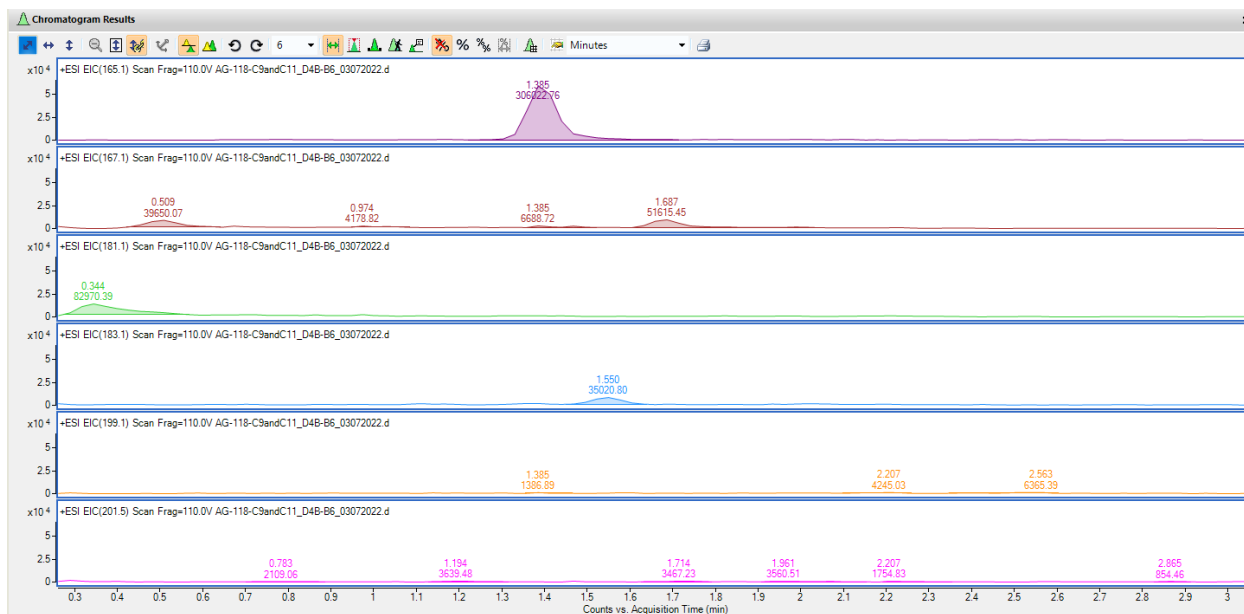
	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



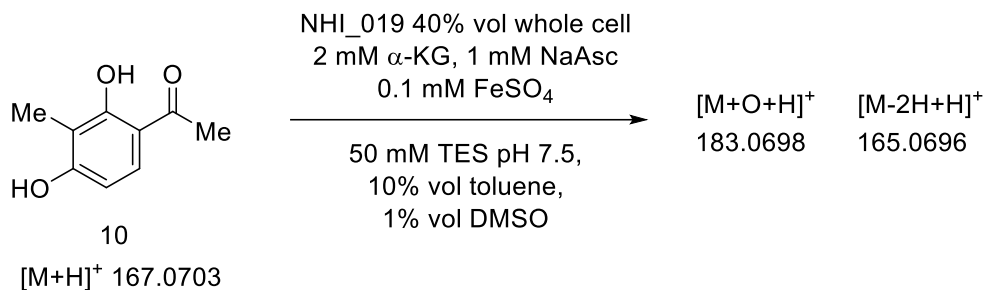
Discovered Reaction 50. Substrate_010 + NHI_018 = hydroxylation and desaturation



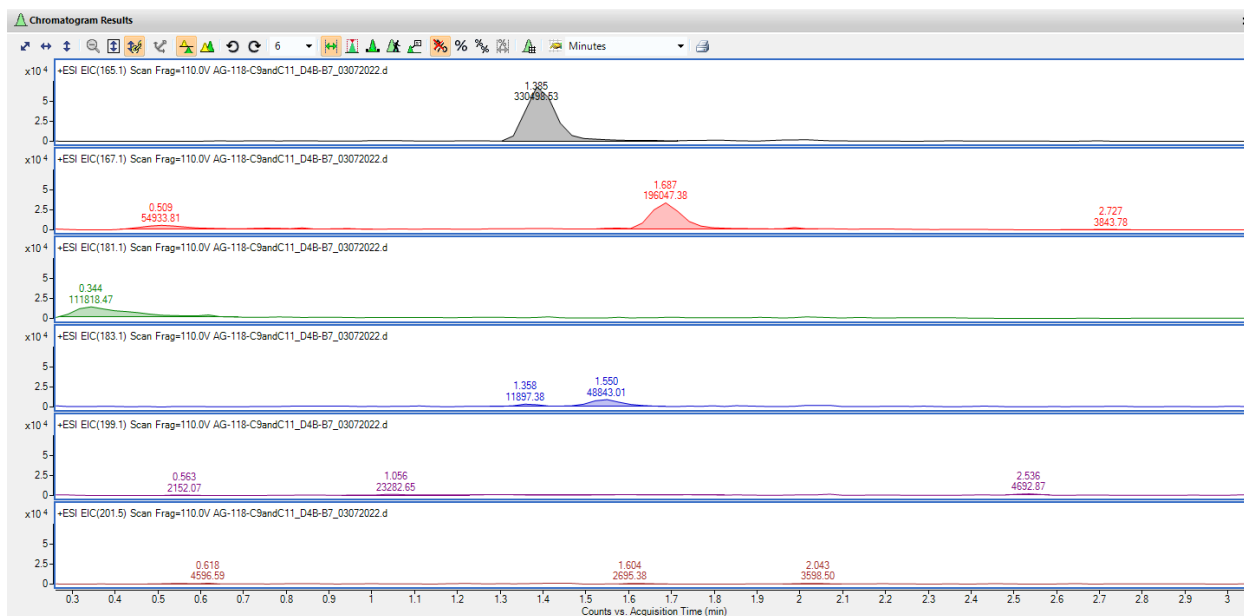
	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



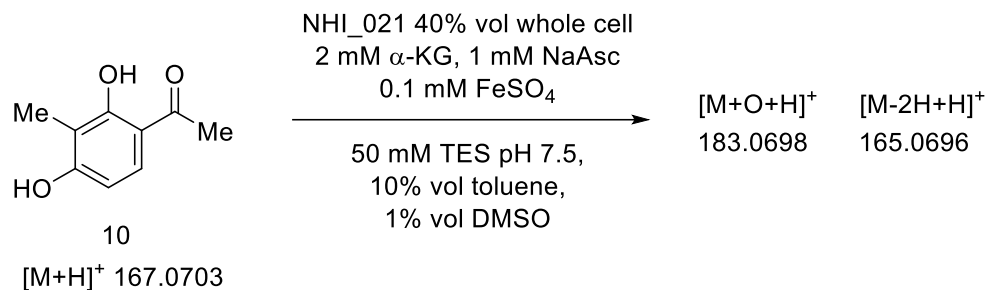
Discovered Reaction 51. Substrate_010 + NHI_019 = hydroxylation and desaturation



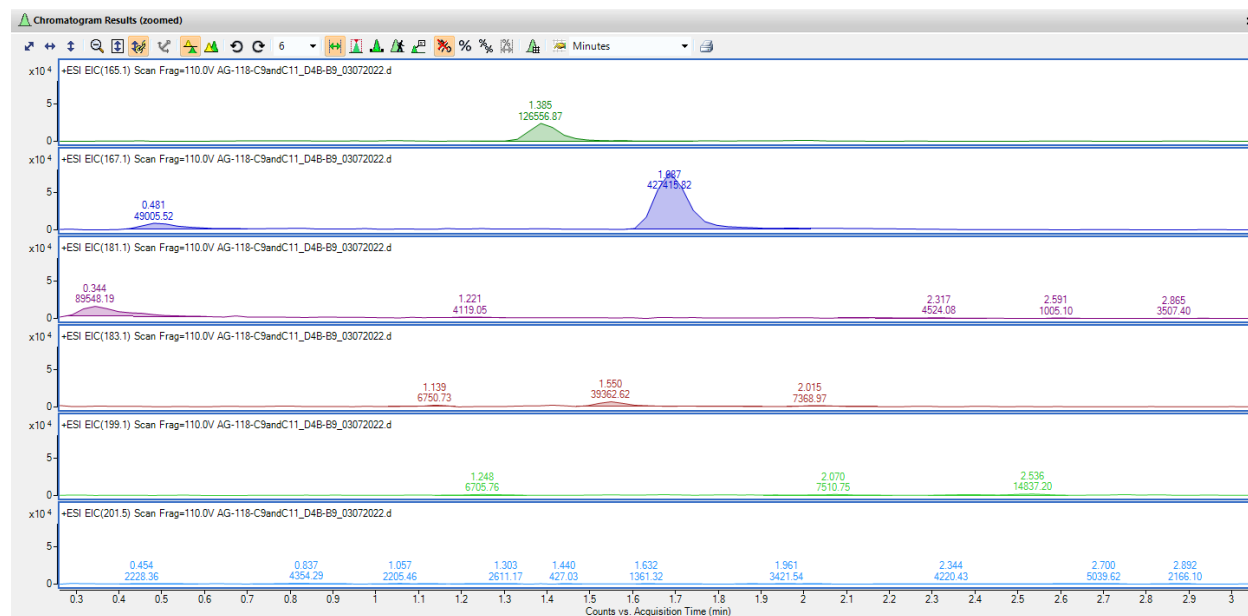
	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



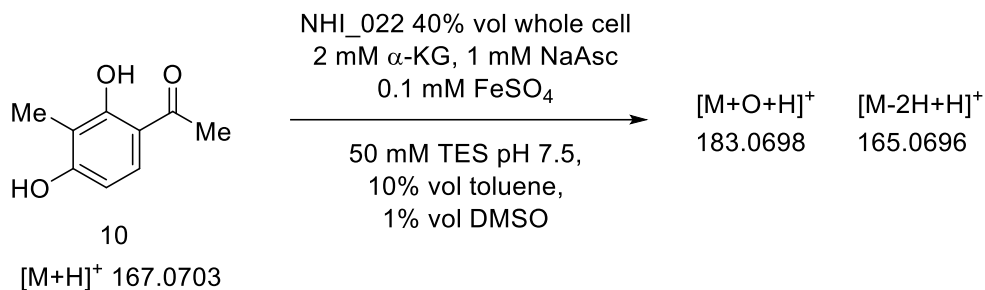
Discovered Reaction 52. Substrate_010 + NHI_021 = hydroxylation and desaturation



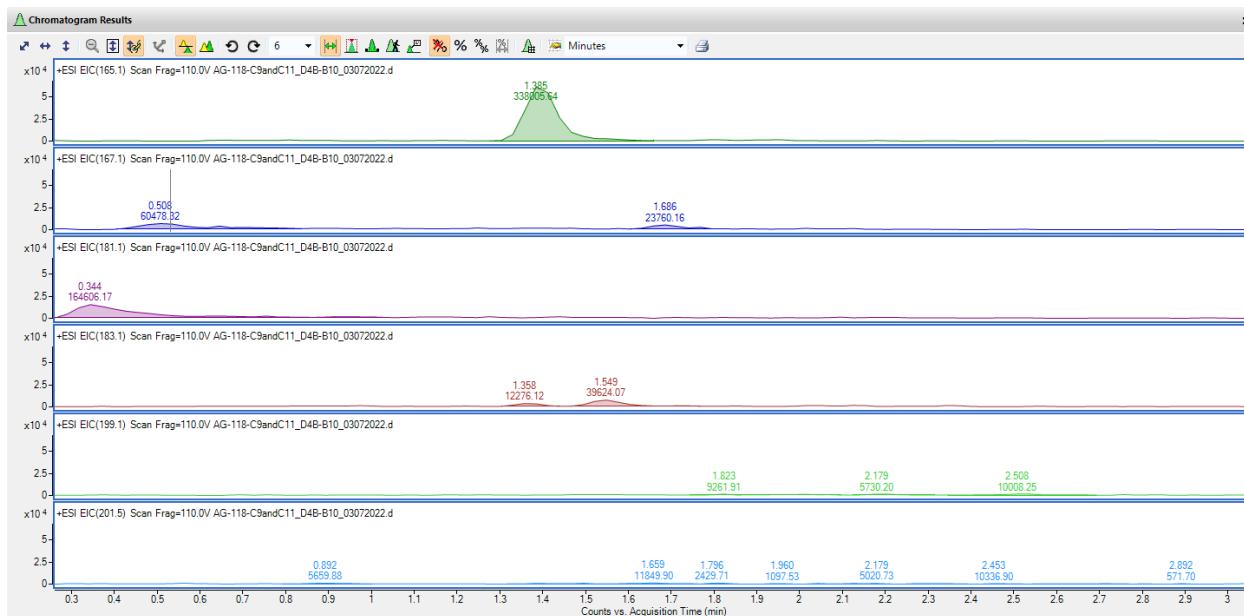
	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



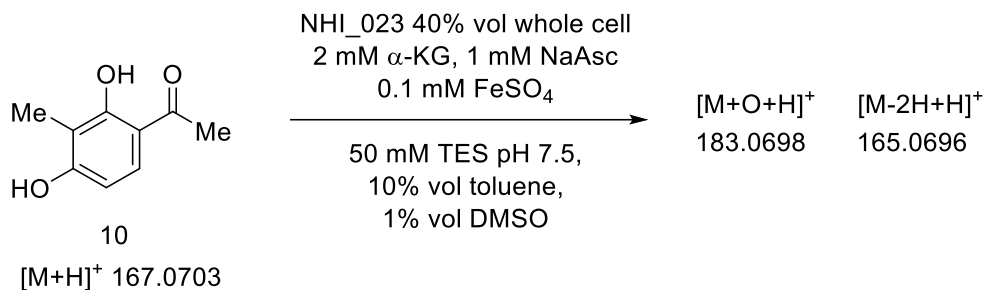
Discovered Reaction 53. Substrate_010 + NHI_022 = hydroxylation and desaturation



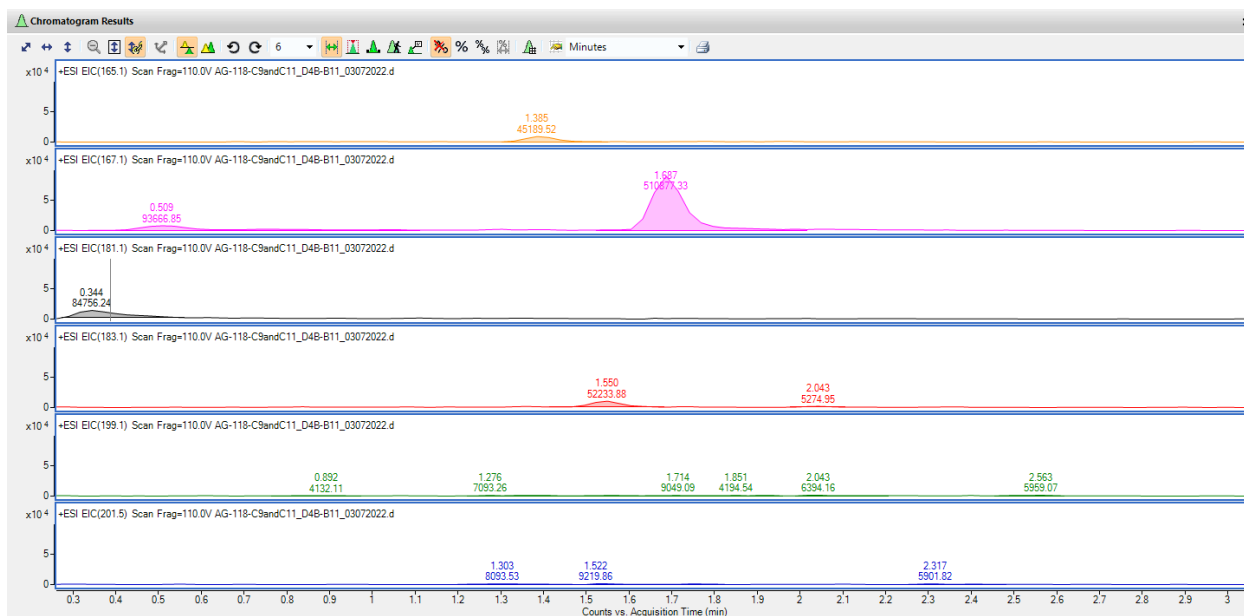
	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



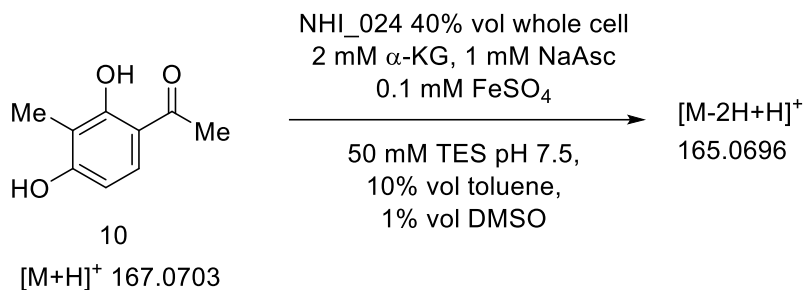
Discovered Reaction 54. Substrate_010 + NHI_023 = hydroxylation and desaturation



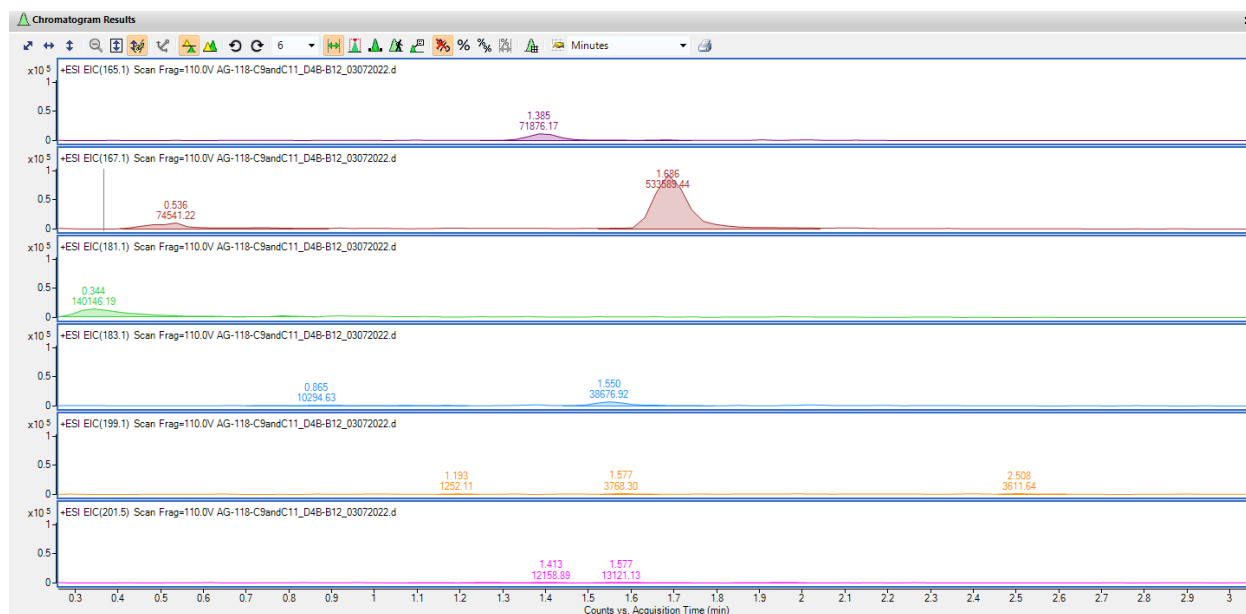
	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



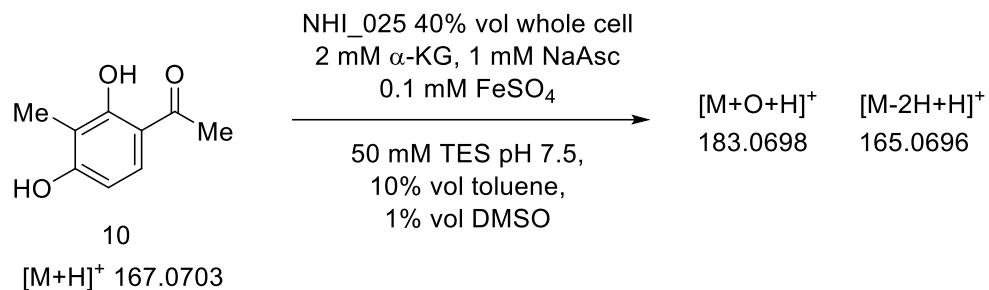
Discovered Reaction 55. Substrate_010 + NHI_024 = desaturation



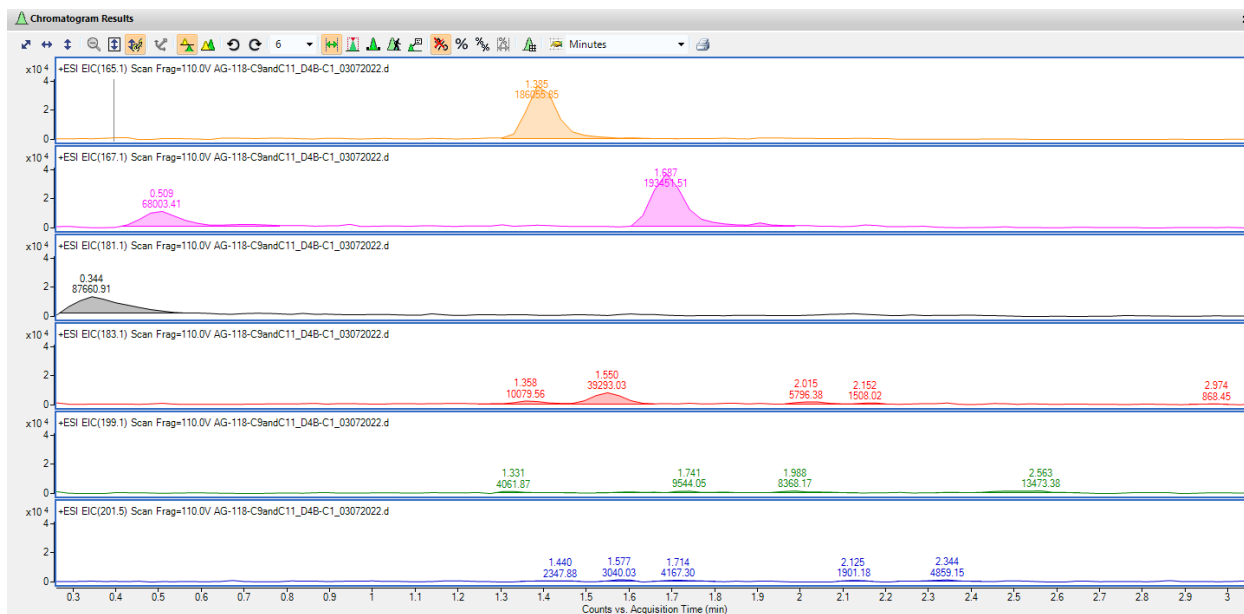
	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



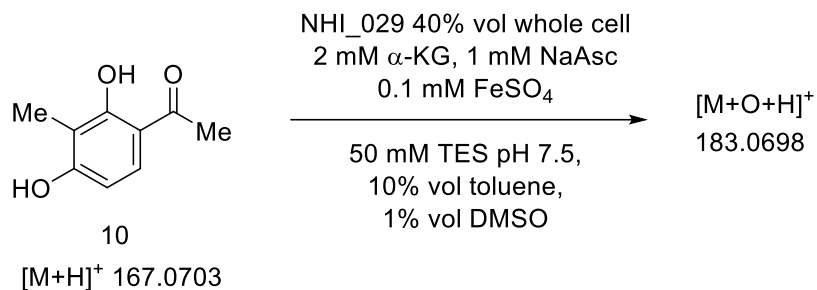
Discovered Reaction 56. Substrate_010 + NHI_025 = hydroxylation and desaturation



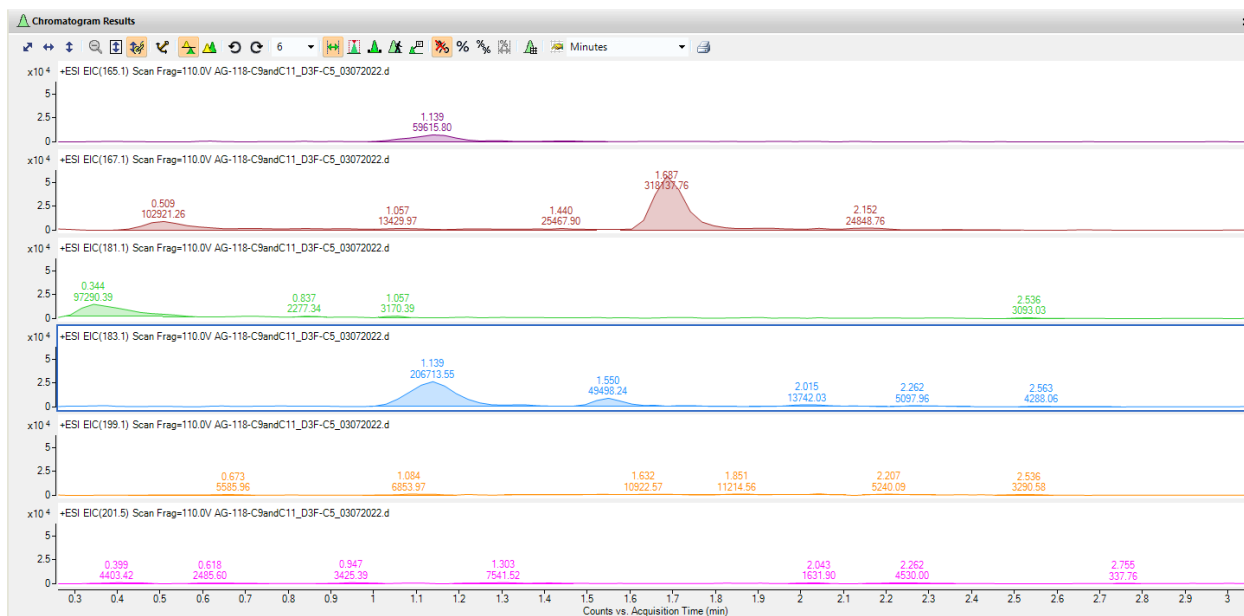
	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



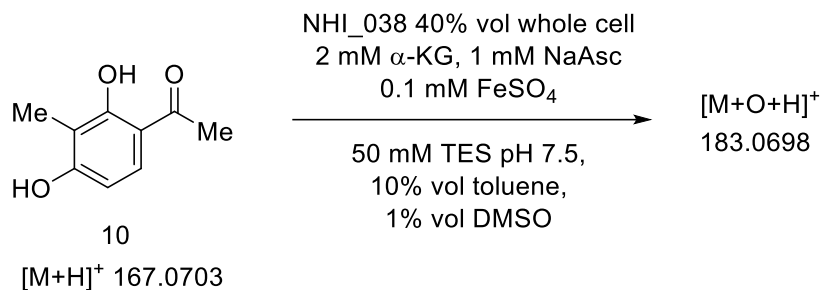
Discovered Reaction 57. Substrate_010 + NHI_029 = hydroxylation



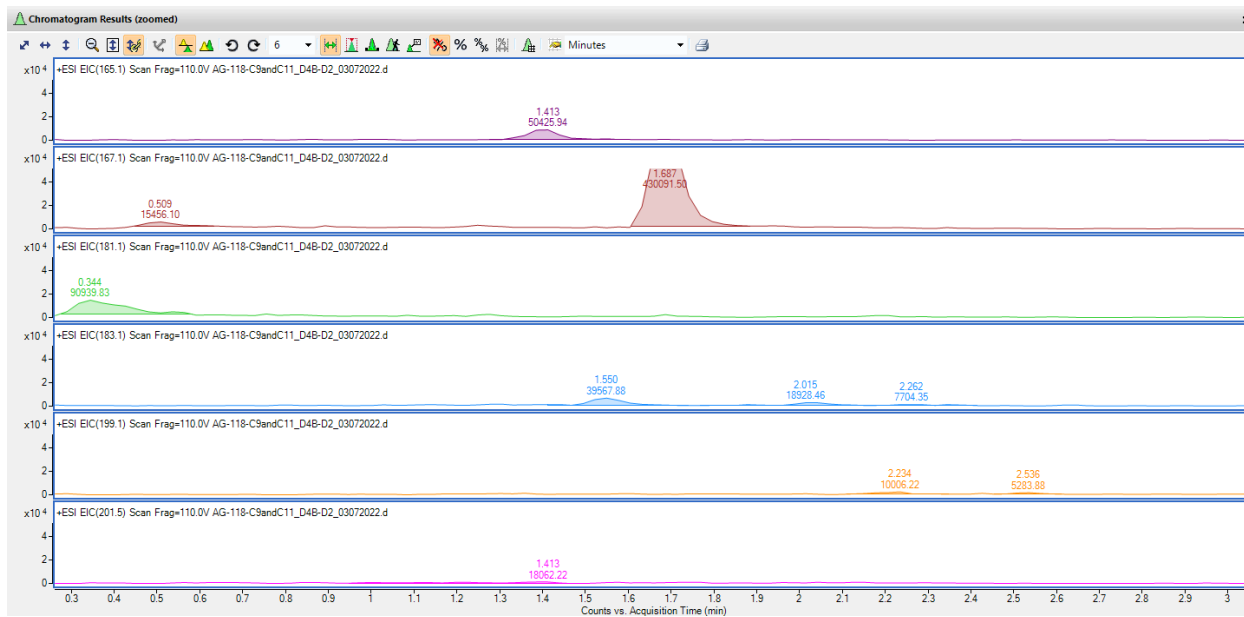
	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



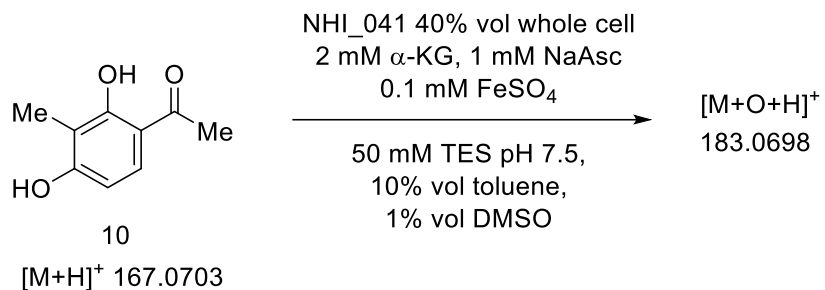
Discovered Reaction 58. Substrate_010 + NHI_038 = hydroxylation



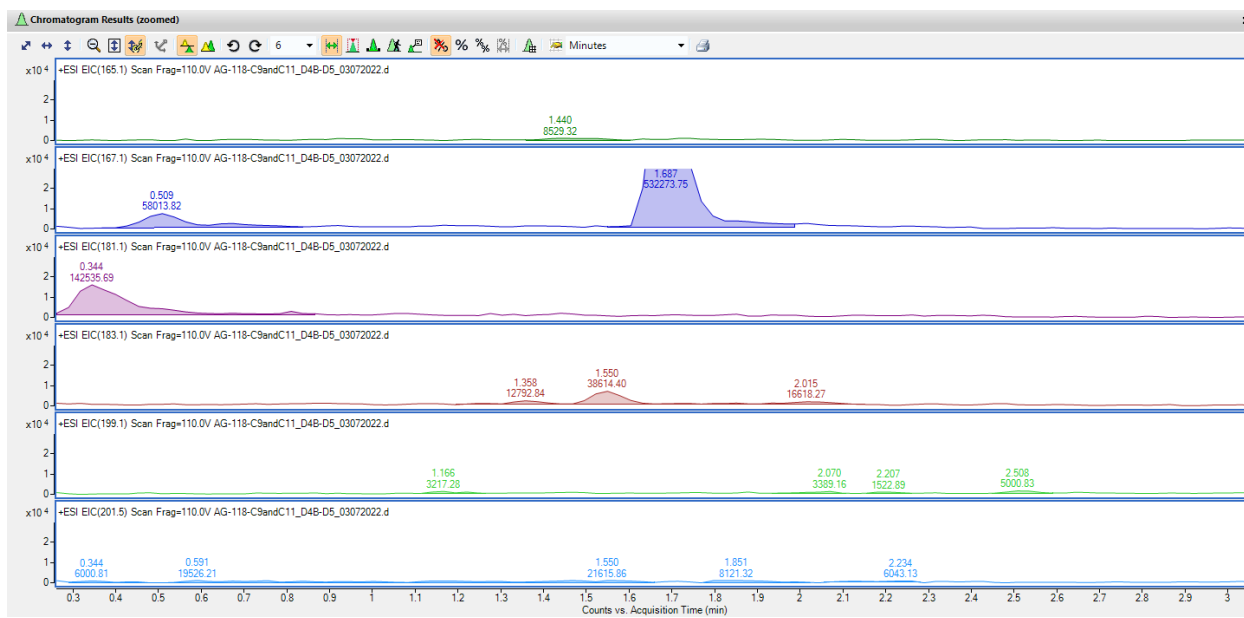
	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



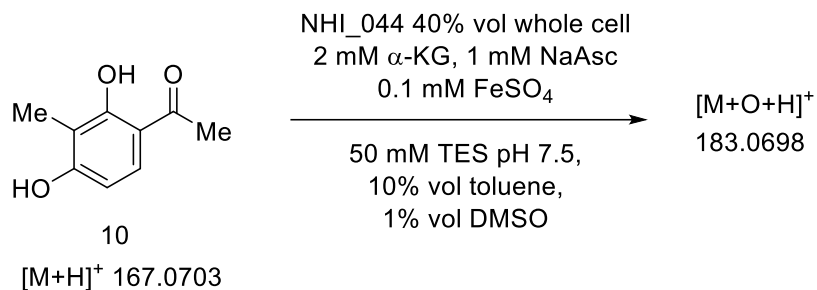
Discovered Reaction 59 .Substrate_010 + NHI_041 = hydroxylation



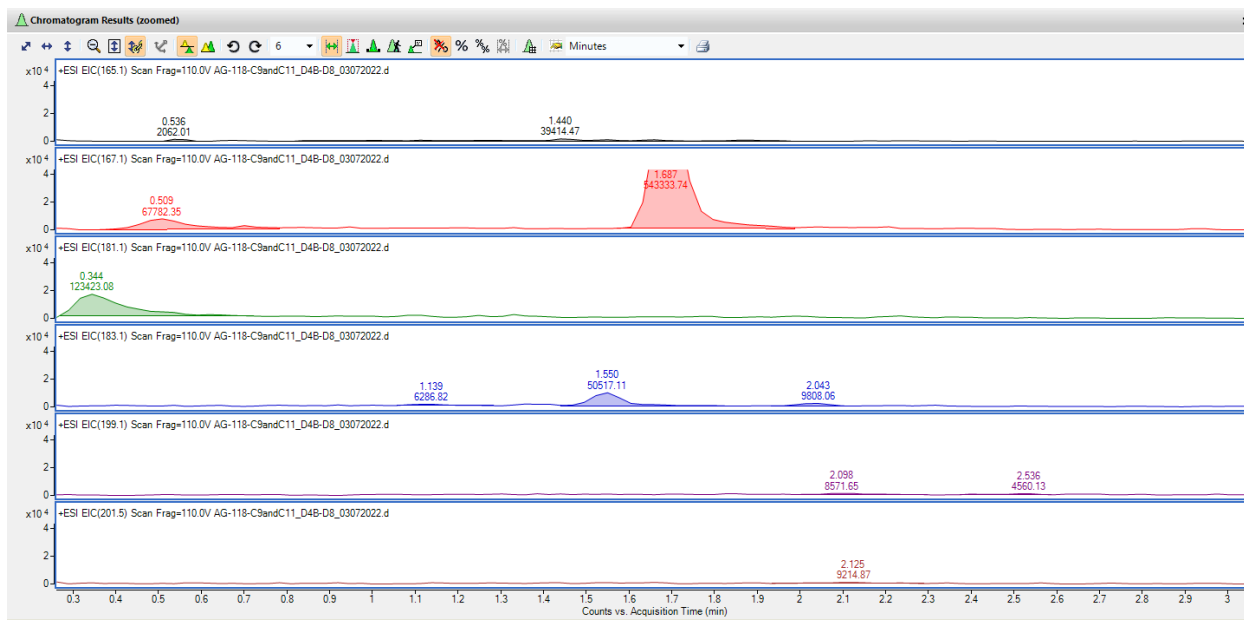
	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



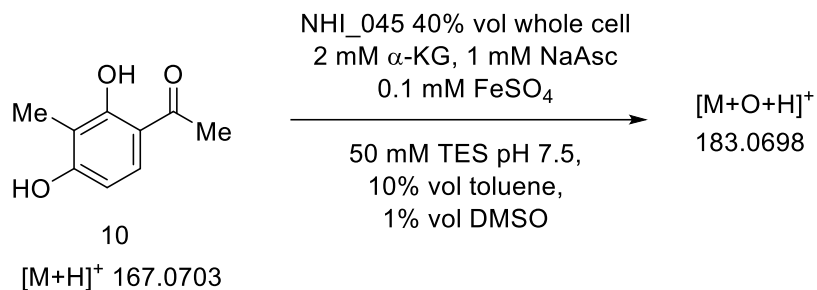
Discovered Reaction 60. Substrate_010 + NHI_044 = hydroxylation



	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



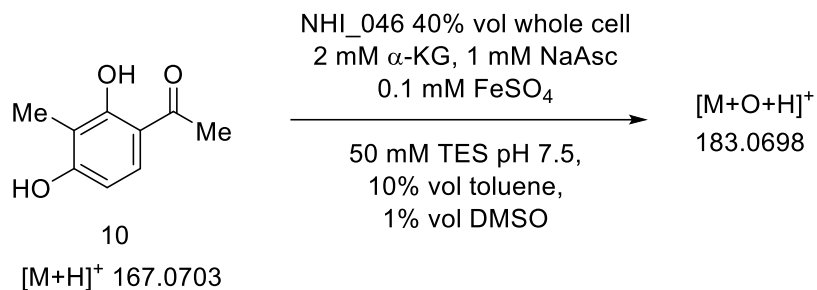
Discovered Reaction 61. Substrate_010 + NHI_045 = hydroxylation



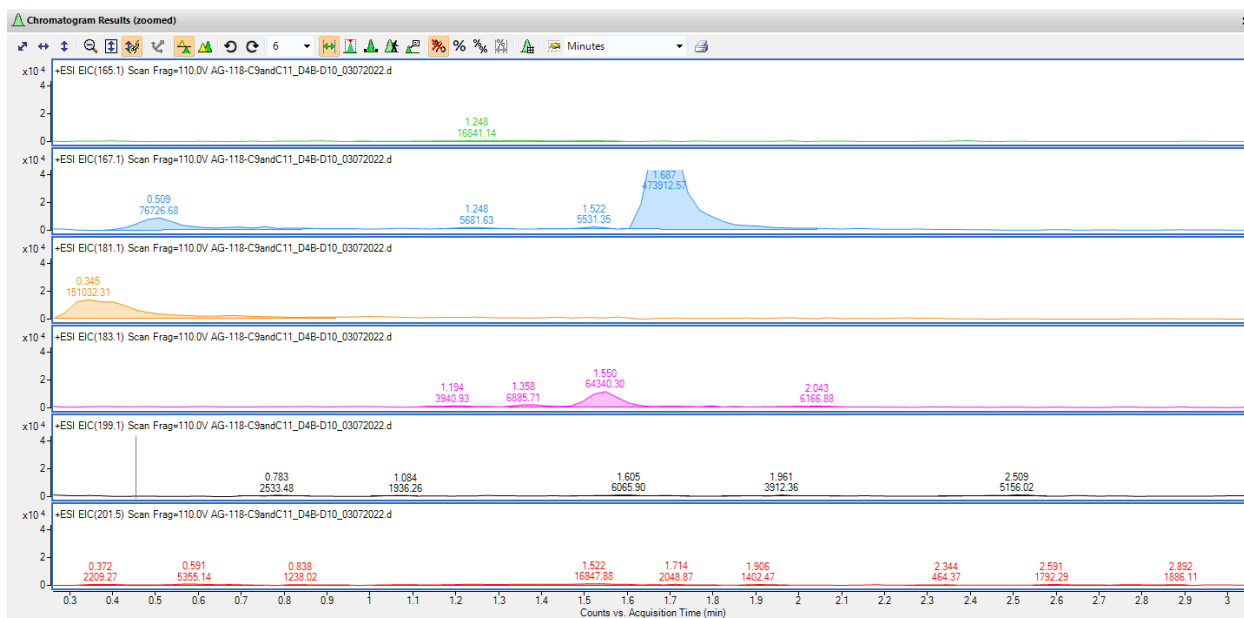
	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



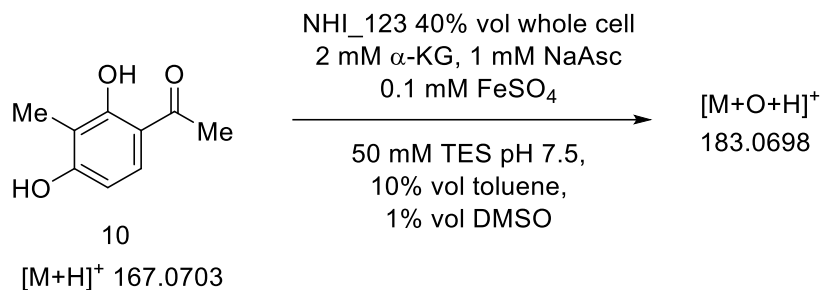
Discovered Reaction 62. Substrate_010 + NHI_046 = hydroxylation



	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



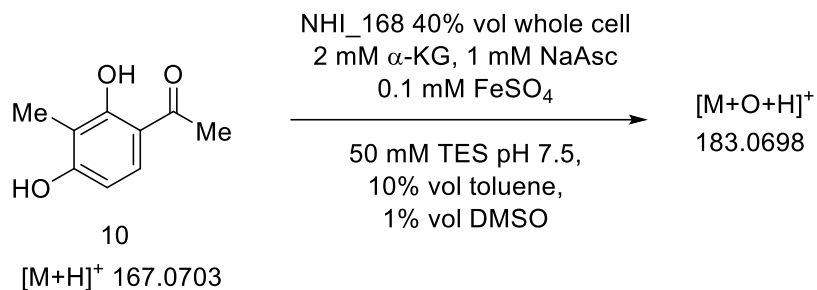
Discovered Reaction 63. Substrate_010 + NHI_123 = hydroxylation



	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



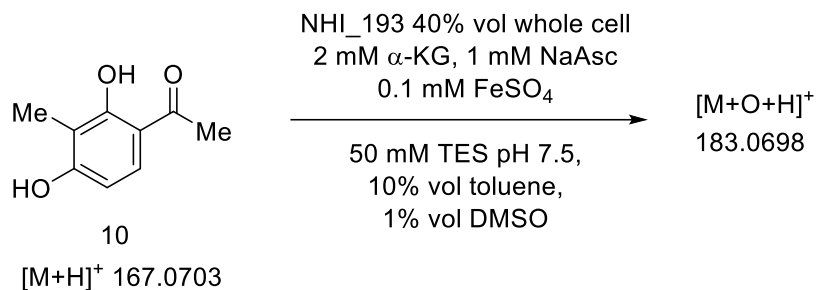
Discovered Reaction 64. Substrate_010 + NHI_168 = hydroxylation



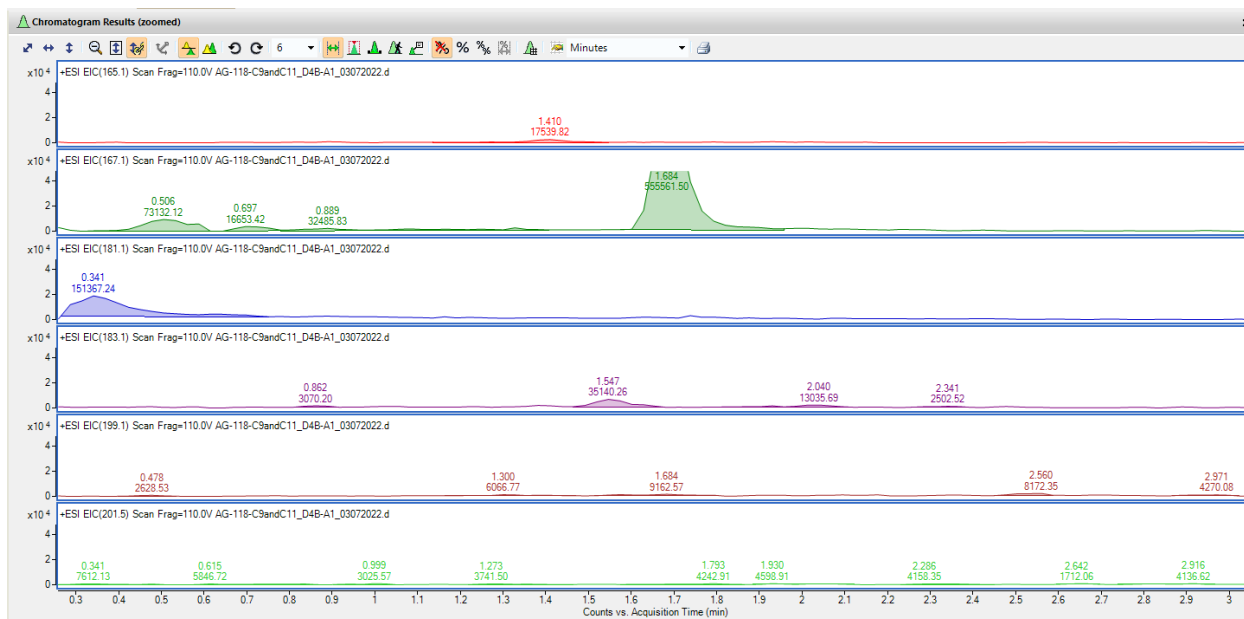
	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



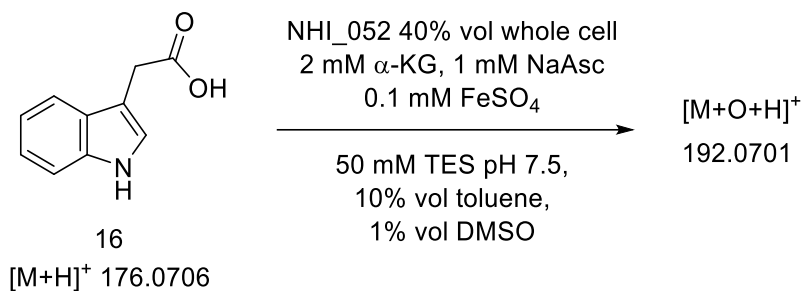
Discovered Reaction 65. Substrate_010 + NHI_193 = hydroxylation



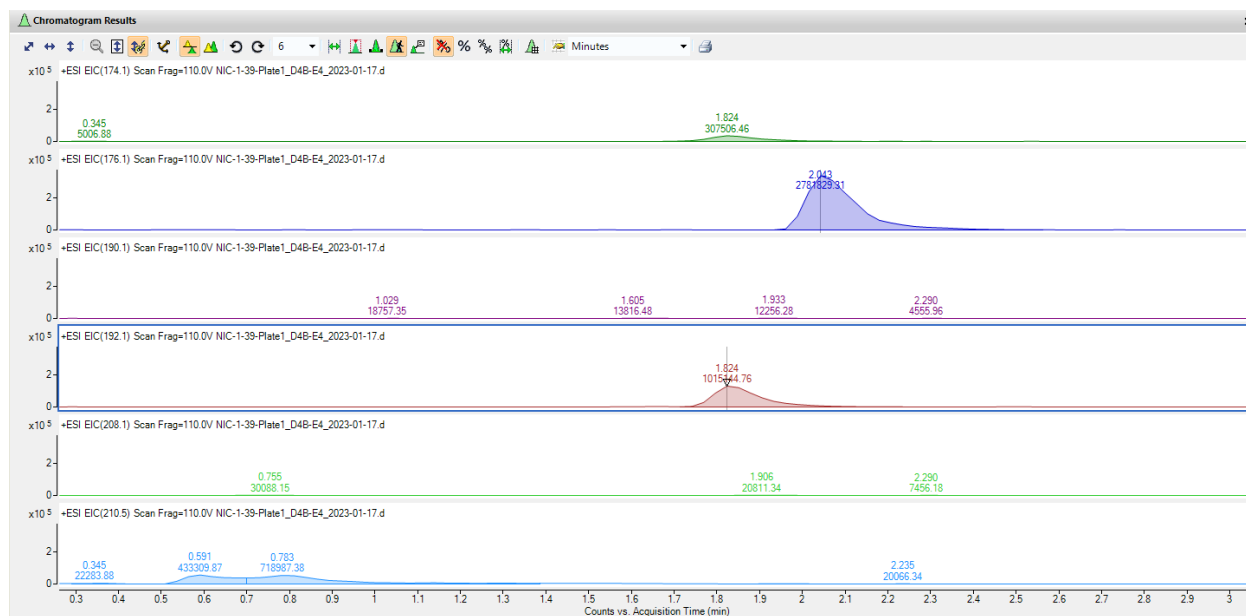
	Neutral	Positive	Negative
desaturation	164.05	165.06	163.04
substrate	166.06	167.07	165.06
oxidation/desaturation	180.05	181.05	179.04
hydroxylation	182.06	183.07	181.05
dihydroxylation	198.06	199.07	197.05
chlorination	200.51	201.52	199.5



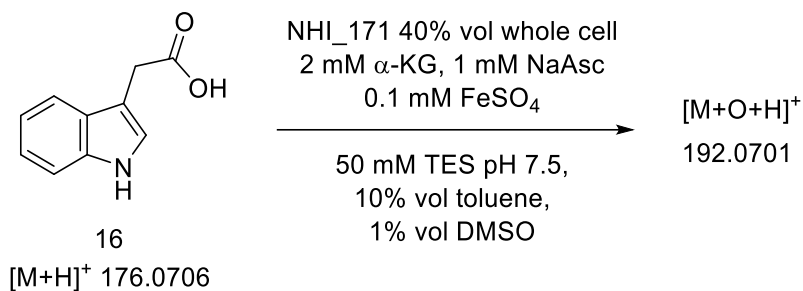
Discovered Reaction 66. Substrate_016 + NHI_052 = hydroxylation



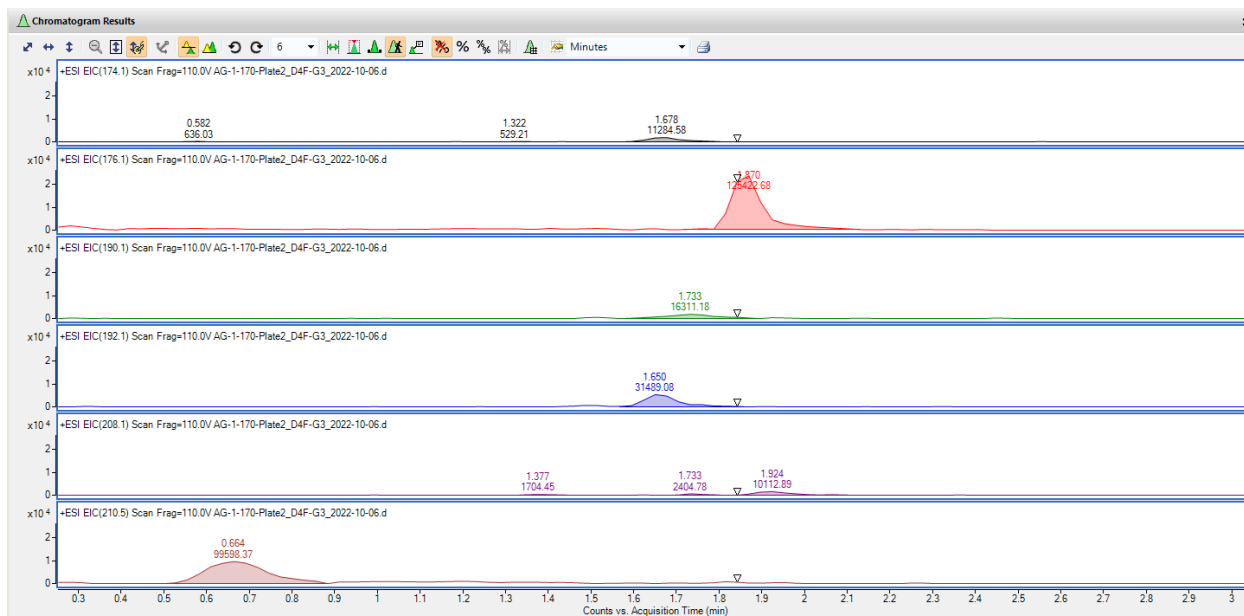
	Neutral	Positive	Negative
desaturation	173.0476	174.0555	172.0398
substrate	175.0633	176.0711	174.0555
oxidation/desaturation	189.0466	190.0545	188.0388
hydroxylation	191.0623	192.0701	190.0545
dihydroxylation	207.0613	208.0691	206.0535
chlorination	209.5085	210.5163	208.5006



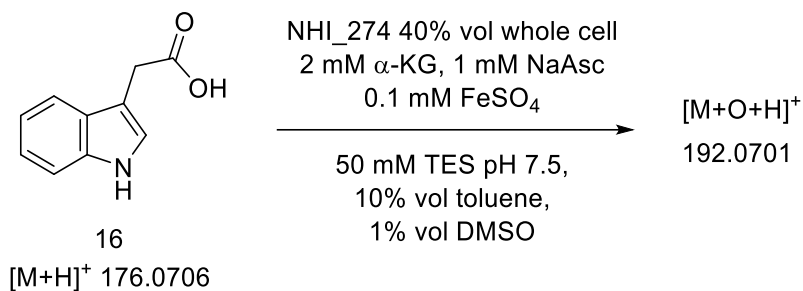
Discovered Reaction 67. Substrate_016 + NHI_171 = hydroxylation



	Neutral	Positive	Negative
desaturation	173.0476	174.0555	172.0398
substrate	175.0633	176.0711	174.0555
oxidation/desaturation	189.0466	190.0545	188.0388
hydroxylation	191.0623	192.0701	190.0545
dihydroxylation	207.0613	208.0691	206.0535
chlorination	209.5085	210.5163	208.5006



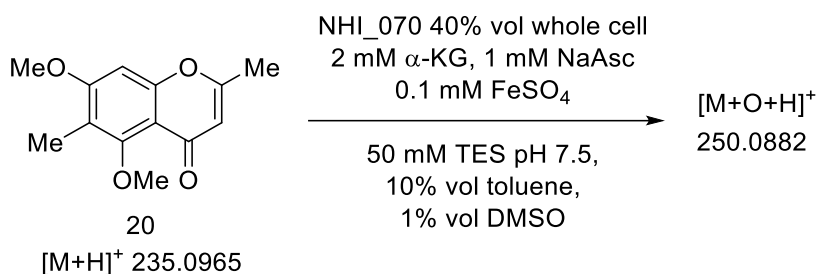
Discovered Reaction 68. Substrate_016 + NHI_274 = hydroxylation



	Neutral	Positive	Negative
desaturation	173.0476	174.0555	172.0398
substrate	175.0633	176.0711	174.0555
oxidation/desaturation	189.0466	190.0545	188.0388
hydroxylation	191.0623	192.0701	190.0545
dihydroxylation	207.0613	208.0691	206.0535
chlorination	209.5085	210.5163	208.5006



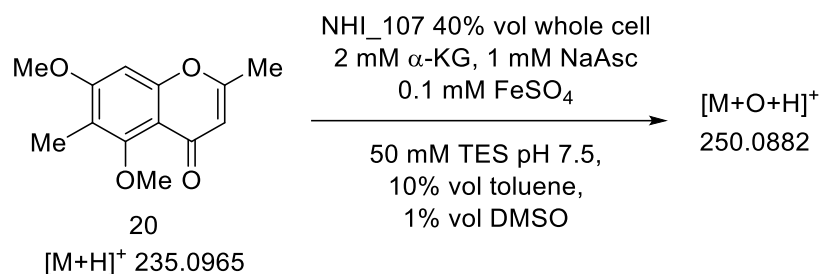
Discovered Reaction 69. Substrate_020 + NHI_070 = hydroxylation



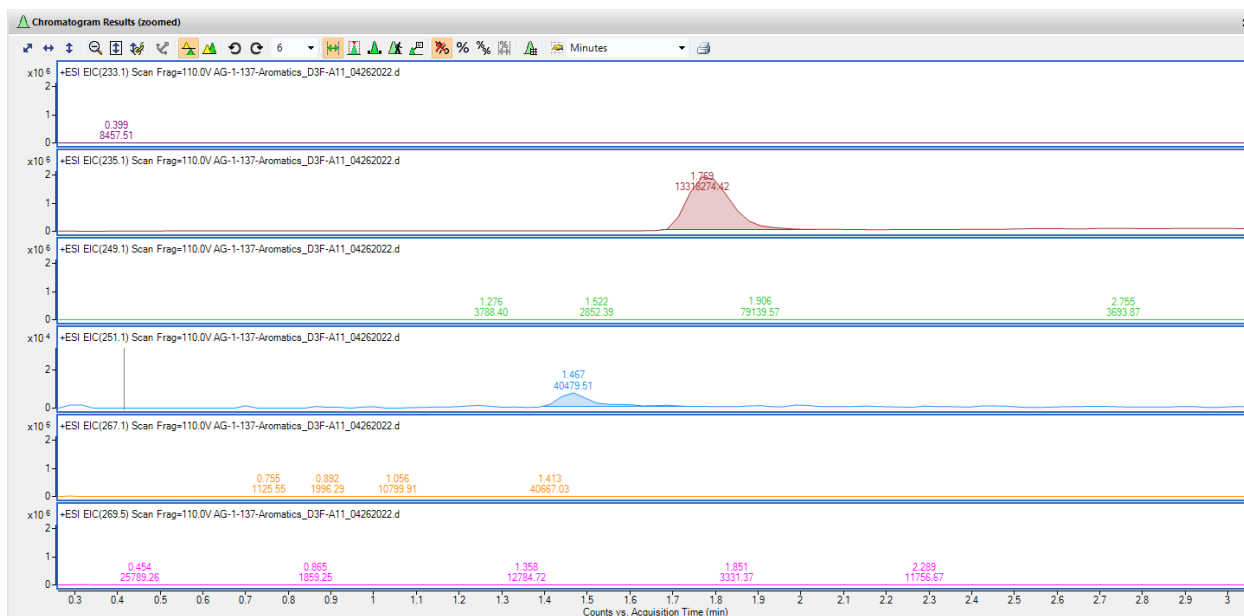
	Neutral	Positive	Negative
desaturation	232.0735	233.0814	231.0657
substrate	234.0892	235.0970	233.0814
oxidation/desaturation	248.0725	249.0804	247.0647
hydroxylation	250.0882	251.0960	249.0804
dihydroxylation	266.0872	267.0950	265.0794
chlorination	268.5344	269.5422	267.5265



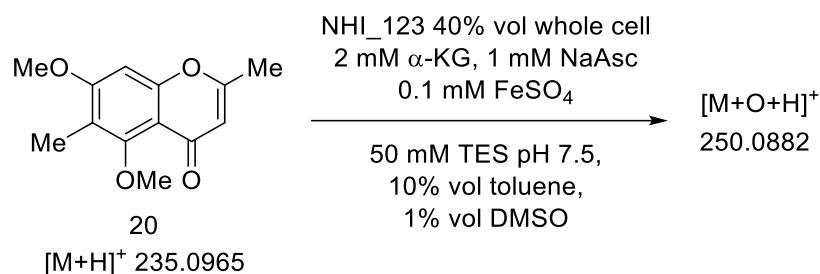
Discovered Reaction 70. Substrate_020 + NHI_107 = hydroxylation



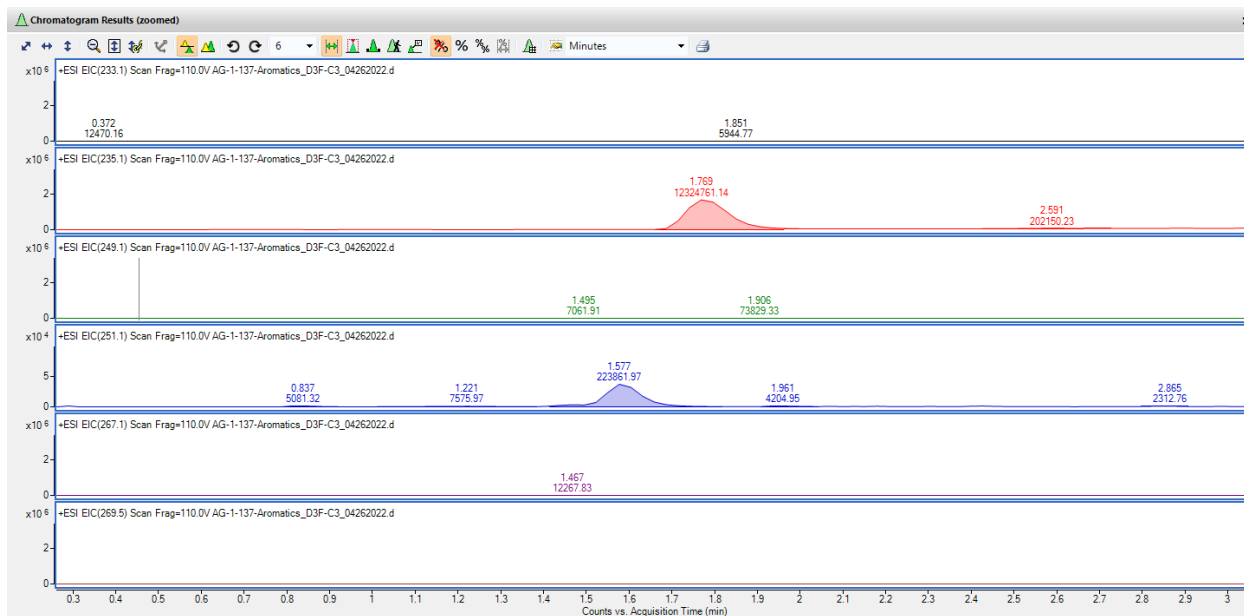
	Neutral	Positive	Negative
desaturation	232.0735	233.0814	231.0657
substrate	234.0892	235.0970	233.0814
oxidation/desaturation	248.0725	249.0804	247.0647
hydroxylation	250.0882	251.0960	249.0804
dihydroxylation	266.0872	267.0950	265.0794
chlorination	268.5344	269.5422	267.5265



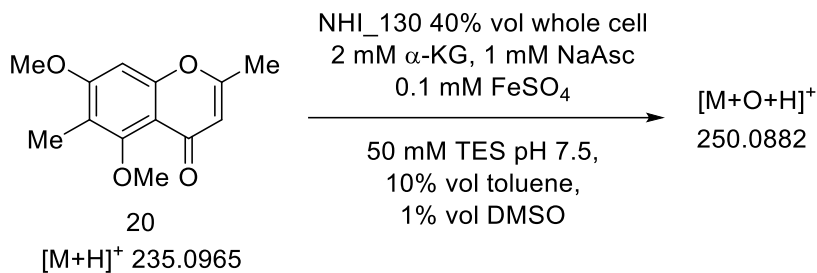
Discovered Reaction 71. Substrate_020 + NHI_123 = hydroxylation



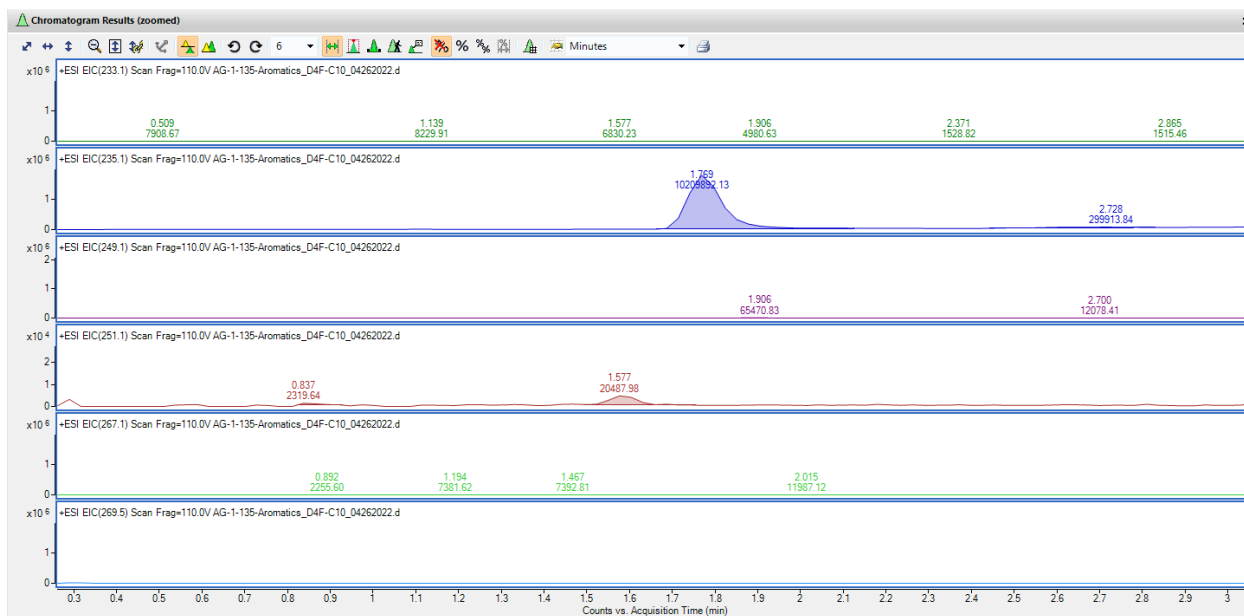
	Neutral	Positive	Negative
desaturation	232.0735	233.0814	231.0657
substrate	234.0892	235.0970	233.0814
oxidation/desaturation	248.0725	249.0804	247.0647
hydroxylation	250.0882	251.0960	249.0804
dihydroxylation	266.0872	267.0950	265.0794
chlorination	268.5344	269.5422	267.5265



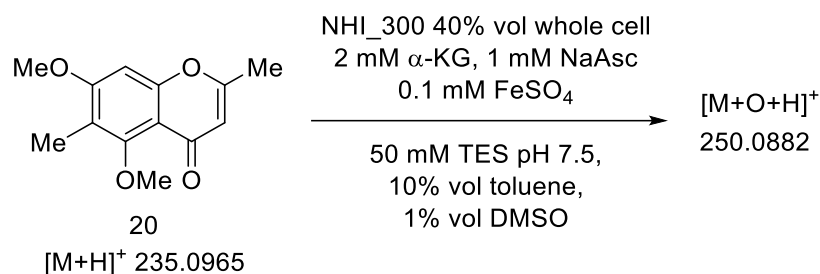
Discovered Reaction 72. Substrate_020 + NHI_130 = hydroxylation



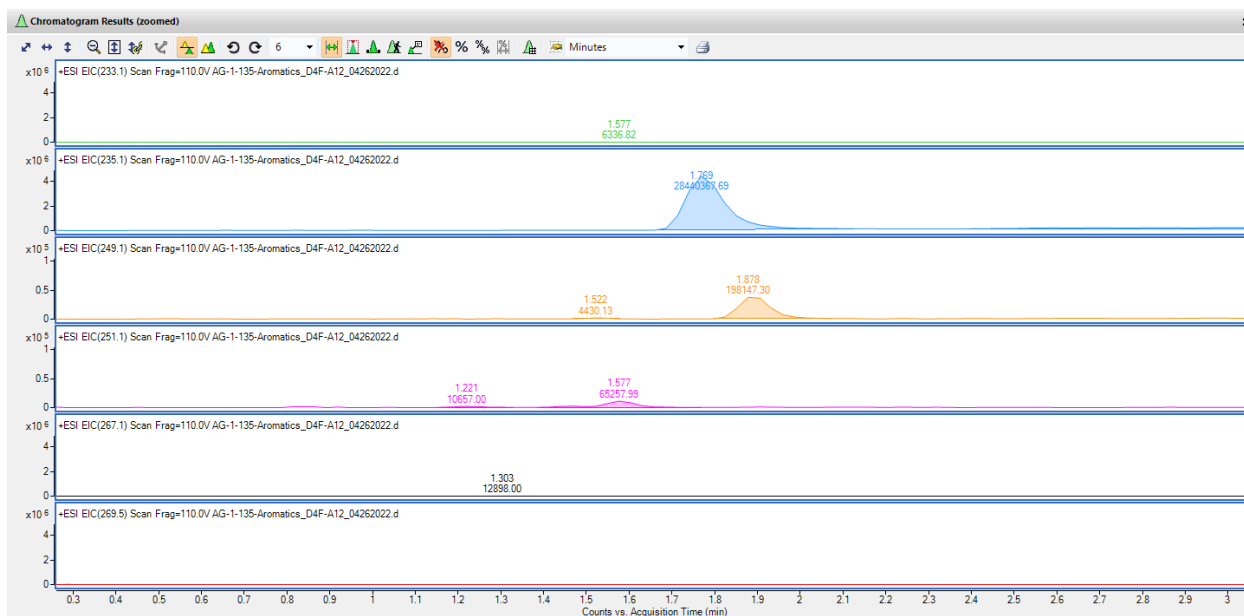
	Neutral	Positive	Negative
desaturation	232.0735	233.0814	231.0657
substrate	234.0892	235.0970	233.0814
oxidation/desaturation	248.0725	249.0804	247.0647
hydroxylation	250.0882	251.0960	249.0804
dihydroxylation	266.0872	267.0950	265.0794
chlorination	268.5344	269.5422	267.5265



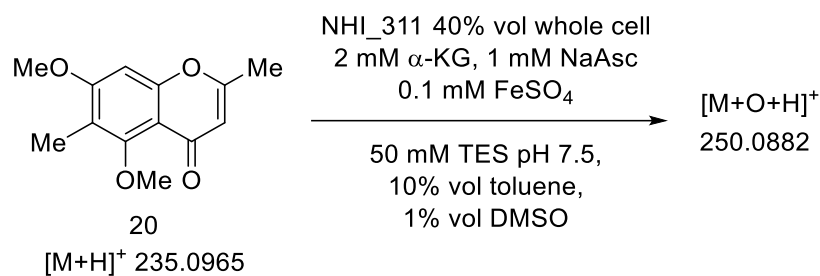
Discovered Reaction 73. Substrate_020 + NHI_300 = hydroxylation



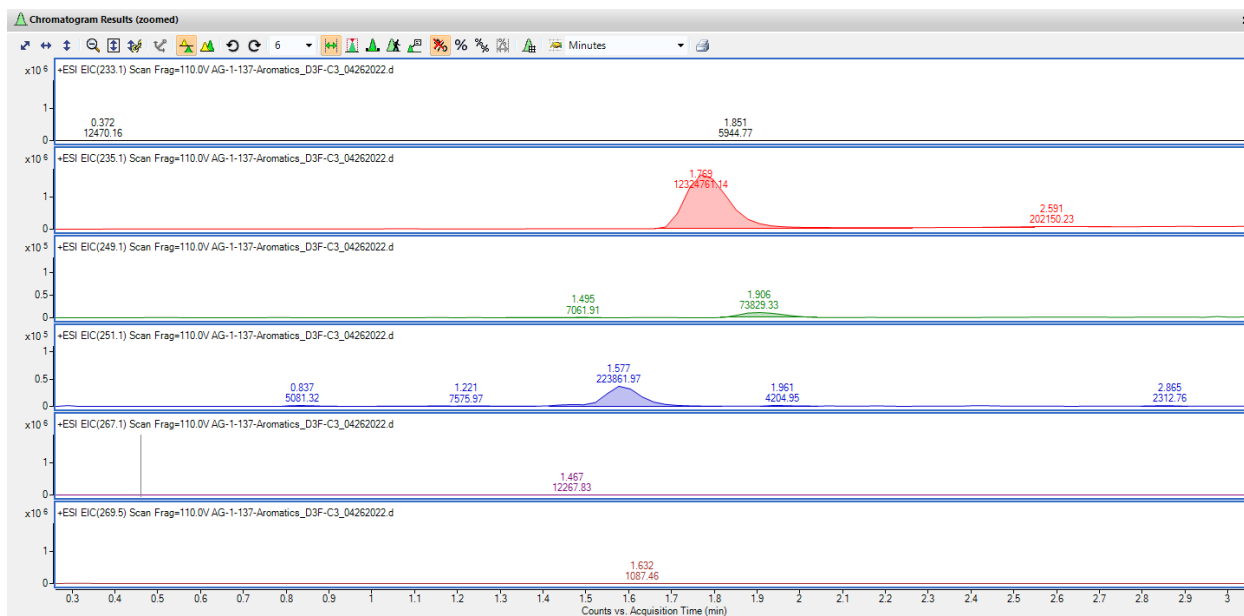
	Neutral	Positive	Negative
desaturation	232.0735	233.0814	231.0657
substrate	234.0892	235.0970	233.0814
oxidation/desaturation	248.0725	249.0804	247.0647
hydroxylation	250.0882	251.0960	249.0804
dihydroxylation	266.0872	267.0950	265.0794
chlorination	268.5344	269.5422	267.5265



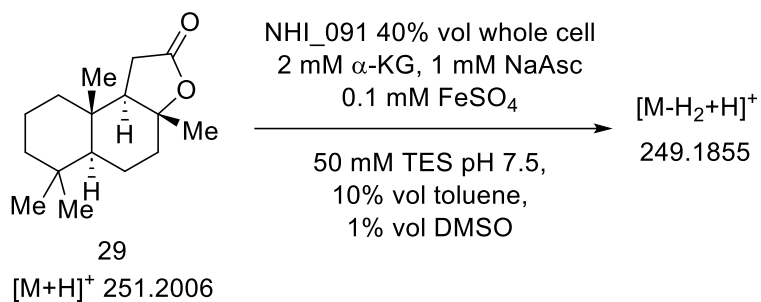
Discovered Reaction 74. Substrate_020 + NHI_311 = hydroxylation



	Neutral	Positive	Negative
desaturation	232.0735	233.0814	231.0657
substrate	234.0892	235.0970	233.0814
oxidation/desaturation	248.0725	249.0804	247.0647
hydroxylation	250.0882	251.0960	249.0804
dihydroxylation	266.0872	267.0950	265.0794
chlorination	268.5344	269.5422	267.5265



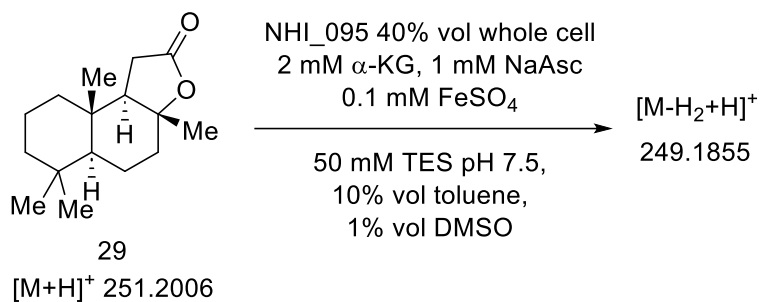
Discovered Reaction 75. Substrate_029 + NHI_091 = desaturation



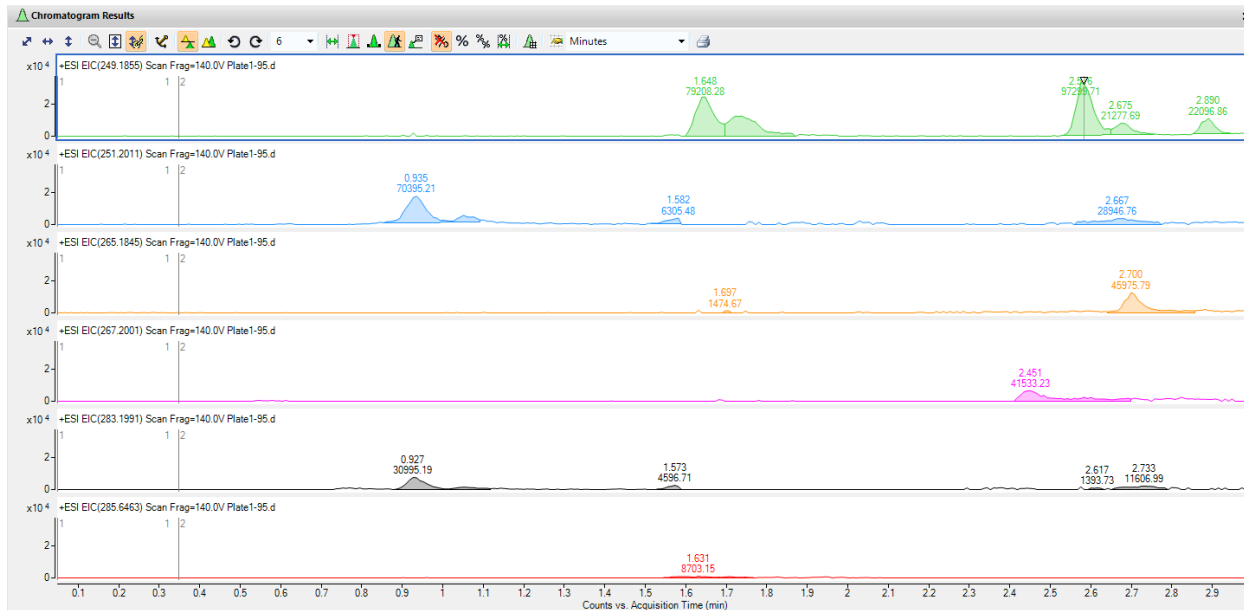
	Neutral	Positive	Negative
desaturation	248.1776	249.1855	247.1698
substrate	250.1933	251.2011	249.1855
oxidation/desaturation	264.1766	265.1845	263.1688
hydroxylation	266.1923	267.2001	265.1845
dihydroxylation	282.1913	283.1991	281.1835
chlorination	284.6385	285.6463	283.6306



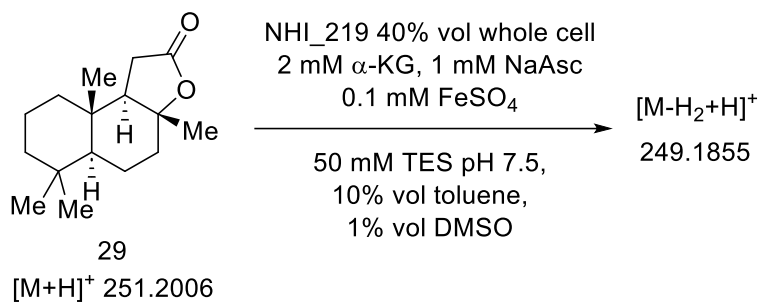
Discovered Reaction 76. Substrate_029 + NHI_095 = desaturation



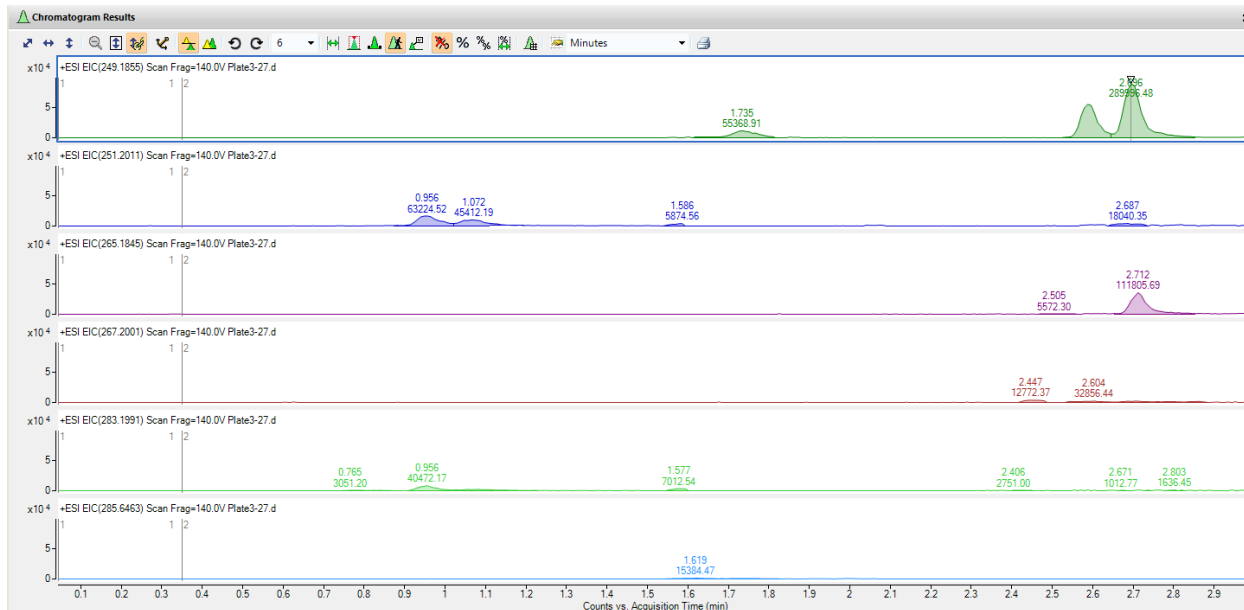
	Neutral	Positive	Negative
desaturation	248.1776	249.1855	247.1698
substrate	250.1933	251.2011	249.1855
oxidation/desaturation	264.1766	265.1845	263.1688
hydroxylation	266.1923	267.2001	265.1845
dihydroxylation	282.1913	283.1991	281.1835
chlorination	284.6385	285.6463	283.6306



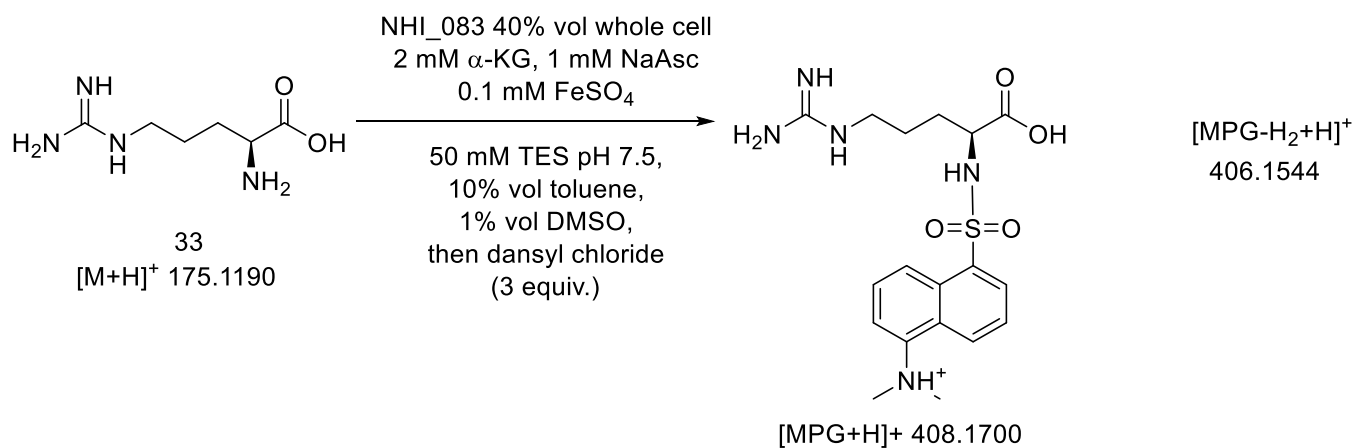
Discovered Reaction 77. Substrate_029 + NHI_219 = desaturation



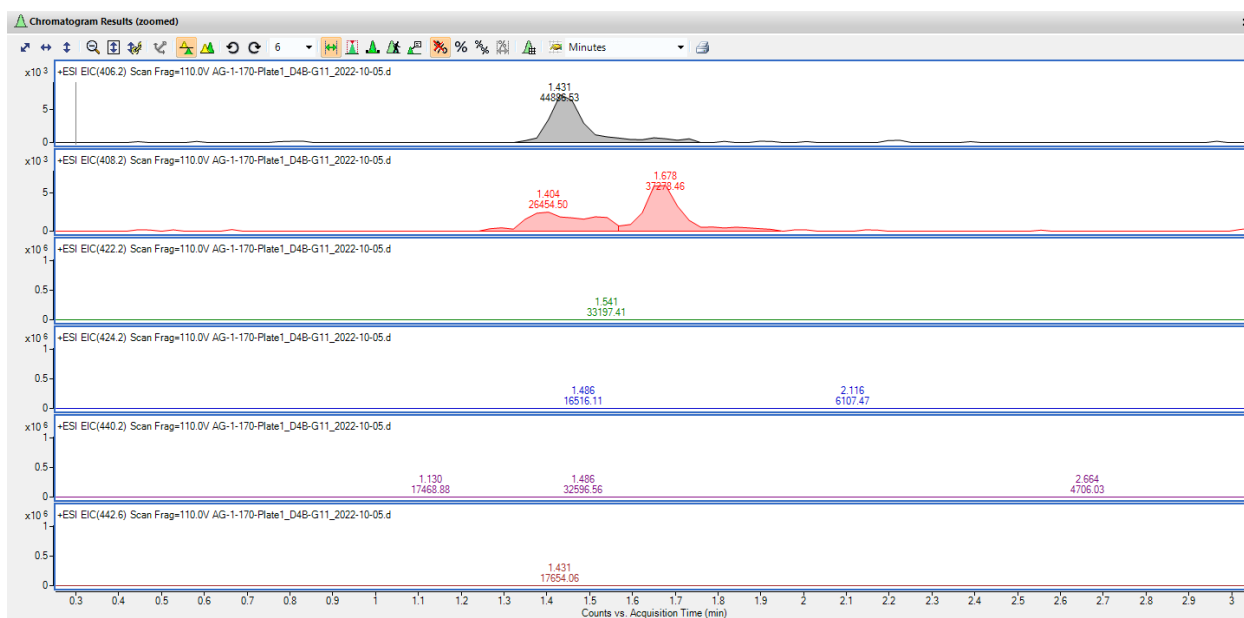
	Neutral	Positive	Negative
desaturation	248.1776	249.1855	247.1698
substrate	250.1933	251.2011	249.1855
oxidation/desaturation	264.1766	265.1845	263.1688
hydroxylation	266.1923	267.2001	265.1845
dihydroxylation	282.1913	283.1991	281.1835
chlorination	284.6385	285.6463	283.6306



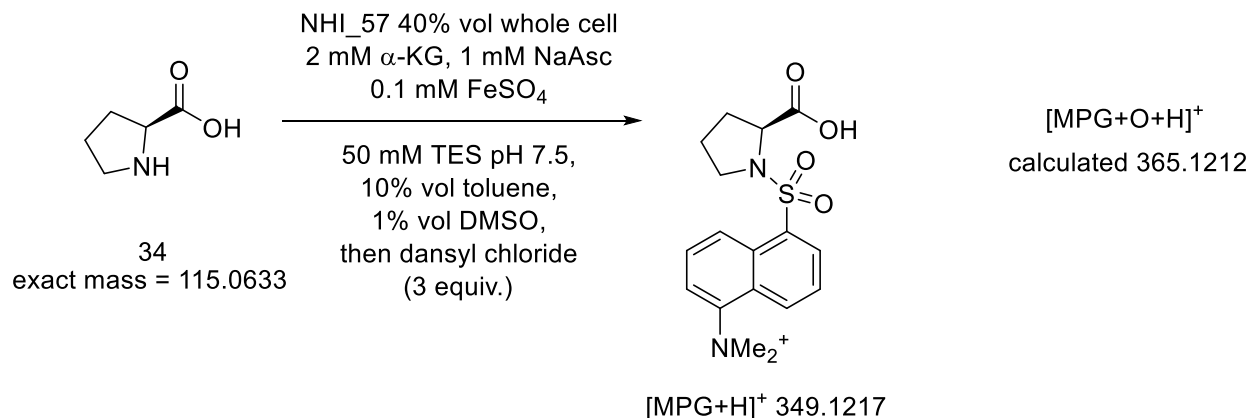
Discovered Reaction 78. Substrate_033 + NHI_083 = desaturation



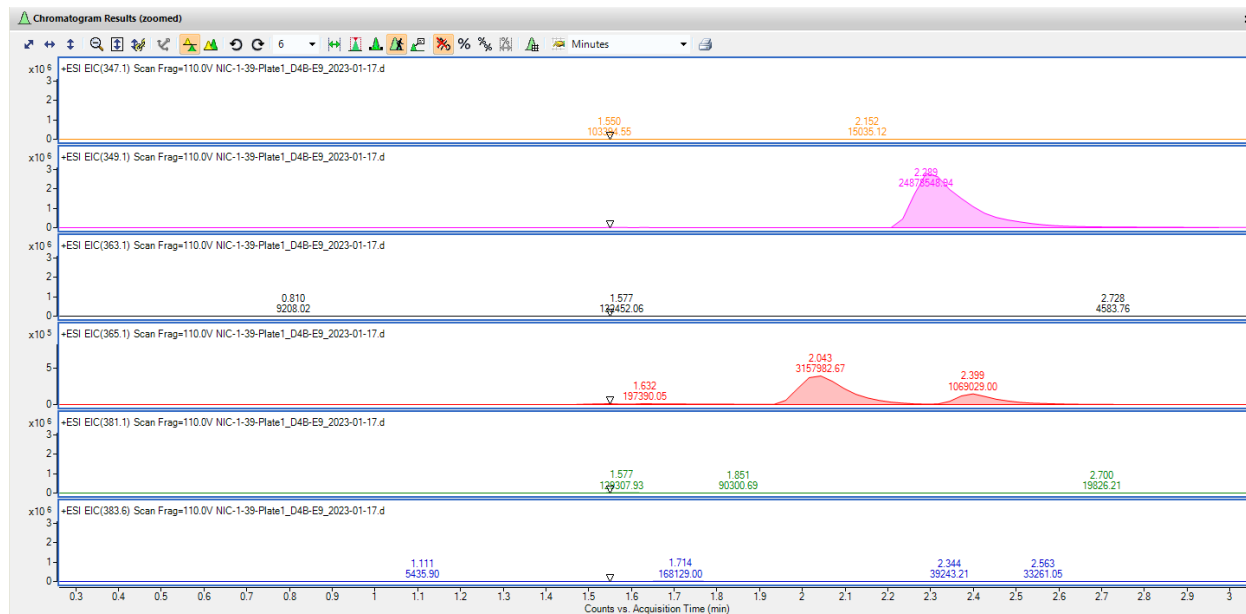
	Neutral	Positive	Negative
Desaturation – PG	405.1470	406.1549	404.1392
Substrate – PG	407.1627	408.1705	406.1549
oxidation/desaturation - PG	421.1460	422.1539	420.1382
Hydroxylation – PG	423.1617	424.1695	422.1539
Dihydroxylation – PG	439.1607	440.1685	438.1529
Chlorination - PG	441.6079	442.6157	440.6000



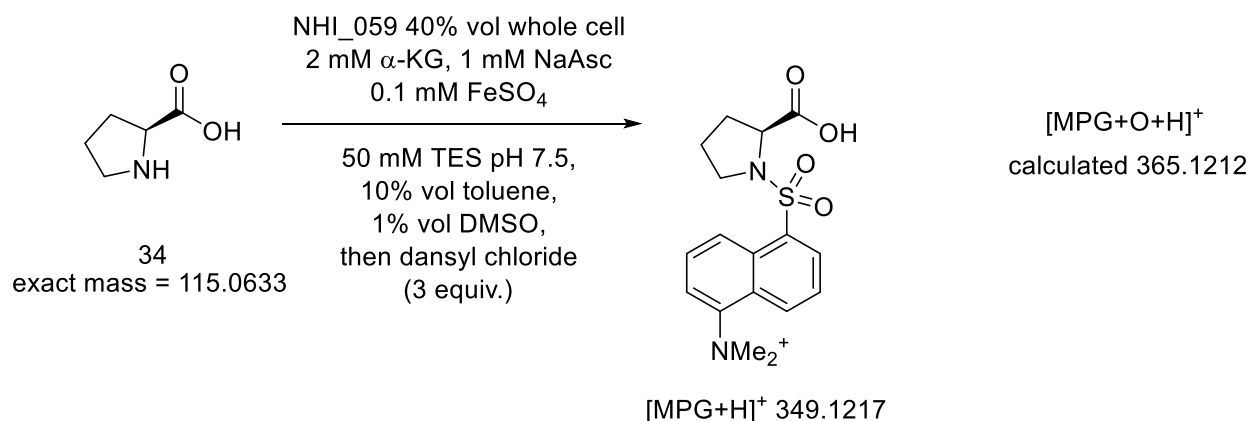
Discovered Reaction 79. Substrate_034 + NHI_057 = hydroxylation



	Neutral	Positive	Negative
Desaturation – PG	346.0987	347.1066	345.0909
Substrate – PG	348.1144	349.1222	347.1066
oxidation/desaturation - PG	362.0977	363.1056	361.0899
Hydroxylation – PG	364.1134	365.1212	363.1056
Dihydroxylation – PG	380.1124	381.1202	379.1046
Chlorination - PG	382.5596	383.5674	381.5517



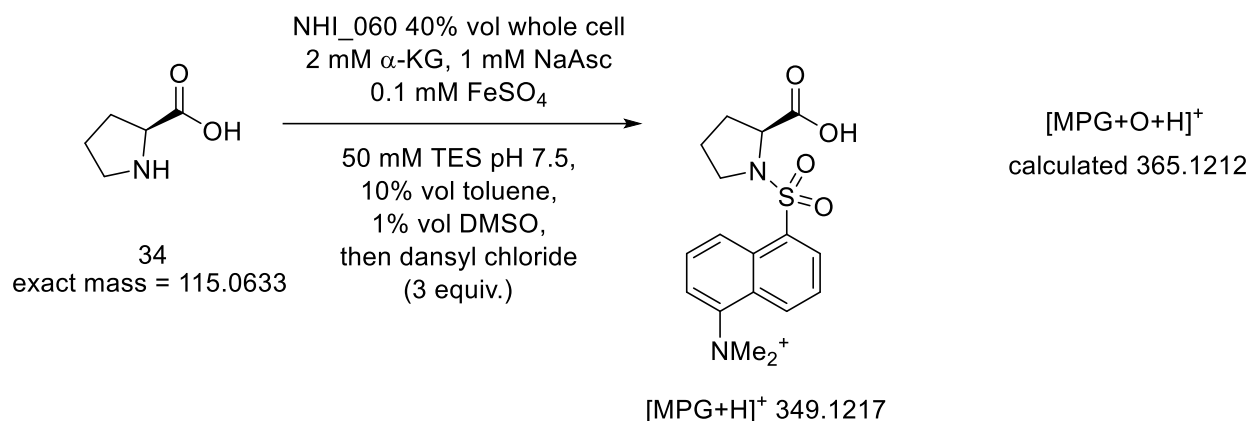
Discovered Reaction 80. Substrate_034 + NHI_059 = hydroxylation



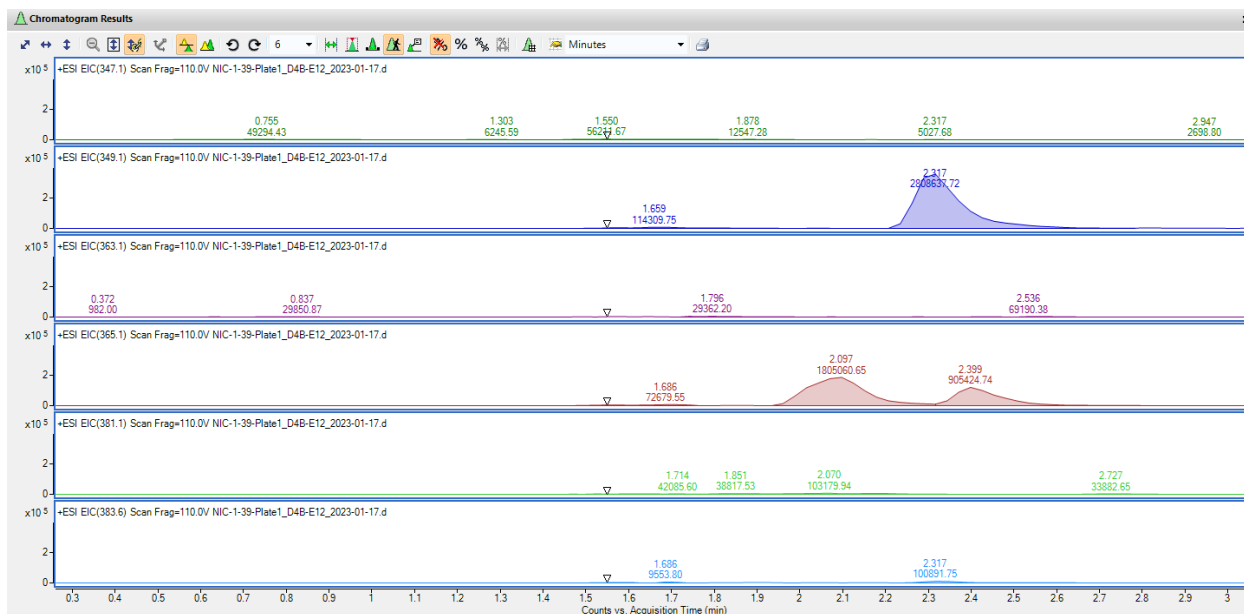
	Neutral	Positive	Negative
Desaturation – PG	346.0987	347.1066	345.0909
Substrate – PG	348.1144	349.1222	347.1066
oxidation/desaturation - PG	362.0977	363.1056	361.0899
Hydroxylation – PG	364.1134	365.1212	363.1056
Dihydroxylation – PG	380.1124	381.1202	379.1046
Chlorination - PG	382.5596	383.5674	381.5517



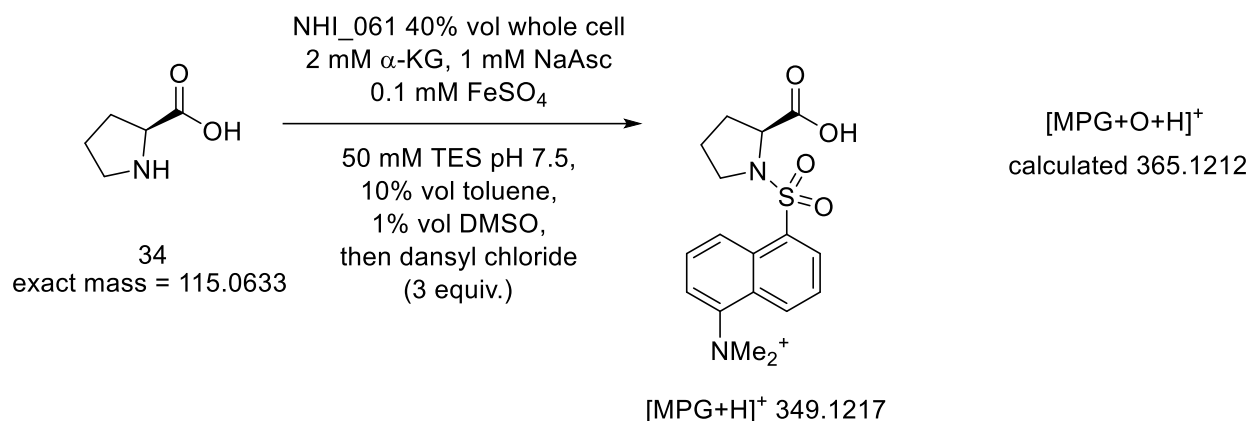
Discovered Reaction 81. Substrate_034 + NHI_060 = hydroxylation



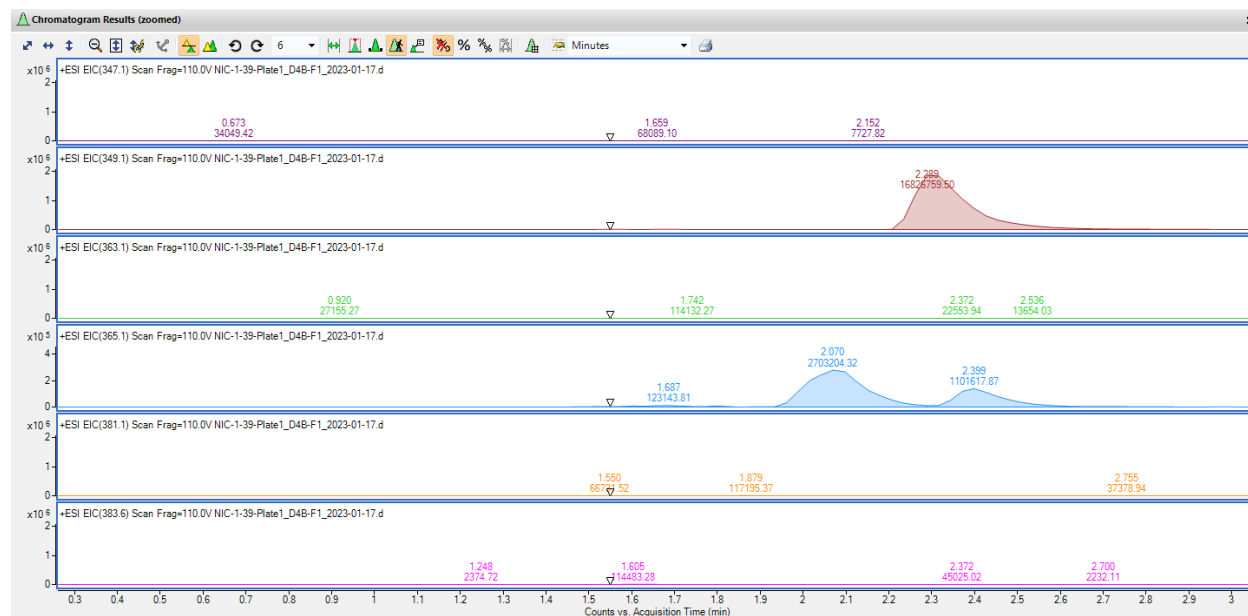
	Neutral	Positive	Negative
Desaturation – PG	346.0987	347.1066	345.0909
Substrate – PG	348.1144	349.1222	347.1066
oxidation/desaturation - PG	362.0977	363.1056	361.0899
Hydroxylation – PG	364.1134	365.1212	363.1056
Dihydroxylation – PG	380.1124	381.1202	379.1046
Chlorination - PG	382.5596	383.5674	381.5517



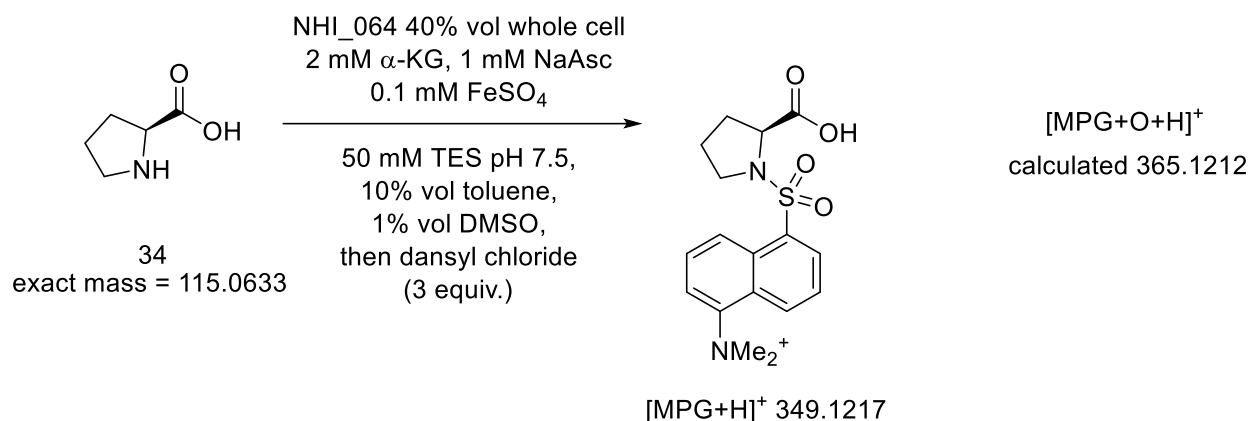
Discovered Reaction 82. Substrate_034 + NHI_061 = hydroxylation



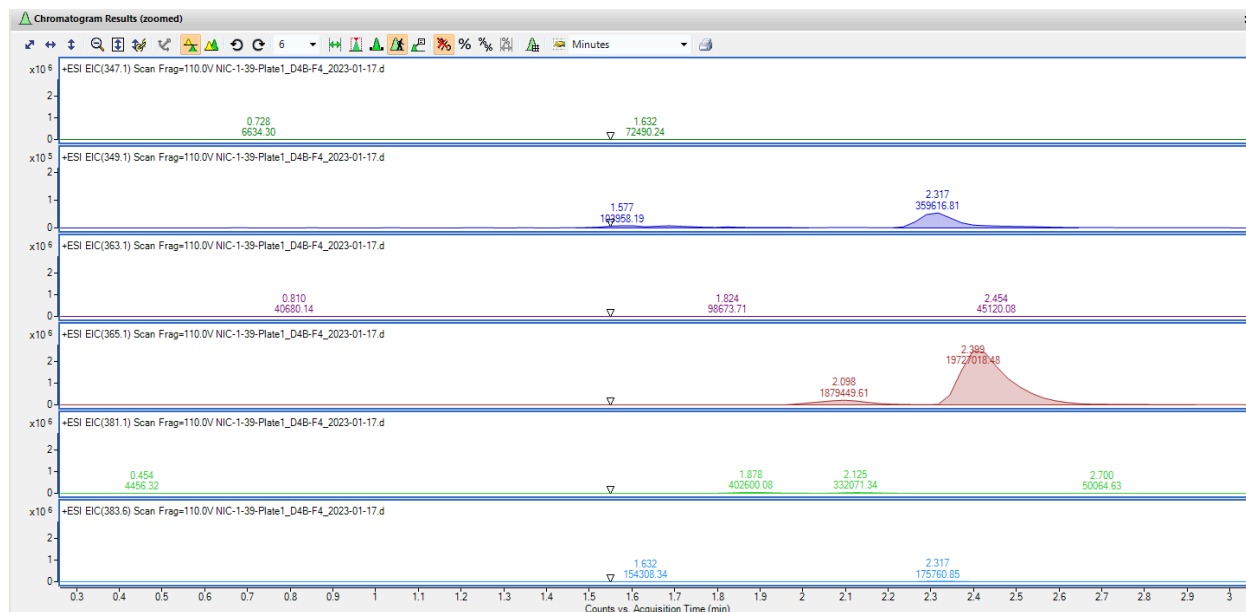
	Neutral	Positive	Negative
Desaturation – PG	346.0987	347.1066	345.0909
Substrate – PG	348.1144	349.1222	347.1066
oxidation/desaturation - PG	362.0977	363.1056	361.0899
Hydroxylation – PG	364.1134	365.1212	363.1056
Dihydroxylation – PG	380.1124	381.1202	379.1046
Chlorination - PG	382.5596	383.5674	381.5517



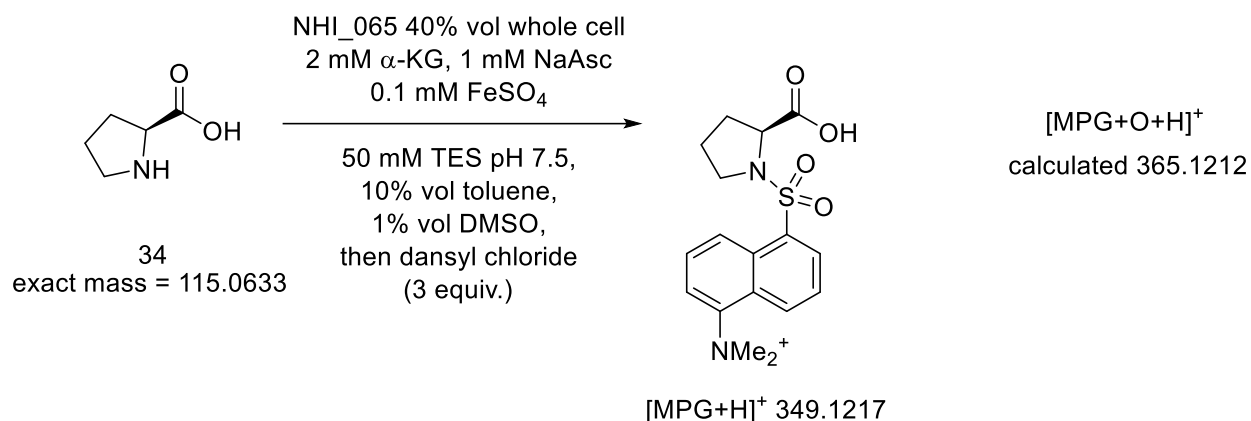
Discovered Reaction 83. Substrate_034 + NHI_064 = hydroxylation



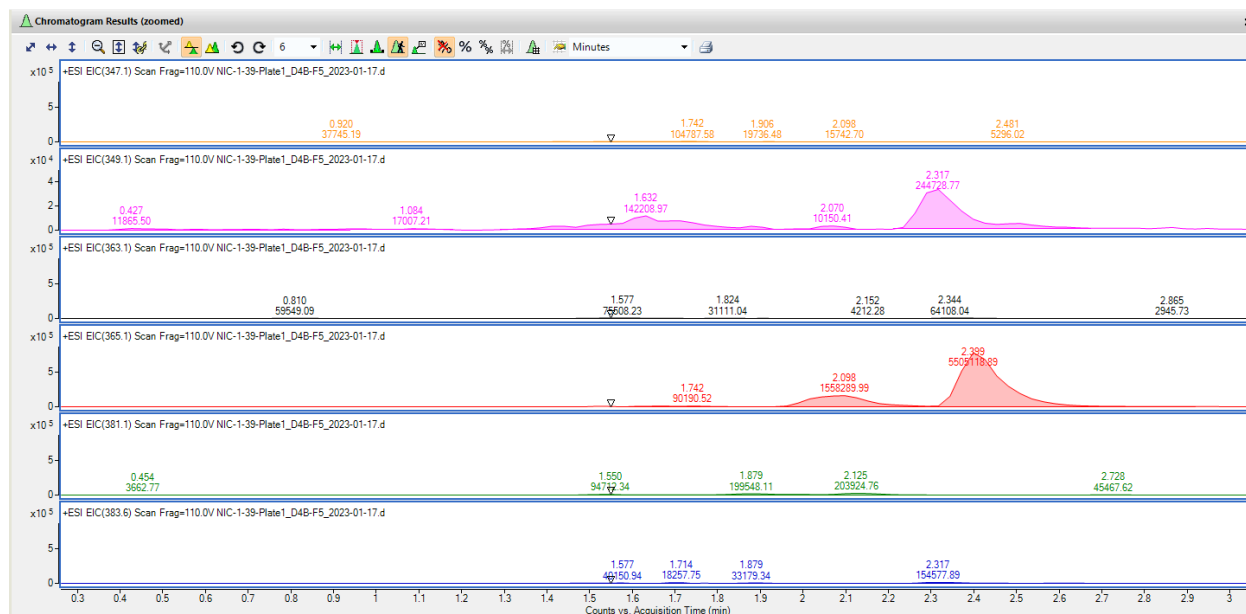
	Neutral	Positive	Negative
Desaturation – PG	346.0987	347.1066	345.0909
Substrate – PG	348.1144	349.1222	347.1066
oxidation/desaturation - PG	362.0977	363.1056	361.0899
Hydroxylation – PG	364.1134	365.1212	363.1056
Dihydroxylation – PG	380.1124	381.1202	379.1046
Chlorination - PG	382.5596	383.5674	381.5517



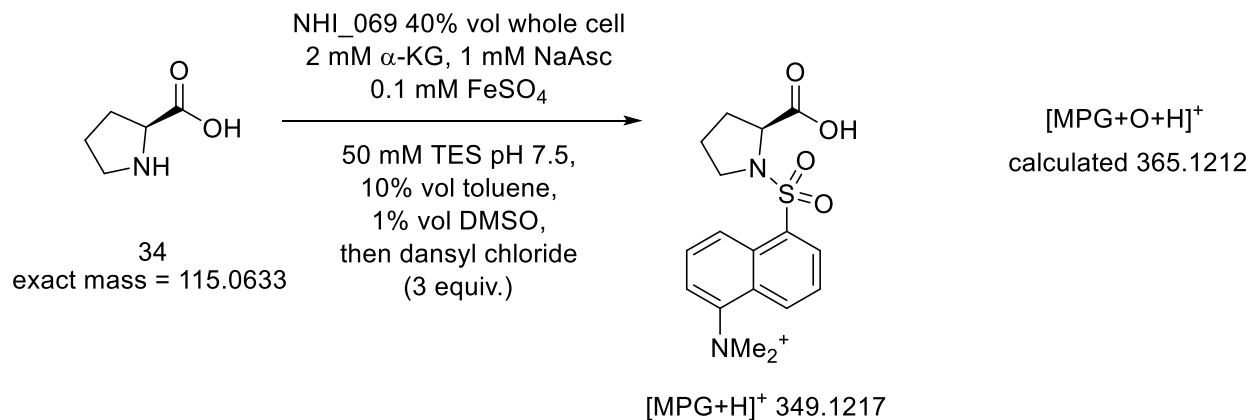
Discovered Reaction 84. Substrate_034 + NHI_065 = hydroxylation



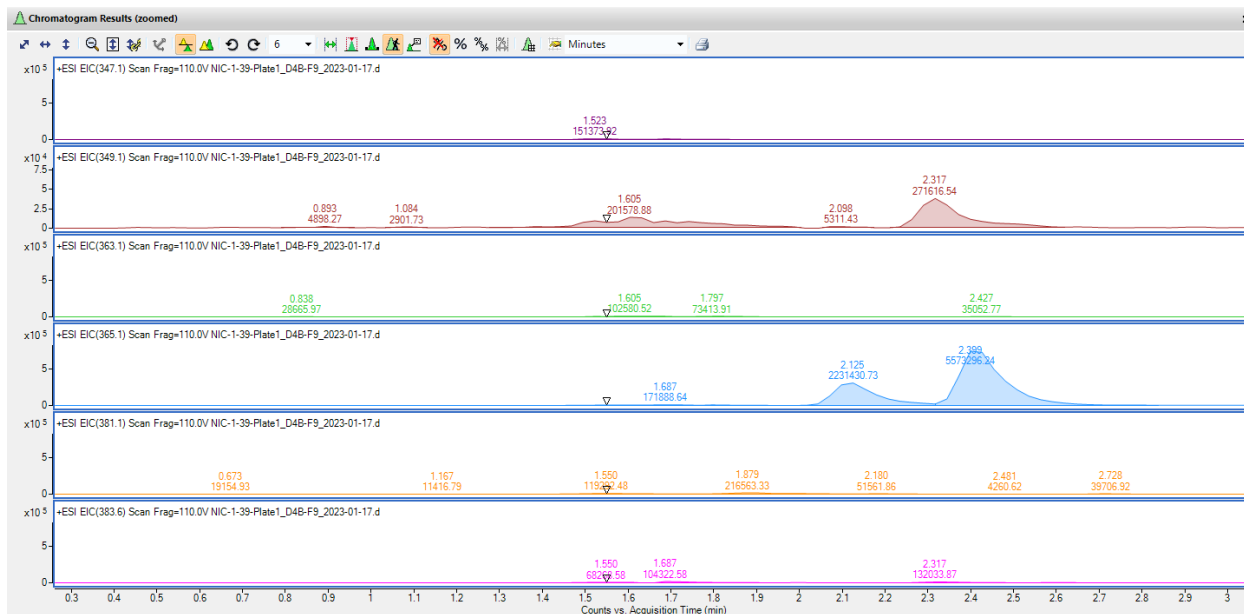
	Neutral	Positive	Negative
Desaturation – PG	346.0987	347.1066	345.0909
Substrate – PG	348.1144	349.1222	347.1066
oxidation/desaturation - PG	362.0977	363.1056	361.0899
Hydroxylation – PG	364.1134	365.1212	363.1056
Dihydroxylation – PG	380.1124	381.1202	379.1046
Chlorination - PG	382.5596	383.5674	381.5517



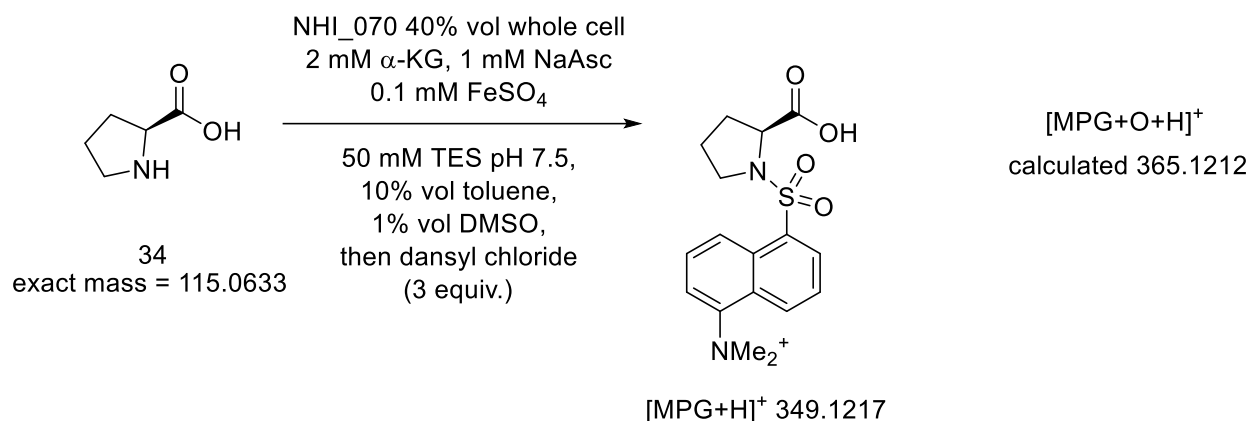
Discovered Reaction 85. Substrate_034 + NHI_069 = hydroxylation



	Neutral	Positive	Negative
Desaturation – PG	346.0987	347.1066	345.0909
Substrate – PG	348.1144	349.1222	347.1066
oxidation/desaturation - PG	362.0977	363.1056	361.0899
Hydroxylation – PG	364.1134	365.1212	363.1056
Dihydroxylation – PG	380.1124	381.1202	379.1046
Chlorination - PG	382.5596	383.5674	381.5517



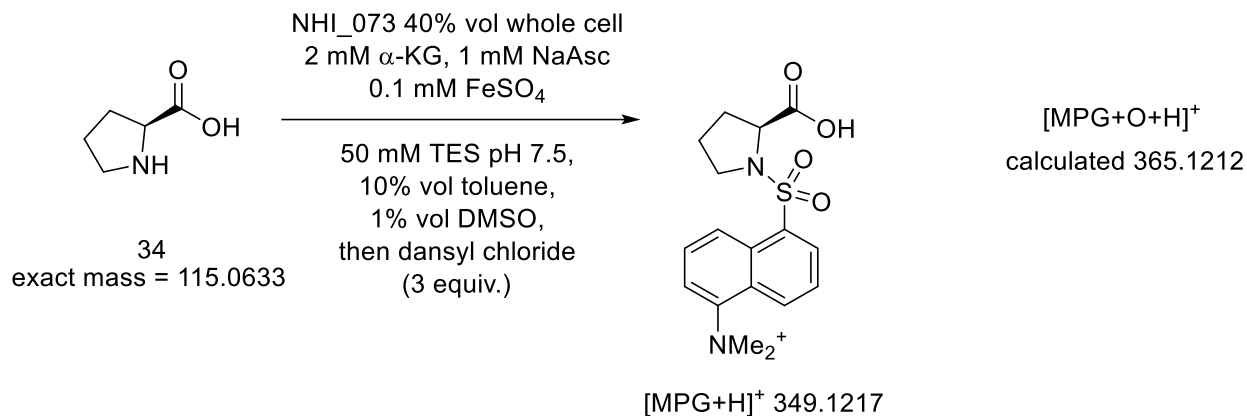
Discovered Reaction 86. Substrate_034 + NHI_070 = hydroxylation



	Neutral	Positive	Negative
Desaturation – PG	346.0987	347.1066	345.0909
Substrate – PG	348.1144	349.1222	347.1066
oxidation/desaturation - PG	362.0977	363.1056	361.0899
Hydroxylation – PG	364.1134	365.1212	363.1056
Dihydroxylation – PG	380.1124	381.1202	379.1046
Chlorination - PG	382.5596	383.5674	381.5517



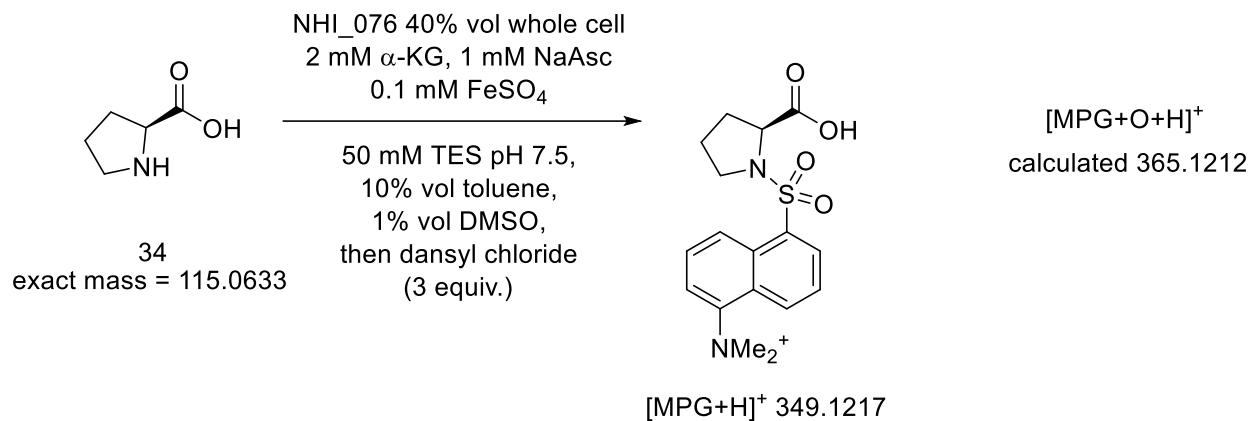
Discovered Reaction 87. Substrate_034 + NHI_073 = hydroxylation



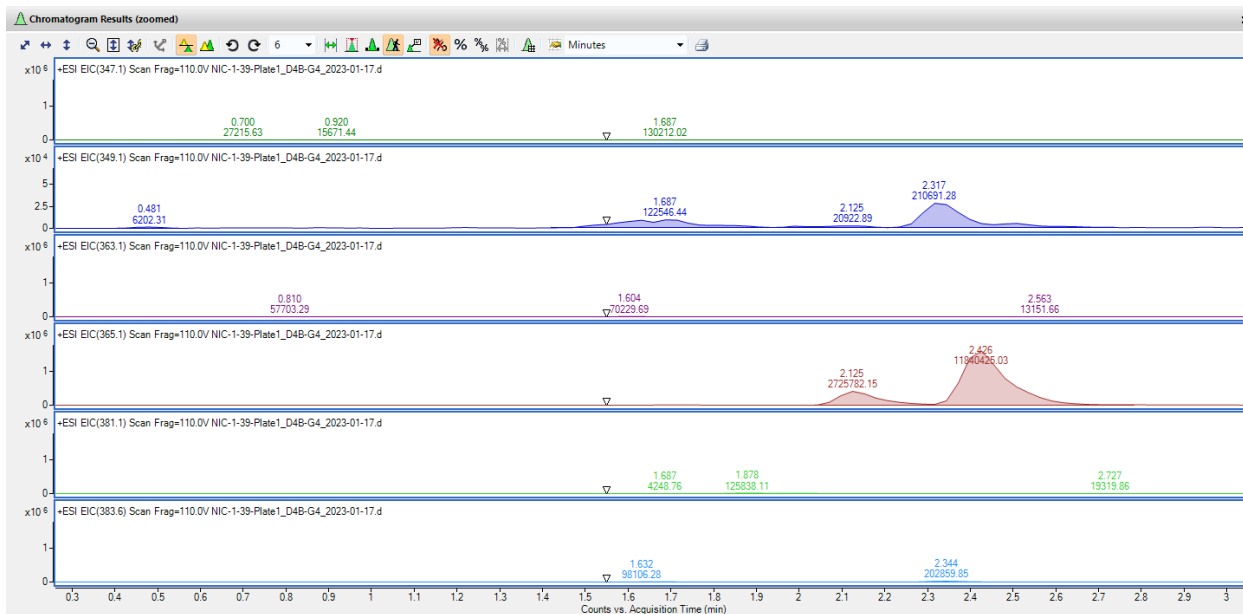
	Neutral	Positive	Negative
Desaturation – PG	346.0987	347.1066	345.0909
Substrate – PG	348.1144	349.1222	347.1066
oxidation/desaturation - PG	362.0977	363.1056	361.0899
Hydroxylation – PG	364.1134	365.1212	363.1056
Dihydroxylation – PG	380.1124	381.1202	379.1046
Chlorination - PG	382.5596	383.5674	381.5517



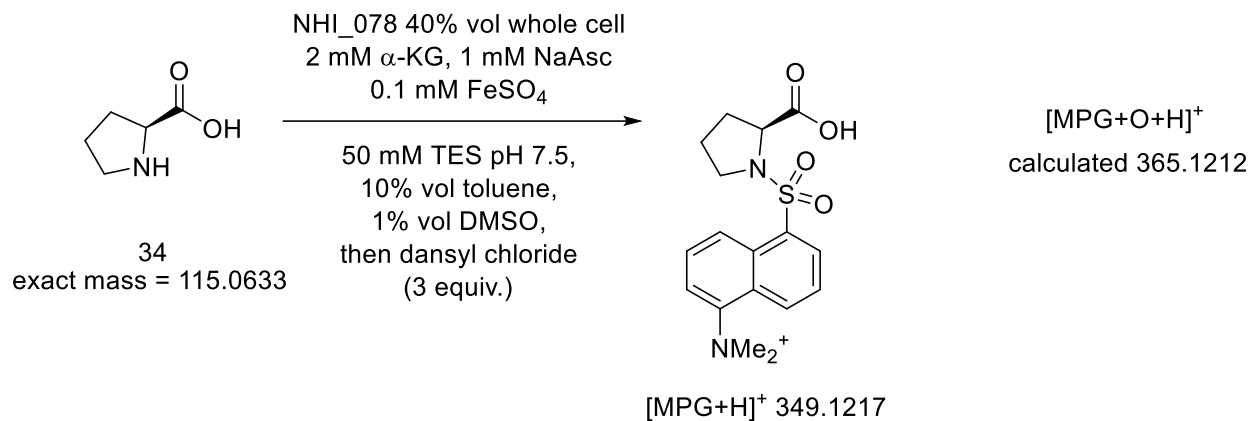
Discovered Reaction 88. Substrate_034 + NHI_076 = hydroxylation



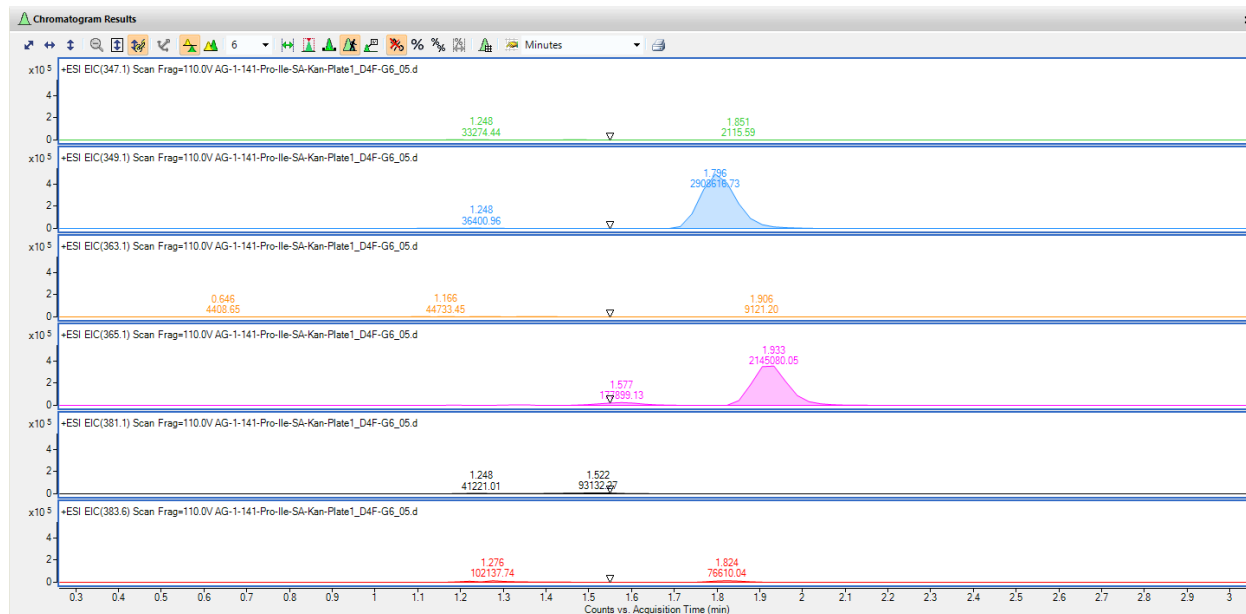
	Neutral	Positive	Negative
Desaturation – PG	346.0987	347.1066	345.0909
Substrate – PG	348.1144	349.1222	347.1066
oxidation/desaturation - PG	362.0977	363.1056	361.0899
Hydroxylation – PG	364.1134	365.1212	363.1056
Dihydroxylation – PG	380.1124	381.1202	379.1046
Chlorination - PG	382.5596	383.5674	381.5517



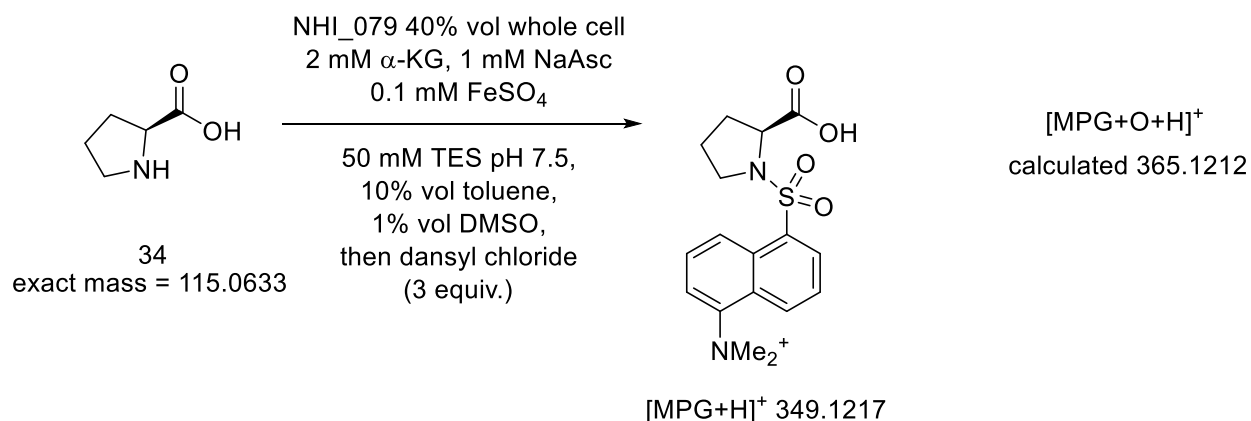
Discovered Reaction 89. Substrate_034 + NHI_078 = hydroxylation



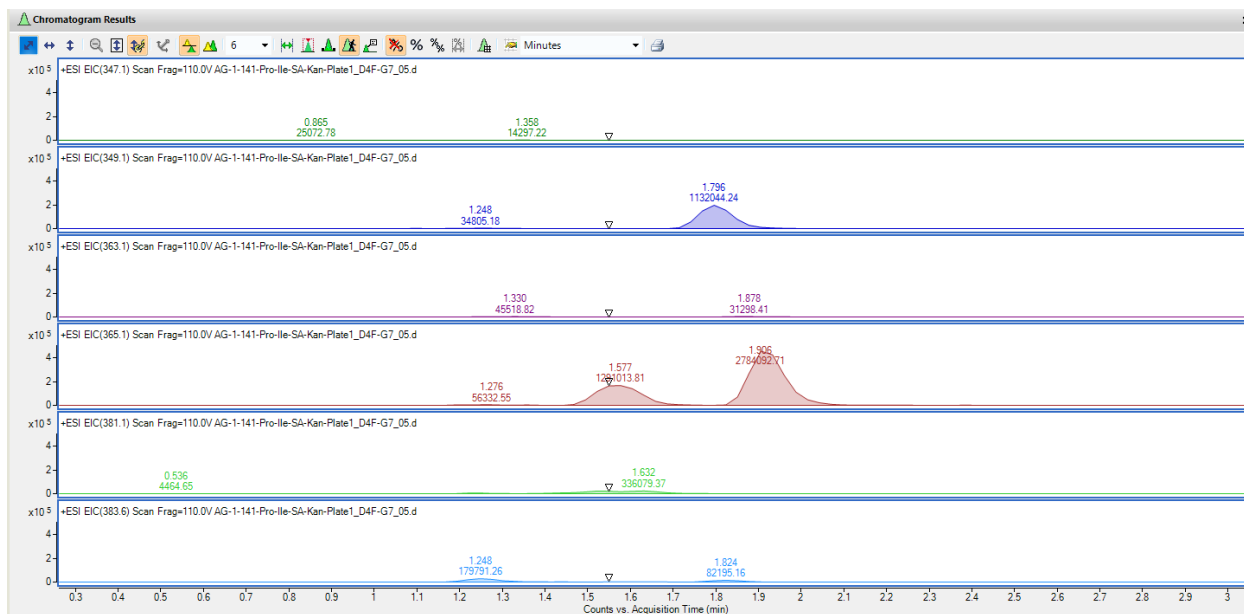
	Neutral	Positive	Negative
Desaturation – PG	346.0987	347.1066	345.0909
Substrate – PG	348.1144	349.1222	347.1066
oxidation/desaturation - PG	362.0977	363.1056	361.0899
Hydroxylation – PG	364.1134	365.1212	363.1056
Dihydroxylation – PG	380.1124	381.1202	379.1046
Chlorination - PG	382.5596	383.5674	381.5517



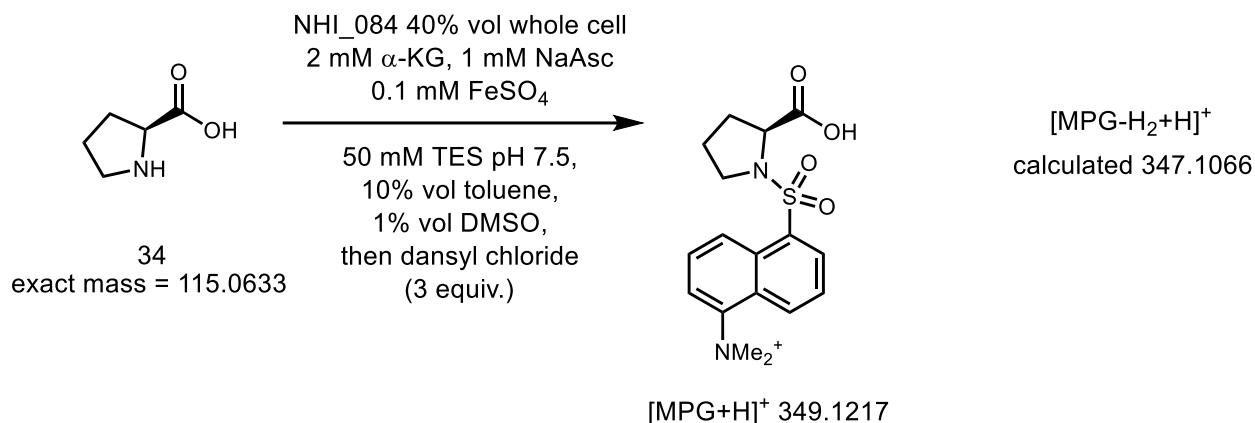
Discovered Reaction 90. Substrate_034 + NHI_079 = hydroxylation



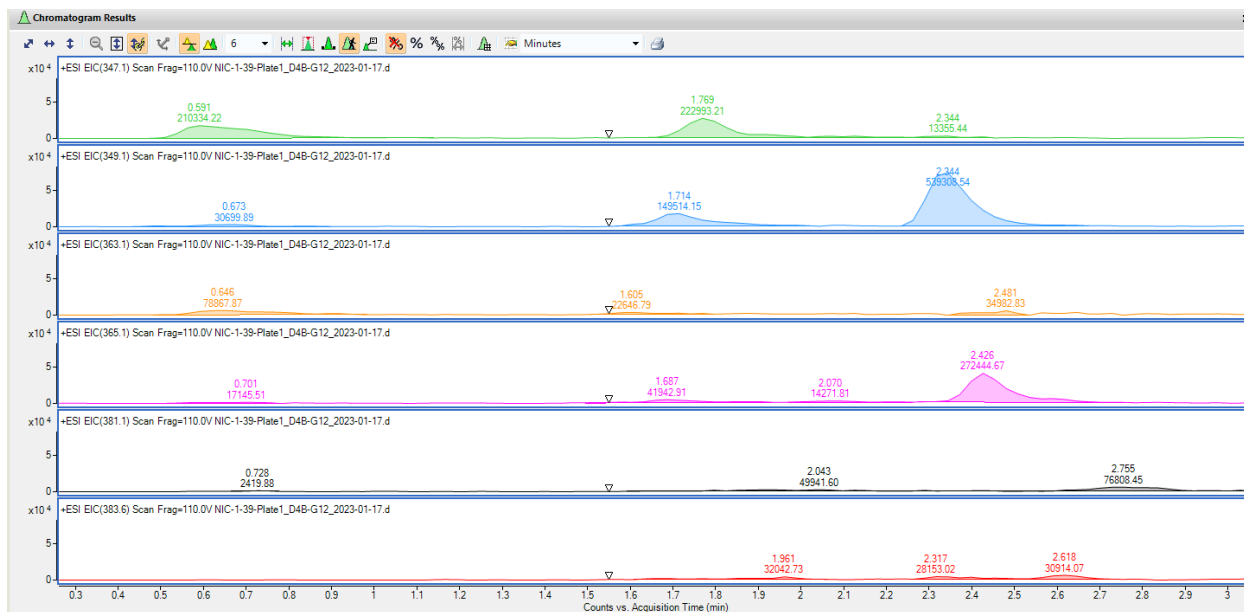
	Neutral	Positive	Negative
Desaturation – PG	346.0987	347.1066	345.0909
Substrate – PG	348.1144	349.1222	347.1066
oxidation/desaturation - PG	362.0977	363.1056	361.0899
Hydroxylation – PG	364.1134	365.1212	363.1056
Dihydroxylation – PG	380.1124	381.1202	379.1046
Chlorination - PG	382.5596	383.5674	381.5517



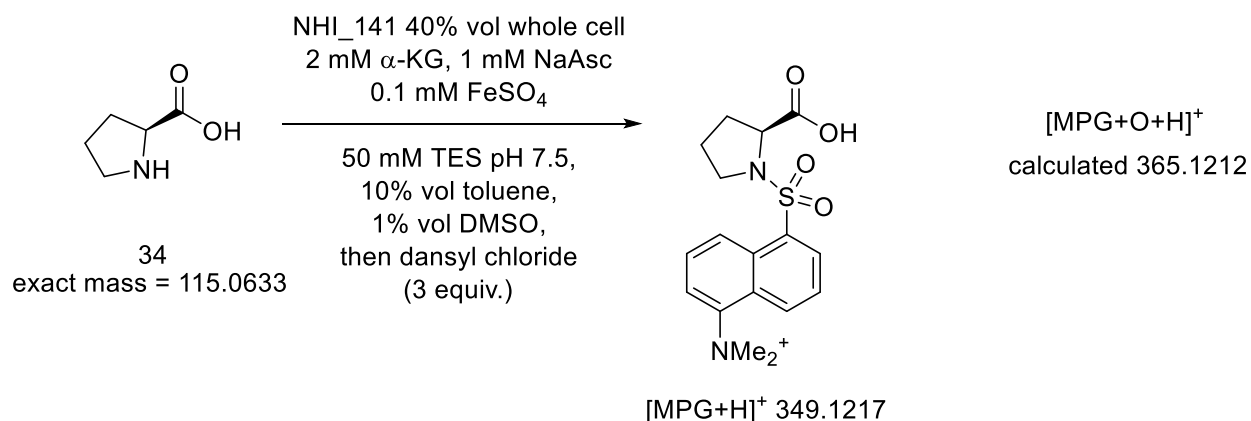
Discovered Reaction 91. Substrate_034 + NHI_084 = desaturation



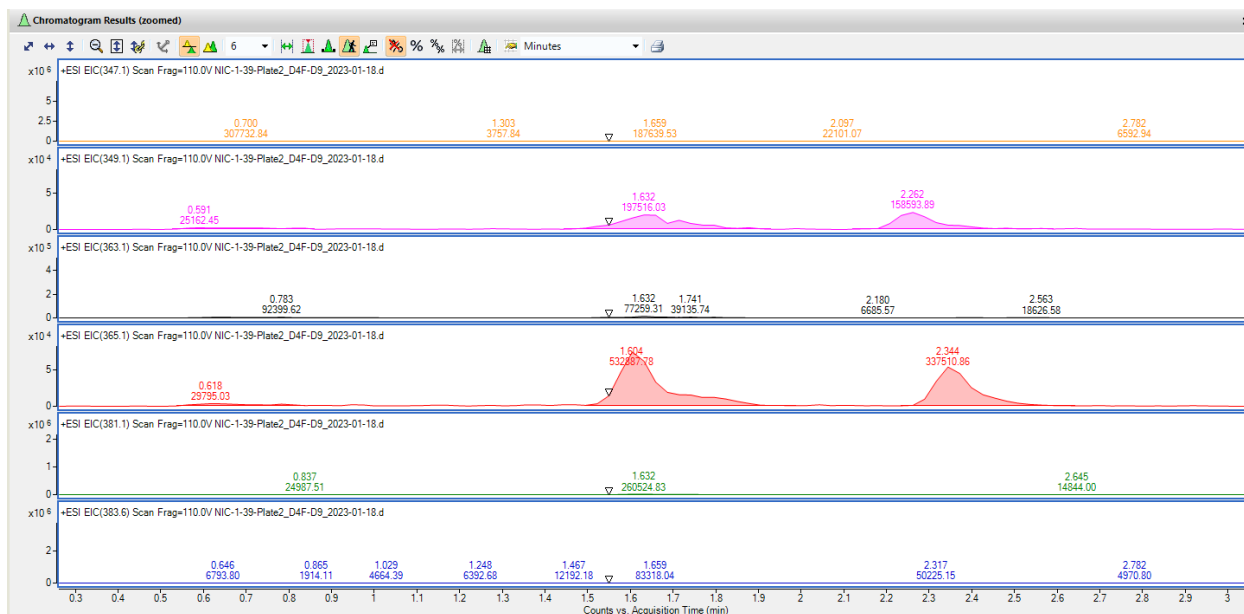
	Neutral	Positive	Negative
Desaturation – PG	346.0987	347.1066	345.0909
Substrate – PG	348.1144	349.1222	347.1066
oxidation/desaturation - PG	362.0977	363.1056	361.0899
Hydroxylation – PG	364.1134	365.1212	363.1056
Dihydroxylation – PG	380.1124	381.1202	379.1046
Chlorination - PG	382.5596	383.5674	381.5517



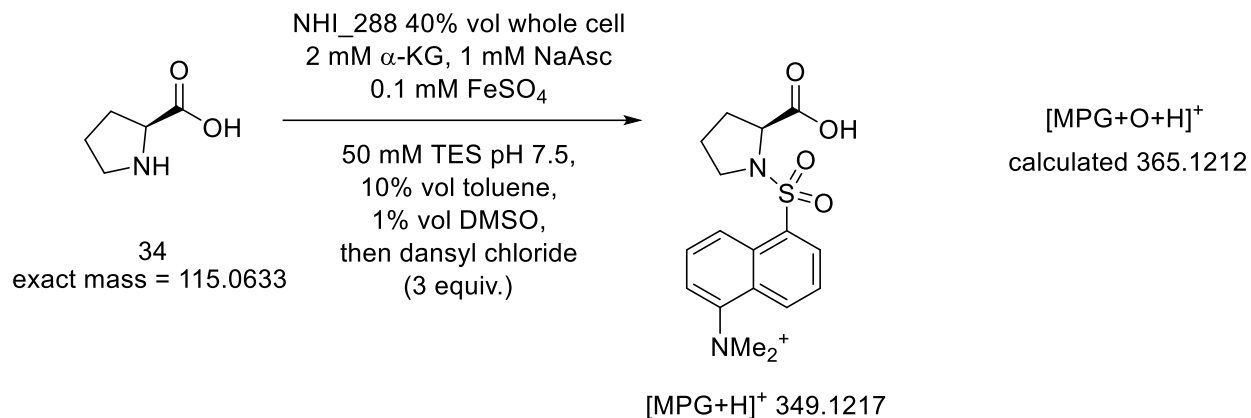
Discovered Reaction 92. Substrate_034 + NHI_141 = hydroxylation



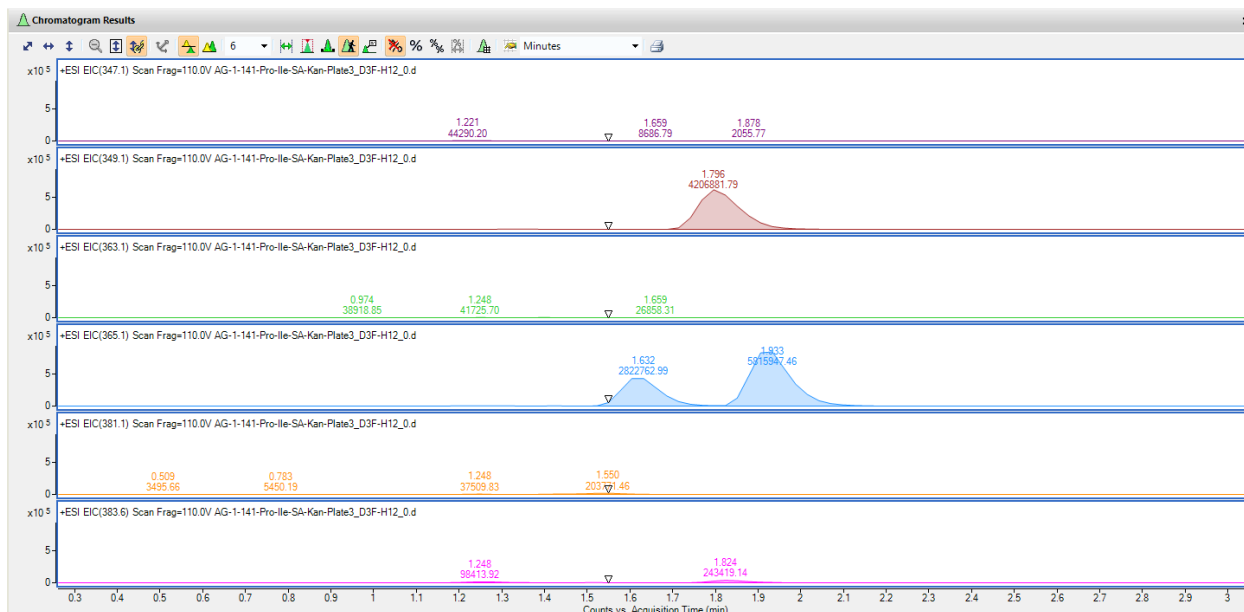
	Neutral	Positive	Negative
Desaturation – PG	346.0987	347.1066	345.0909
Substrate – PG	348.1144	349.1222	347.1066
oxidation/desaturation - PG	362.0977	363.1056	361.0899
Hydroxylation – PG	364.1134	365.1212	363.1056
Dihydroxylation – PG	380.1124	381.1202	379.1046
Chlorination - PG	382.5596	383.5674	381.5517



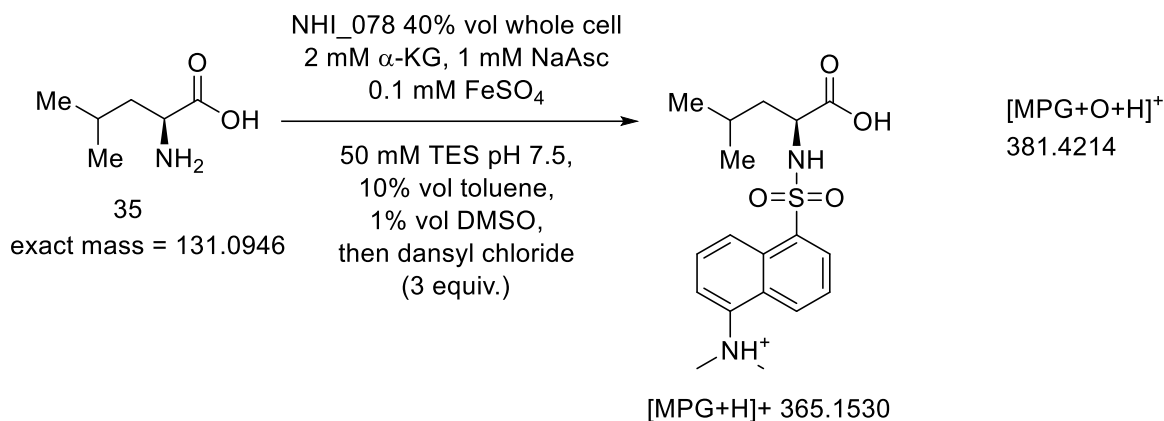
Discovered Reaction 93. Substrate_034 + NHI_288 = hydroxylation



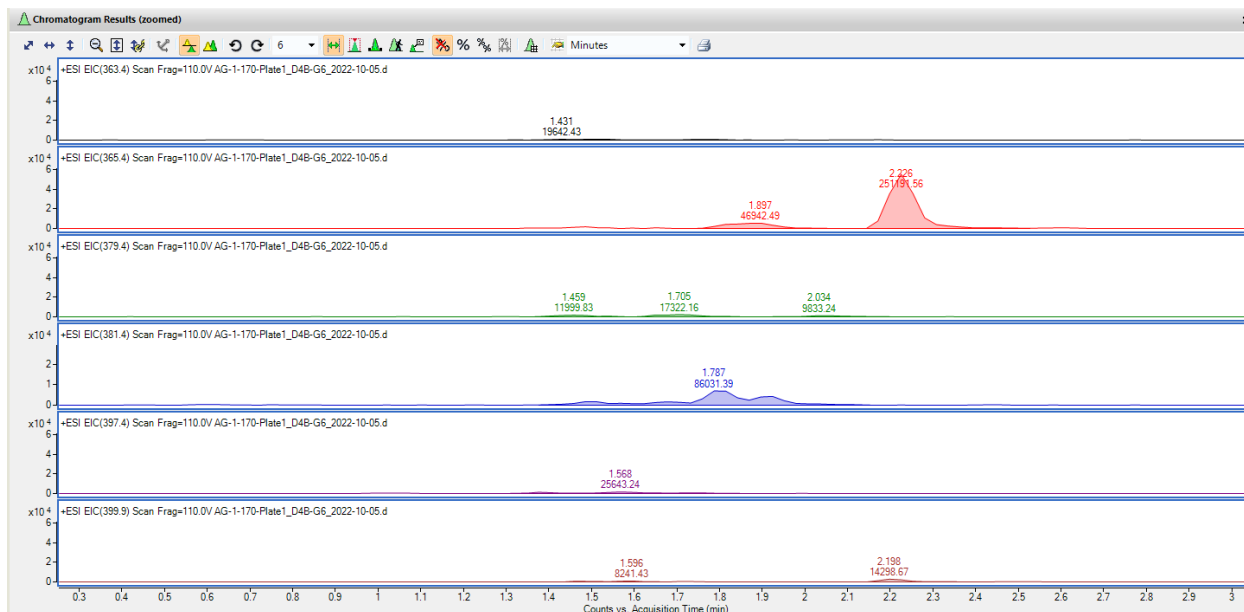
	Neutral	Positive	Negative
Desaturation – PG	346.0987	347.1066	345.0909
Substrate – PG	348.1144	349.1222	347.1066
oxidation/desaturation - PG	362.0977	363.1056	361.0899
Hydroxylation – PG	364.1134	365.1212	363.1056
Dihydroxylation – PG	380.1124	381.1202	379.1046
Chlorination - PG	382.5596	383.5674	381.5517



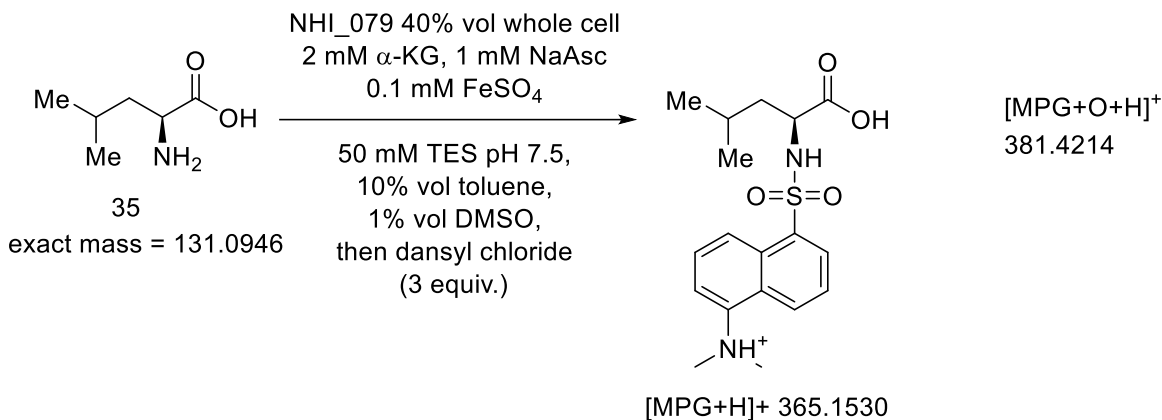
Discovered Reaction 94. Substrate_035 + NHI_078 = hydroxylation



	Neutral	Positive	Negative
Desaturation – PG	362.3988	363.4067	361.3910
Substrate – PG	364.4145	365.4223	363.4067
oxidation/desaturation - PG	378.3978	379.4057	377.3900
Hydroxylation – PG	380.4135	381.4213	379.4057
Dihydroxylation – PG	396.4125	397.4203	395.4047
Chlorination - PG	398.8597	399.8675	397.8518



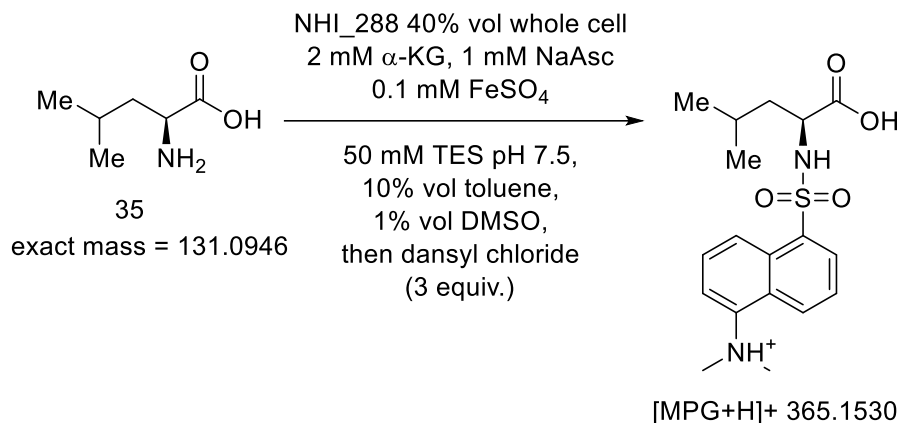
Discovered Reaction 95. Substrate_035 + NHI_079 = hydroxylation



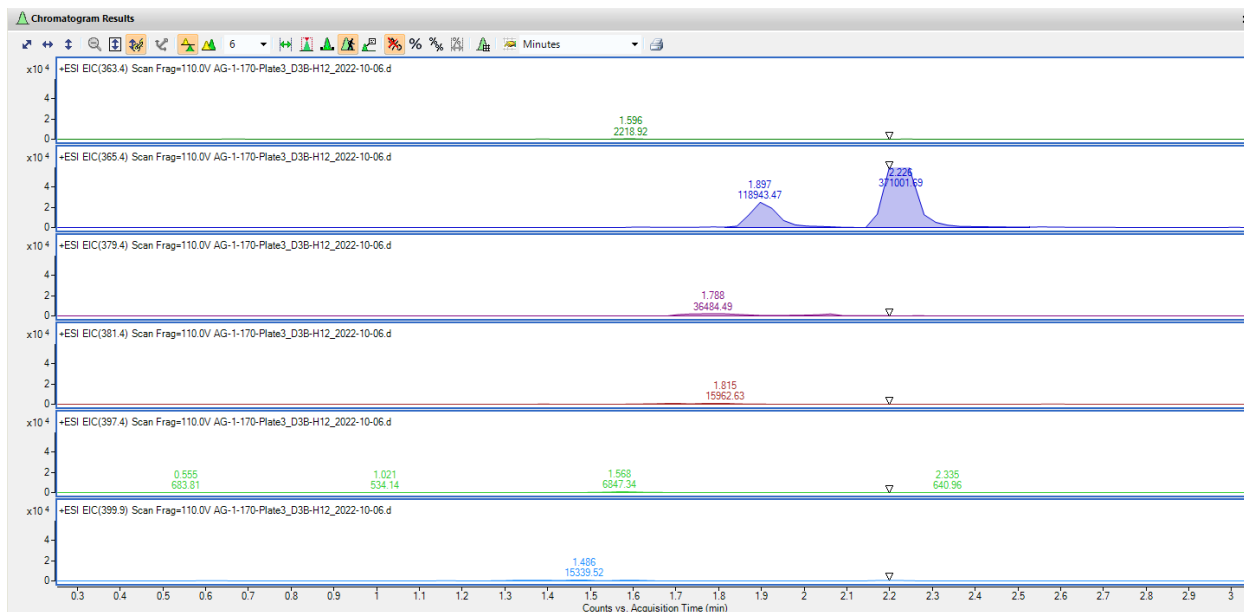
	Neutral	Positive	Negative
Desaturation – PG	362.3988	363.4067	361.3910
Substrate – PG	364.4145	365.4223	363.4067
oxidation/desaturation - PG	378.3978	379.4057	377.3900
Hydroxylation – PG	380.4135	381.4213	379.4057
Dihydroxylation – PG	396.4125	397.4203	395.4047
Chlorination - PG	398.8597	399.8675	397.8518



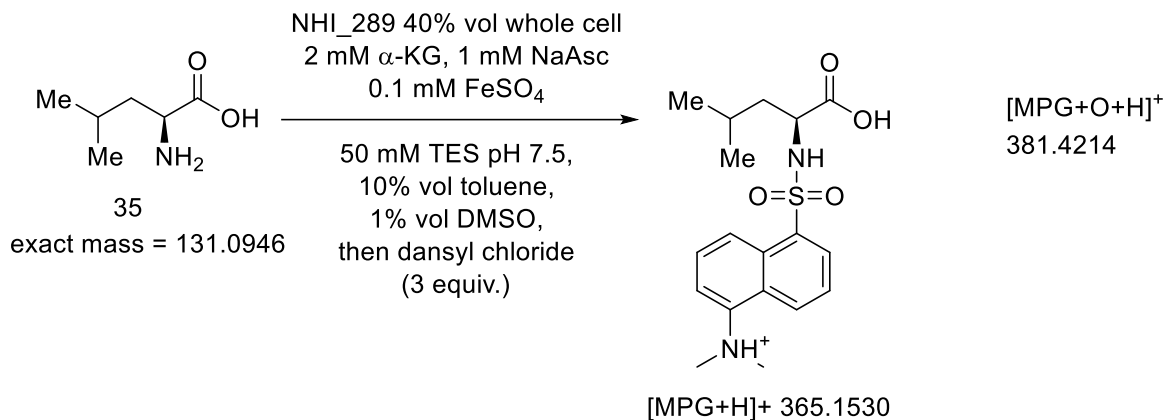
Discovered Reaction 96. Substrate_035 + NHI_288 = rearrangement



	Neutral	Positive	Negative
Desaturation – PG	362.3988	363.4067	361.3910
Substrate – PG	364.4145	365.4223	363.4067
oxidation/desaturation - PG	378.3978	379.4057	377.3900
Hydroxylation – PG	380.4135	381.4213	379.4057
Dihydroxylation – PG	396.4125	397.4203	395.4047
Chlorination - PG	398.8597	399.8675	397.8518



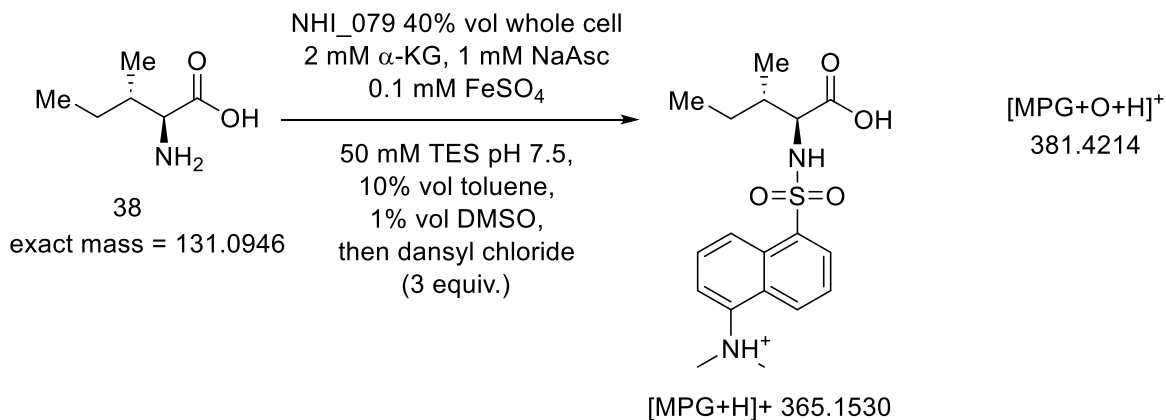
Discovered Reaction 97. Substrate_035 + NHI_289 = hydroxylation



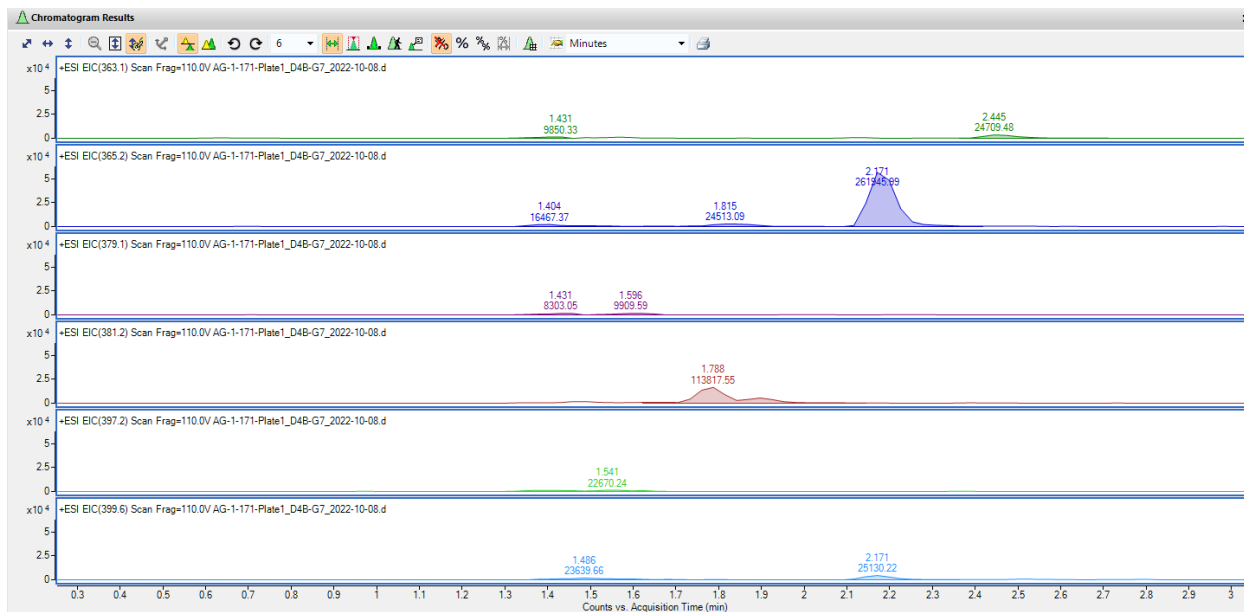
	Neutral	Positive	Negative
Desaturation – PG	362.3988	363.4067	361.3910
Substrate – PG	364.4145	365.4223	363.4067
oxidation/desaturation - PG	378.3978	379.4057	377.3900
Hydroxylation – PG	380.4135	381.4213	379.4057
Dihydroxylation – PG	396.4125	397.4203	395.4047
Chlorination - PG	398.8597	399.8675	397.8518



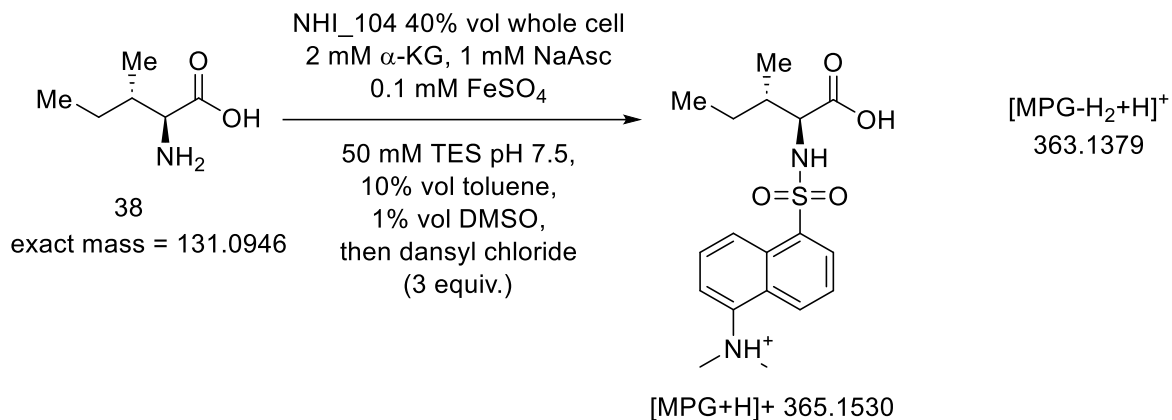
Discovered Reaction 98. Substrate_038 + NHI_079 = hydroxylation



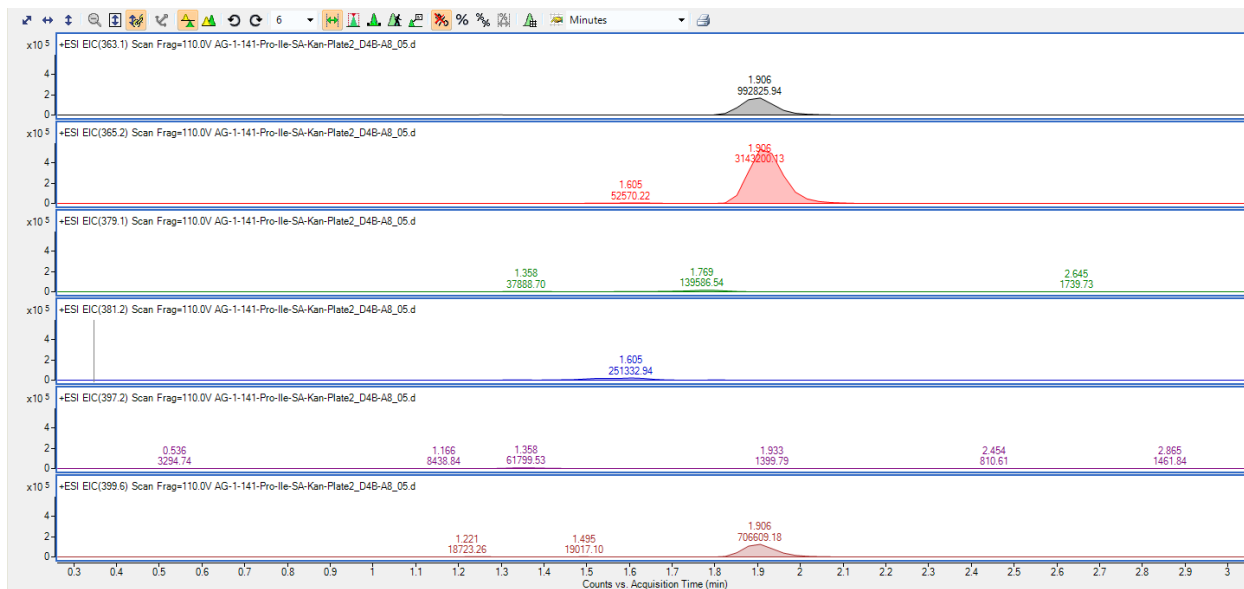
	Neutral	Positive	Negative
Desaturation – PG	362.1300	363.1379	361.1222
Substrate – PG	364.1457	365.1535	363.1379
oxidation/desaturation - PG	378.1290	379.1369	377.1212
Hydroxylation – PG	380.1447	381.1525	379.1369
Dihydroxylation – PG	396.1437	397.1515	395.1359
Chlorination - PG	398.5909	399.5987	397.5830



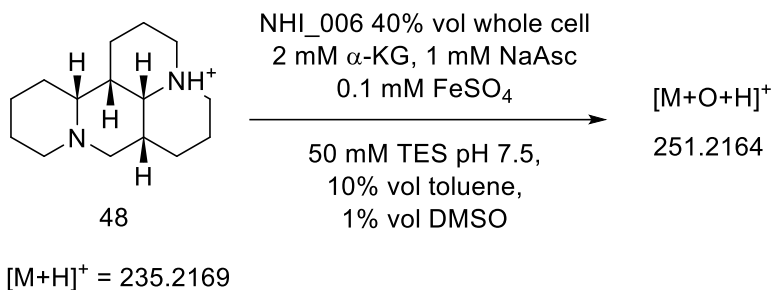
Discovered Reaction 99. Substrate_038 + NHI_104 = desaturation



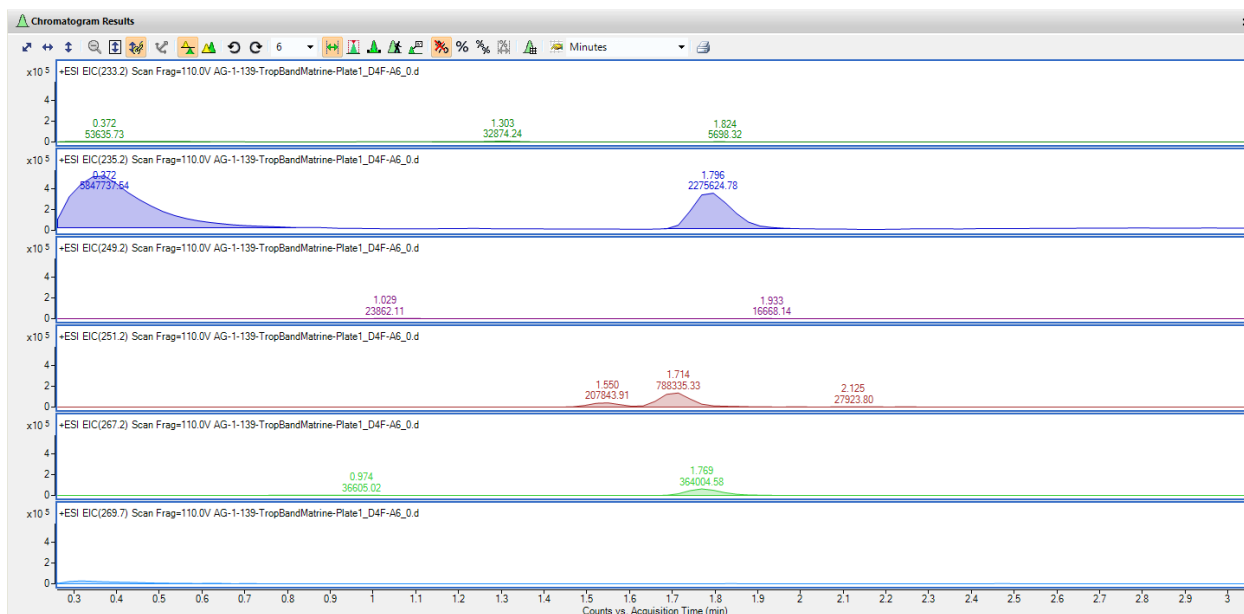
	Neutral	Positive	Negative
Desaturation – PG	362.1300	363.1379	361.1222
Substrate – PG	364.1457	365.1535	363.1379
oxidation/desaturation - PG	378.1290	379.1369	377.1212
Hydroxylation – PG	380.1447	381.1525	379.1369
Dihydroxylation – PG	396.1437	397.1515	395.1359
Chlorination - PG	398.5909	399.5987	397.5830



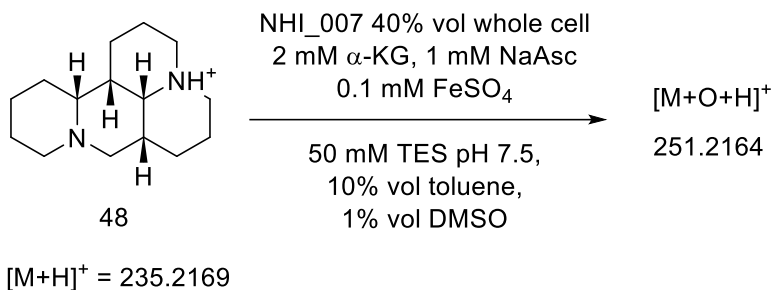
Discovered Reaction 100. Substrate_048 + NHI_006 = hydroxylation



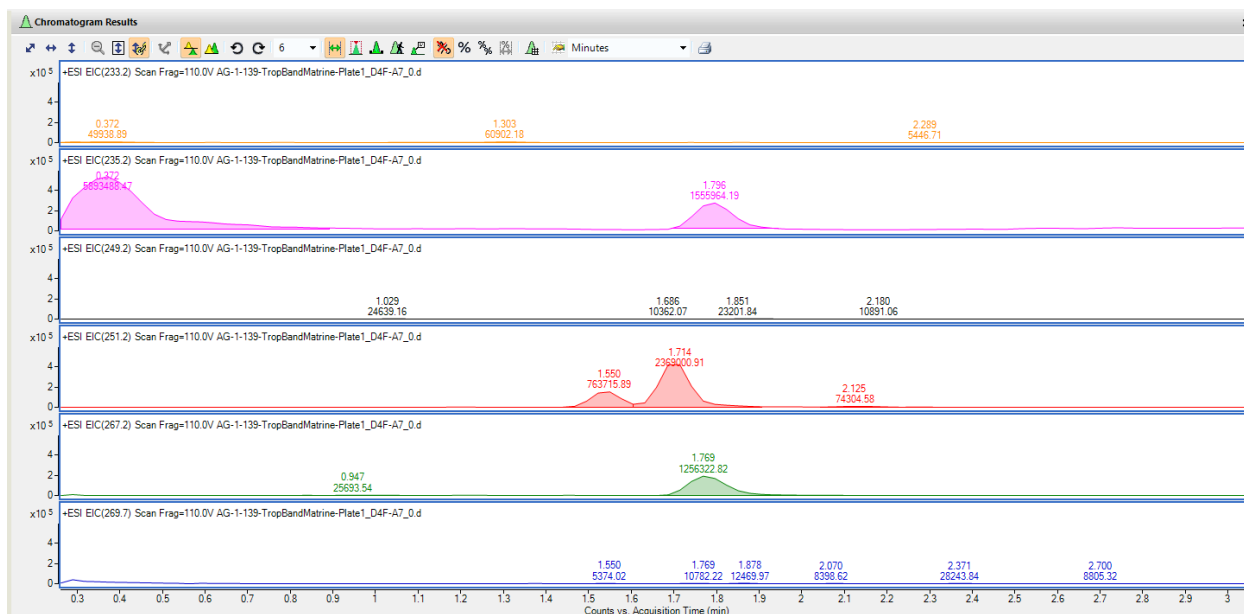
	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



Discovered Reaction 101. Substrate_048 + NHI_007 = hydroxylation



	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469

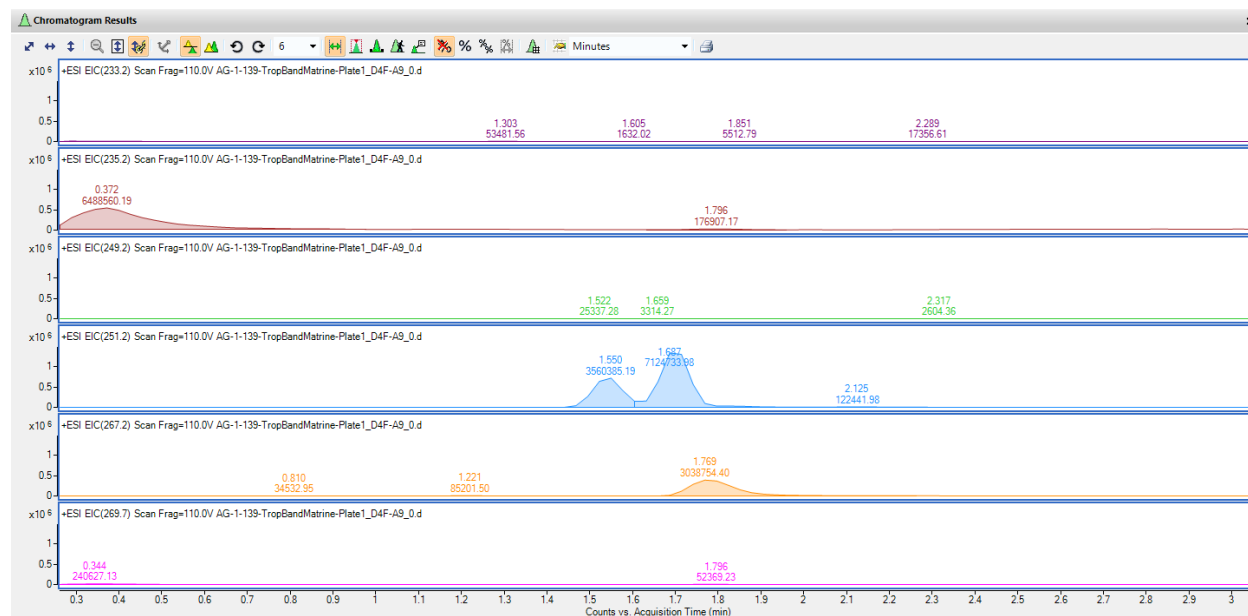


Discovered Reaction 102. Substrate_048 + NHI_009 = hydroxylation

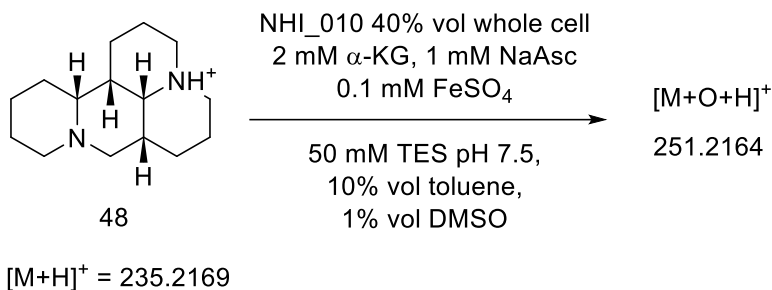


$[M+H]^+ = 235.2169$

	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



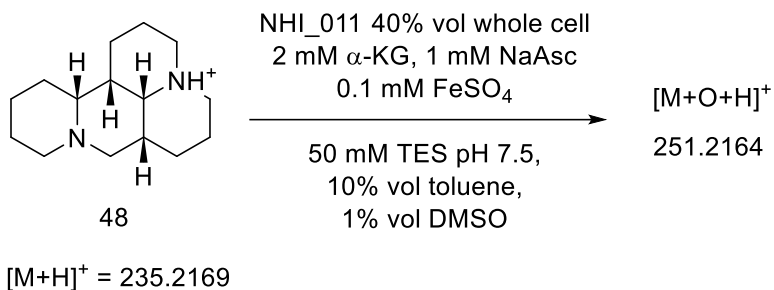
Discovered Reaction 103. Substrate_048 + NHI_010 = hydroxylation



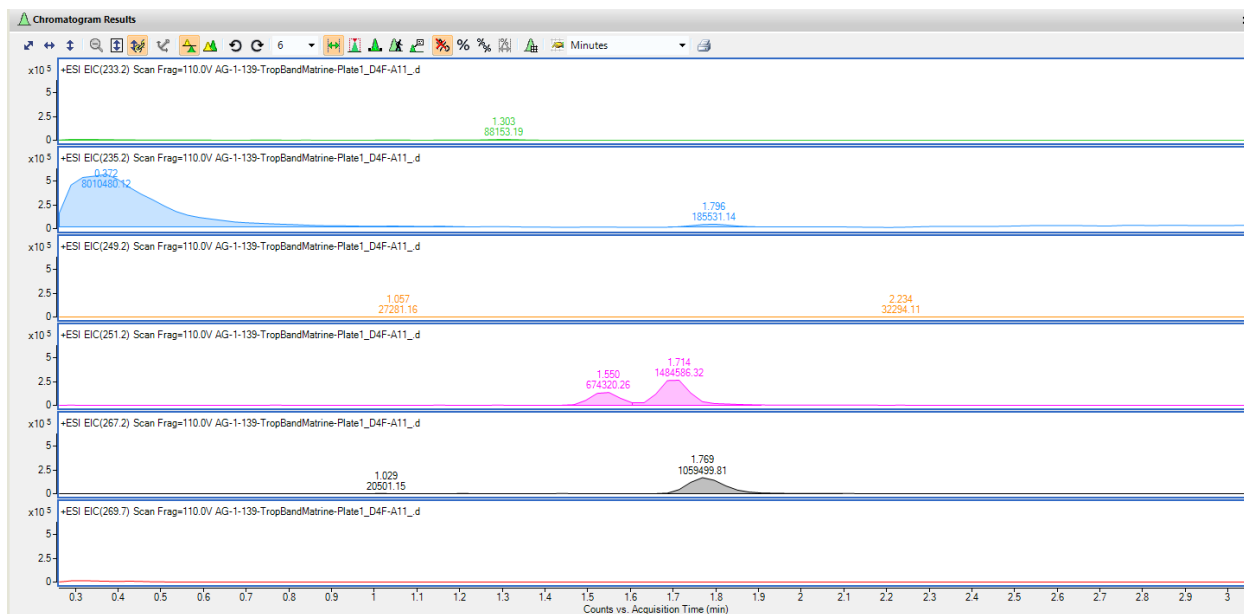
	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



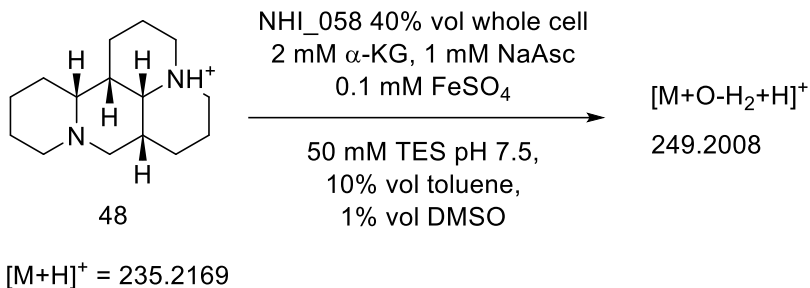
Discovered Reaction 104. Substrate_048 + NHI_011 = hydroxylation



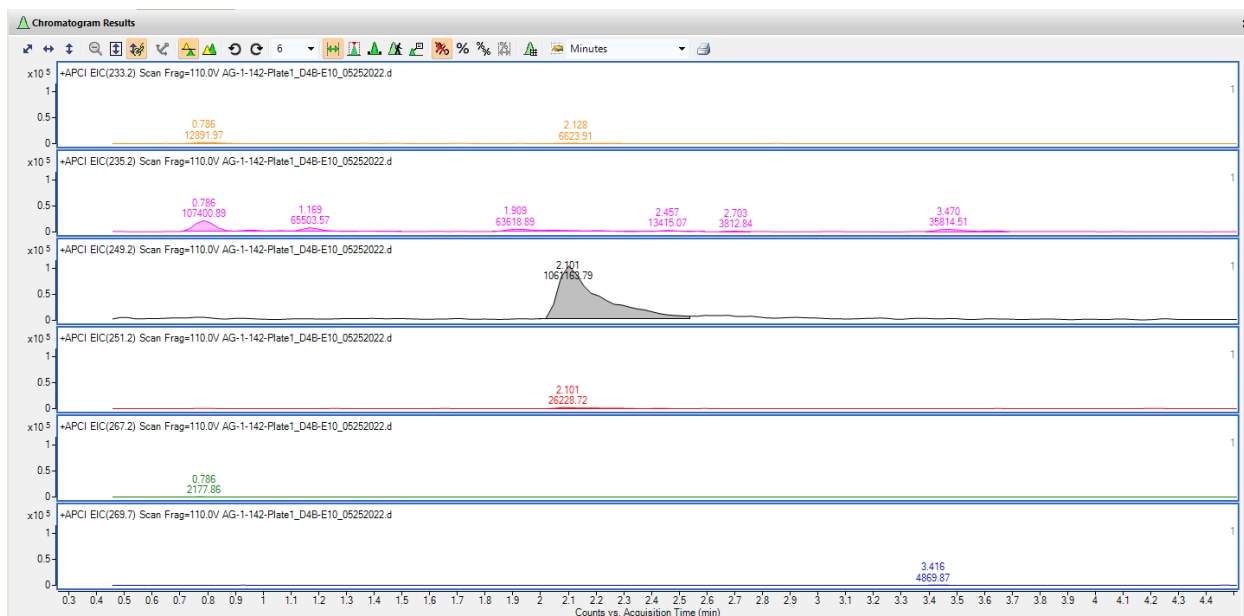
	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



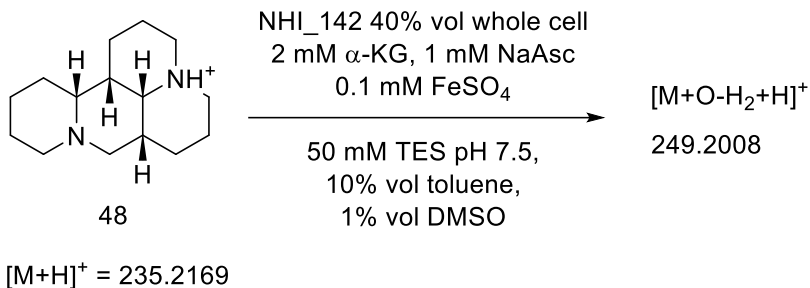
Discovered Reaction 105. Substrate_048 + NHI_058 = hydroxylation/desaturation



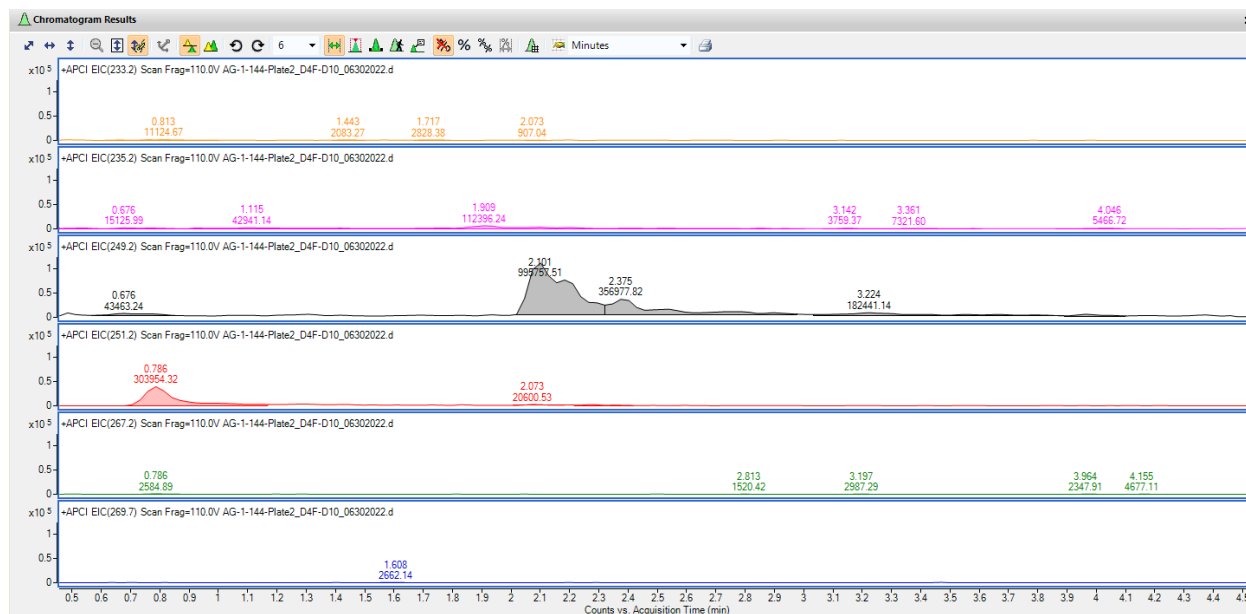
	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



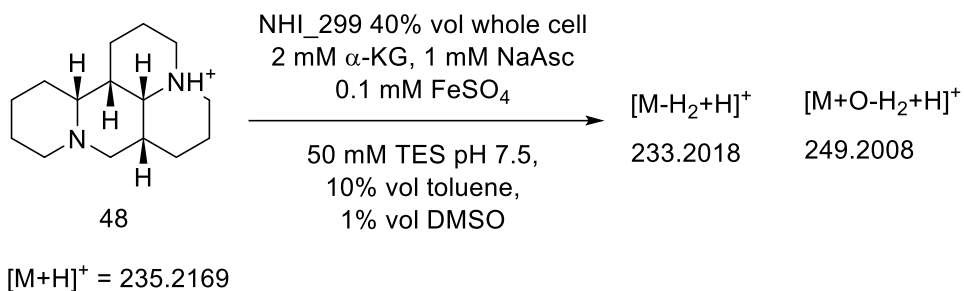
Discovered Reaction 106. Substrate_048 + NHI_142 = hydroxylation/desaturation



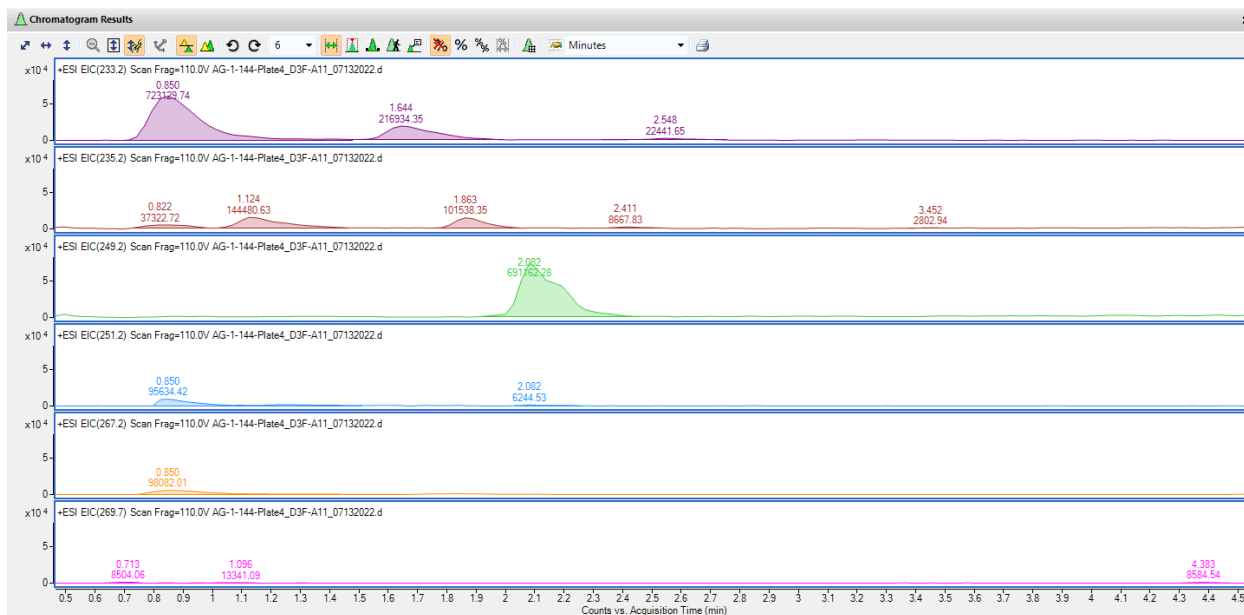
	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



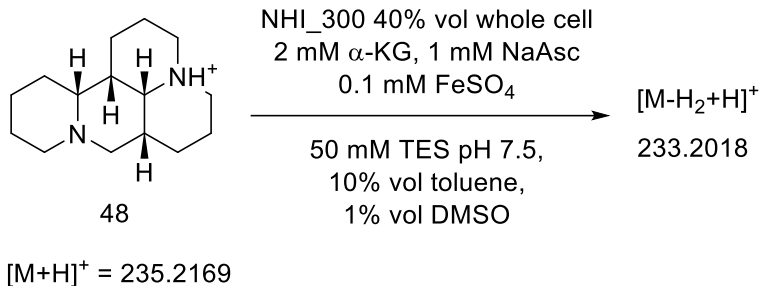
Discovered Reaction 107. Substrate_048 + NHI_299 = desaturation and oxidation/desaturation



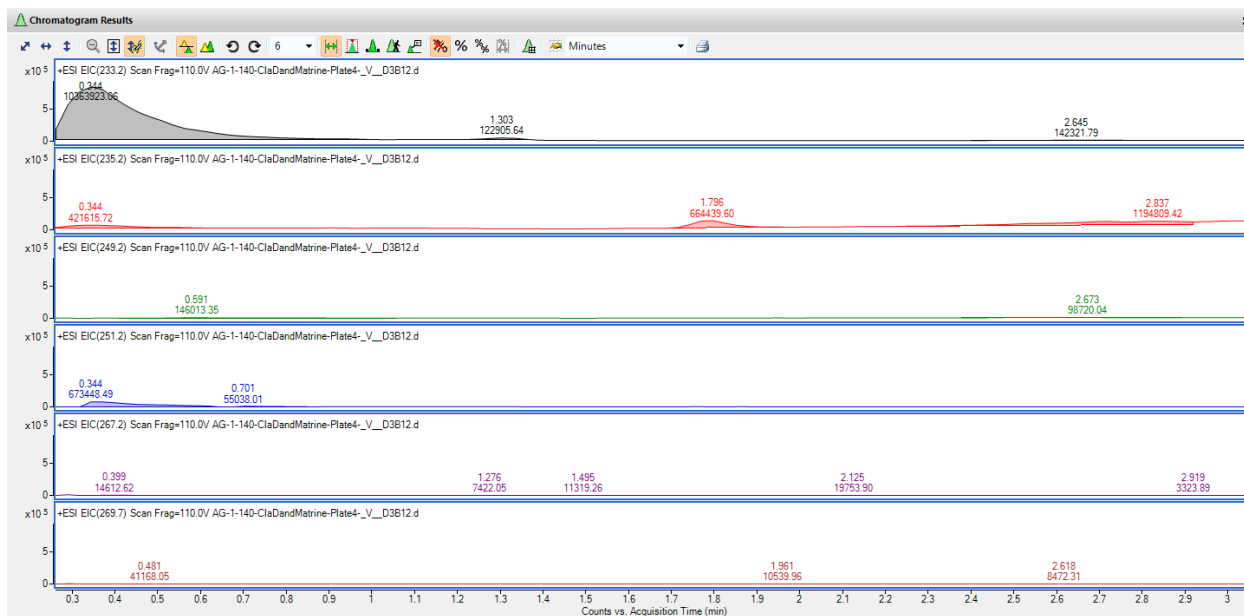
	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



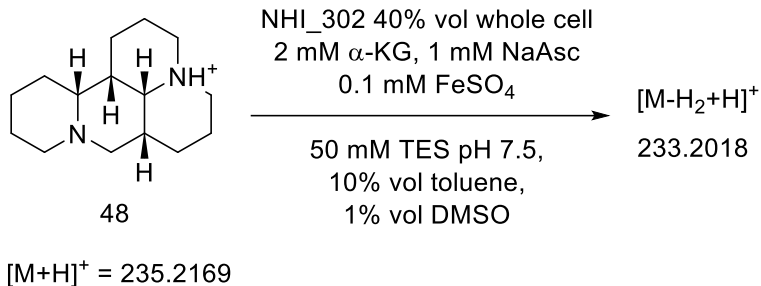
Discovered Reaction 108. Substrate_048 + NHI_300 = desaturation



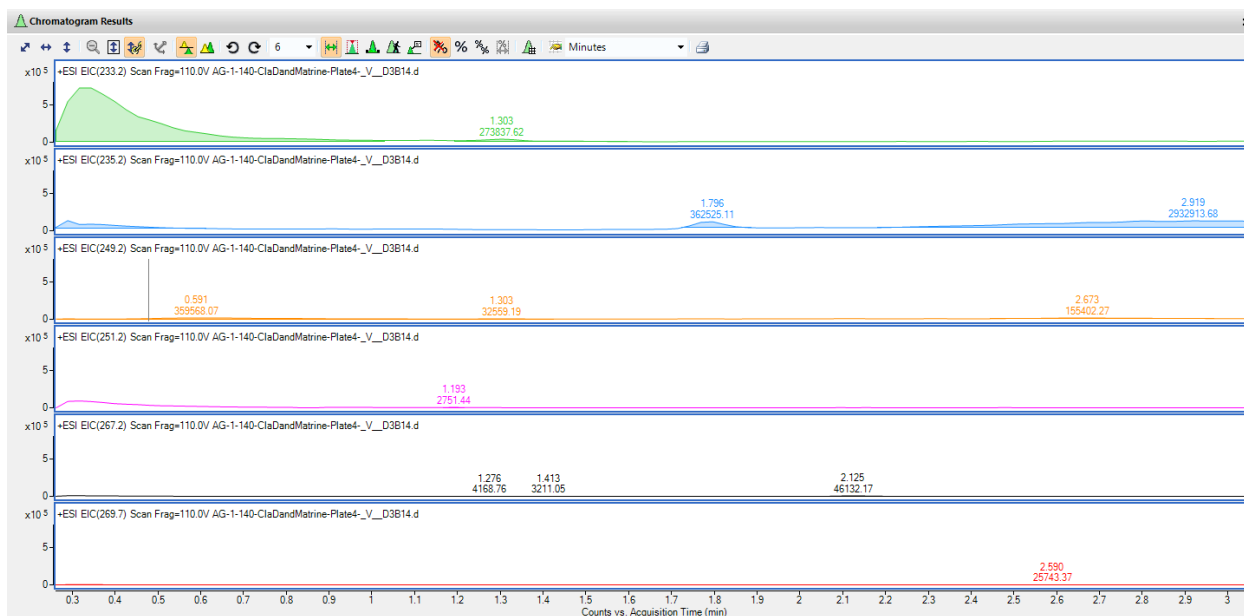
	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



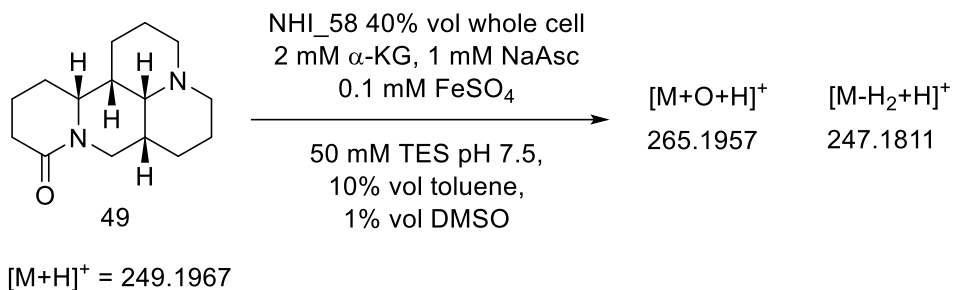
Discovered Reaction 109. Substrate_048 + NHI_302 = desaturation



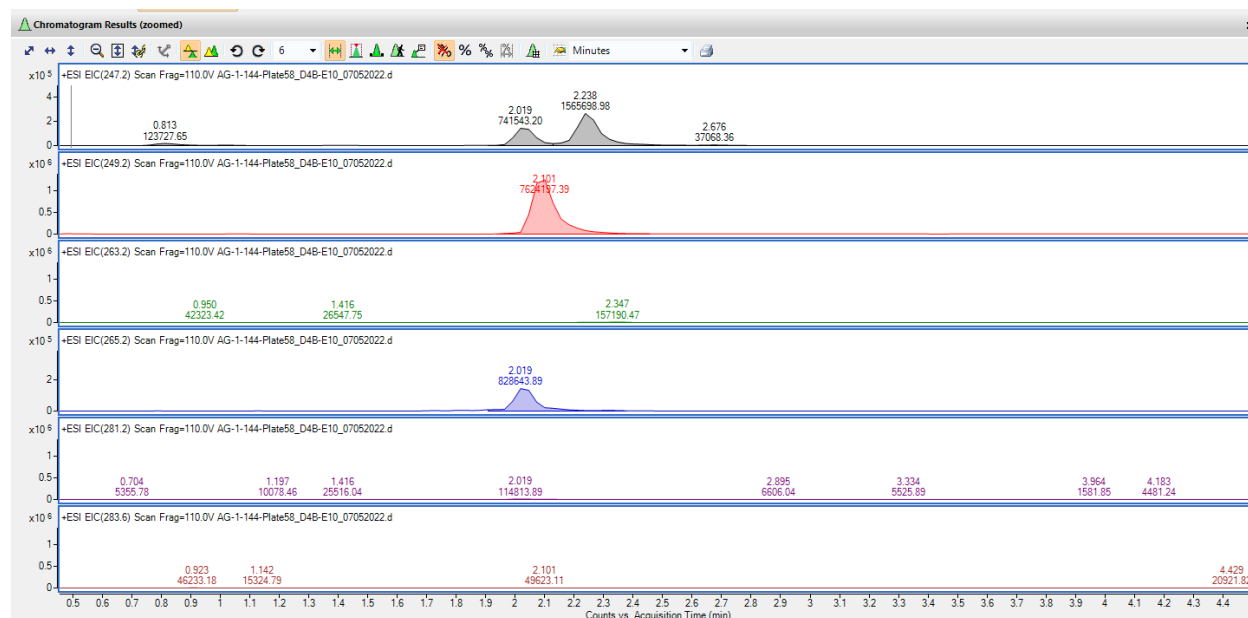
	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



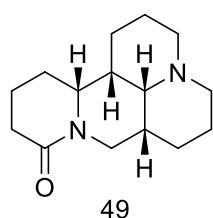
Discovered Reaction 110. Substrate_049 + NHI_058 = hydroxylation and desaturation



	Neutral	Positive	Negative
desaturation	246.1732	247.1811	245.1654
substrate	248.1889	249.1967	247.1811
oxidation/desaturation	262.1722	263.1801	261.1644
hydroxylation	264.1879	265.1957	263.1801
dihydroxylation	280.1869	281.1947	279.1791
chlorination	282.6341	283.6419	281.6262



Discovered Reaction 111. Substrate_049 + NHI_142 = desaturation



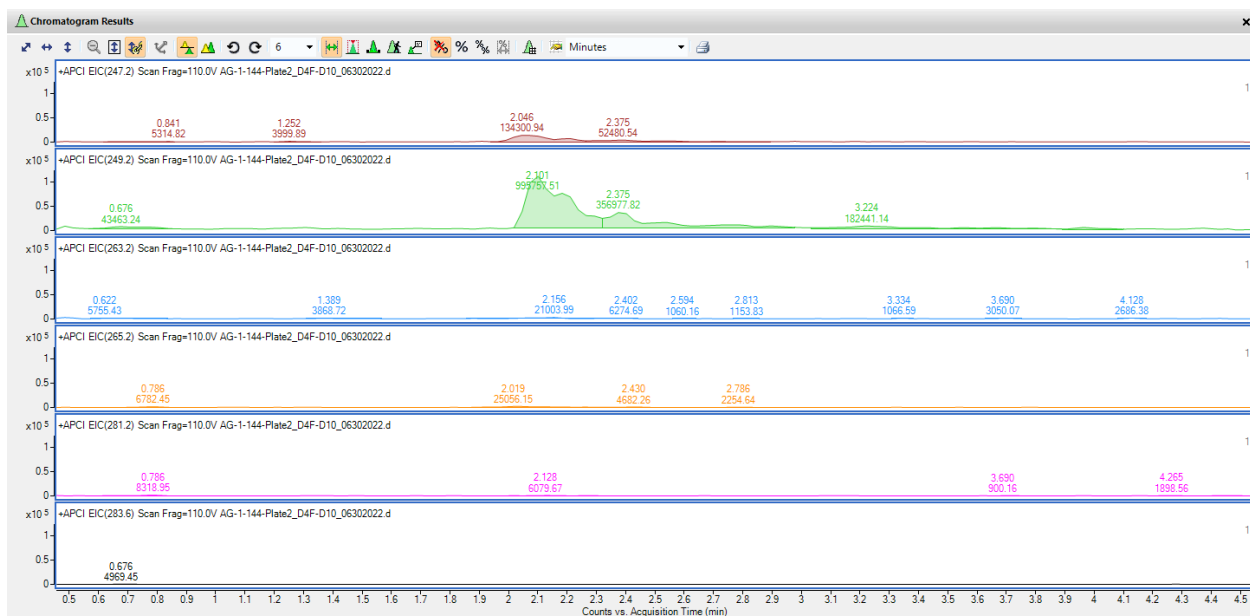
NHI_142 40% vol whole cell
2 mM α -KG, 1 mM NaAsc
0.1 mM FeSO_4

50 mM TES pH 7.5,
10% vol toluene,
1% vol DMSO

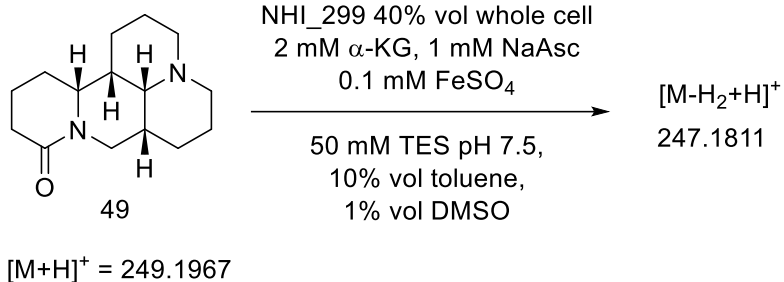
$[\text{M}-\text{H}_2+\text{H}]^+$
247.1811

$[\text{M}+\text{H}]^+ = 249.1967$

	Neutral	Positive	Negative
desaturation	246.1732	247.1811	245.1654
substrate	248.1889	249.1967	247.1811
oxidation/desaturation	262.1722	263.1801	261.1644
hydroxylation	264.1879	265.1957	263.1801
dihydroxylation	280.1869	281.1947	279.1791
chlorination	282.6341	283.6419	281.6262



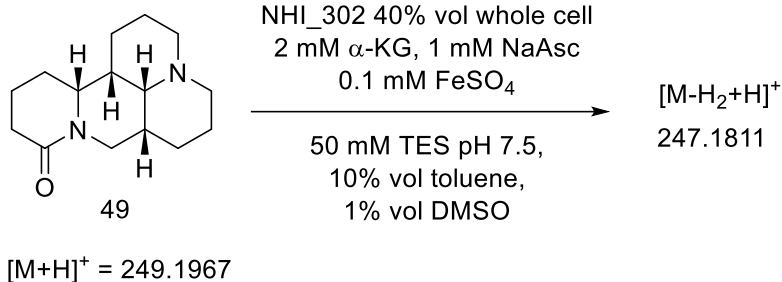
Discovered Reaction 112. Substrate_049 + NHI_299 = desaturation



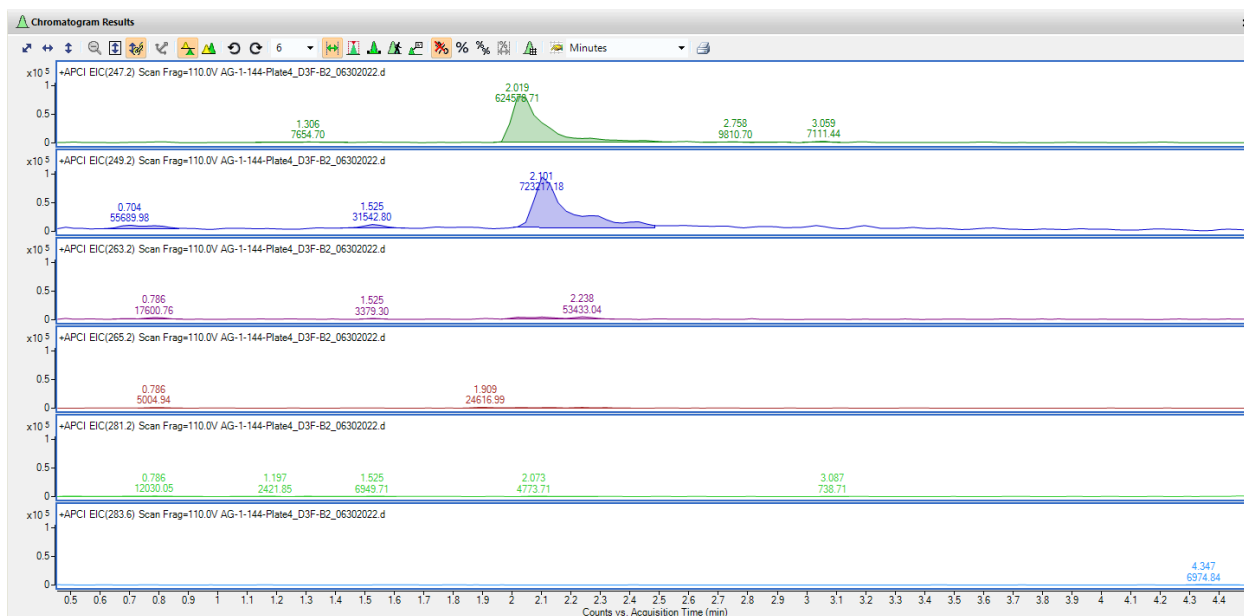
	Neutral	Positive	Negative
desaturation	246.1732	247.1811	245.1654
substrate	248.1889	249.1967	247.1811
oxidation/desaturation	262.1722	263.1801	261.1644
hydroxylation	264.1879	265.1957	263.1801
dihydroxylation	280.1869	281.1947	279.1791
chlorination	282.6341	283.6419	281.6262



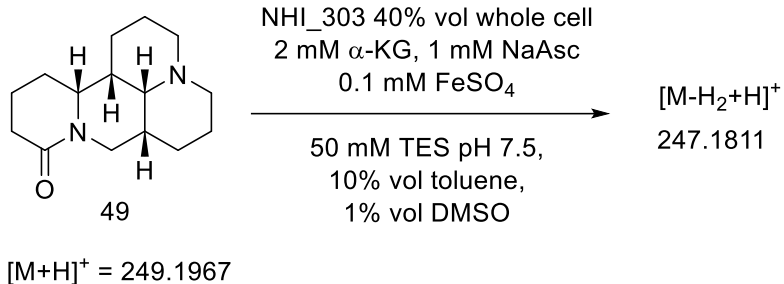
Discovered Reaction 113. Substrate_049 + NHI_302 = desaturation



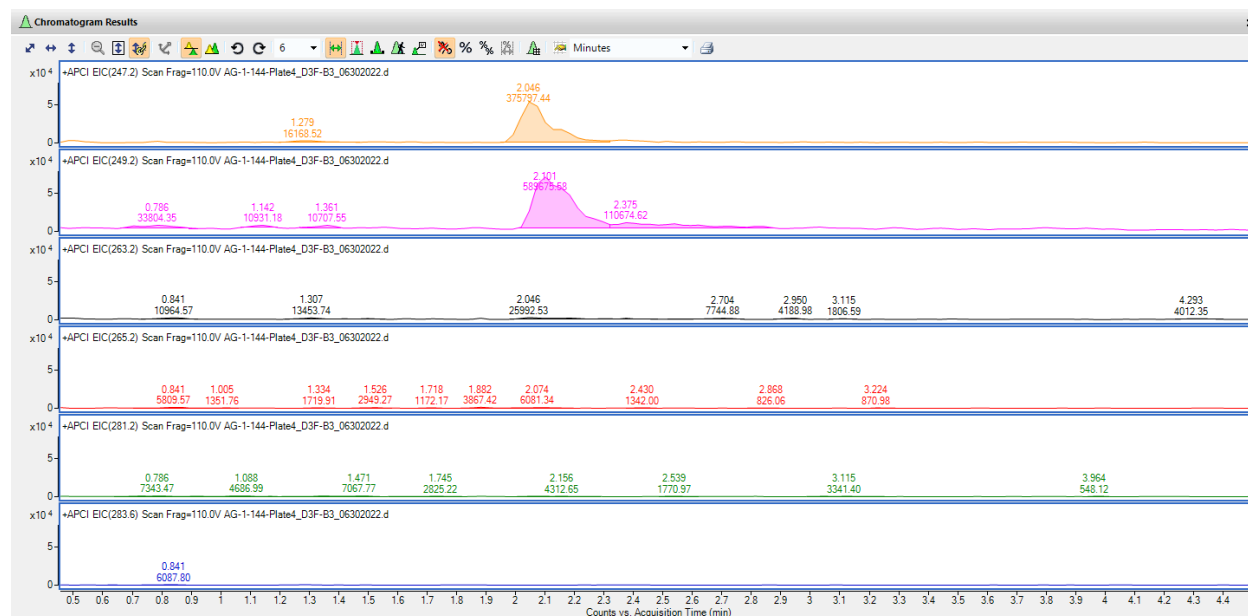
	Neutral	Positive	Negative
desaturation	246.1732	247.1811	245.1654
substrate	248.1889	249.1967	247.1811
oxidation/desaturation	262.1722	263.1801	261.1644
hydroxylation	264.1879	265.1957	263.1801
dihydroxylation	280.1869	281.1947	279.1791
chlorination	282.6341	283.6419	281.6262



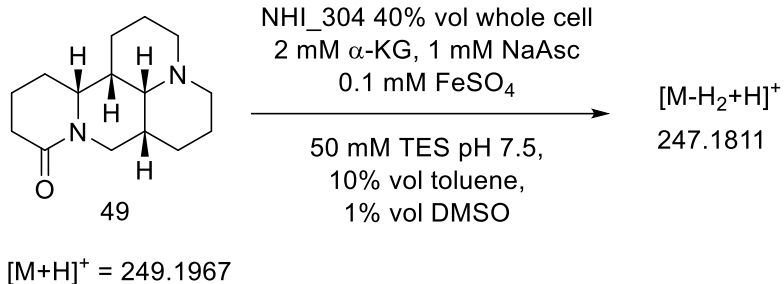
Discovered Reaction 114. Substrate_049 + NHI_303 = desaturation



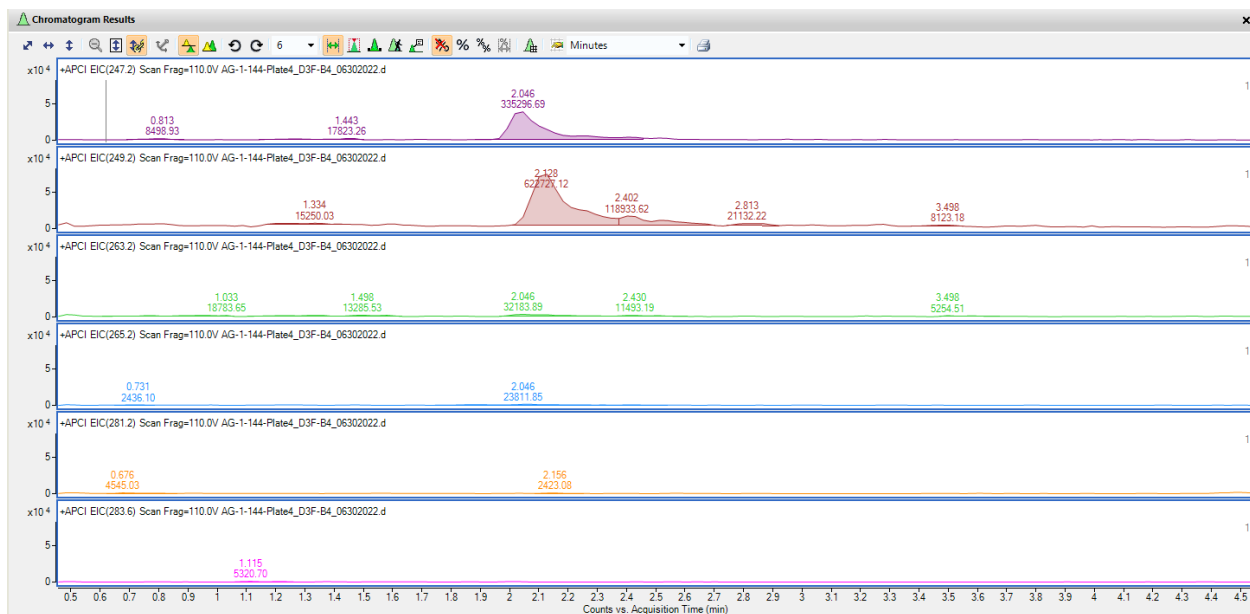
	Neutral	Positive	Negative
desaturation	246.1732	247.1811	245.1654
substrate	248.1889	249.1967	247.1811
oxidation/desaturation	262.1722	263.1801	261.1644
hydroxylation	264.1879	265.1957	263.1801
dihydroxylation	280.1869	281.1947	279.1791
chlorination	282.6341	283.6419	281.6262



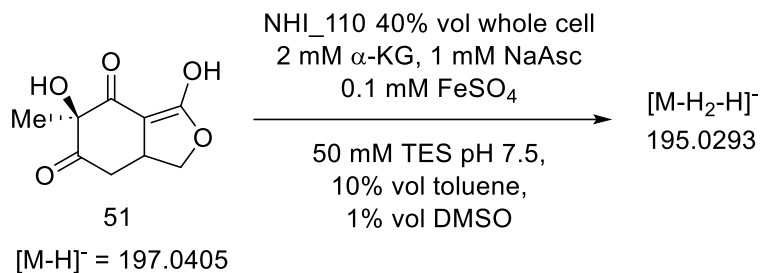
Discovered Reaction 115. Substrate_049 + NHI_304 = desaturation



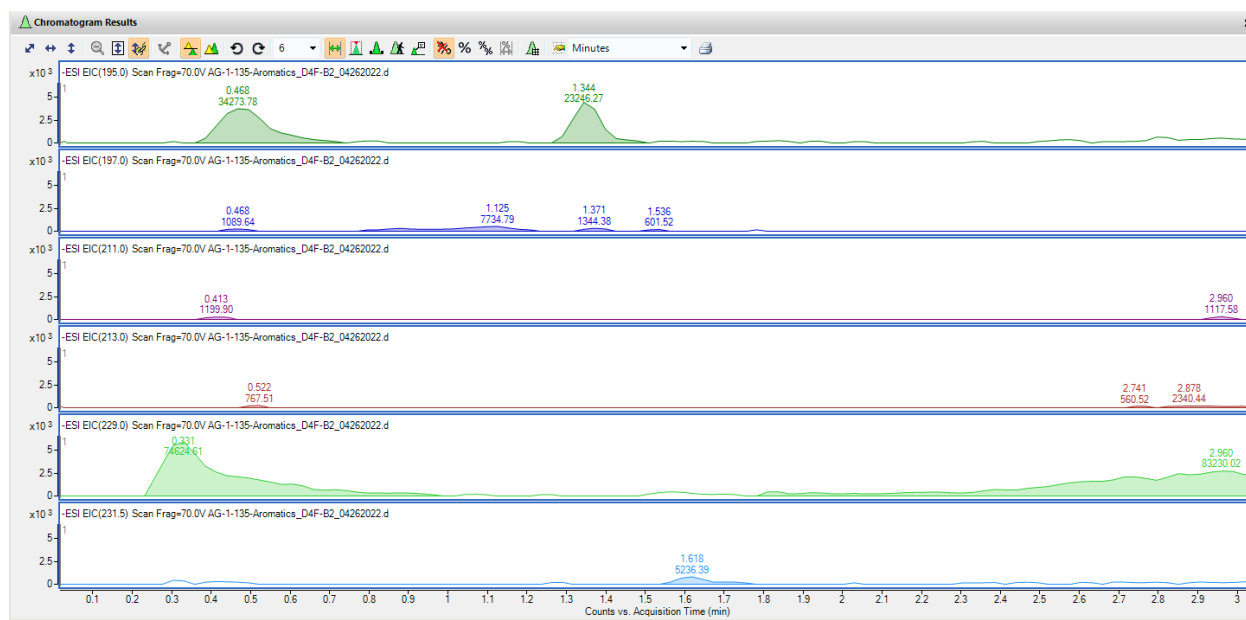
	Neutral	Positive	Negative
desaturation	246.1732	247.1811	245.1654
substrate	248.1889	249.1967	247.1811
oxidation/desaturation	262.1722	263.1801	261.1644
hydroxylation	264.1879	265.1957	263.1801
dihydroxylation	280.1869	281.1947	279.1791
chlorination	282.6341	283.6419	281.6262



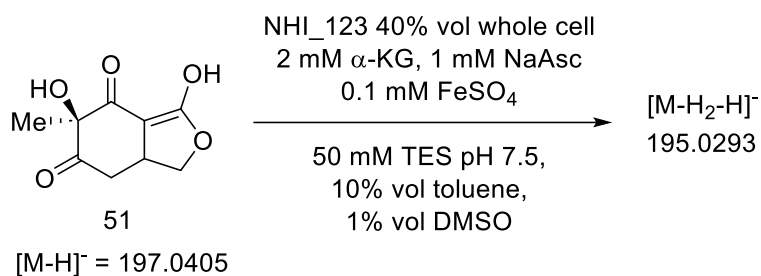
Discovered Reaction 116. Substrate_051 + NHI_110 = desaturation



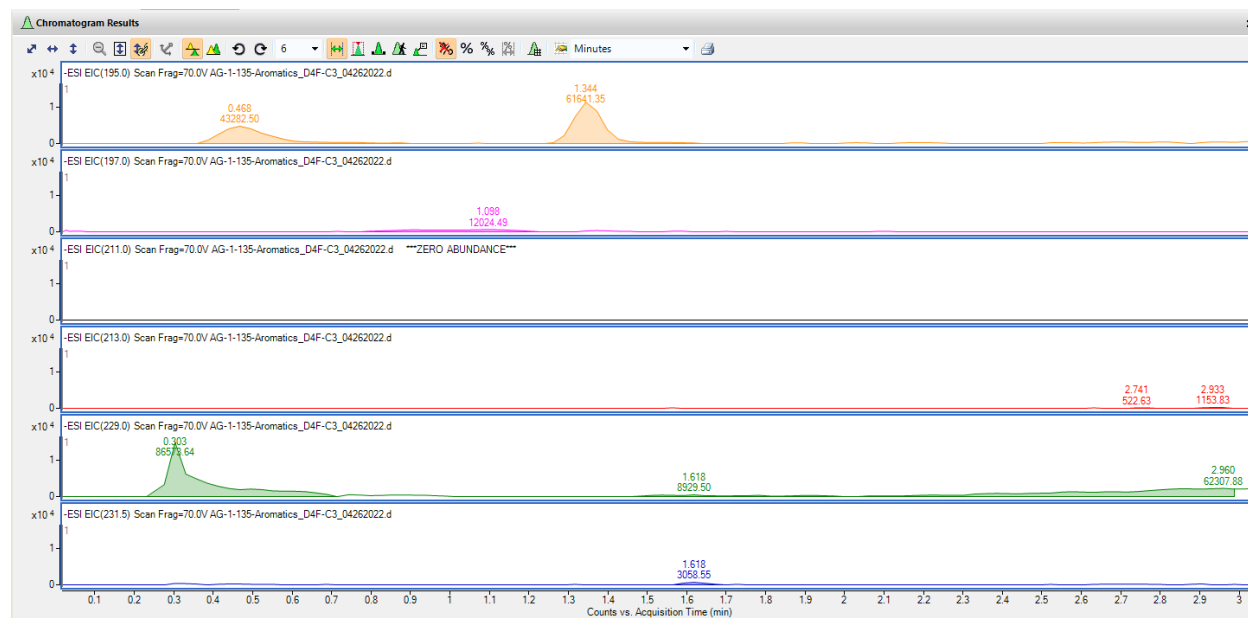
	Neutral	Positive	Negative
desaturation	196.0371	197.0450	195.0293
substrate	198.0528	199.0606	197.0450
oxidation/desaturation	212.0361	213.0440	211.0283
hydroxylation	214.0518	215.0596	213.0440
dihydroxylation	230.0508	231.0586	229.0430
chlorination	232.4980	233.5058	231.4901



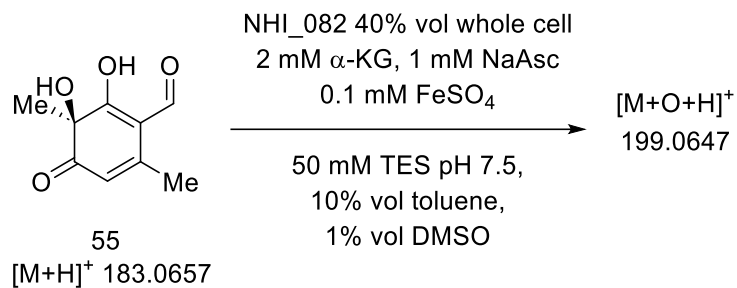
Discovered Reaction 117. Substrate_051 + NHI_123 = desaturation



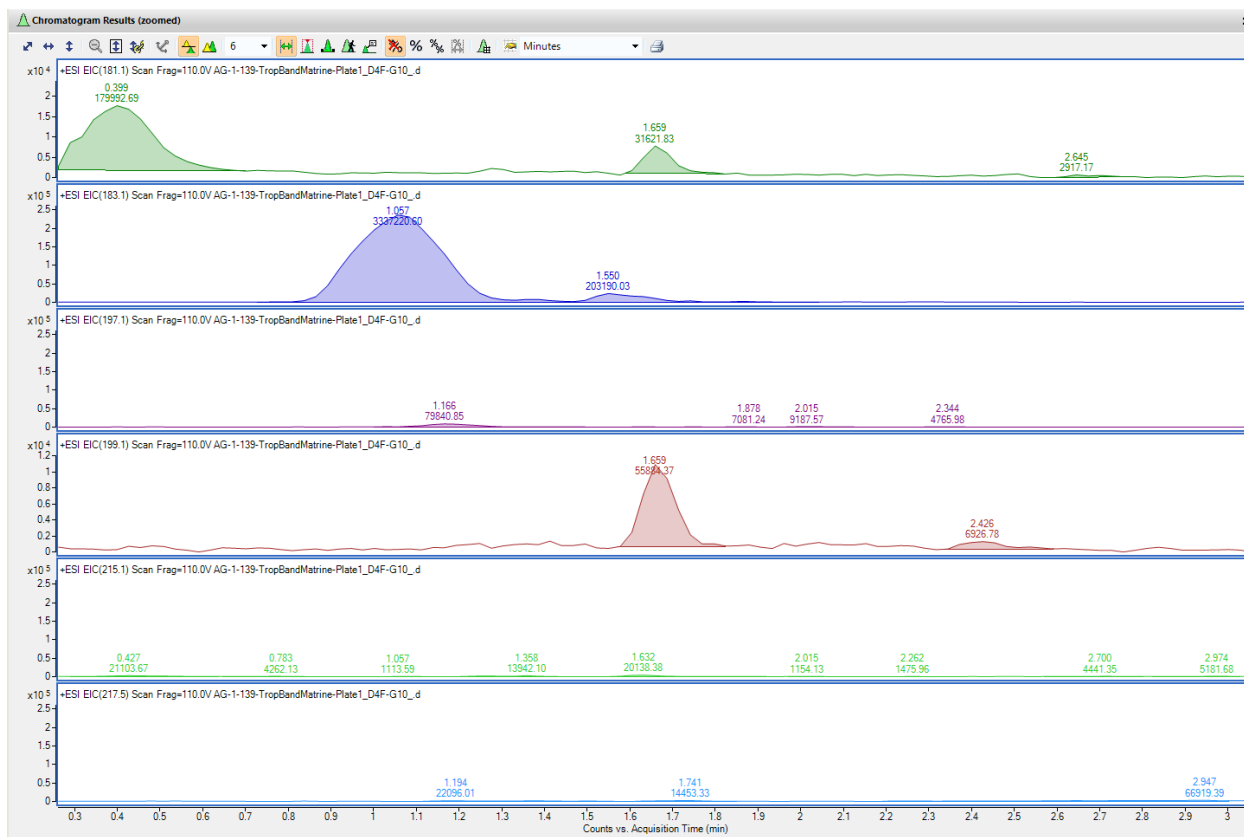
	Neutral	Positive	Negative
desaturation	196.0371	197.0450	195.0293
substrate	198.0528	199.0606	197.0450
oxidation/desaturation	212.0361	213.0440	211.0283
hydroxylation	214.0518	215.0596	213.0440
dihydroxylation	230.0508	231.0586	229.0430
chlorination	232.4980	233.5058	231.4901



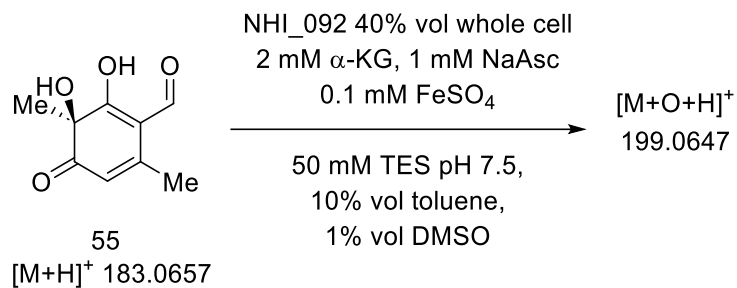
Discovered Reaction 118. Substrate_055 + NHI_082 = hydroxylation



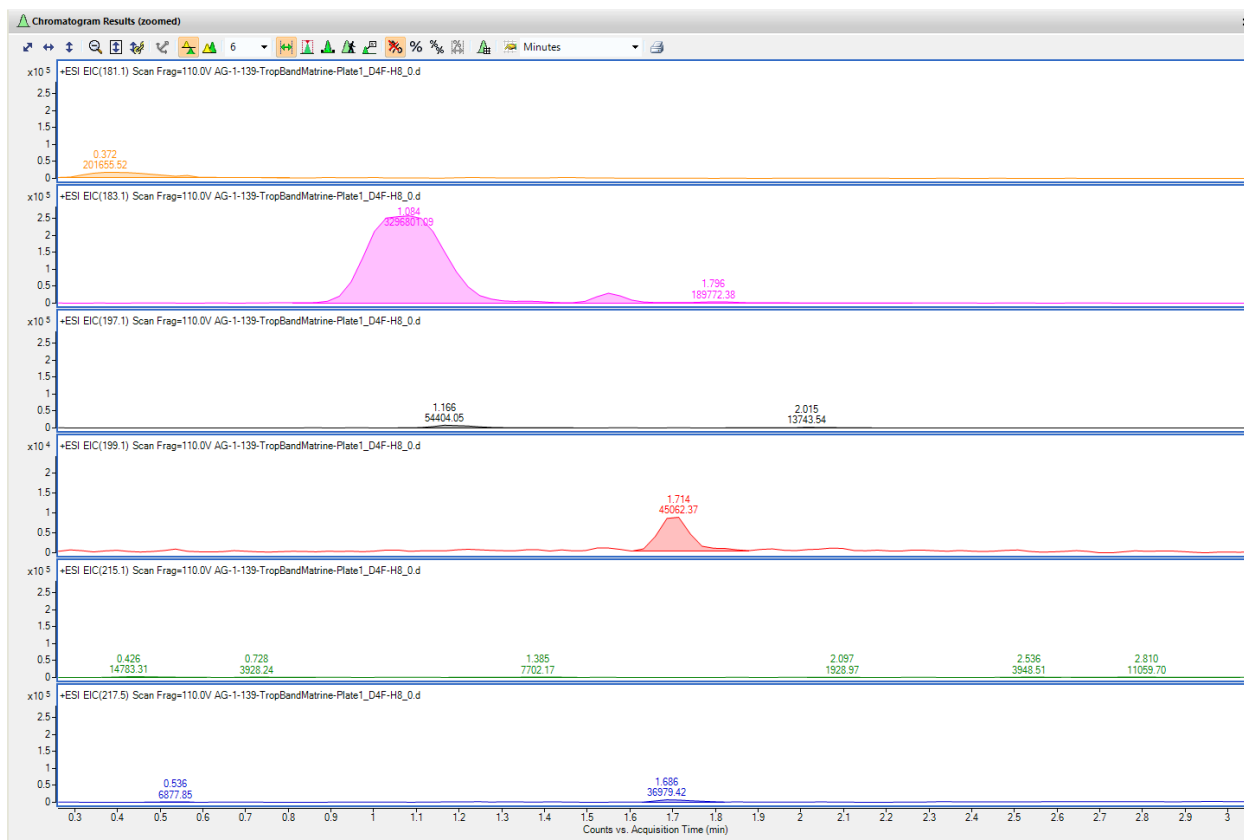
	Neutral	Positive	Negative
desaturation	180.0422	181.0501	179.0344
substrate	182.0579	183.0657	181.0501
oxidation/desaturation	196.0412	197.0491	195.0334
hydroxylation	198.0569	199.0647	197.0491
dihydroxylation	214.0559	215.0637	213.0481
chlorination	216.5031	217.5109	215.4952



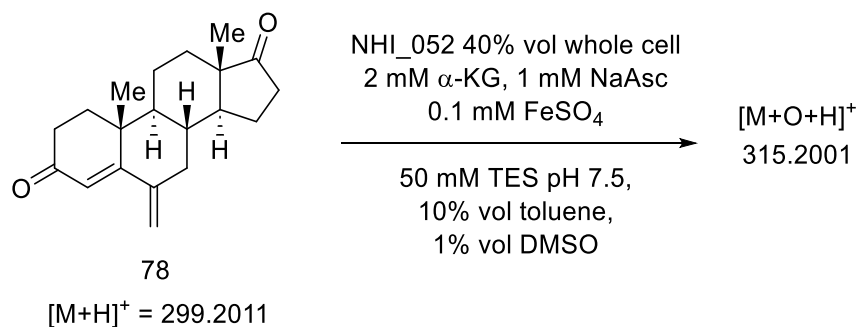
Discovered Reaction 119. Substrate_055 + NHI_092 = hydroxylation



	Neutral	Positive	Negative
desaturation	180.0422	181.0501	179.0344
substrate	182.0579	183.0657	181.0501
oxidation/desaturation	196.0412	197.0491	195.0334
hydroxylation	198.0569	199.0647	197.0491
dihydroxylation	214.0559	215.0637	213.0481
chlorination	216.5031	217.5109	215.4952



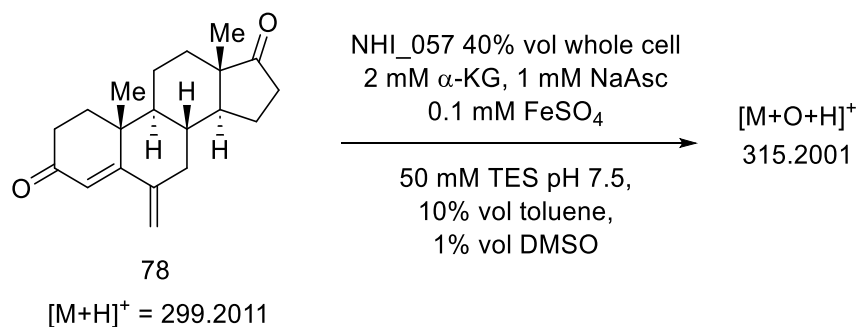
Discovered Reaction 120. Substrate_078 + NHI_052 = hydroxylation



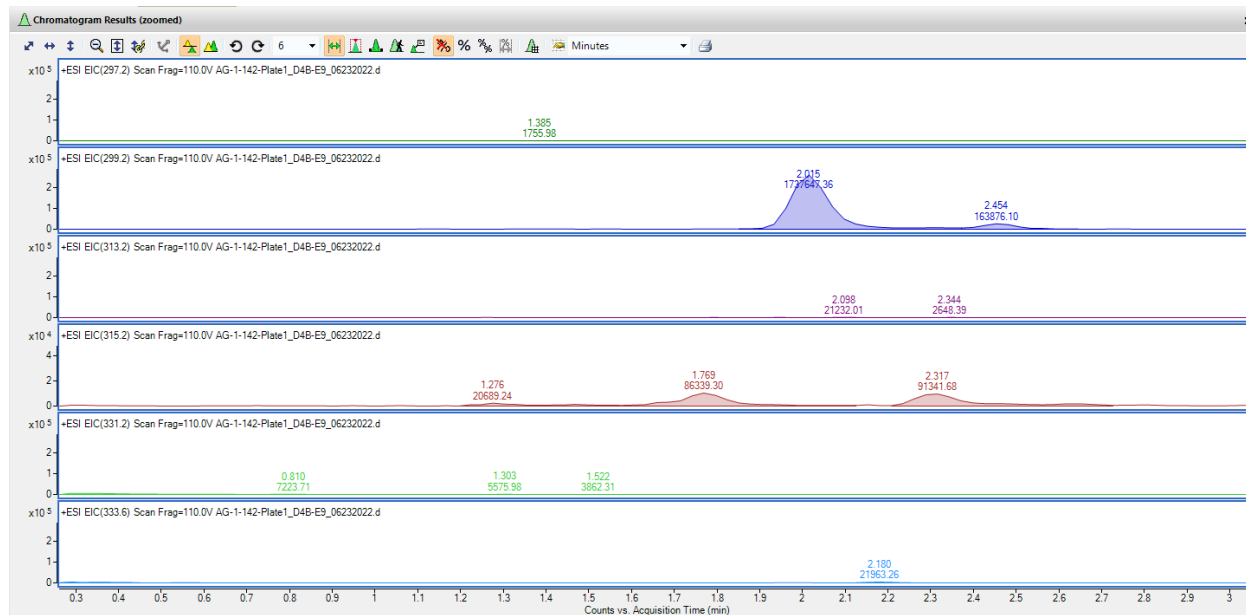
	Neutral	Positive	Negative
desaturation	296.1776	297.1855	295.1698
substrate	298.1933	299.2011	297.1855
oxidation/desaturation	312.1766	313.1845	311.1688
hydroxylation	314.1923	315.2001	313.1845
dihydroxylation	330.1913	331.1991	329.1835
chlorination	332.6385	333.6463	331.6306



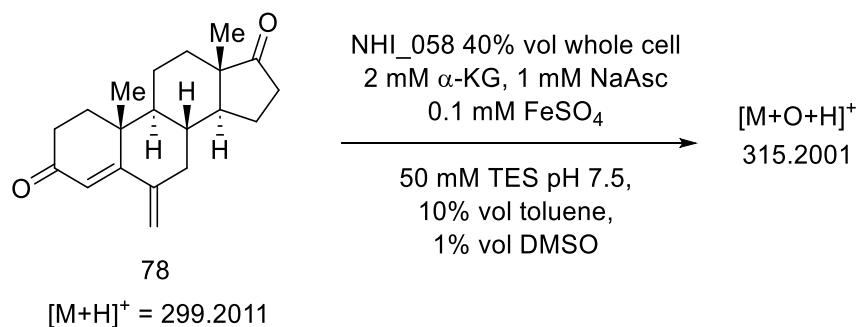
Discovered Reaction 121. Substrate_078 + NHI_057 = hydroxylation



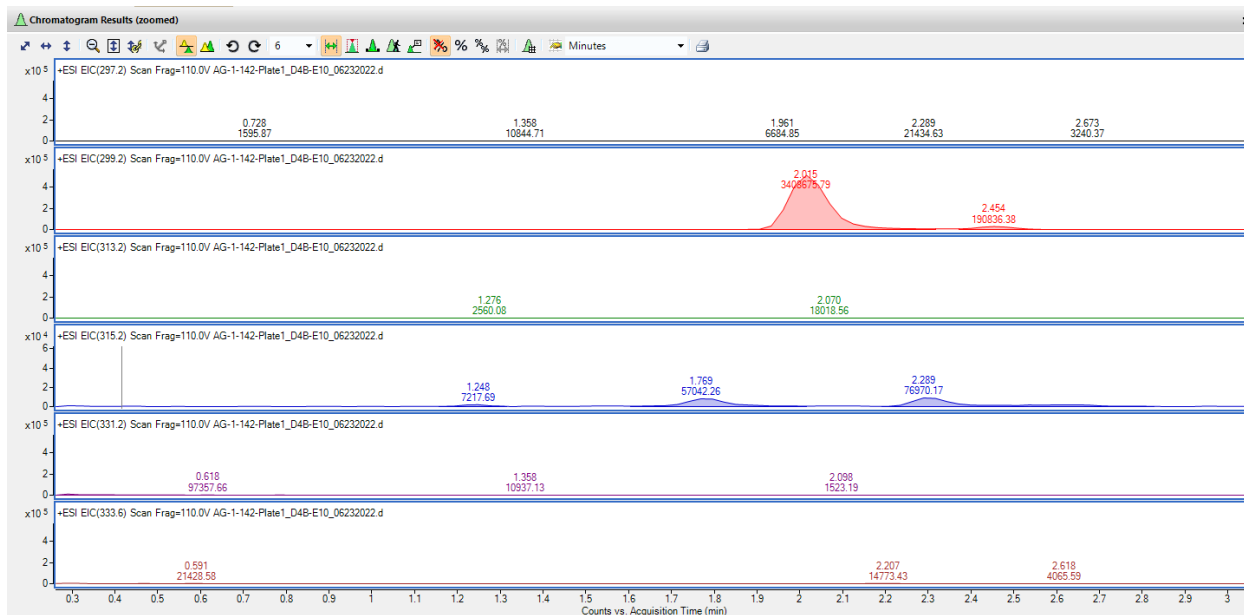
	Neutral	Positive	Negative
desaturation	296.1776	297.1855	295.1698
substrate	298.1933	299.2011	297.1855
oxidation/desaturation	312.1766	313.1845	311.1688
hydroxylation	314.1923	315.2001	313.1845
dihydroxylation	330.1913	331.1991	329.1835
chlorination	332.6385	333.6463	331.6306



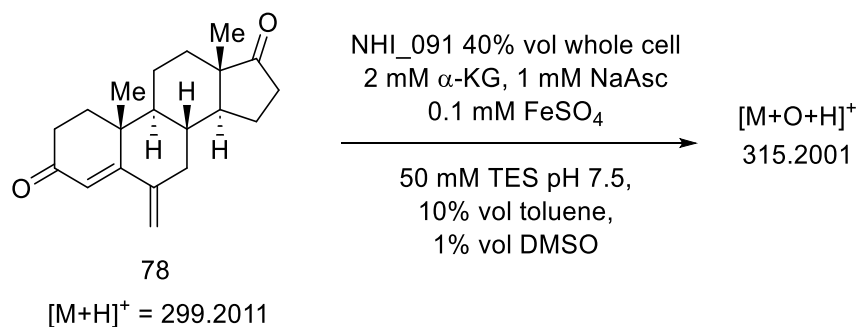
Discovered Reaction 122. Substrate_078 + NHI_058 = hydroxylation



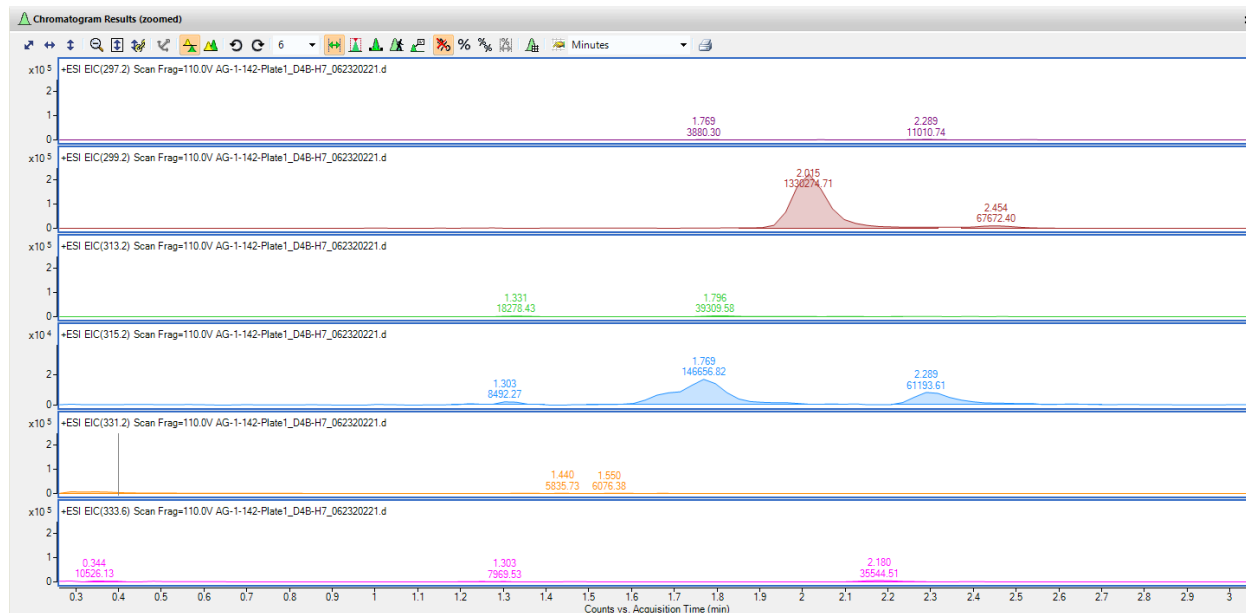
	Neutral	Positive	Negative
desaturation	296.1776	297.1855	295.1698
substrate	298.1933	299.2011	297.1855
oxidation/desaturation	312.1766	313.1845	311.1688
hydroxylation	314.1923	315.2001	313.1845
dihydroxylation	330.1913	331.1991	329.1835
chlorination	332.6385	333.6463	331.6306



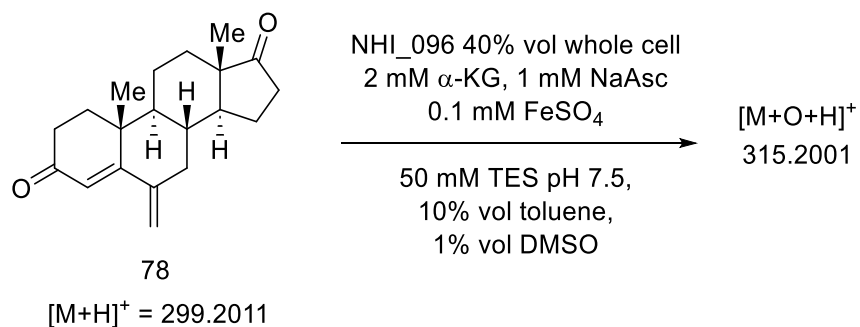
Discovered Reaction 123. Substrate_078 + NHI_091 = hydroxylation



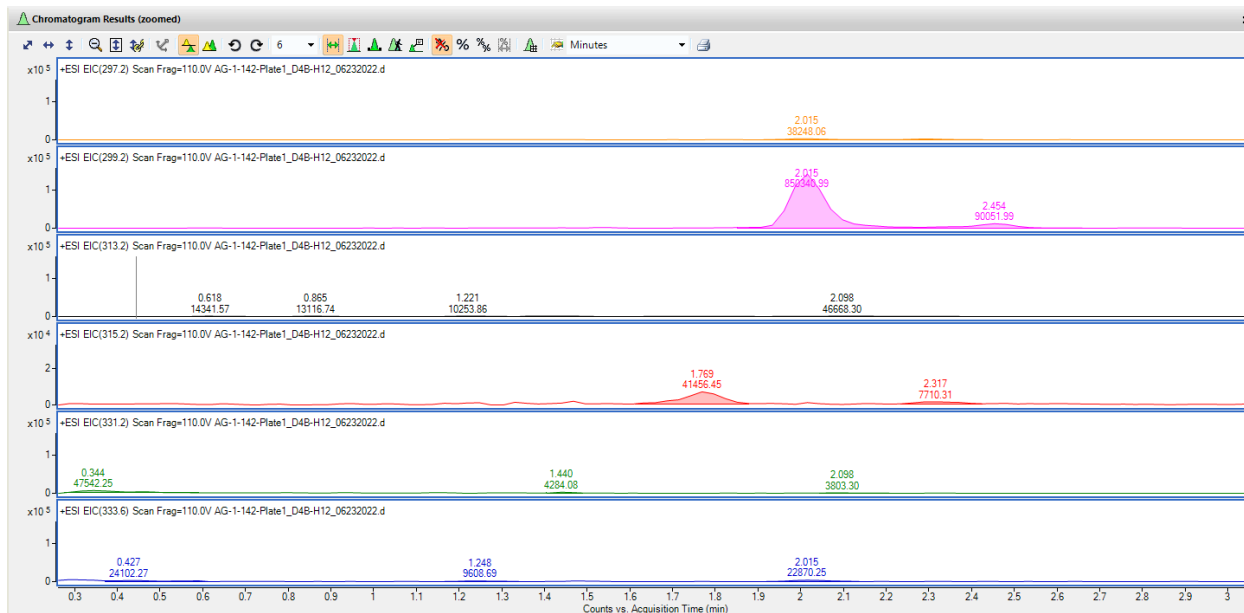
	Neutral	Positive	Negative
desaturation	296.1776	297.1855	295.1698
substrate	298.1933	299.2011	297.1855
oxidation/desaturation	312.1766	313.1845	311.1688
hydroxylation	314.1923	315.2001	313.1845
dihydroxylation	330.1913	331.1991	329.1835
chlorination	332.6385	333.6463	331.6306



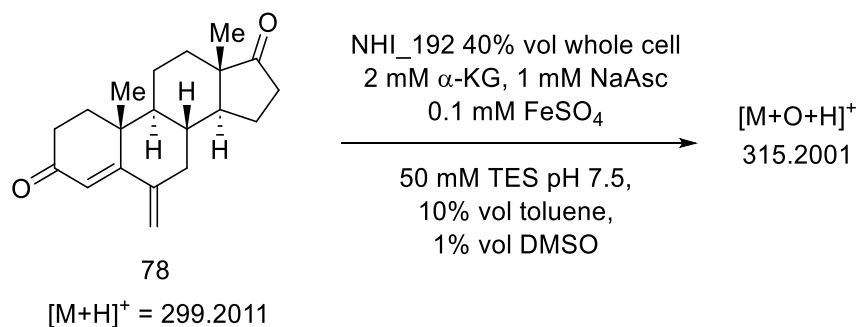
Discovered Reaction 124. Substrate_078 + NHI_096 = hydroxylation



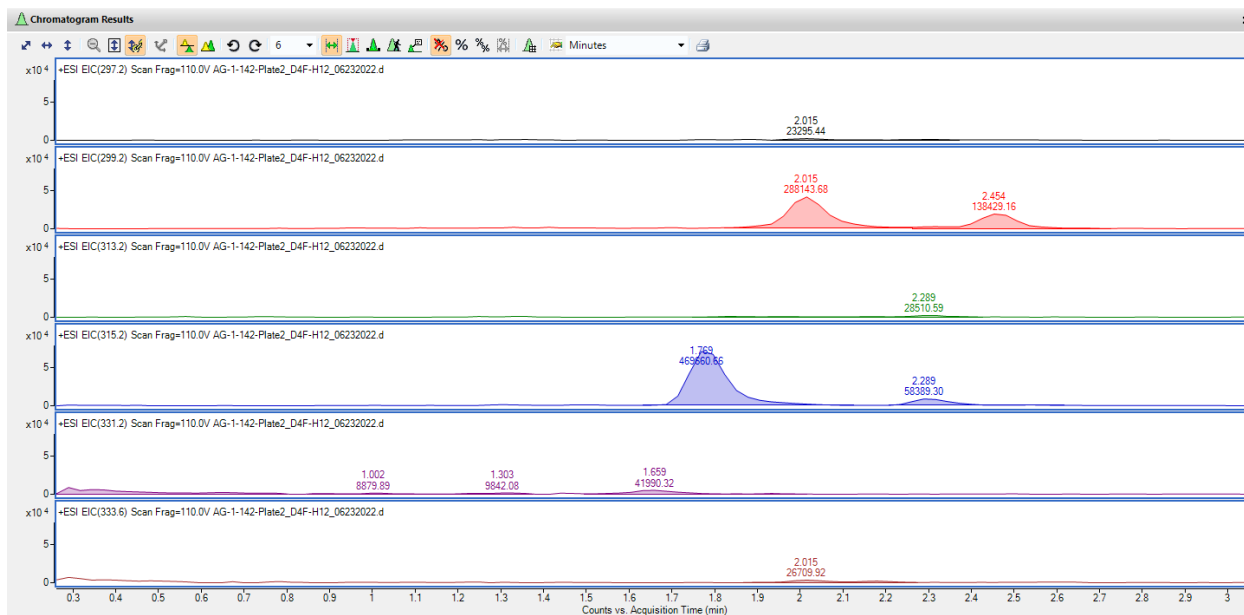
	Neutral	Positive	Negative
desaturation	296.1776	297.1855	295.1698
substrate	298.1933	299.2011	297.1855
oxidation/desaturation	312.1766	313.1845	311.1688
hydroxylation	314.1923	315.2001	313.1845
dihydroxylation	330.1913	331.1991	329.1835
chlorination	332.6385	333.6463	331.6306



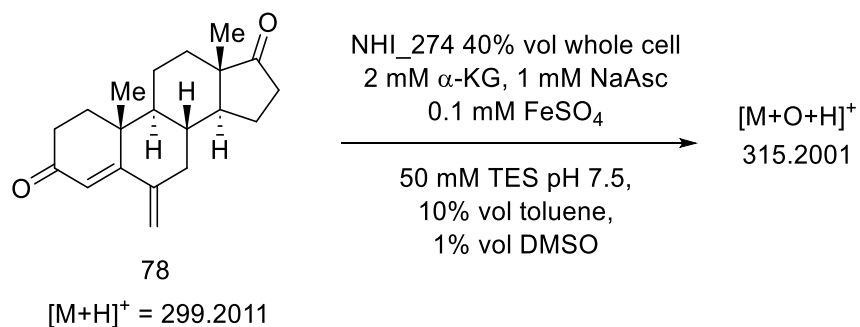
Discovered Reaction 125. Substrate_078 + NHI_192 = hydroxylation



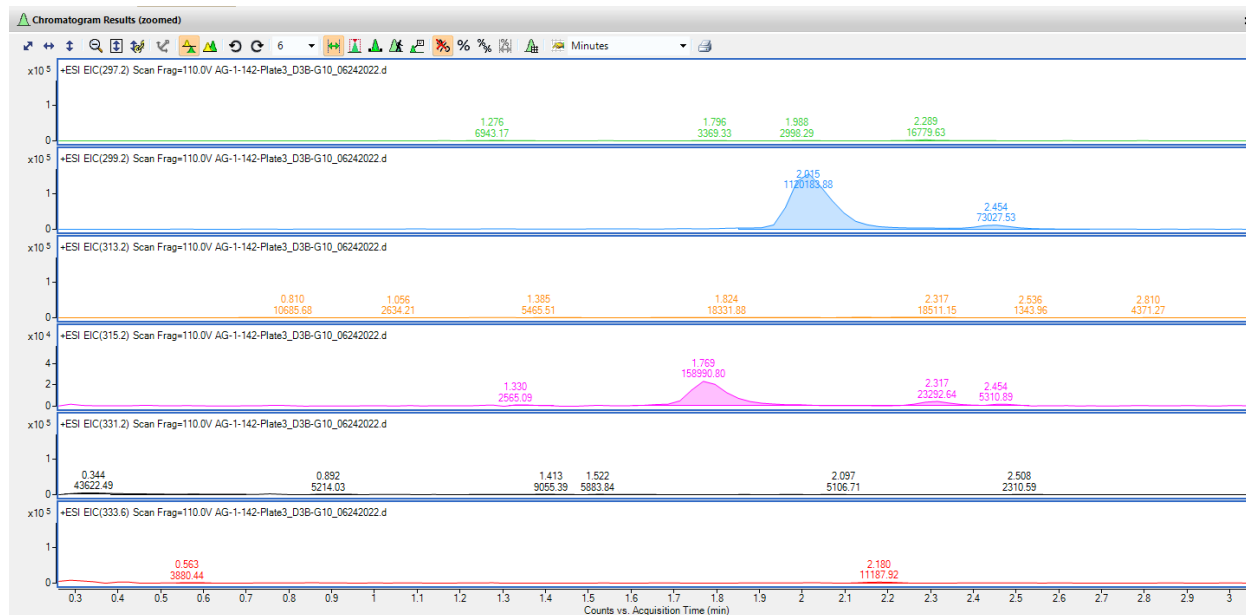
	Neutral	Positive	Negative
desaturation	296.1776	297.1855	295.1698
substrate	298.1933	299.2011	297.1855
oxidation/desaturation	312.1766	313.1845	311.1688
hydroxylation	314.1923	315.2001	313.1845
dihydroxylation	330.1913	331.1991	329.1835
chlorination	332.6385	333.6463	331.6306



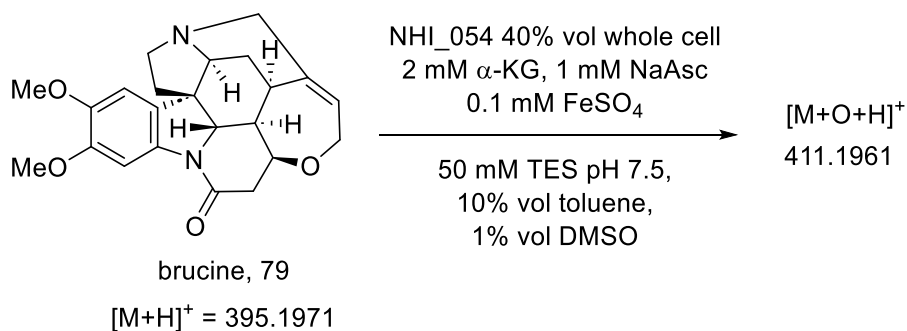
Discovered Reaction 126. Substrate_078 + NHI_274 = hydroxylation



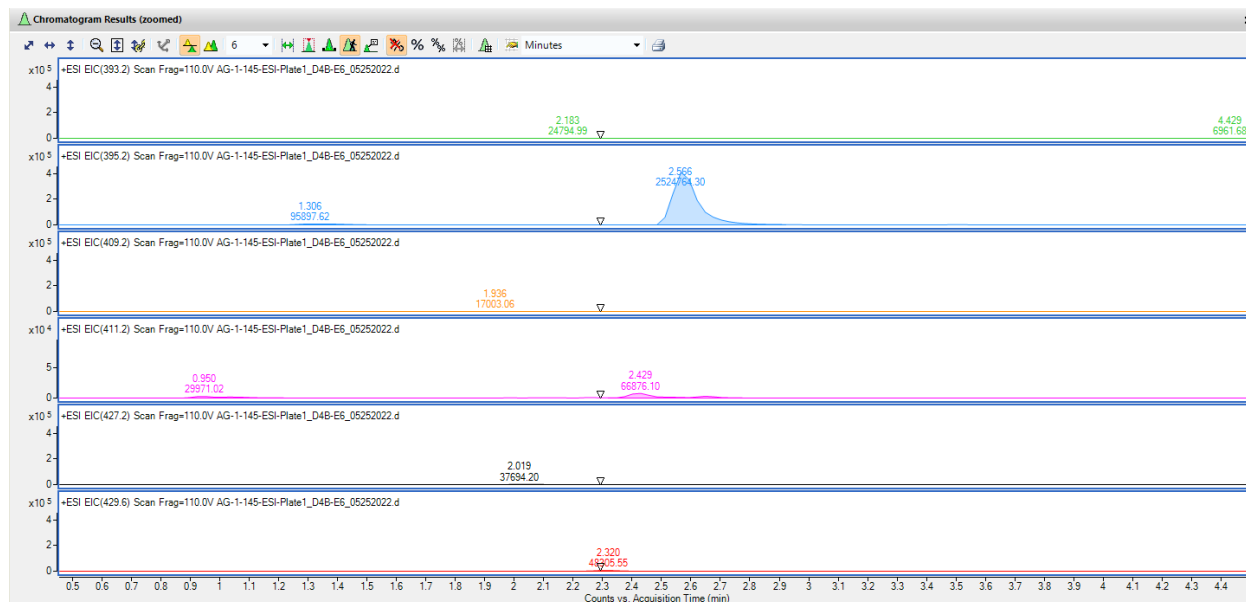
	Neutral	Positive	Negative
desaturation	296.1776	297.1855	295.1698
substrate	298.1933	299.2011	297.1855
oxidation/desaturation	312.1766	313.1845	311.1688
hydroxylation	314.1923	315.2001	313.1845
dihydroxylation	330.1913	331.1991	329.1835
chlorination	332.6385	333.6463	331.6306



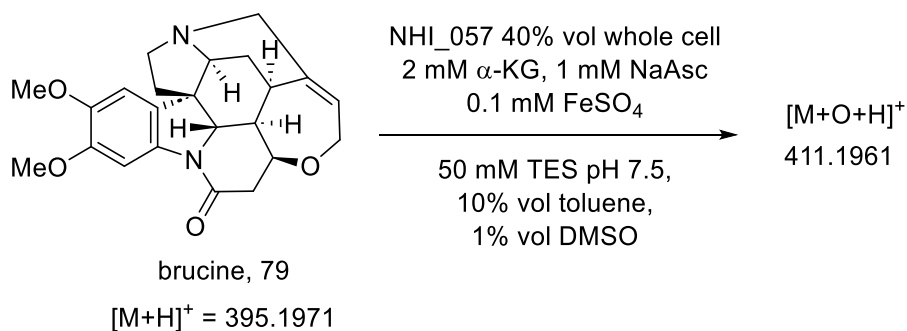
Discovered Reaction 127. Substrate_079 + NHI_054 = hydroxylation



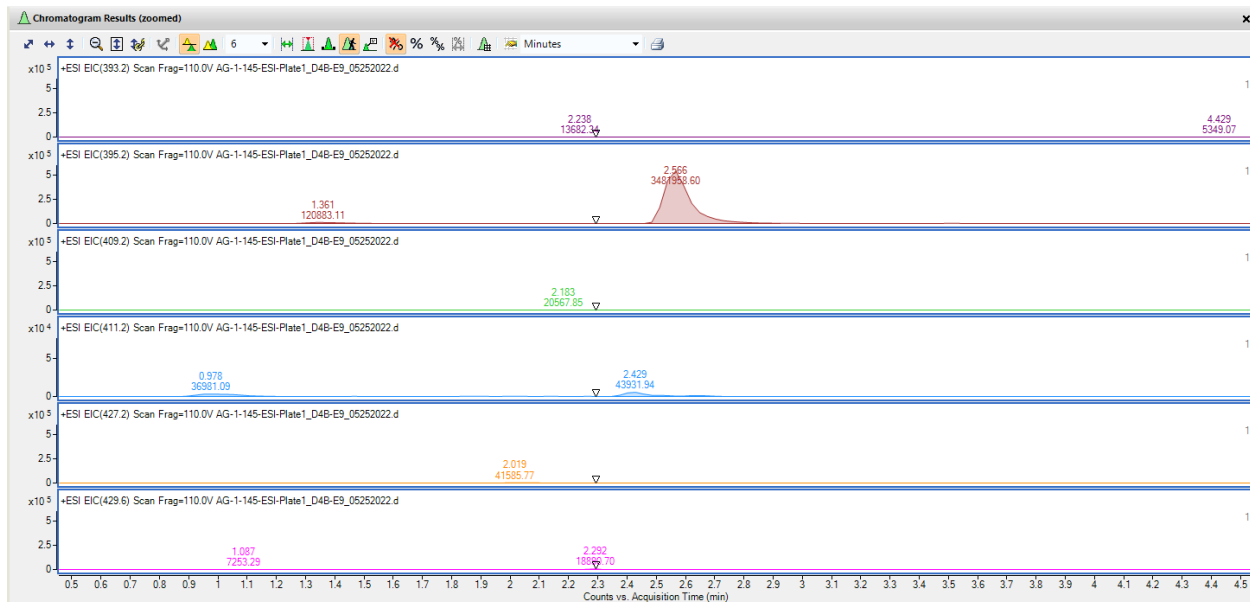
	Neutral	Positive	Negative
desaturation	392.1736	393.1815	391.1658
substrate	394.1893	395.1971	393.1815
oxidation/desaturation	408.1726	409.1805	407.1648
hydroxylation	410.1883	411.1961	409.1805
dihydroxylation	426.1873	427.1951	425.1795
chlorination	428.6345	429.6423	427.6266



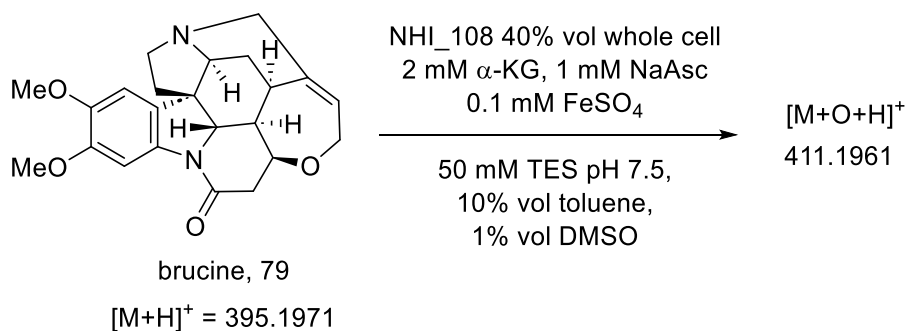
Discovered Reaction 128. Substrate_079 + NHI_057 = hydroxylation



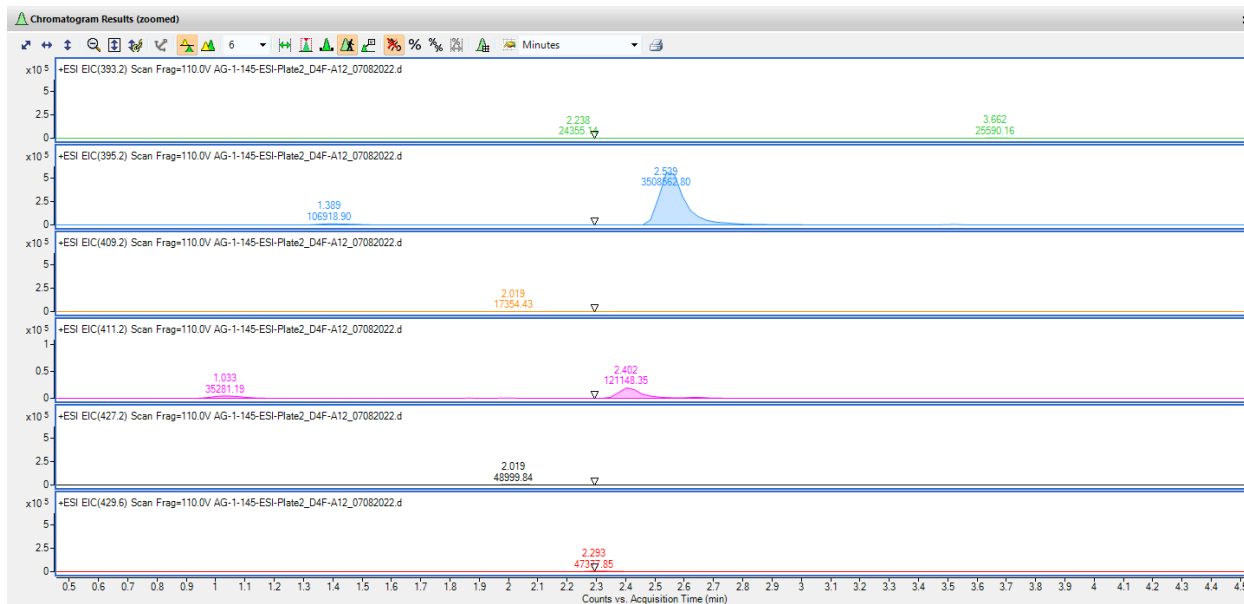
	Neutral	Positive	Negative
desaturation	392.1736	393.1815	391.1658
substrate	394.1893	395.1971	393.1815
oxidation/desaturation	408.1726	409.1805	407.1648
hydroxylation	410.1883	411.1961	409.1805
dihydroxylation	426.1873	427.1951	425.1795
chlorination	428.6345	429.6423	427.6266



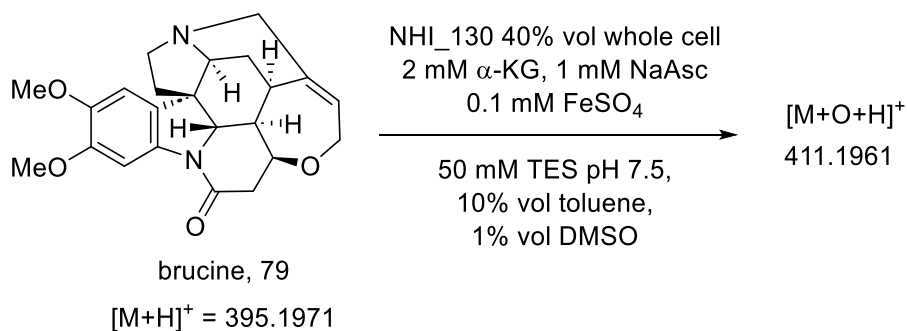
Discovered Reaction 129. Substrate_079 + NHI_108 = hydroxylation



	Neutral	Positive	Negative
desaturation	392.1736	393.1815	391.1658
substrate	394.1893	395.1971	393.1815
oxidation/desaturation	408.1726	409.1805	407.1648
hydroxylation	410.1883	411.1961	409.1805
dihydroxylation	426.1873	427.1951	425.1795
chlorination	428.6345	429.6423	427.6266



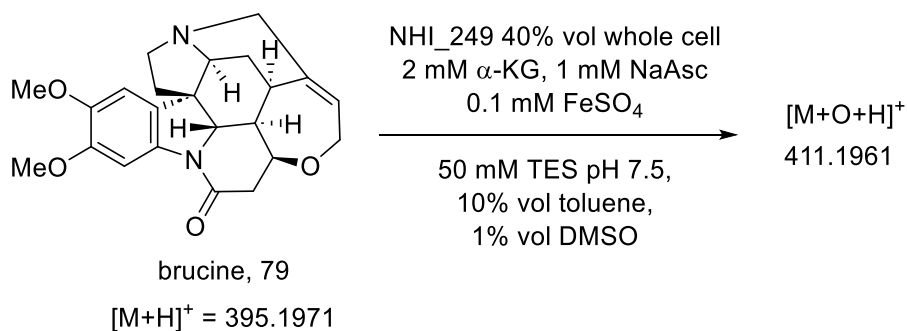
Discovered Reaction 130. Substrate_079 + NHI_130 = hydroxylation



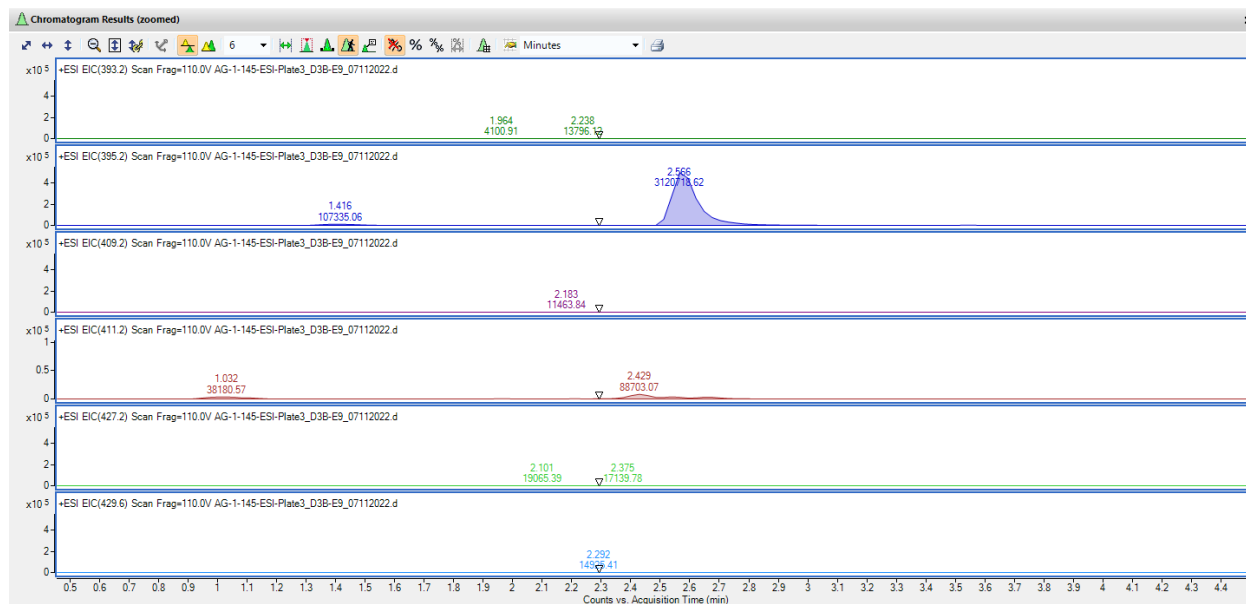
	Neutral	Positive	Negative
desaturation	392.1736	393.1815	391.1658
substrate	394.1893	395.1971	393.1815
oxidation/desaturation	408.1726	409.1805	407.1648
hydroxylation	410.1883	411.1961	409.1805
dihydroxylation	426.1873	427.1951	425.1795
chlorination	428.6345	429.6423	427.6266



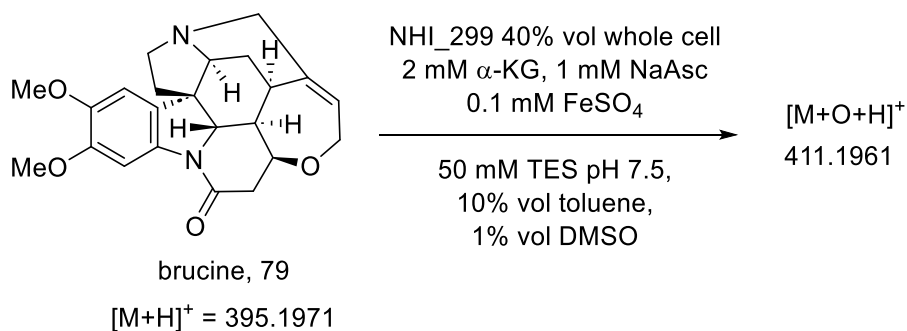
Discovered Reaction 131. Substrate_079 + NHI_249 = hydroxylation



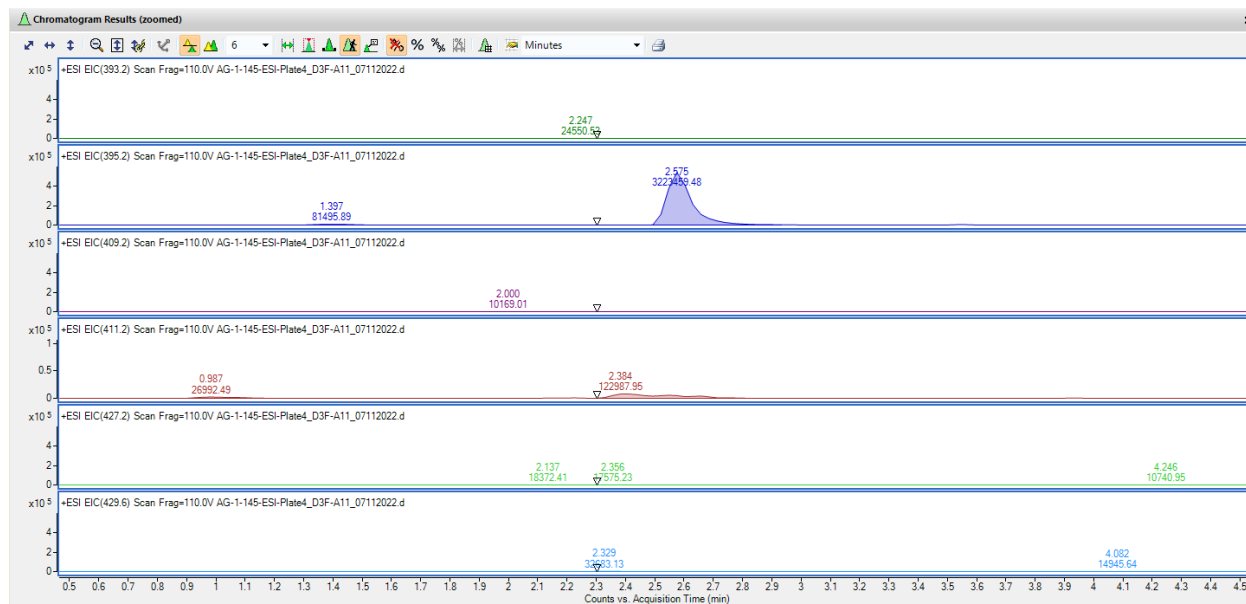
	Neutral	Positive	Negative
desaturation	392.1736	393.1815	391.1658
substrate	394.1893	395.1971	393.1815
oxidation/desaturation	408.1726	409.1805	407.1648
hydroxylation	410.1883	411.1961	409.1805
dihydroxylation	426.1873	427.1951	425.1795
chlorination	428.6345	429.6423	427.6266



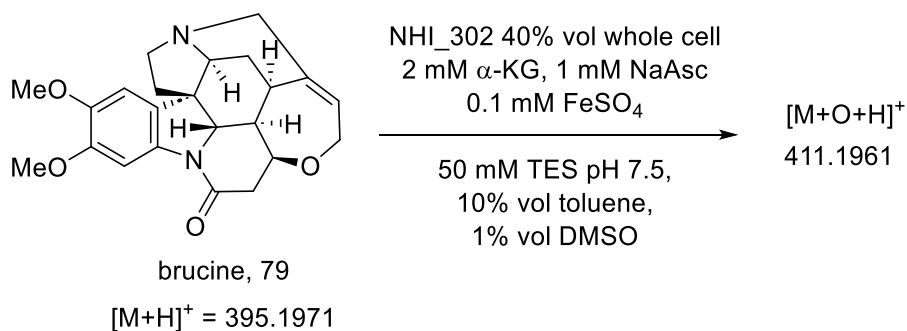
Discovered Reaction 132. Substrate_079 + NHI_299 = hydroxylation



	Neutral	Positive	Negative
desaturation	392.1736	393.1815	391.1658
substrate	394.1893	395.1971	393.1815
oxidation/desaturation	408.1726	409.1805	407.1648
hydroxylation	410.1883	411.1961	409.1805
dihydroxylation	426.1873	427.1951	425.1795
chlorination	428.6345	429.6423	427.6266



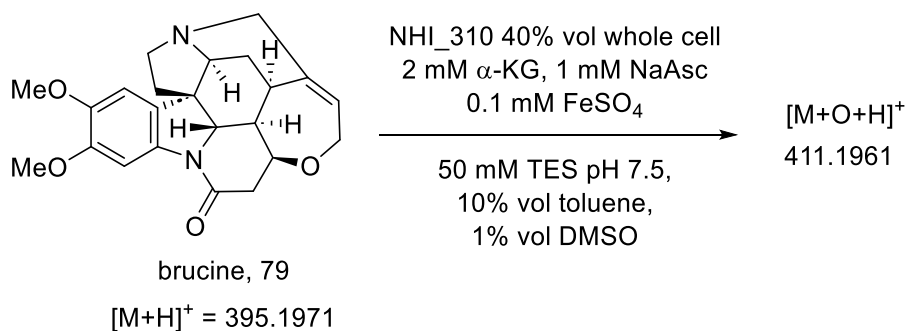
Discovered Reaction 133. Substrate_079 + NHI_302 = hydroxylation



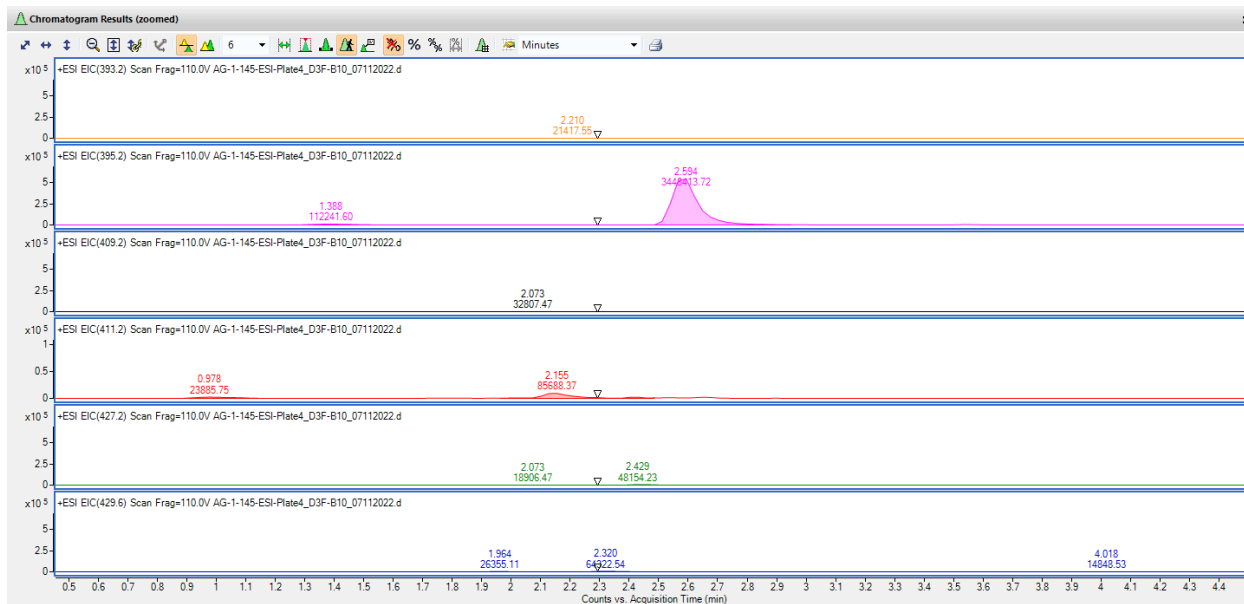
	Neutral	Positive	Negative
desaturation	392.1736	393.1815	391.1658
substrate	394.1893	395.1971	393.1815
oxidation/desaturation	408.1726	409.1805	407.1648
hydroxylation	410.1883	411.1961	409.1805
dihydroxylation	426.1873	427.1951	425.1795
chlorination	428.6345	429.6423	427.6266



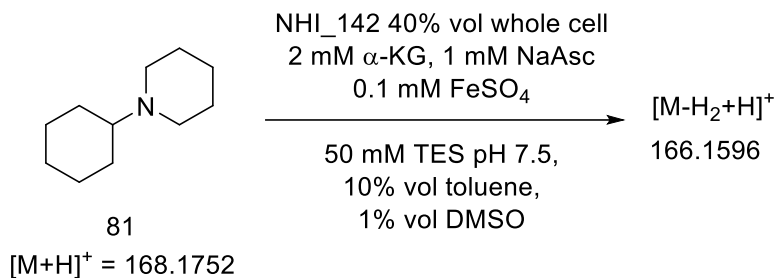
Discovered Reaction 134. Substrate_079 + NHI_310 = hydroxylation



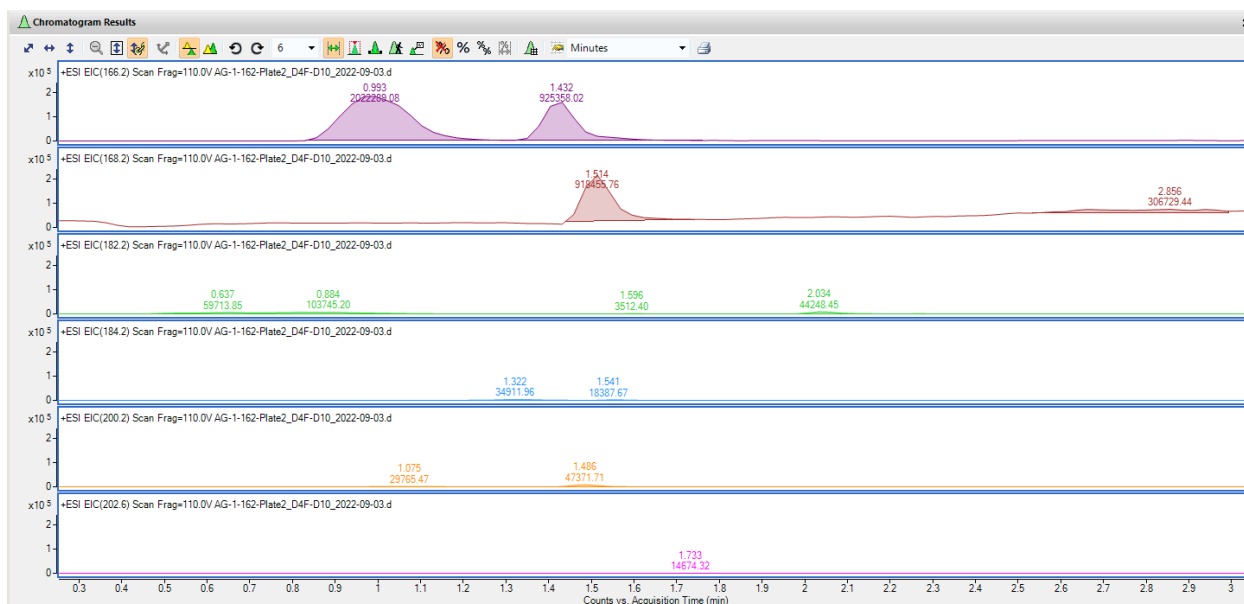
	Neutral	Positive	Negative
desaturation	392.1736	393.1815	391.1658
substrate	394.1893	395.1971	393.1815
oxidation/desaturation	408.1726	409.1805	407.1648
hydroxylation	410.1883	411.1961	409.1805
dihydroxylation	426.1873	427.1951	425.1795
chlorination	428.6345	429.6423	427.6266



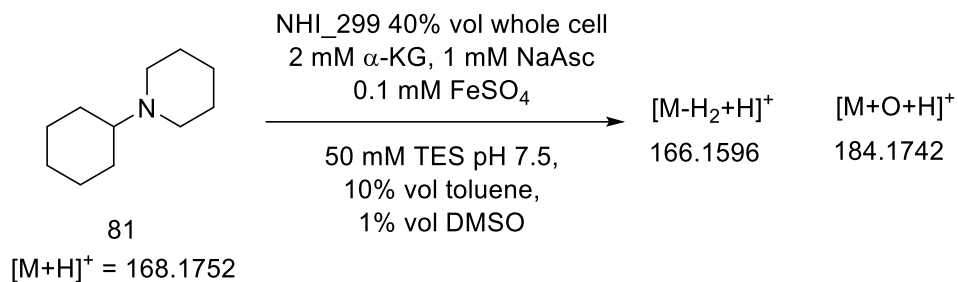
Discovered Reaction 135. Substrate_081 + NHI_142 = desaturation



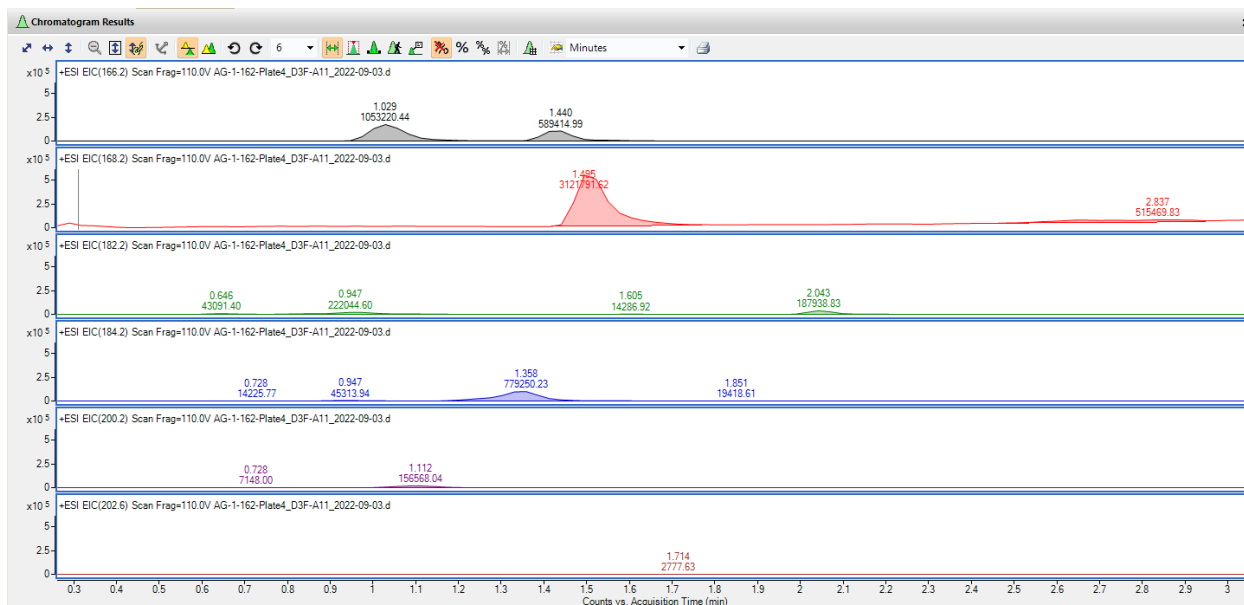
	Neutral	Positive	Negative
desaturation	165.1517	166.1596	164.1439
substrate	167.1674	168.1752	166.1596
oxidation/desaturation	181.1507	182.1586	180.1429
hydroxylation	183.1664	184.1742	182.1586
dihydroxylation	199.1654	200.1732	198.1576
chlorination	201.6126	202.6204	200.6047



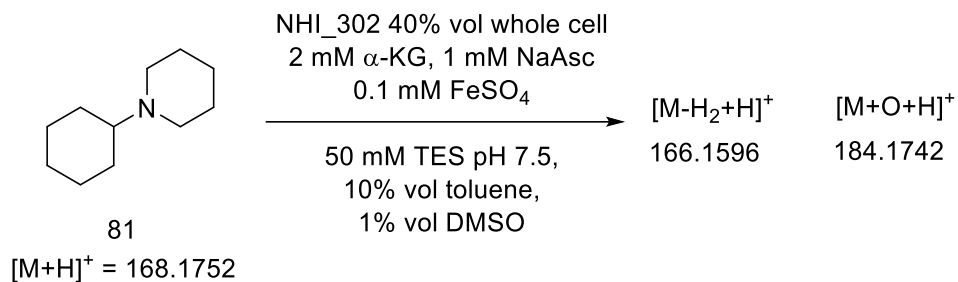
Discovered Reaction 136. Substrate_081 + NHI_299 = hydroxylation and desaturation



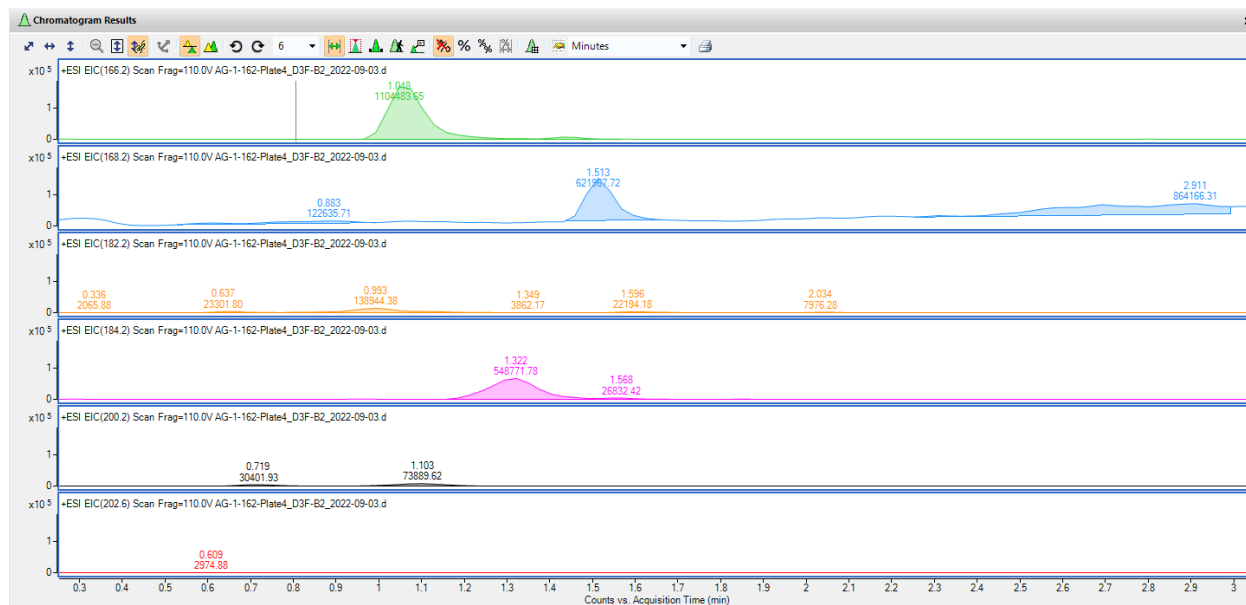
	Neutral	Positive	Negative
desaturation	165.1517	166.1596	164.1439
substrate	167.1674	168.1752	166.1596
oxidation/desaturation	181.1507	182.1586	180.1429
hydroxylation	183.1664	184.1742	182.1586
dihydroxylation	199.1654	200.1732	198.1576
chlorination	201.6126	202.6204	200.6047



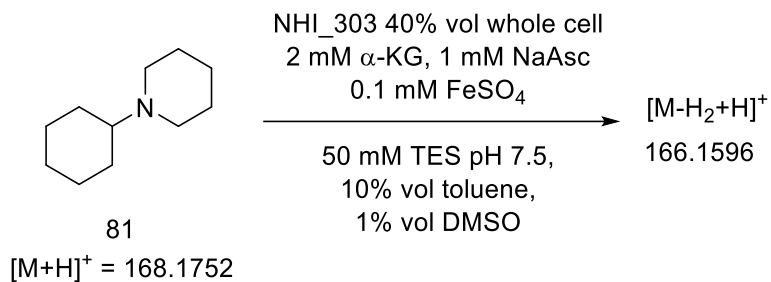
Discovered Reaction 137. Substrate_081 + NHI_302 = hydroxylation and desaturation



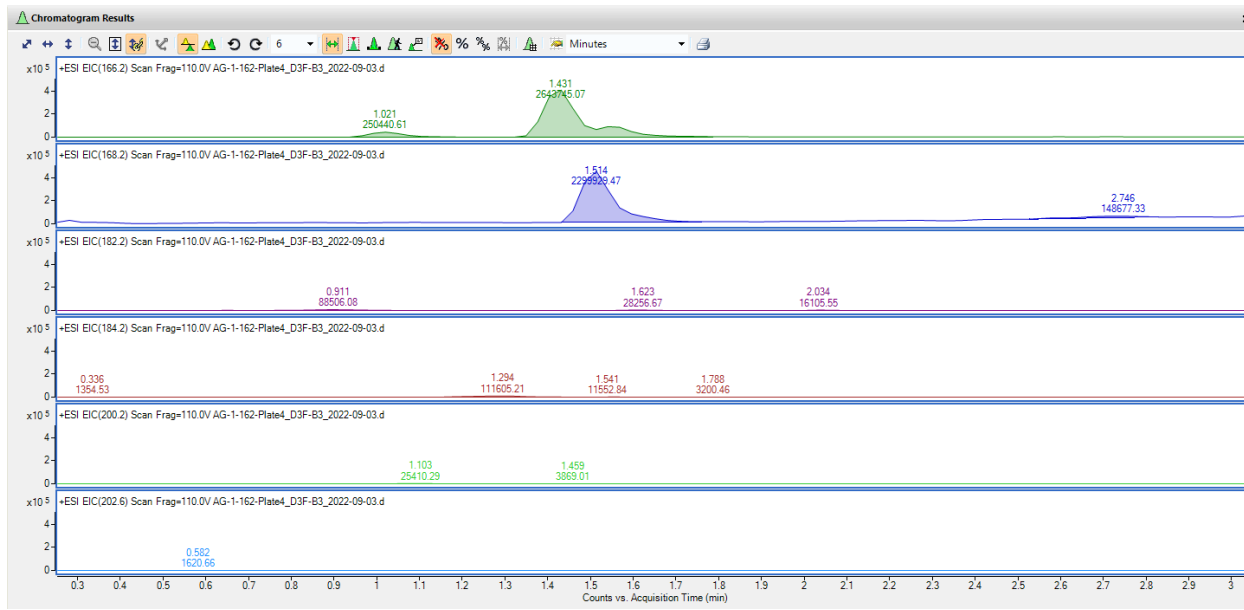
	Neutral	Positive	Negative
desaturation	165.1517	166.1596	164.1439
substrate	167.1674	168.1752	166.1596
oxidation/desaturation	181.1507	182.1586	180.1429
hydroxylation	183.1664	184.1742	182.1586
dihydroxylation	199.1654	200.1732	198.1576
chlorination	201.6126	202.6204	200.6047



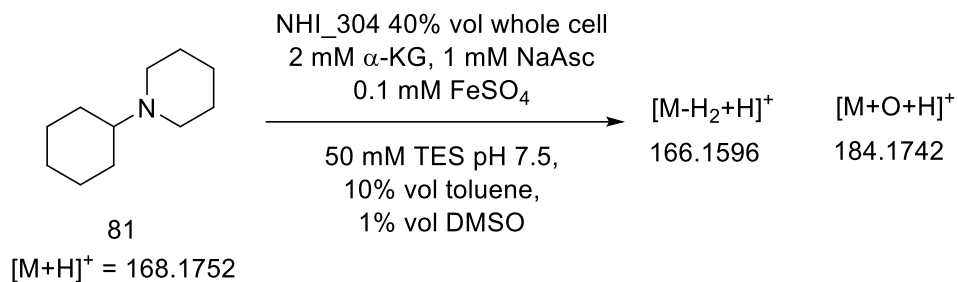
Discovered Reaction 138. Substrate_081 + NHI_303 = desaturation



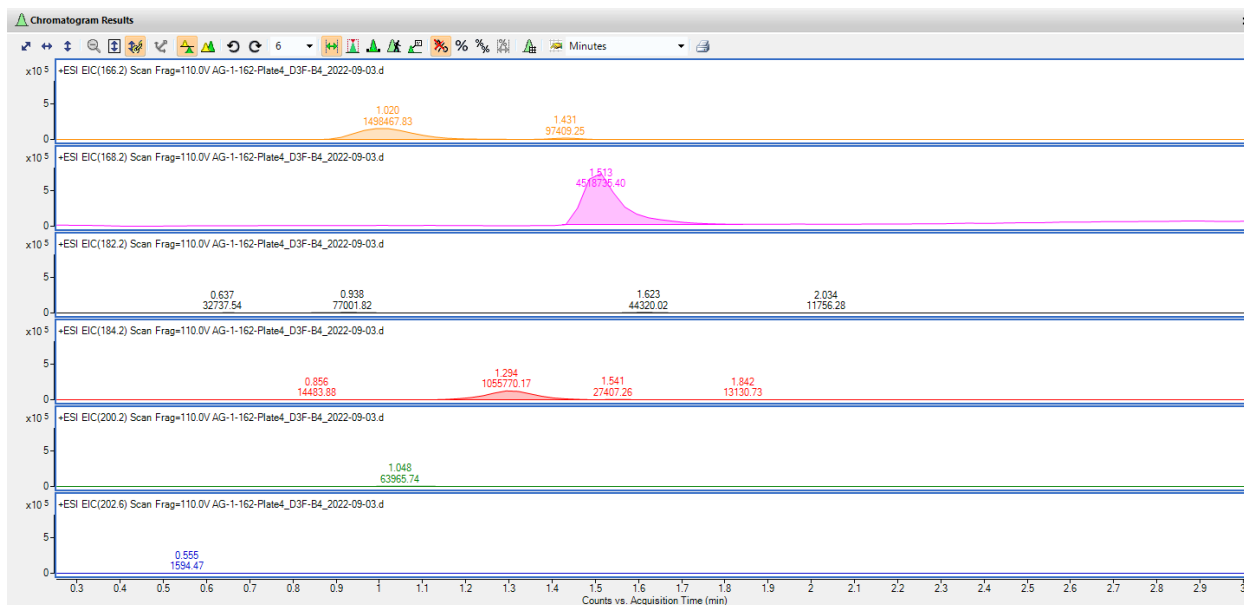
	Neutral	Positive	Negative
desaturation	165.1517	166.1596	164.1439
substrate	167.1674	168.1752	166.1596
oxidation/desaturation	181.1507	182.1586	180.1429
hydroxylation	183.1664	184.1742	182.1586
dihydroxylation	199.1654	200.1732	198.1576
chlorination	201.6126	202.6204	200.6047



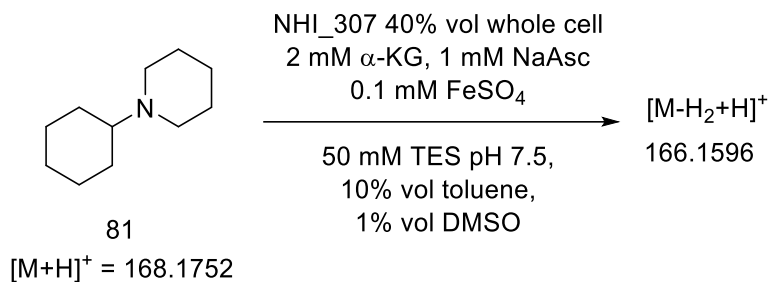
Discovered Reaction 139. Substrate_081 + NHI_304 = hydroxylation and desaturation



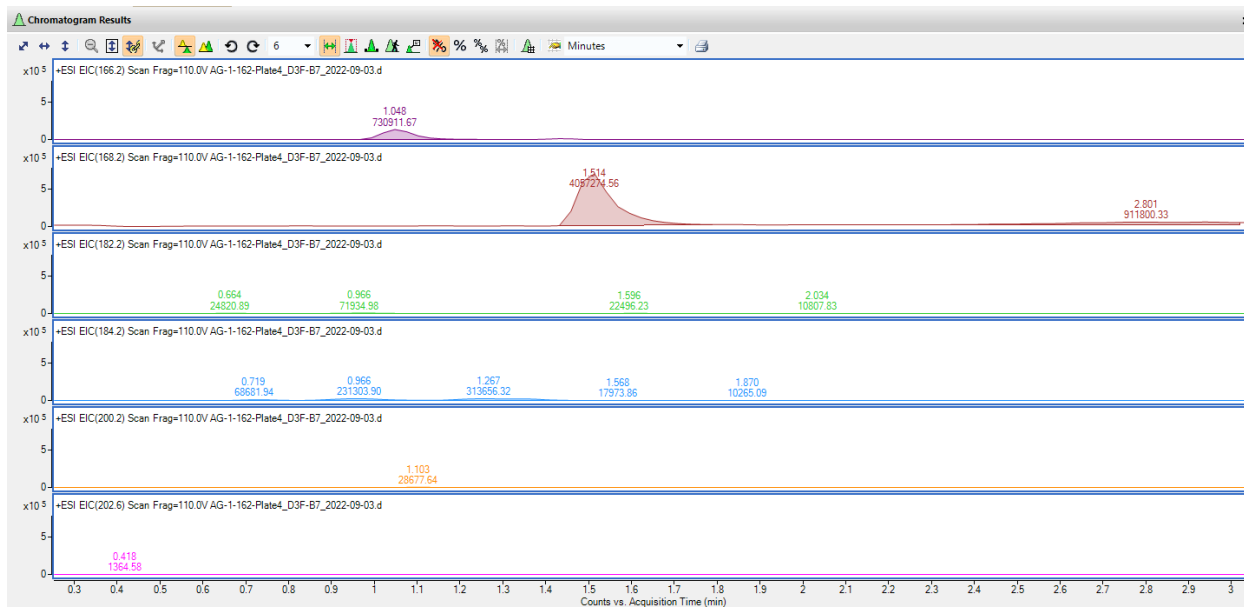
	Neutral	Positive	Negative
desaturation	165.1517	166.1596	164.1439
substrate	167.1674	168.1752	166.1596
oxidation/desaturation	181.1507	182.1586	180.1429
hydroxylation	183.1664	184.1742	182.1586
dihydroxylation	199.1654	200.1732	198.1576
chlorination	201.6126	202.6204	200.6047



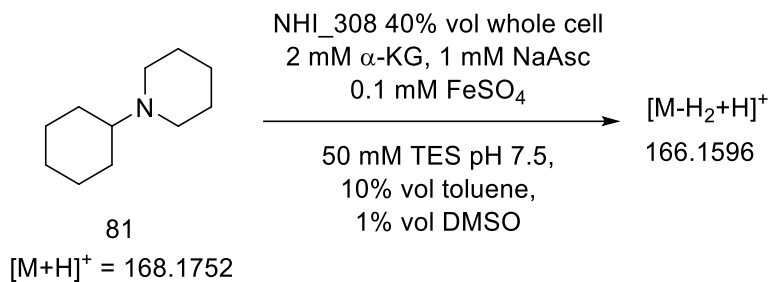
Discovered Reaction 140. Substrate_081 + NHI_307 = desaturation



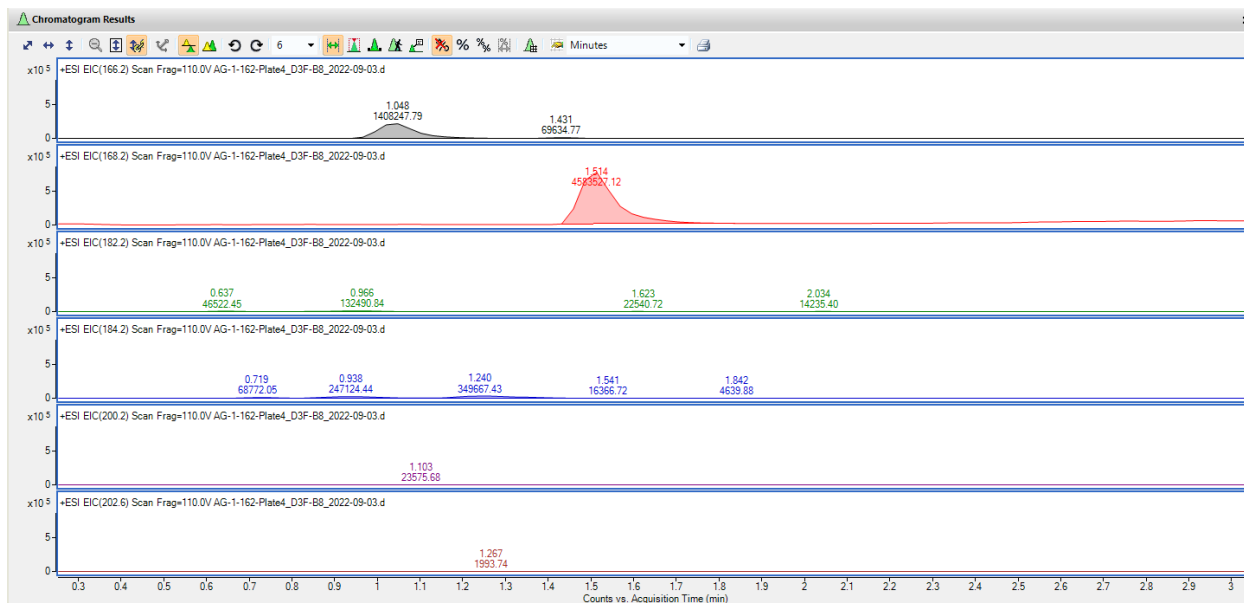
	Neutral	Positive	Negative
desaturation	165.1517	166.1596	164.1439
substrate	167.1674	168.1752	166.1596
oxidation/desaturation	181.1507	182.1586	180.1429
hydroxylation	183.1664	184.1742	182.1586
dihydroxylation	199.1654	200.1732	198.1576
chlorination	201.6126	202.6204	200.6047



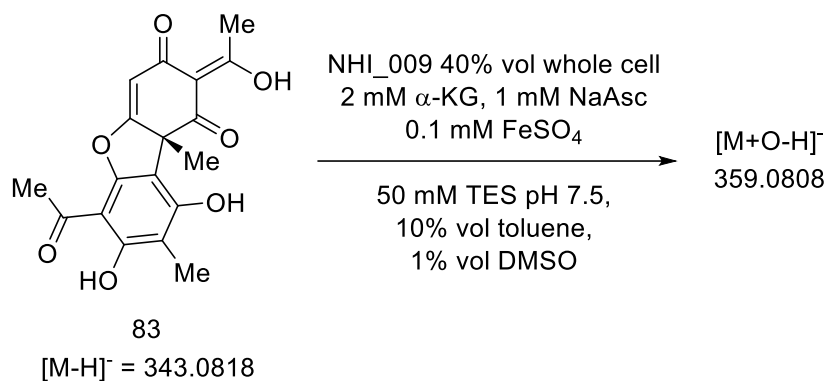
Discovered Reaction 141. Substrate_081 + NHI_308 = desaturation



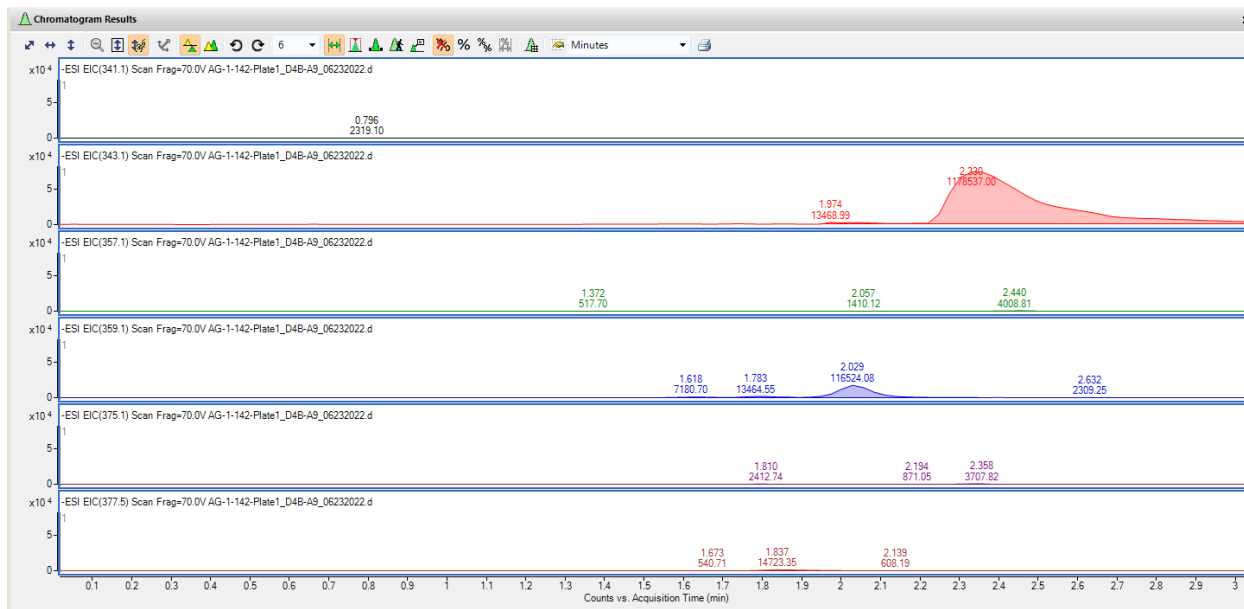
	Neutral	Positive	Negative
desaturation	165.1517	166.1596	164.1439
substrate	167.1674	168.1752	166.1596
oxidation/desaturation	181.1507	182.1586	180.1429
hydroxylation	183.1664	184.1742	182.1586
dihydroxylation	199.1654	200.1732	198.1576
chlorination	201.6126	202.6204	200.6047



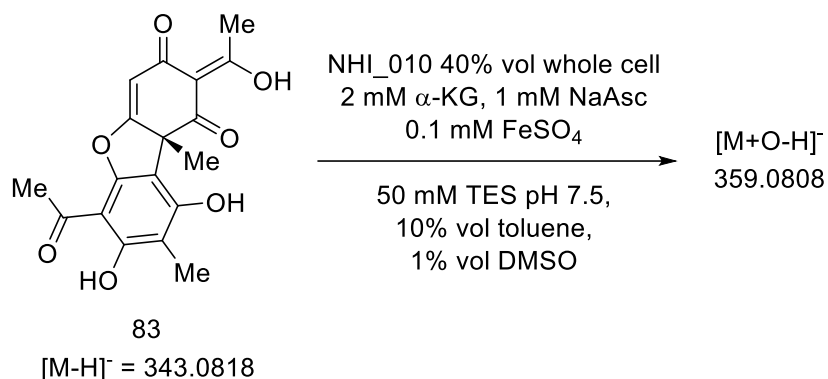
Discovered Reaction 142. Substrate_083 + NHI_009 = hydroxylation



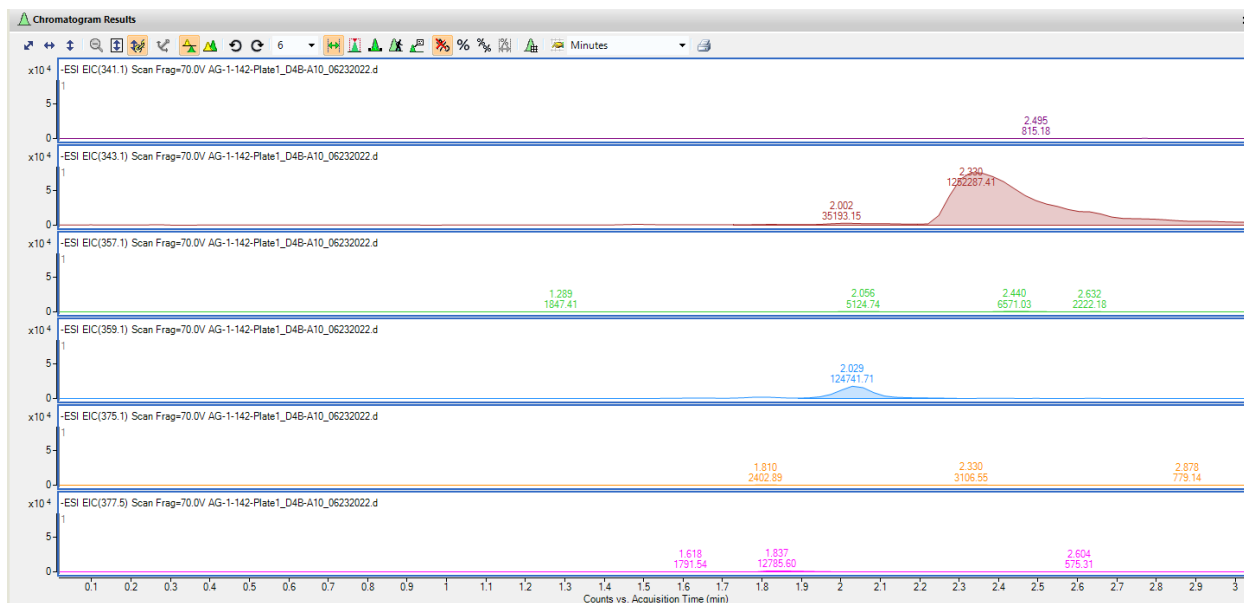
	Neutral	Positive	Negative
desaturation	342.0739	343.0818	341.0661
substrate	344.0896	345.0974	343.0818
oxidation/desaturation	358.0729	359.0808	357.0651
hydroxylation	360.0886	361.0964	359.0808
dihydroxylation	376.0876	377.0954	375.0798
chlorination	378.5348	379.5426	377.5269



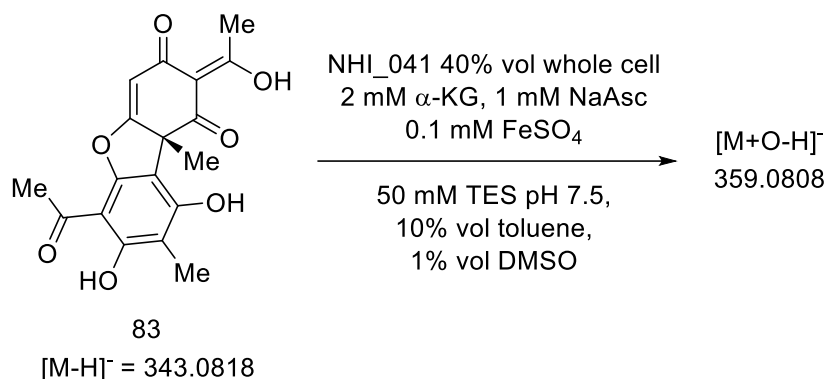
Discovered Reaction 143. Substrate_083 + NHI_010 = hydroxylation



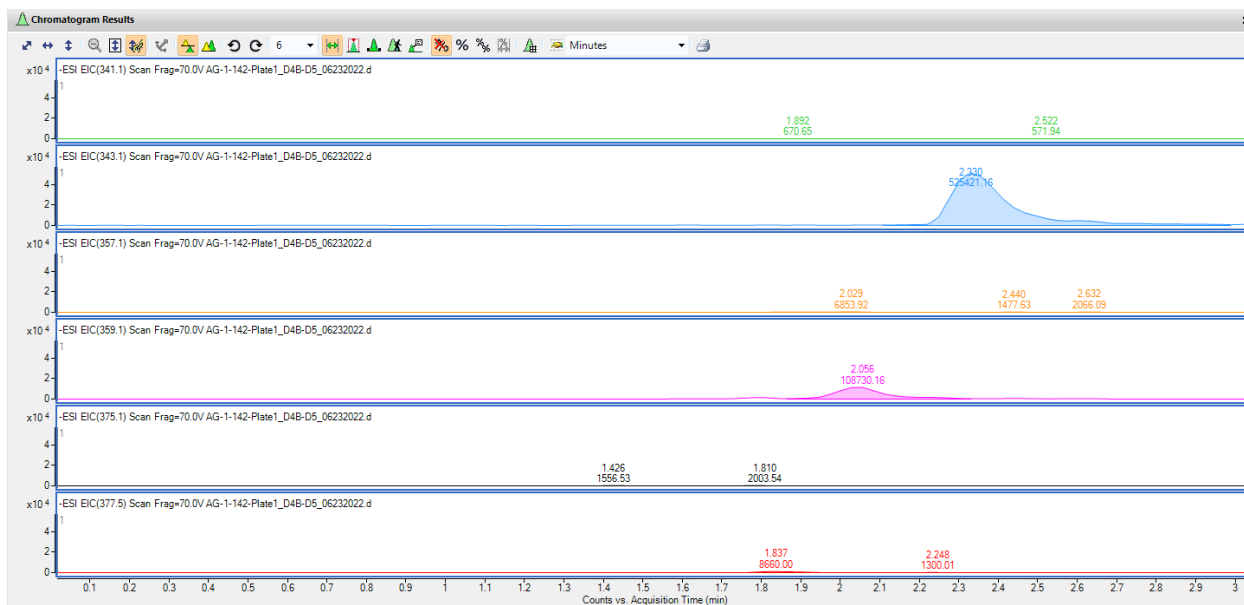
	Neutral	Positive	Negative
desaturation	342.0739	343.0818	341.0661
substrate	344.0896	345.0974	343.0818
oxidation/desaturation	358.0729	359.0808	357.0651
hydroxylation	360.0886	361.0964	359.0808
dihydroxylation	376.0876	377.0954	375.0798
chlorination	378.5348	379.5426	377.5269



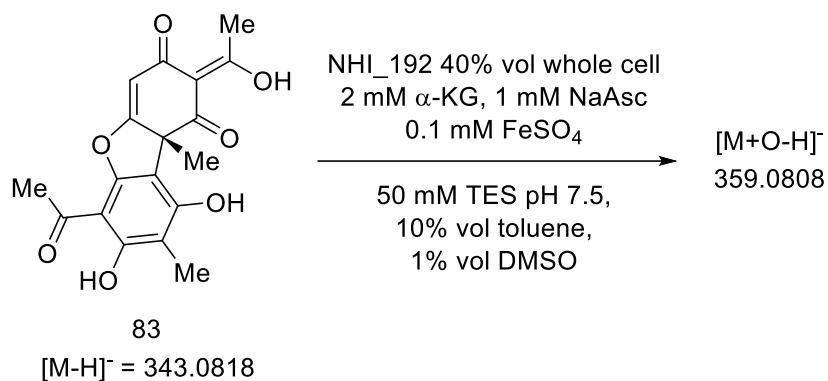
Discovered Reaction 144. Substrate_083 + NHI_041 = hydroxylation



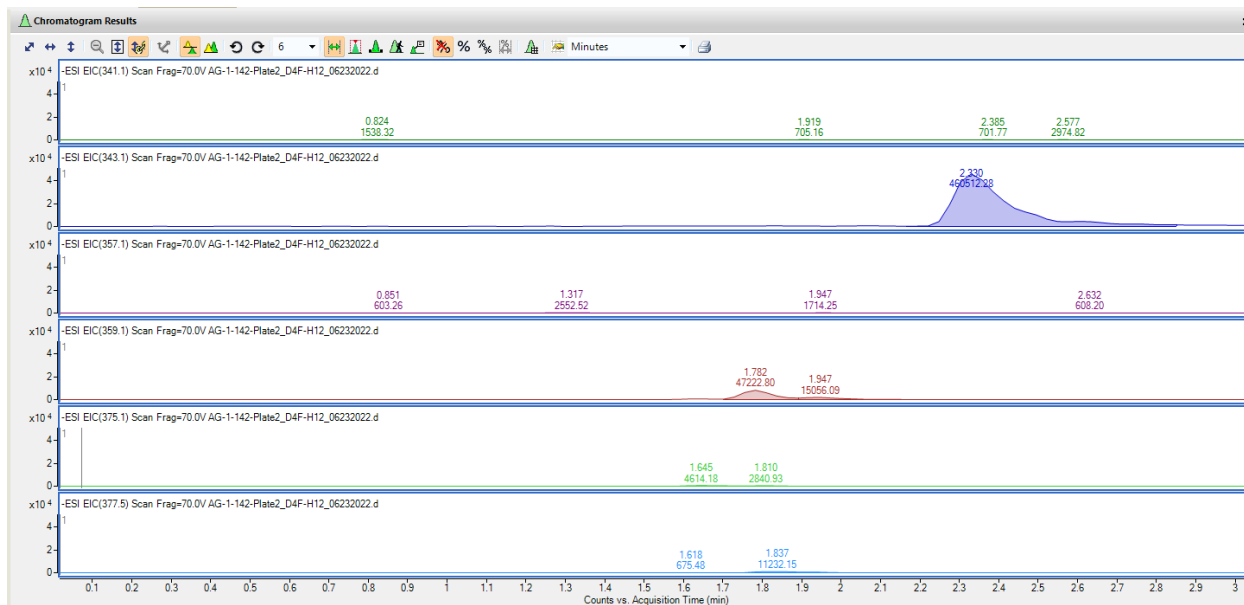
	Neutral	Positive	Negative
desaturation	342.0739	343.0818	341.0661
substrate	344.0896	345.0974	343.0818
oxidation/desaturation	358.0729	359.0808	357.0651
hydroxylation	360.0886	361.0964	359.0808
dihydroxylation	376.0876	377.0954	375.0798
chlorination	378.5348	379.5426	377.5269



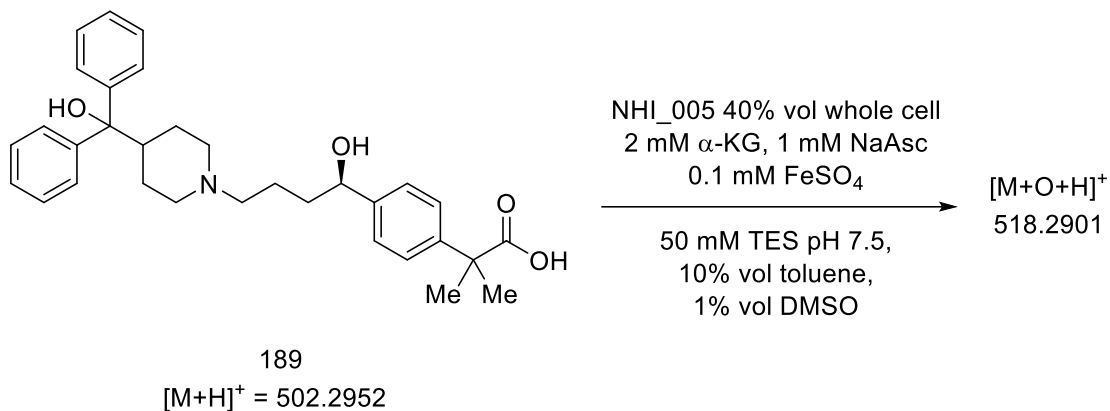
Discovered Reaction 145. Substrate_083 + NHI_192 = hydroxylation



	Neutral	Positive	Negative
desaturation	342.0739	343.0818	341.0661
substrate	344.0896	345.0974	343.0818
oxidation/desaturation	358.0729	359.0808	357.0651
hydroxylation	360.0886	361.0964	359.0808
dihydroxylation	376.0876	377.0954	375.0798
chlorination	378.5348	379.5426	377.5269



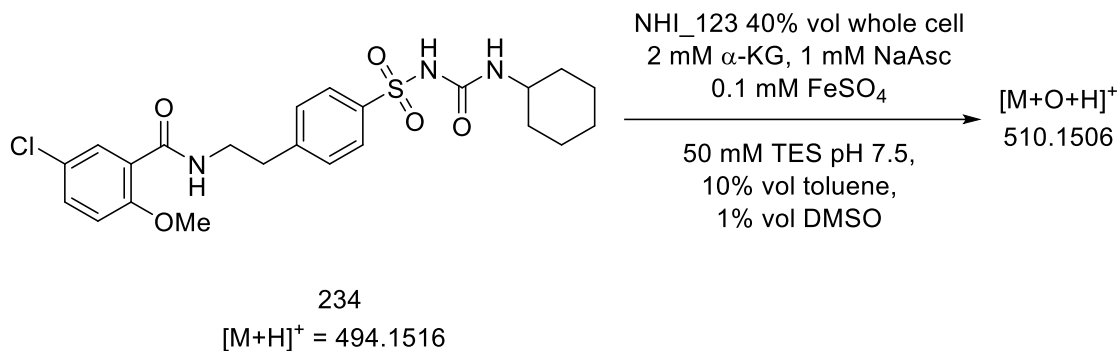
Discovered Reaction 146. Substrate_189 + NHI_005 = hydroxylation



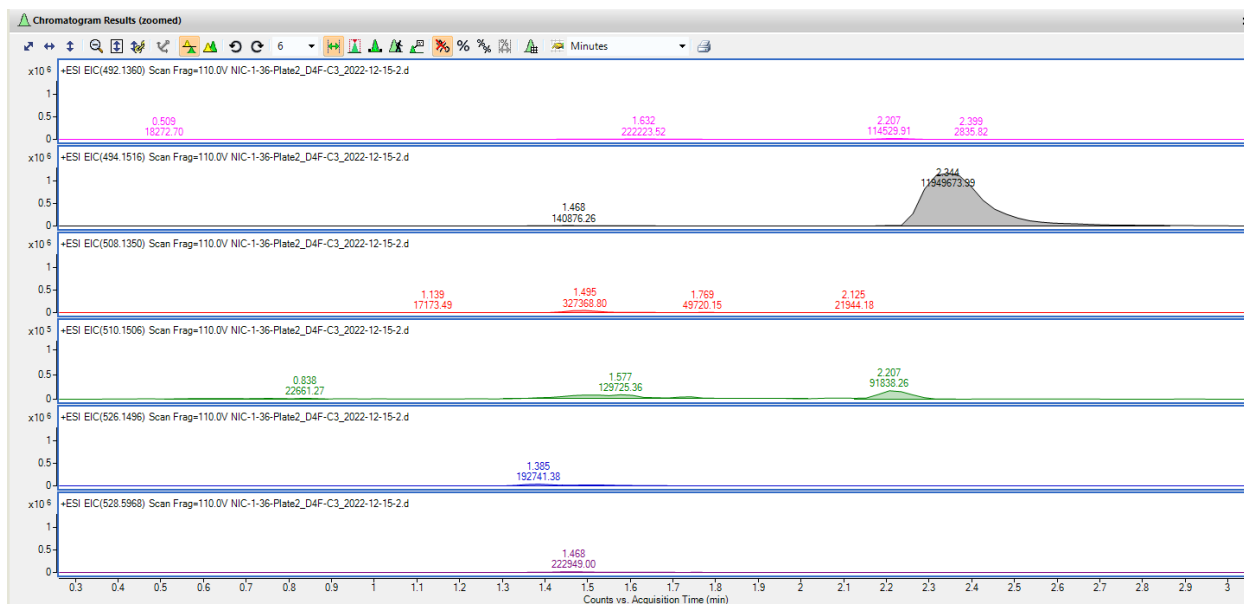
	Neutral	Positive	Negative
desaturation	499.2722	500.28007	498.2644
substrate	501.2879	502.2957	500.2801
oxidation/desaturation	515.2671	516.27497	514.2593
hydroxylation	517.2828	518.29063	516.275
dihydroxylation	533.2777	534.28553	532.2699
chlorination	535.249	536.2568	534.2411



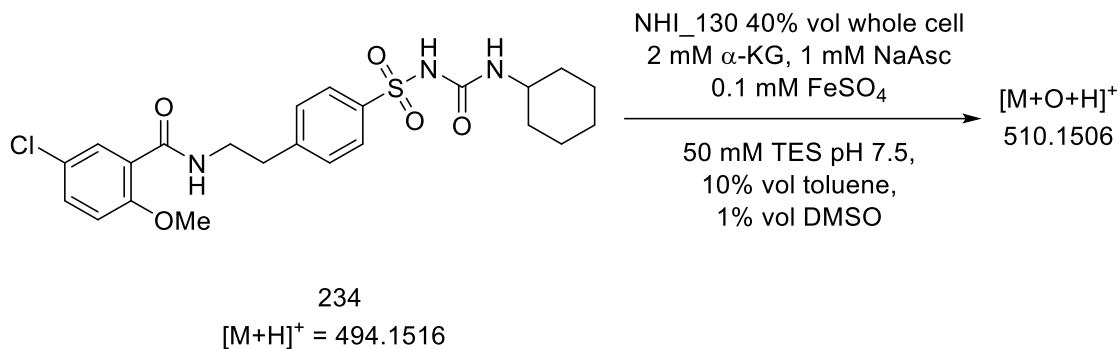
Discovered Reaction 147. Substrate_234 + NHI_123 = hydroxylation



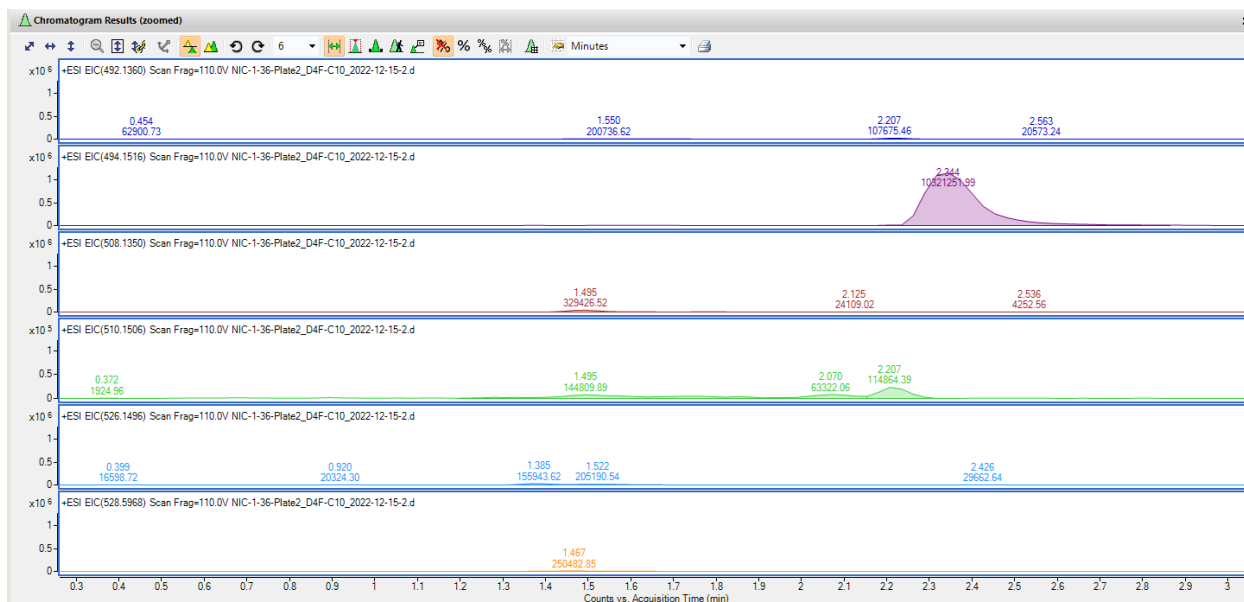
	Neutral	Positive	Negative
desaturation	491.1281	492.1360	490.1203
substrate	493.1438	494.1516	492.1360
oxidation/desaturation	507.1271	508.1350	506.1193
hydroxylation	509.1428	510.1506	508.1350
dihydroxylation	525.1418	526.1496	524.1340
chlorination	527.5890	528.5968	526.5811



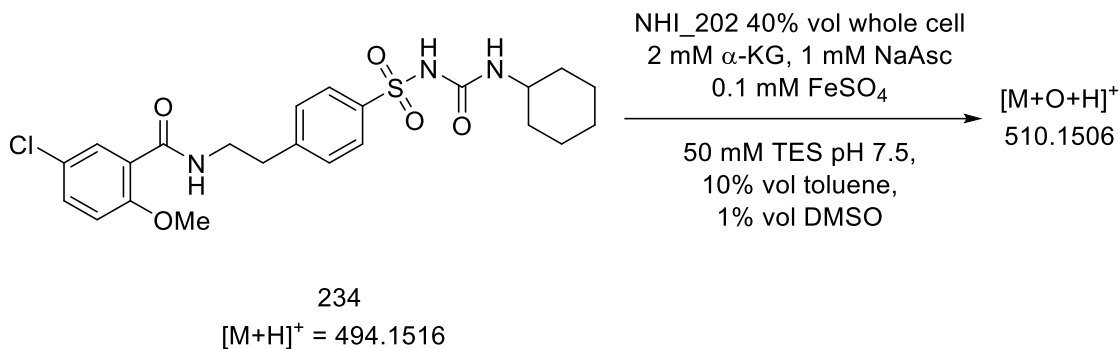
Discovered Reaction 148. Substrate_234 + NHI_130 = hydroxylation



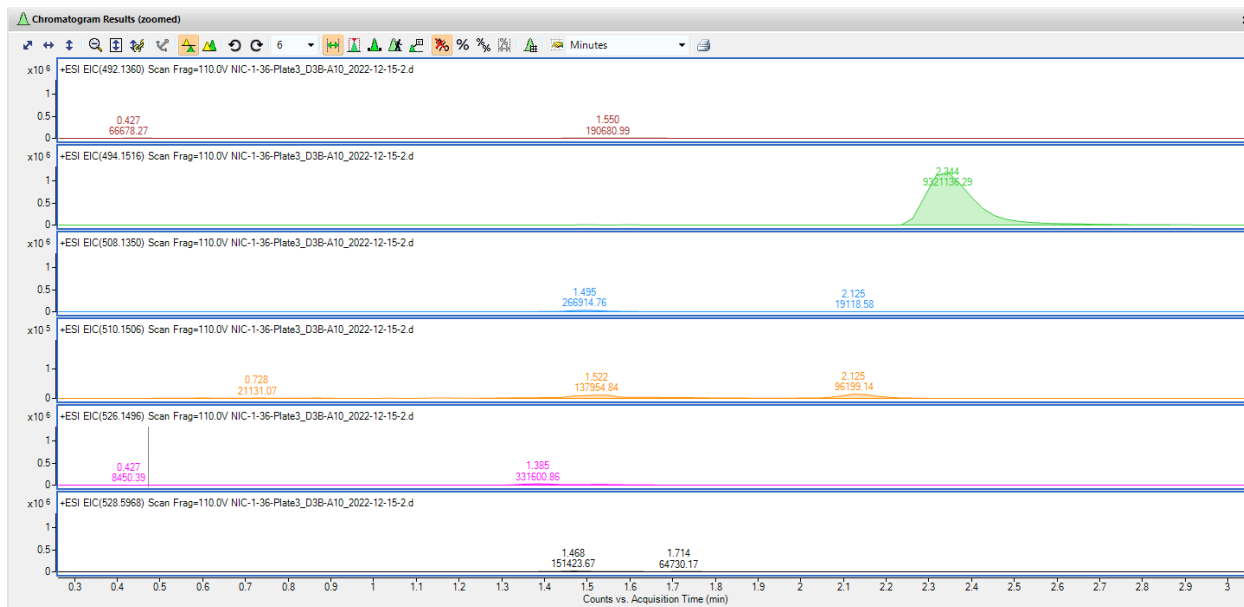
	Neutral	Positive	Negative
desaturation	491.1281	492.1360	490.1203
substrate	493.1438	494.1516	492.1360
oxidation/desaturation	507.1271	508.1350	506.1193
hydroxylation	509.1428	510.1506	508.1350
dihydroxylation	525.1418	526.1496	524.1340
chlorination	527.5890	528.5968	526.5811



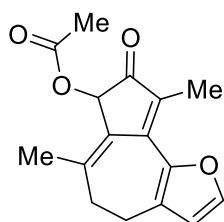
Discovered Reaction 149. Substrate_234 + NHI_202 = hydroxylation



	Neutral	Positive	Negative
desaturation	491.1281	492.1360	490.1203
substrate	493.1438	494.1516	492.1360
oxidation/desaturation	507.1271	508.1350	506.1193
hydroxylation	509.1428	510.1506	508.1350
dihydroxylation	525.1418	526.1496	524.1340
chlorination	527.5890	528.5968	526.5811



Discovered Reaction 150. Substrate_341 + NHI_309 = hydroxylation



341

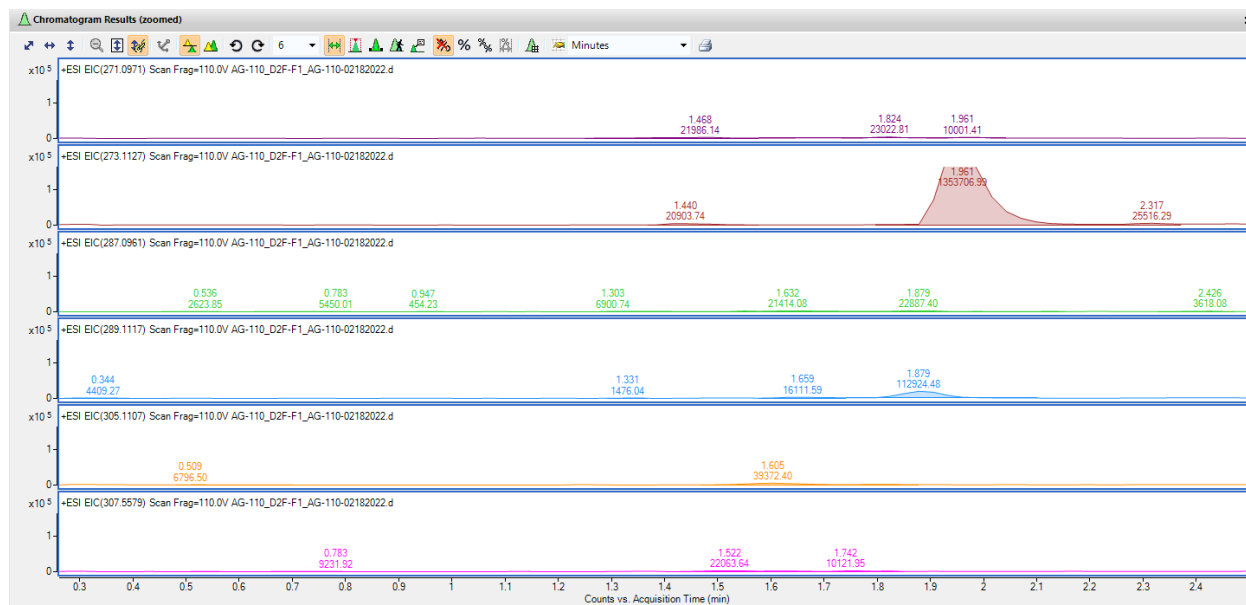
$[M+H]^+ = 273.1127$

NHI_309 40% vol whole cell
2 mM α -KG, 1 mM NaAsc
0.1 mM FeSO₄

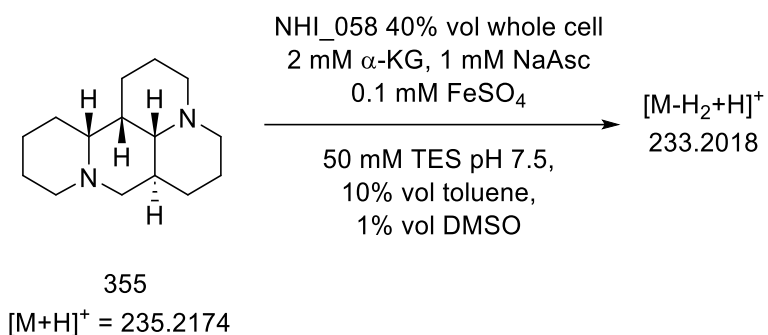
50 mM TES pH 7.5,
10% vol toluene,
1% vol DMSO

$[M+O+H]^+$
289.1117

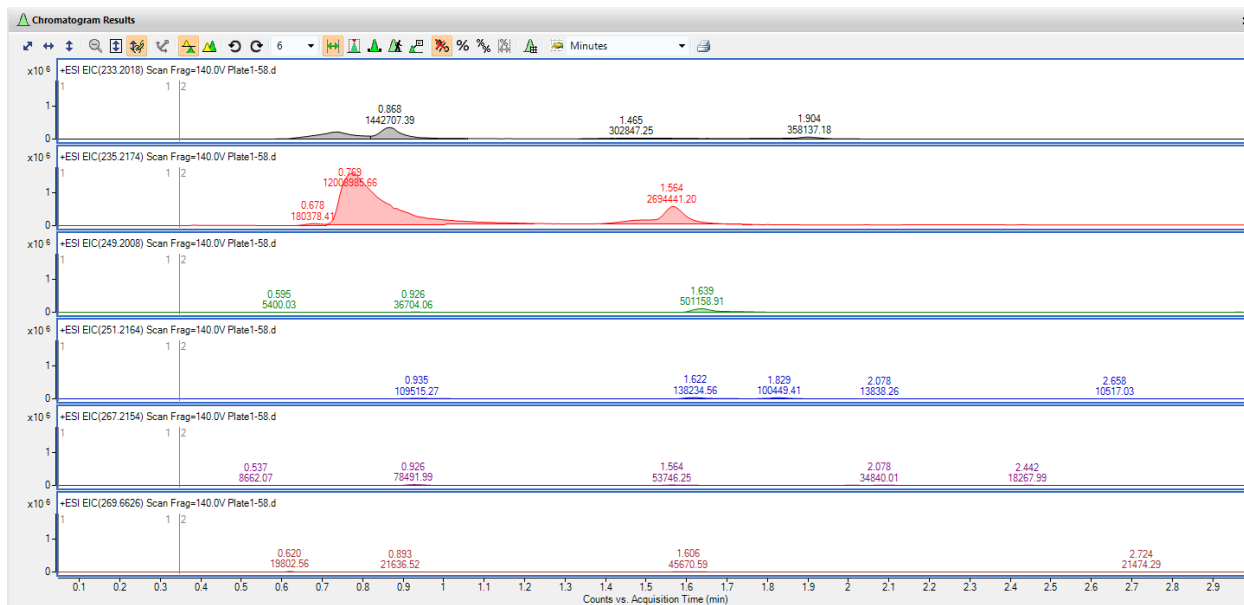
	Neutral	Positive	Negative
desaturation	270.0892	271.0971	269.0814
substrate	272.1049	273.1127	271.0971
oxidation/desaturation	286.0882	287.0961	285.0804
hydroxylation	288.1039	289.1117	287.0961
dihydroxylation	304.1029	305.1107	303.0951
chlorination	306.5501	307.5579	305.5422



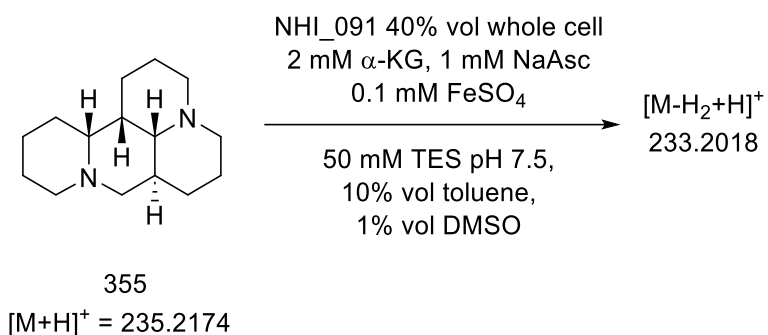
Discovered Reaction 151. Substrate_355 + NHI_058 = desaturation



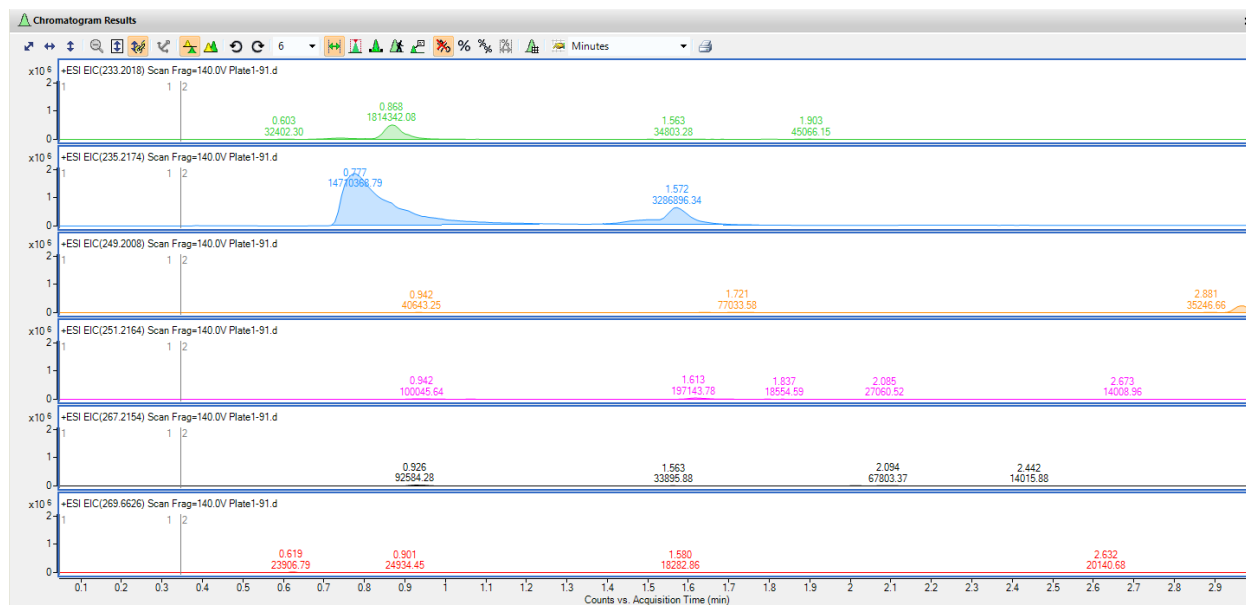
	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



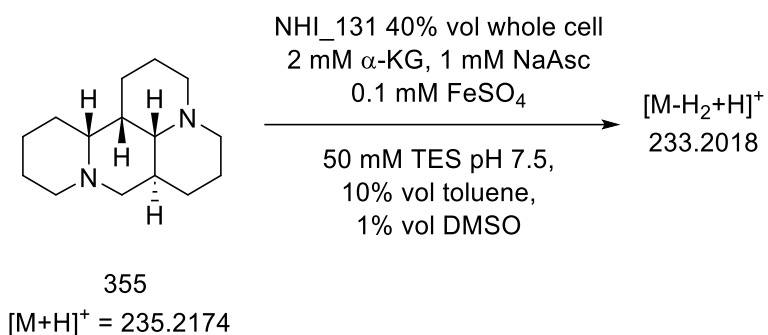
Discovered Reaction 152. Substrate_355 + NHI_091 = desaturation



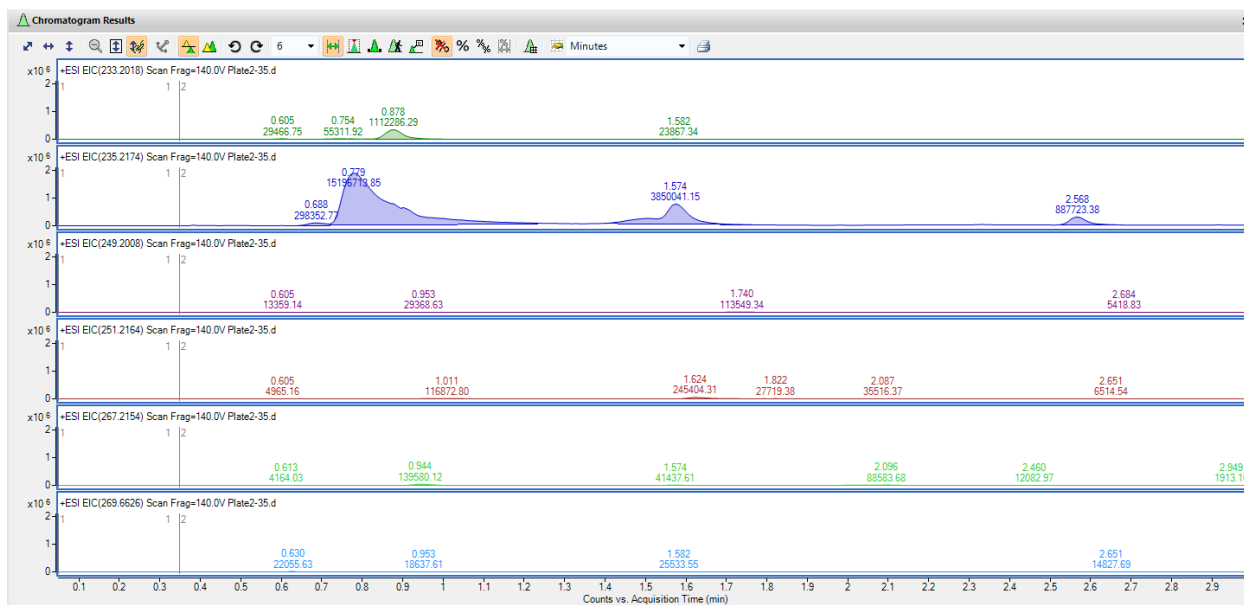
	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



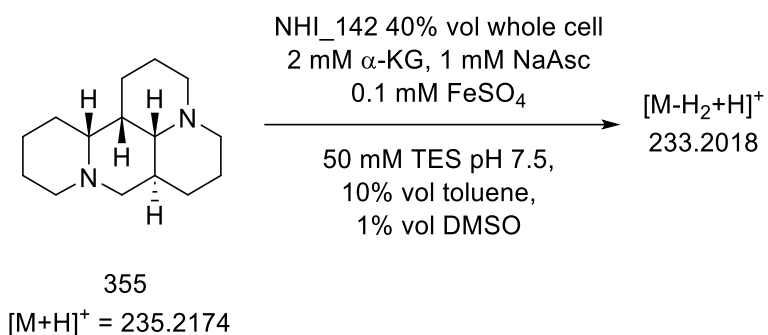
Discovered Reaction 153. Substrate **355** + NHI_131 = desaturation



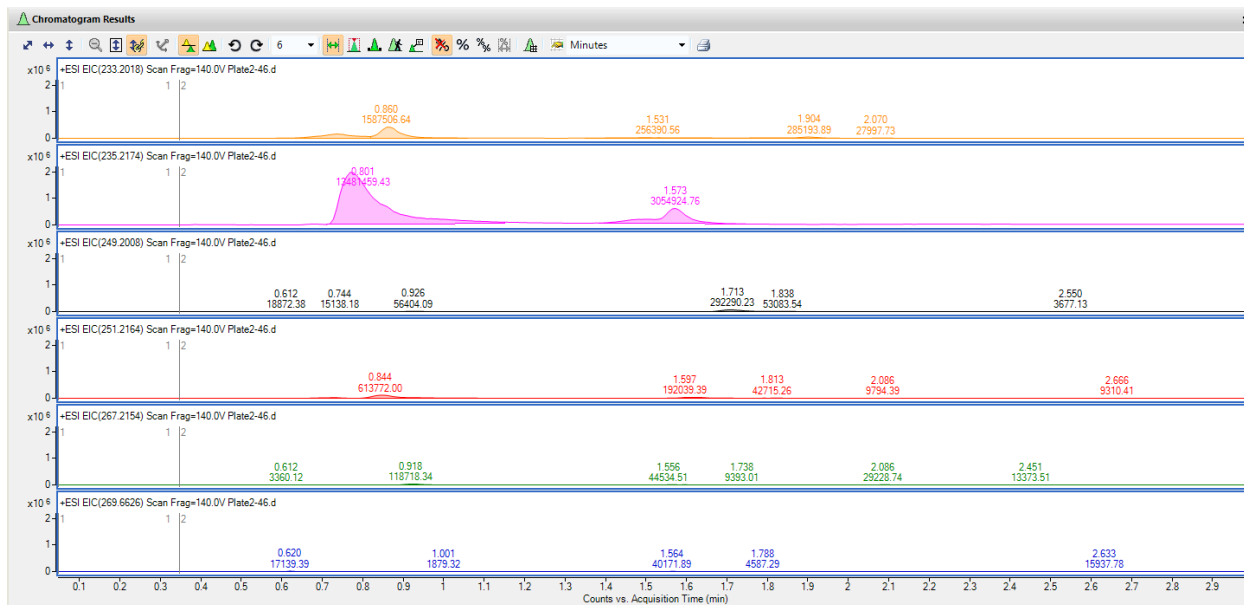
	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



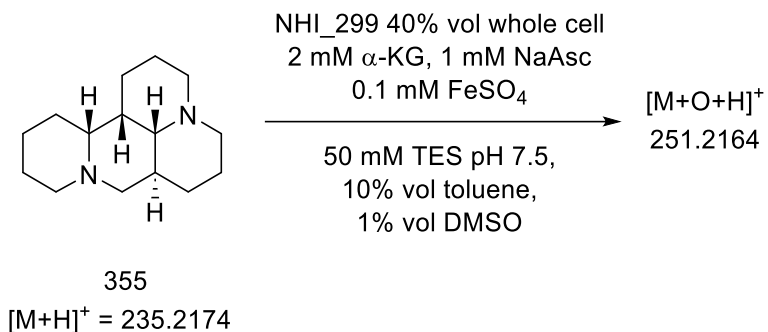
Discovered Reaction 154. Substrate_355 + NHI_142 = desaturation



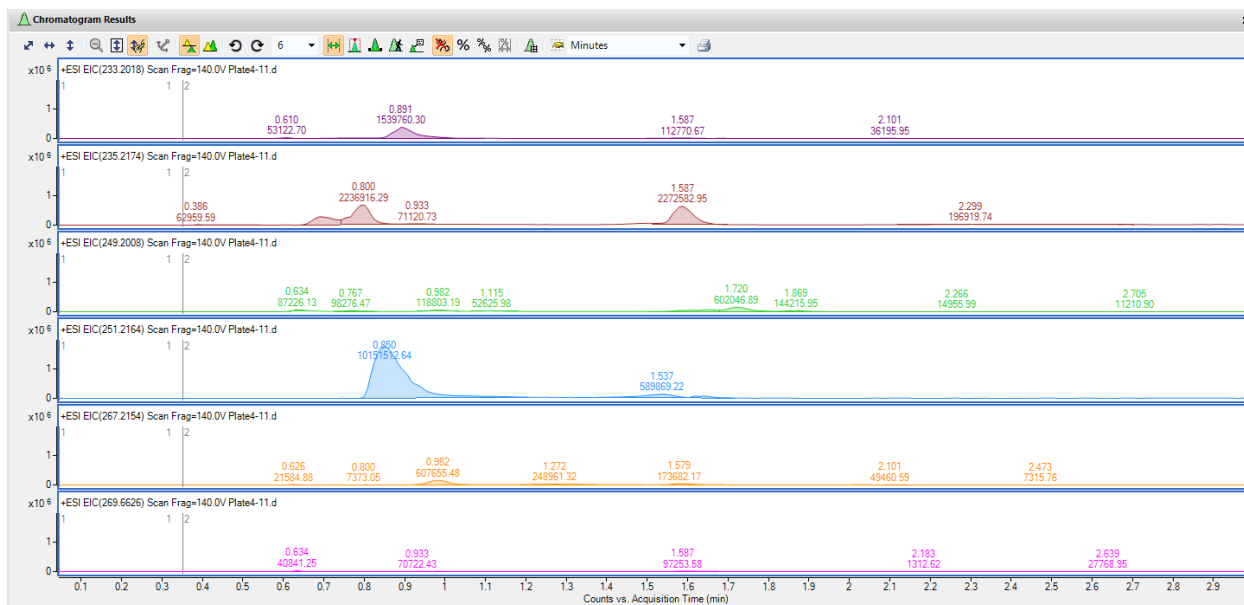
	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



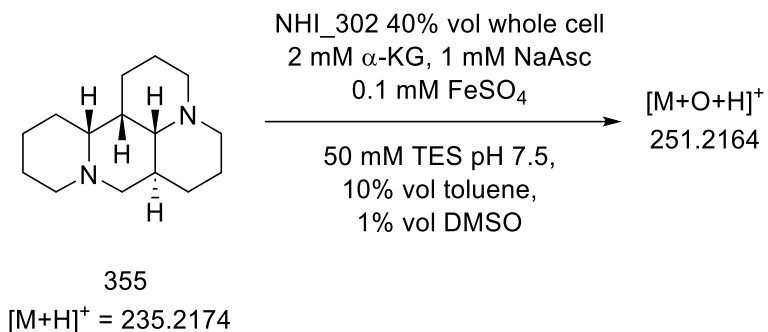
Discovered Reaction 155. Substrate **355** + NHI 299 = hydroxylation



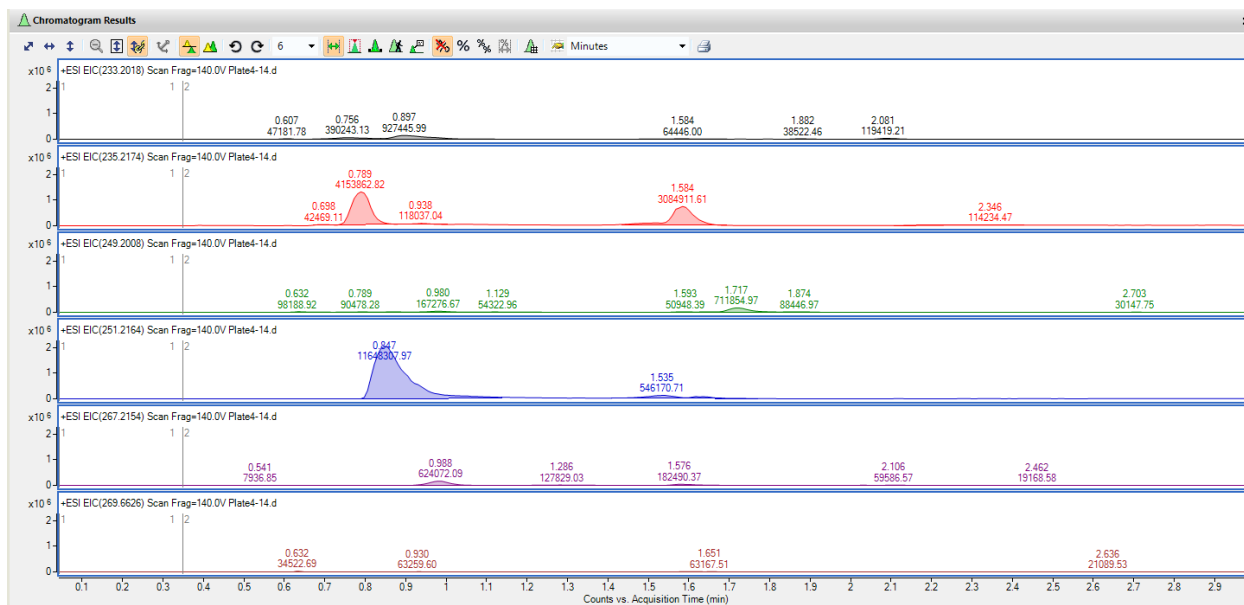
	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



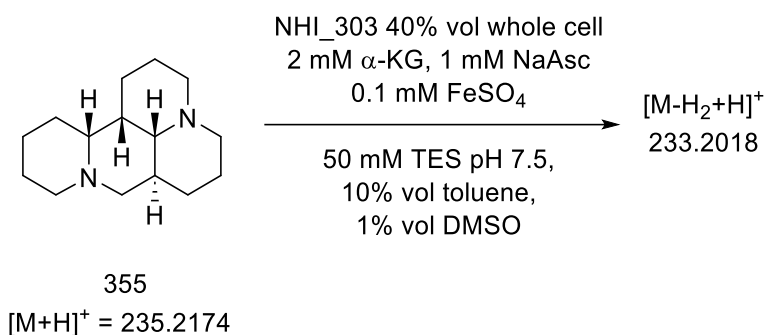
Discovered Reaction 156. Substrate_355 + NHI_302 = hydroxylation



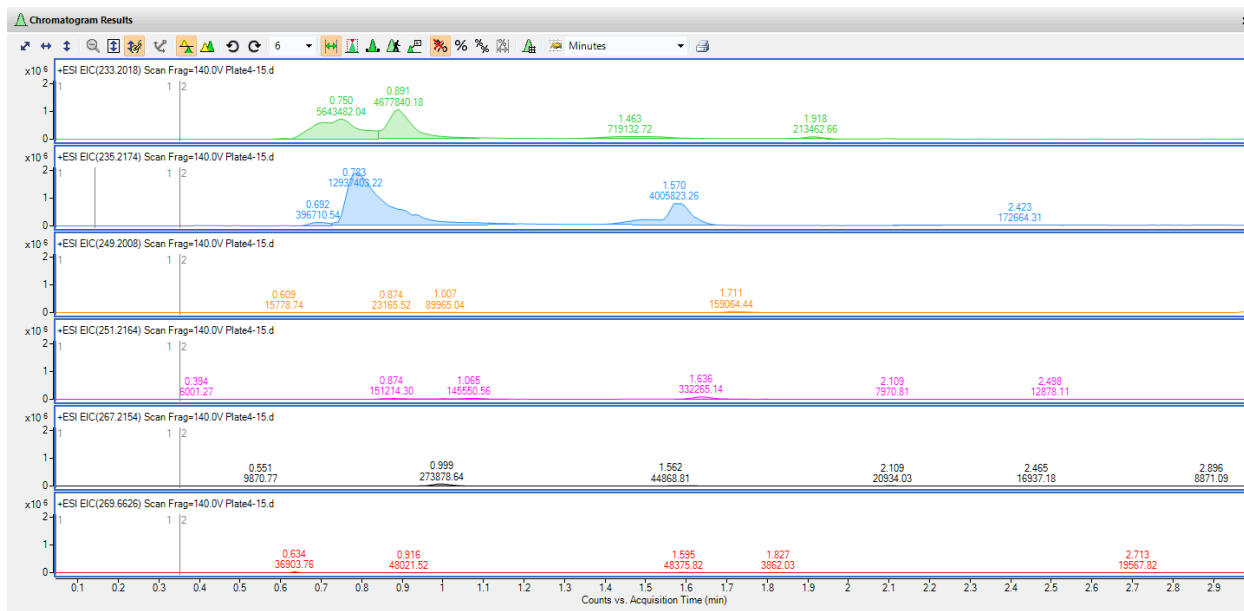
	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



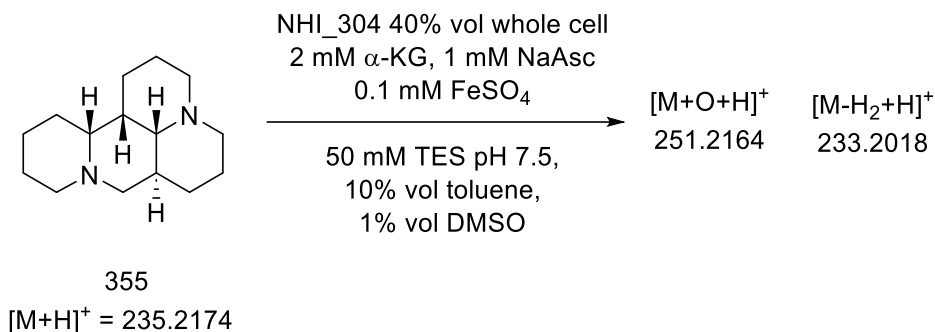
Discovered Reaction 157. Substrate_355 + NHI_303 = desaturation



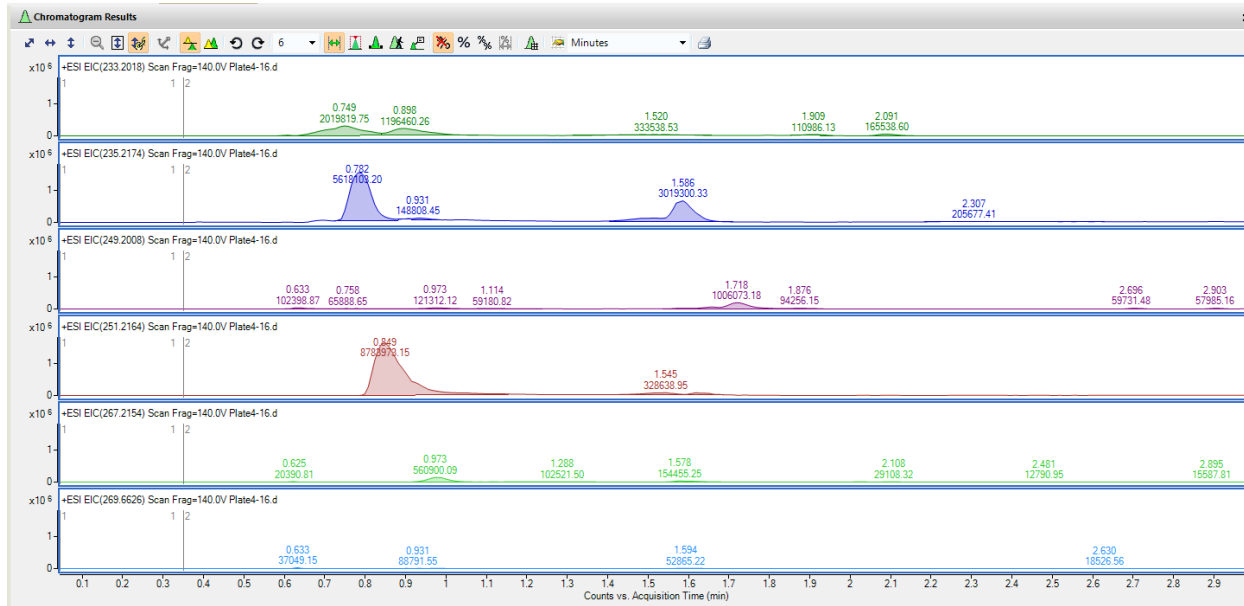
	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



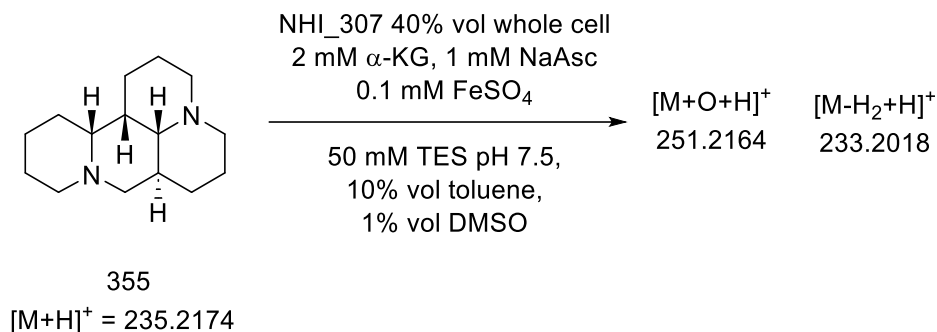
Discovered Reaction 158. Substrate_355 + NHI_304 = hydroxylation and desaturation



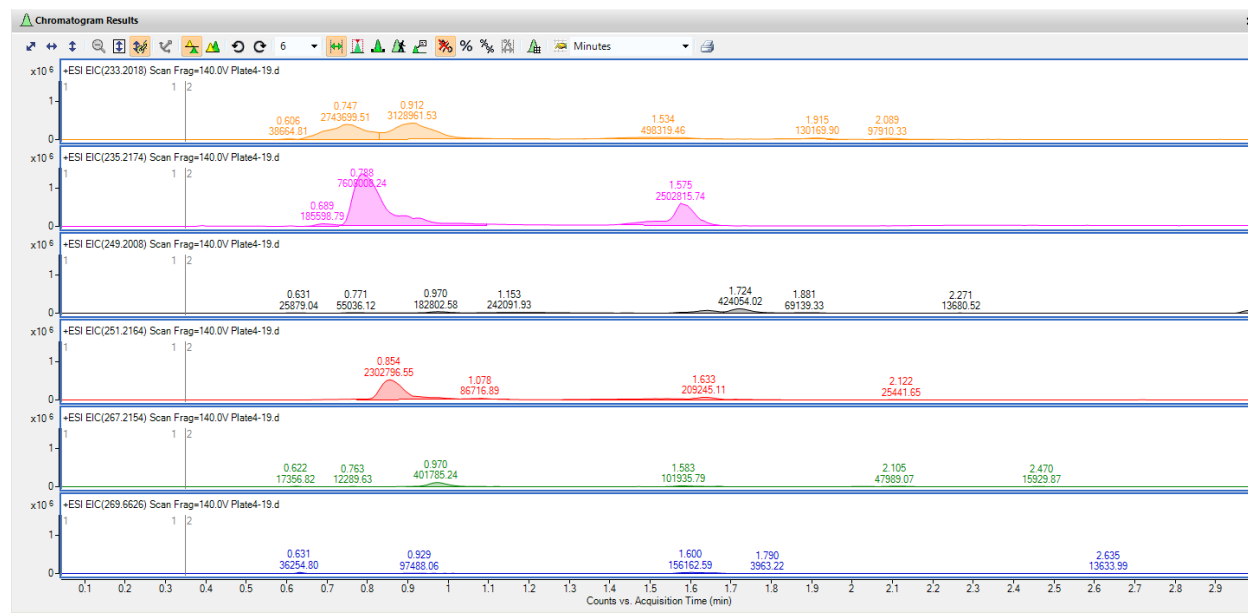
	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



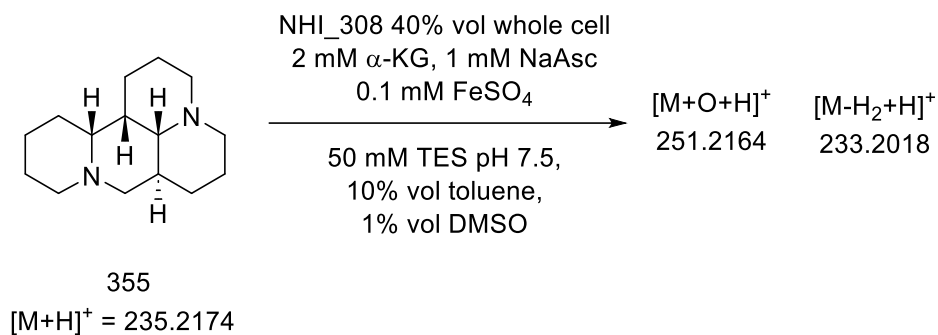
Discovered Reaction 159. Substrate_355 + NHI_307 = hydroxylation and desaturation



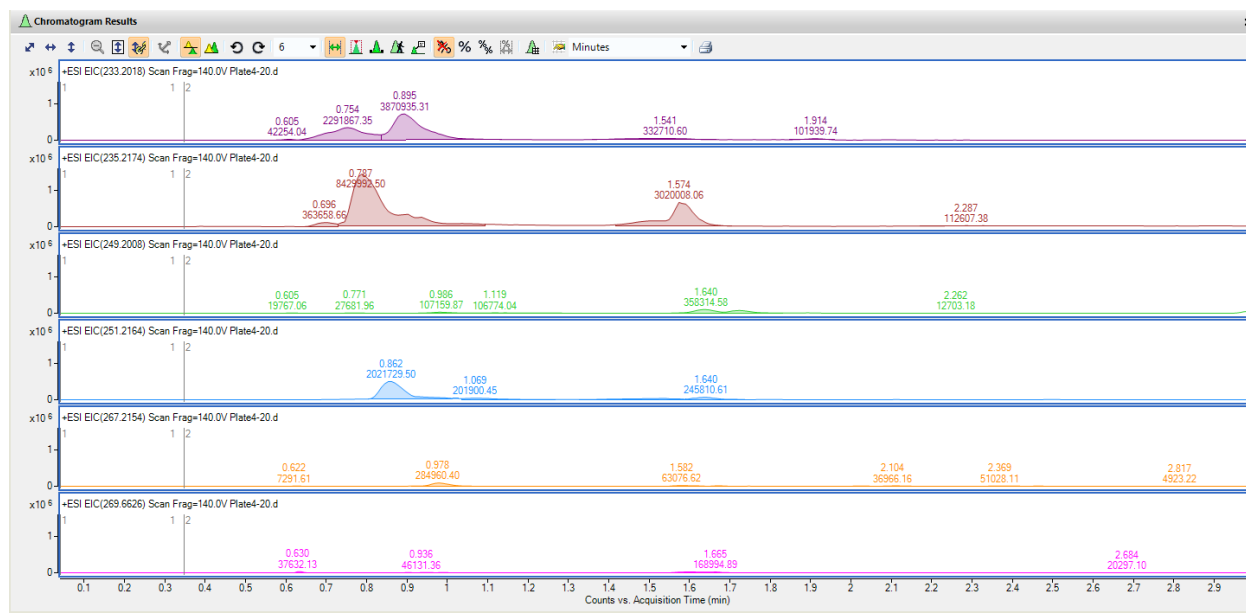
	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



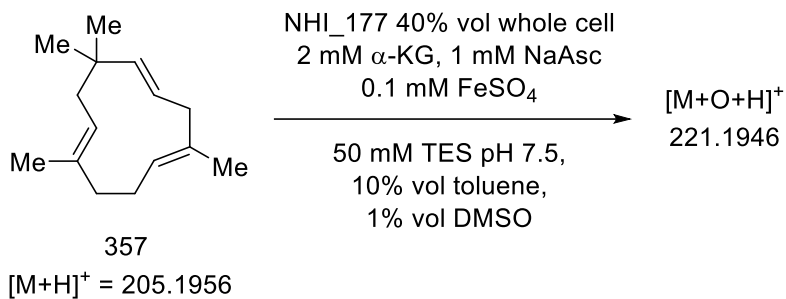
Discovered Reaction 160. Substrate **355** + NHI_308 = hydroxylation and desaturation



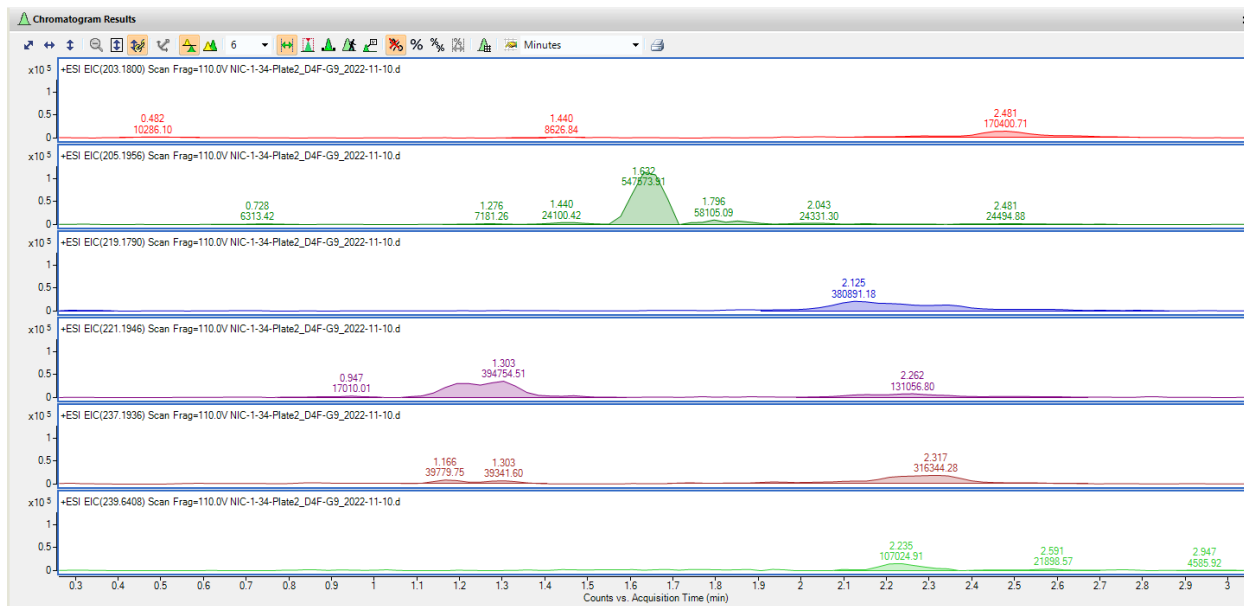
	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



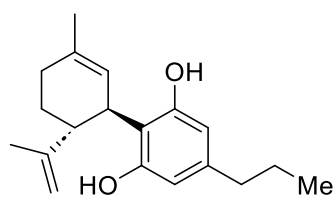
Discovered Reaction 161.Substrate_357 + NHI_177 = hydroxylation



	Neutral	Positive	Negative
desaturation	202.1721	203.1800	201.1643
substrate	204.1878	205.1956	203.1800
oxidation/desaturation	218.1711	219.1790	217.1633
hydroxylation	220.1868	221.1946	219.1790
dihydroxylation	236.1858	237.1936	235.1780
chlorination	238.6330	239.6408	237.6251



Discovered Reaction 162.Substrate_359 + NHI_072 = hydroxylation



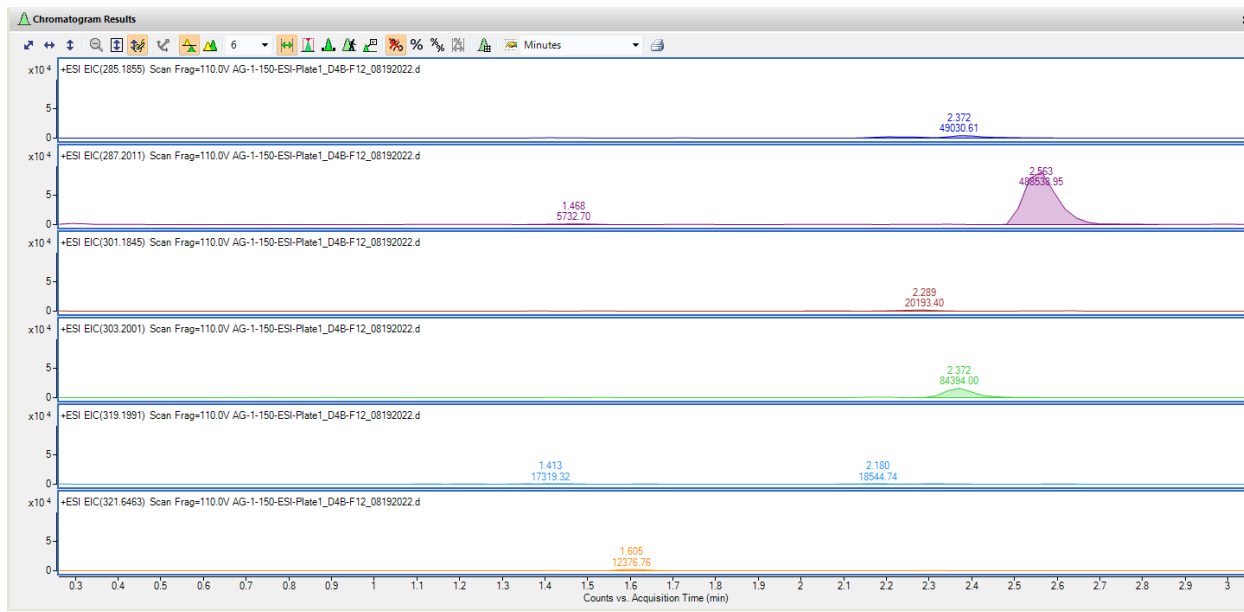
359, cannabidavarin
[M+H]⁺ = 287.2011

NHI_072 40% vol whole cell
2 mM α-KG, 1 mM NaAsc
0.1 mM FeSO₄

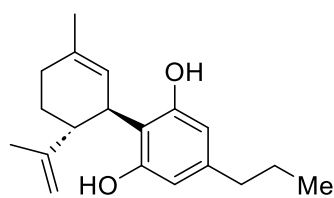
50 mM TES pH 7.5,
10% vol toluene,
1% vol DMSO

[M+O+H]⁺
303.2001

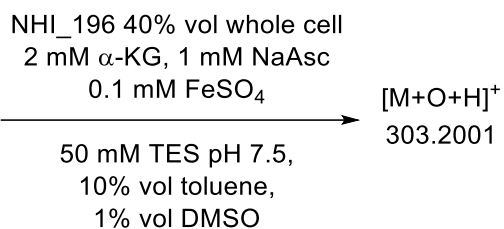
	Neutral	Positive	Negative
desaturation	284.1776	285.1855	283.1698
substrate	286.1933	287.2011	285.1855
oxidation/desaturation	300.1766	301.1845	299.1688
hydroxylation	302.1923	303.2001	301.1845
dihydroxylation	318.1913	319.1991	317.1835
chlorination	320.6385	321.6463	319.6306



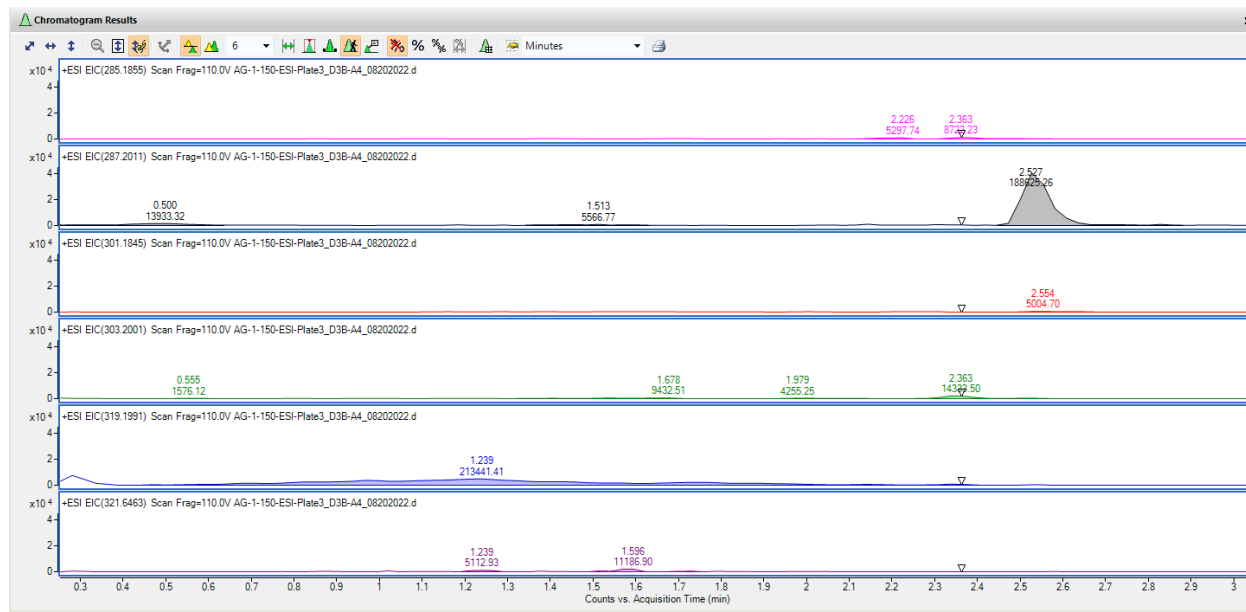
Discovered Reaction 163.Substrate_359 + NHI_196 = hydroxylation



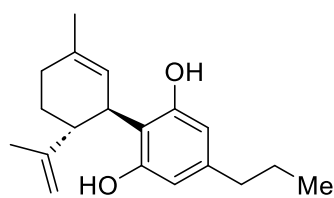
359, cannabidavarin
[M+H]⁺ = 287.2011



	Neutral	Positive	Negative
desaturation	284.1776	285.1855	283.1698
substrate	286.1933	287.2011	285.1855
oxidation/desaturation	300.1766	301.1845	299.1688
hydroxylation	302.1923	303.2001	301.1845
dihydroxylation	318.1913	319.1991	317.1835
chlorination	320.6385	321.6463	319.6306



Discovered Reaction 164.Substrate_359 + NHI_197 = hydroxylation



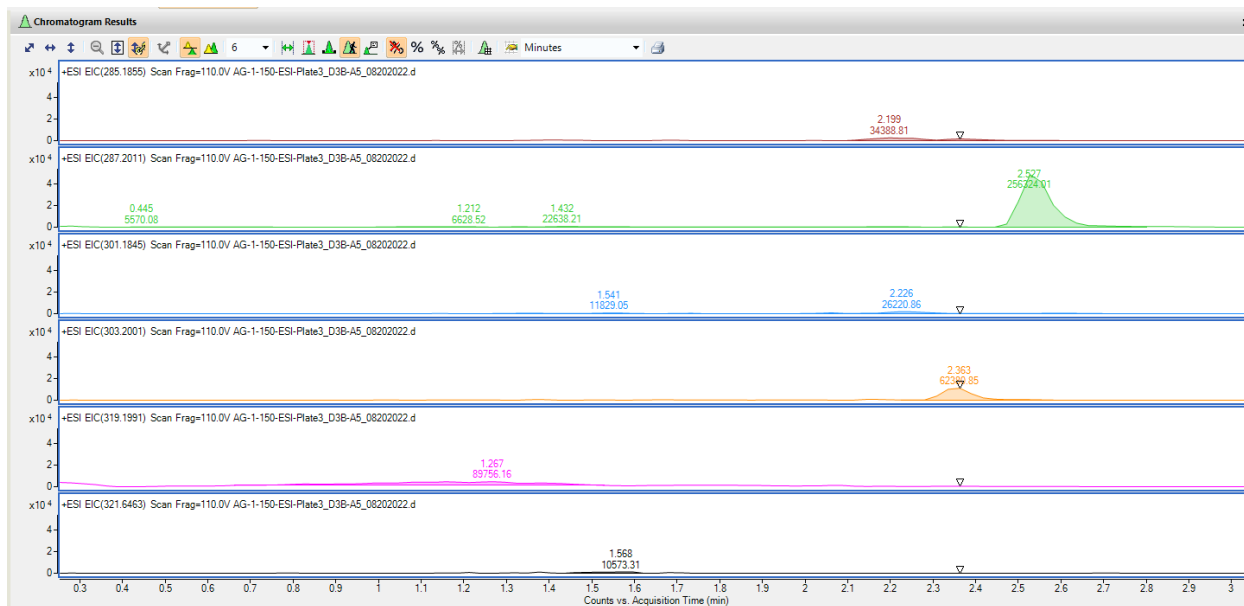
359, cannabidavarin
[M+H]⁺ = 287.2011

NHI_197 40% vol whole cell
2 mM α -KG, 1 mM NaAsc
0.1 mM FeSO₄

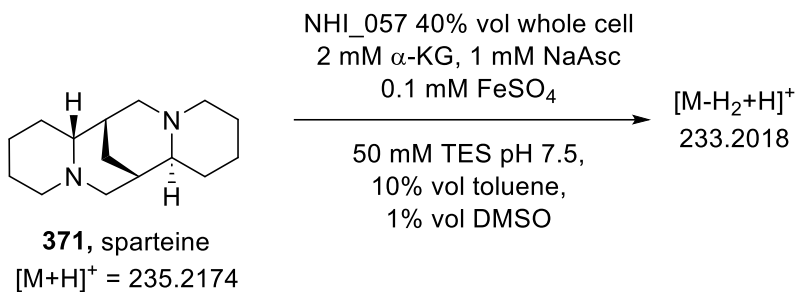
50 mM TES pH 7.5,
10% vol toluene,
1% vol DMSO

[M+O+H]⁺
303.2001

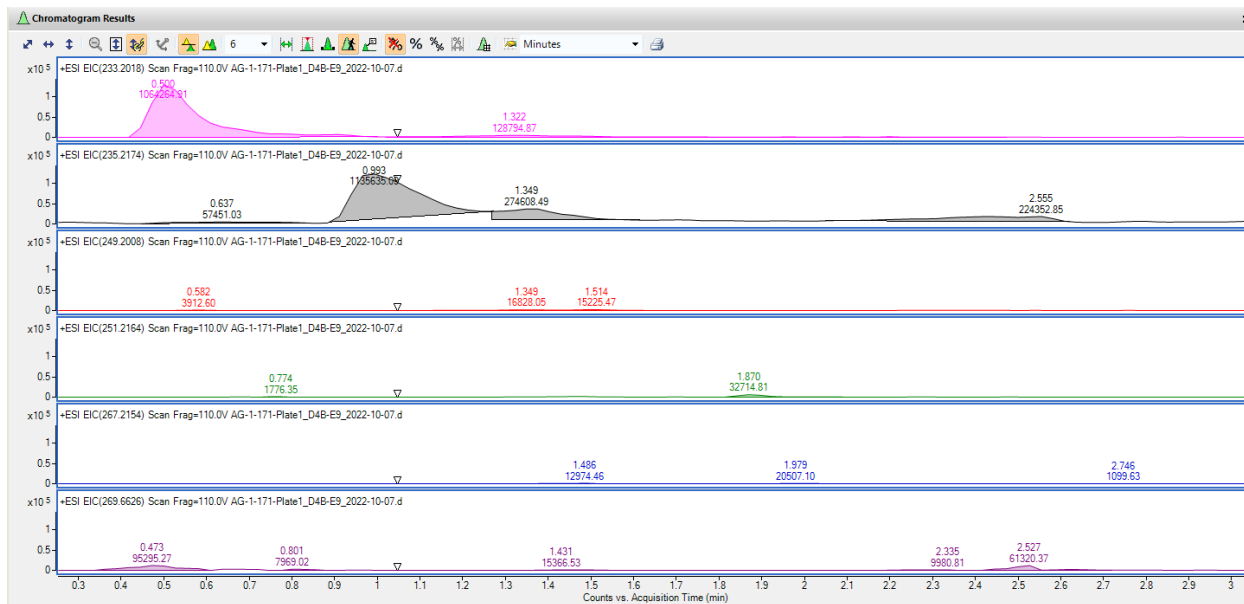
	Neutral	Positive	Negative
desaturation	284.1776	285.1855	283.1698
substrate	286.1933	287.2011	285.1855
oxidation/desaturation	300.1766	301.1845	299.1688
hydroxylation	302.1923	303.2001	301.1845
dihydroxylation	318.1913	319.1991	317.1835
chlorination	320.6385	321.6463	319.6306



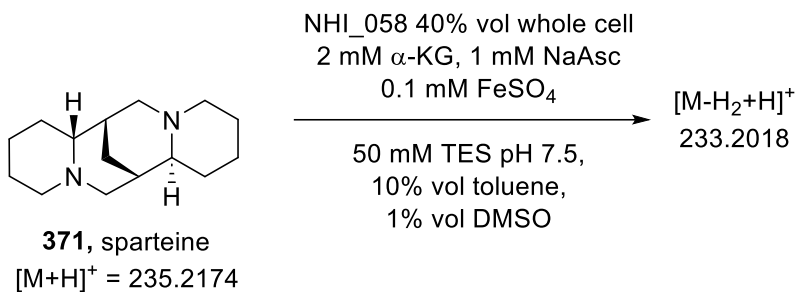
Discovered Reaction 165. Substrate_371 + NHI_057 = desaturation



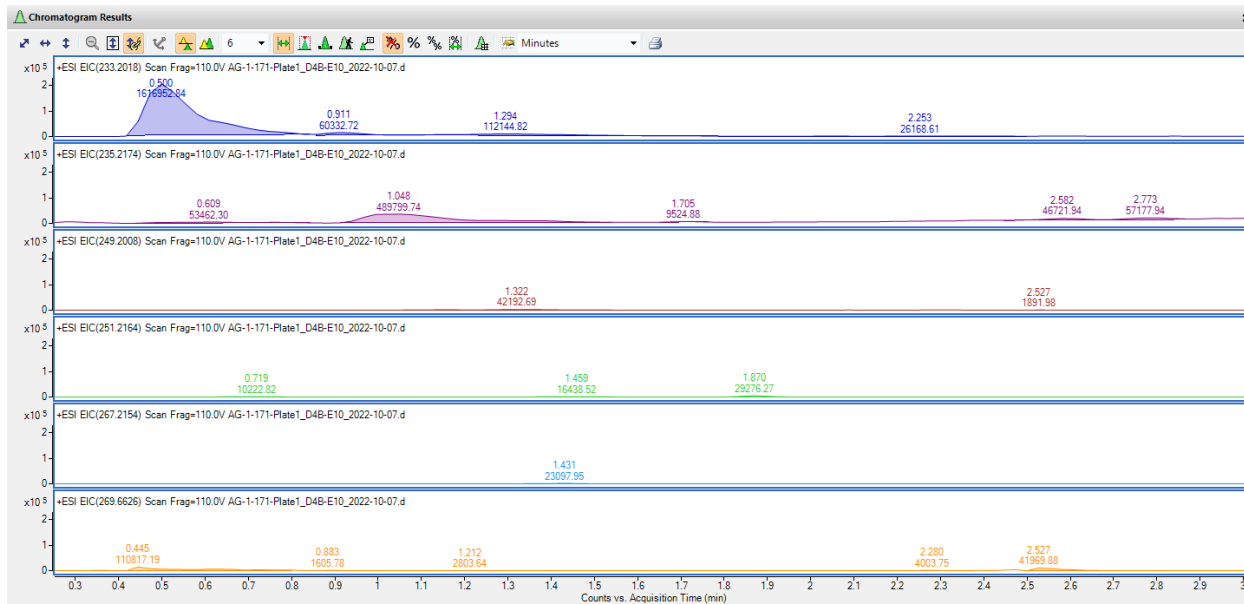
	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



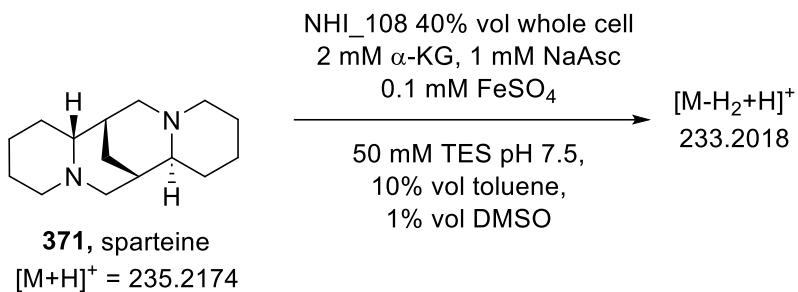
Discovered Reaction 166. Substrate_371 + NHI_058 = desaturation



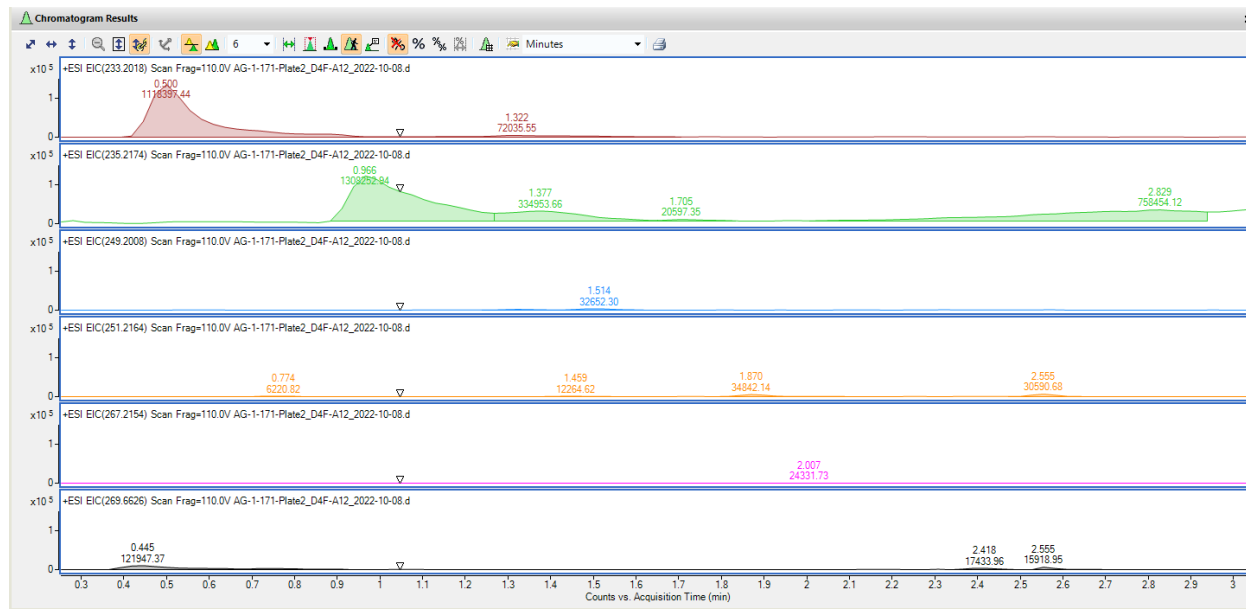
	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



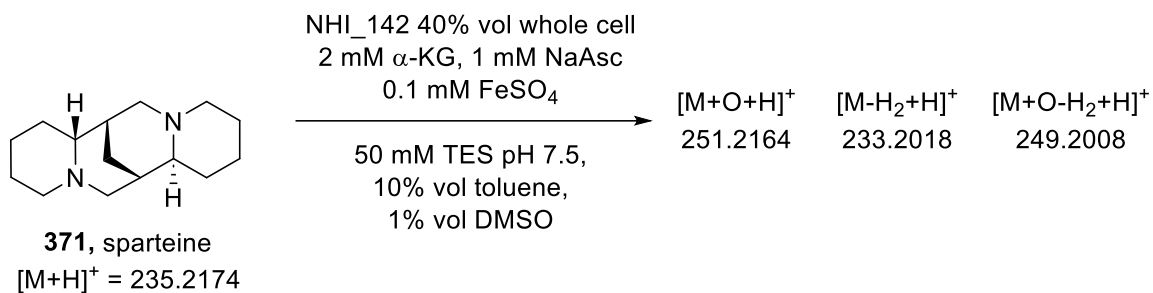
Discovered Reaction 167. Substrate_371 + NHI_108 = hydroxylation



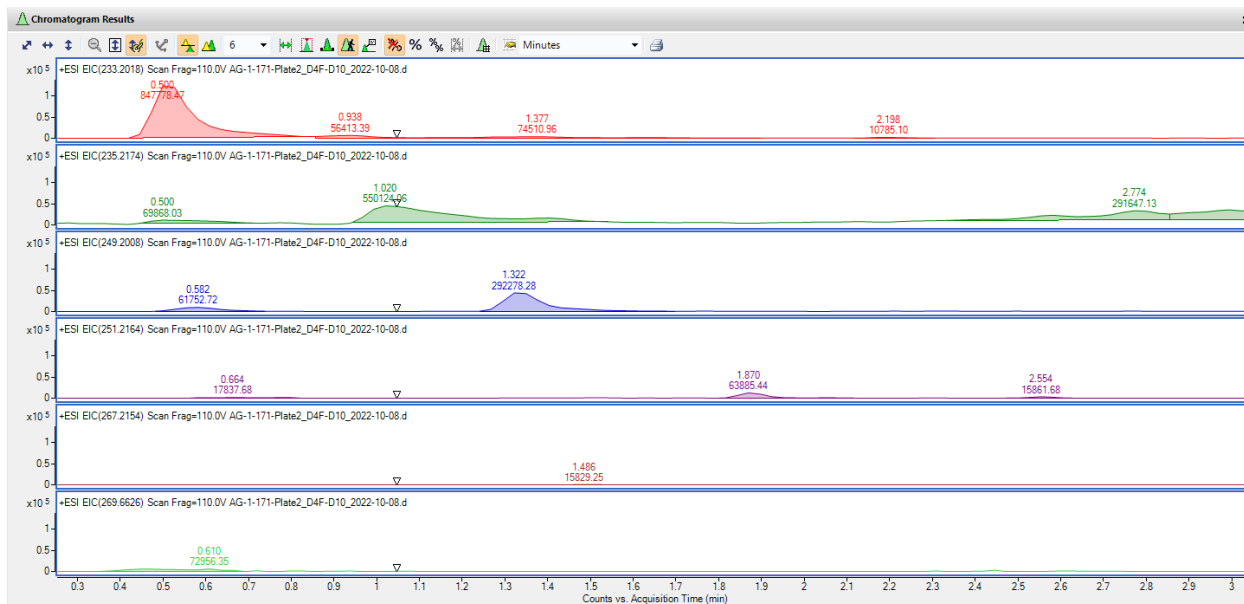
	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



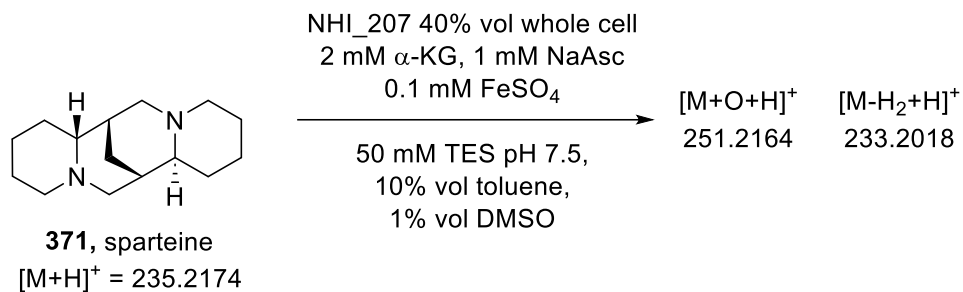
Discovered Reaction 168. Substrate_371 + NHI_142 = hydroxylation, desaturation, and oxidation/desaturation



	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



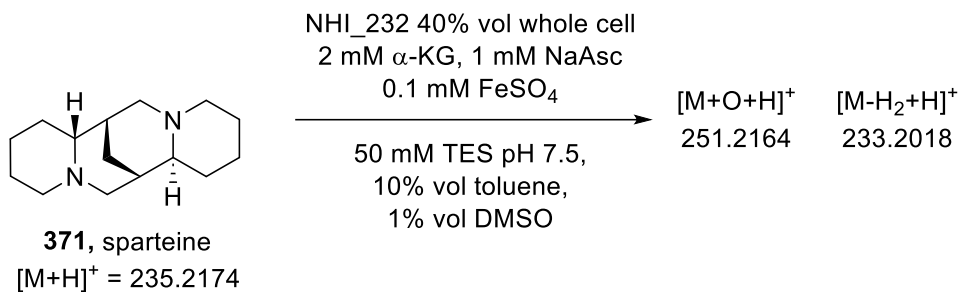
Discovered Reaction 169. Substrate_371 + NHI_207 = hydroxylation and desaturation



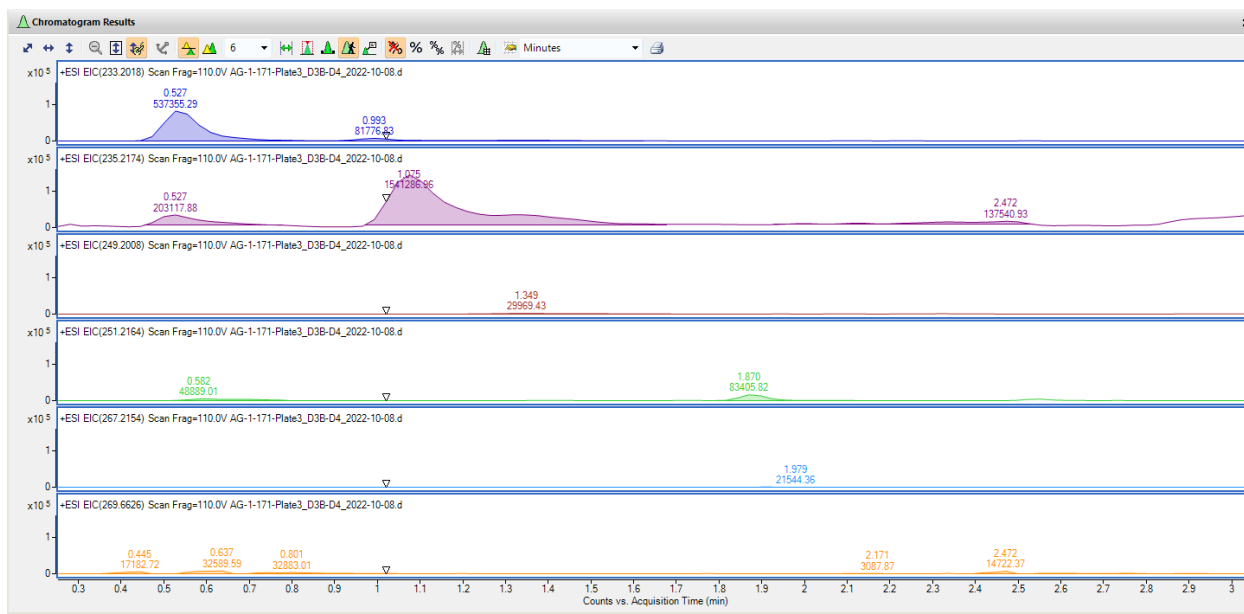
	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



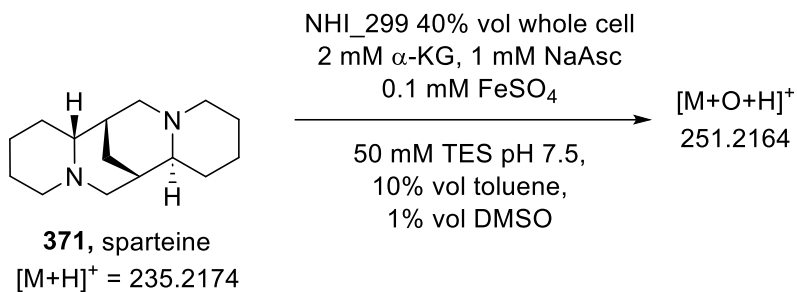
Discovered Reaction 170. Substrate **371** + NHI_232 = desaturation and hydroxylation



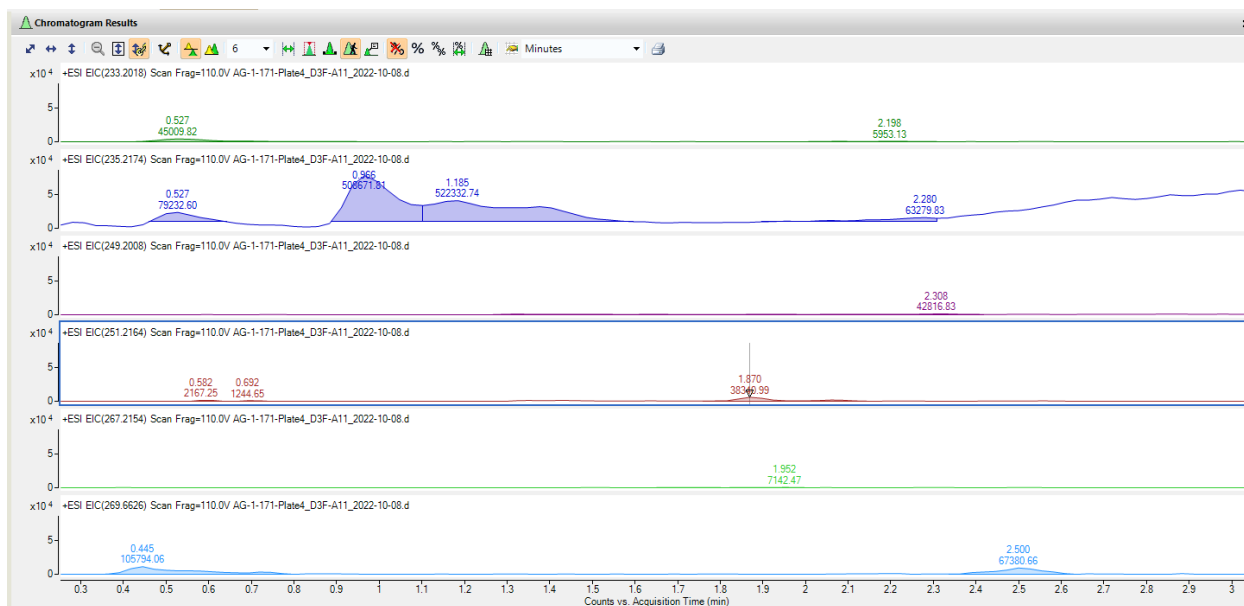
	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



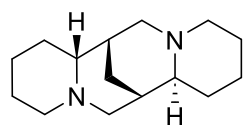
Discovered Reaction 171. Substrate_371 + NHI_299 = hydroxylation



	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



Discovered Reaction 172. Substrate_371 + NHI_302 = desaturation



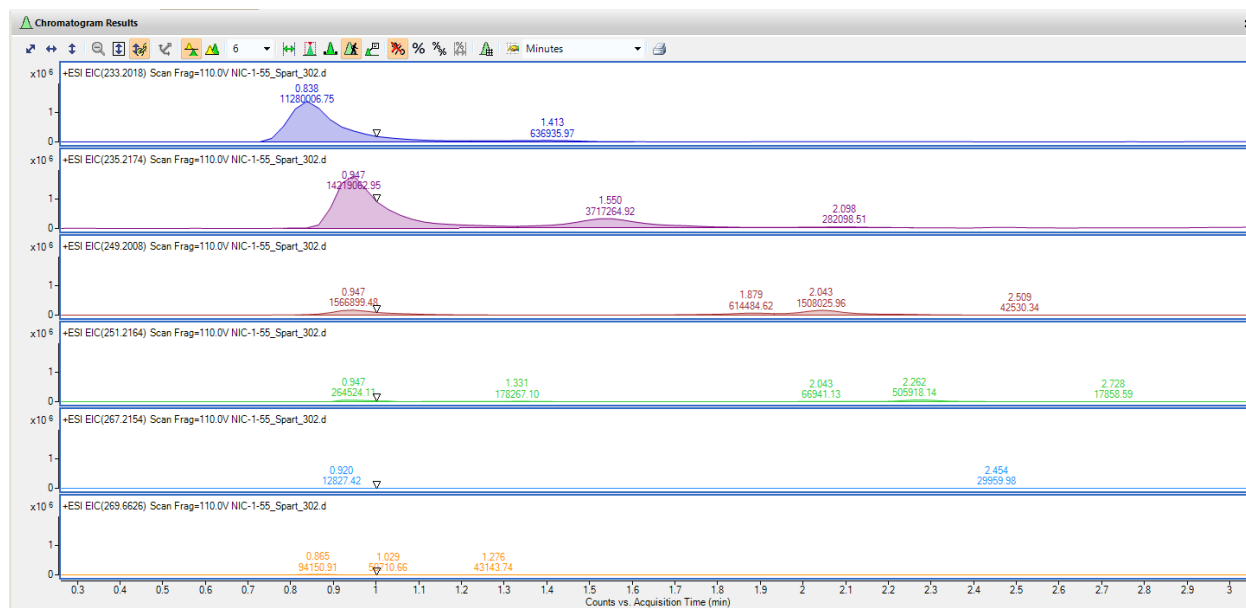
371, sparteine
 $[M+H]^+ = 235.2174$

NHI_302 40% vol whole cell
 2 mM α -KG, 1 mM NaAsc
 0.1 mM $FeSO_4$

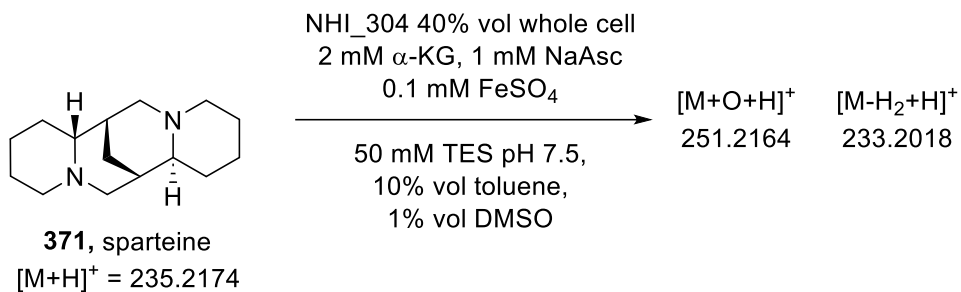
50 mM TES pH 7.5,
 10% vol toluene,
 1% vol DMSO

$[M-H_2+H]^+$
 233.2018

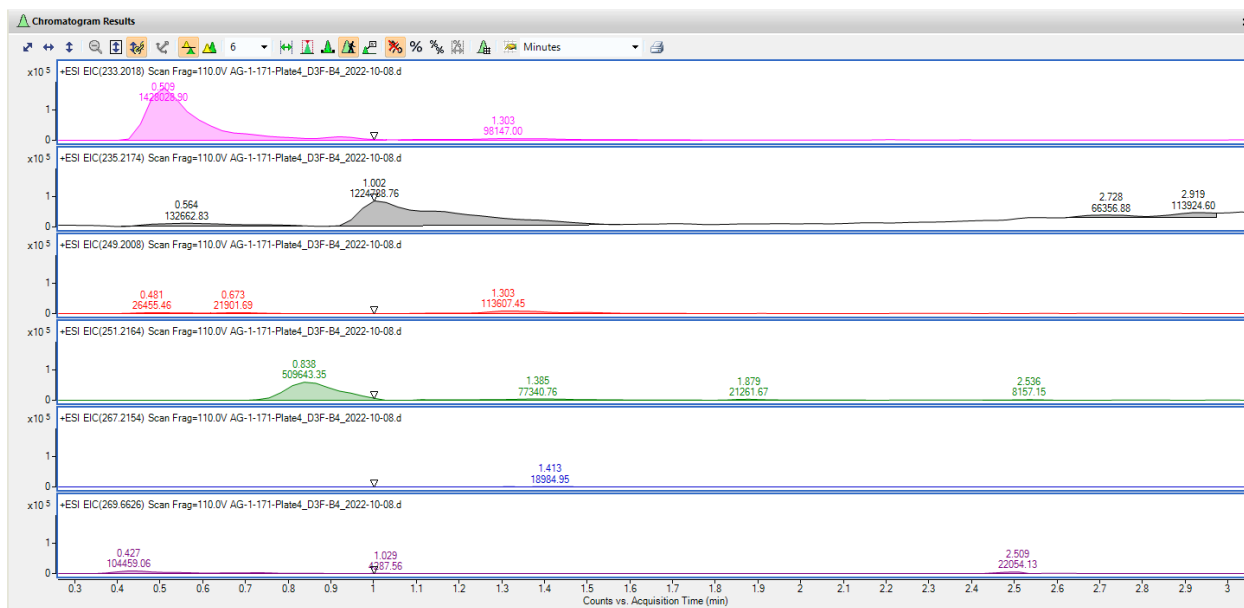
	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



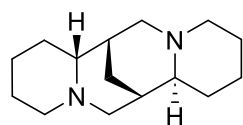
Discovered Reaction 173. Substrate **371** + NHI_304 = hydroxylation and desaturation



	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



Discovered Reaction 174. Substrate_371 + NHI_305 = desaturation



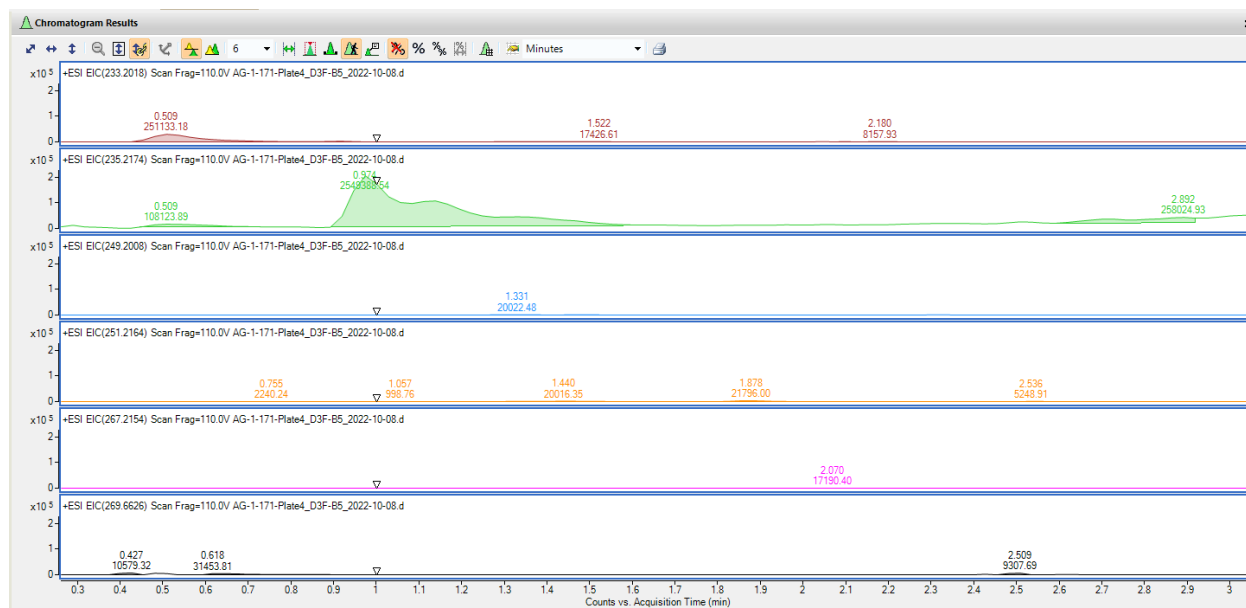
371, sparteine
 $[M+H]^+ = 235.2174$

NHI_305 40% vol whole cell
 2 mM α -KG, 1 mM NaAsc
 0.1 mM $FeSO_4$

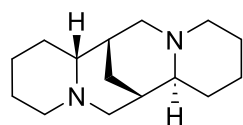
50 mM TES pH 7.5,
 10% vol toluene,
 1% vol DMSO

$[M-H_2+H]^+$
 233.2018

	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



Discovered Reaction 175. Substrate_371 + NHI_306 = desaturation



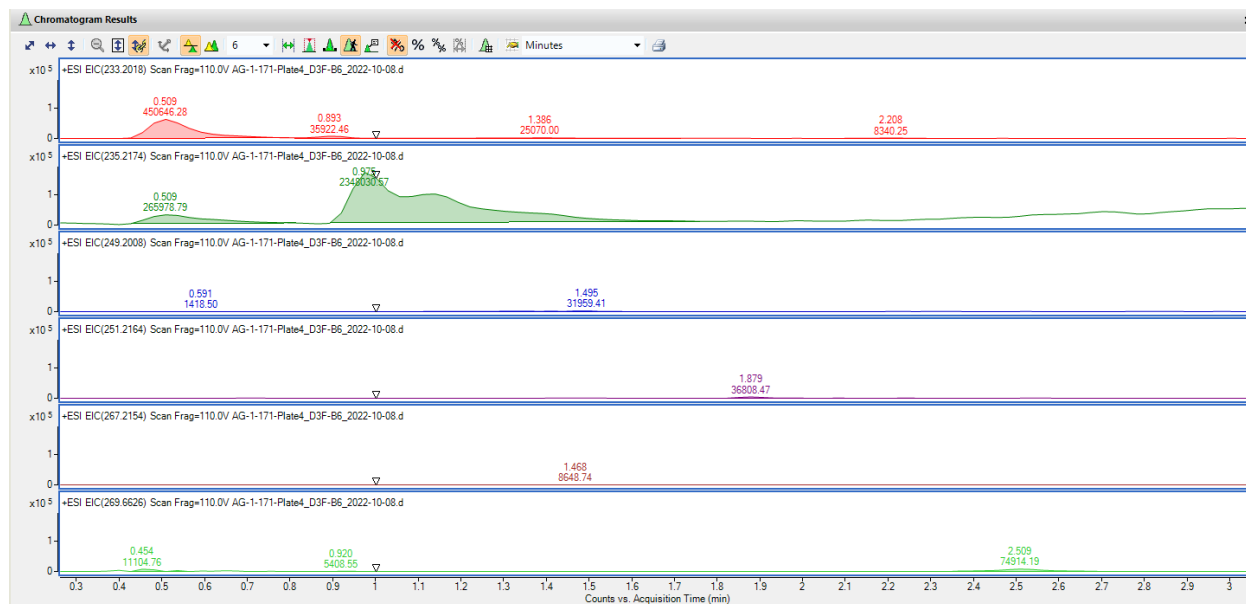
371, sparteine
 $[M+H]^+ = 235.2174$

NHI_306 40% vol whole cell
 2 mM α -KG, 1 mM NaAsc
 0.1 mM FeSO₄

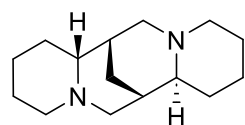
50 mM TES pH 7.5,
 10% vol toluene,
 1% vol DMSO

$[M-H_2+H]^+$
 233.2018

	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



Discovered Reaction 176. Substrate_371 + NHI_307 = desaturation



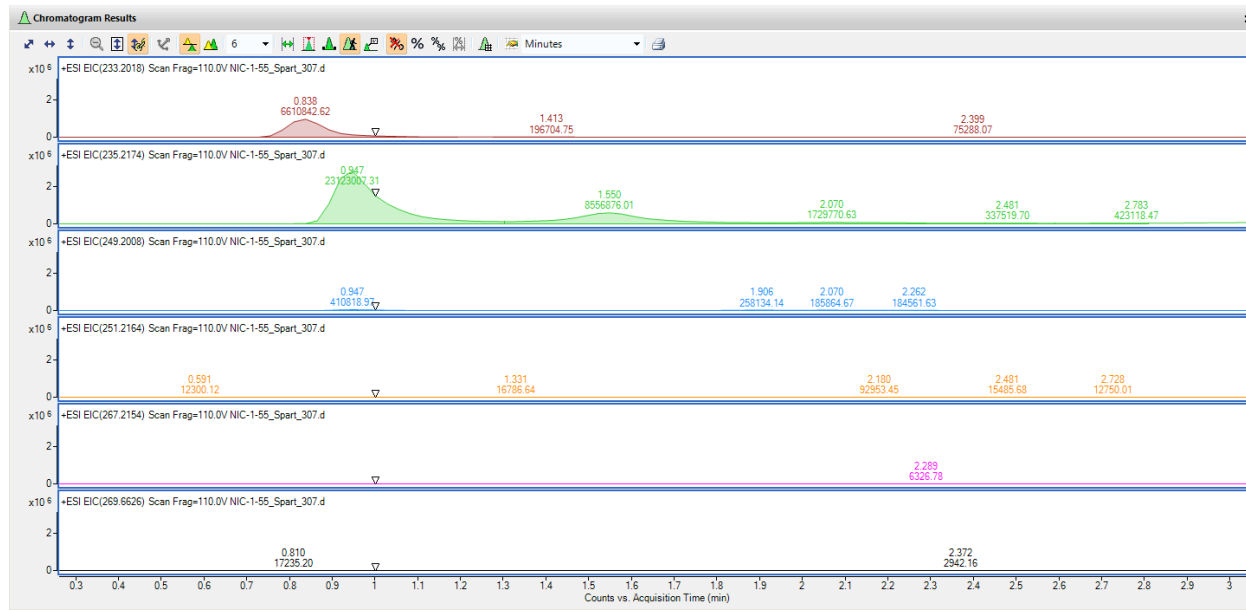
371, sparteine
 $[M+H]^+ = 235.2174$

NHI_307 40% vol whole cell
 2 mM α -KG, 1 mM NaAsc
 0.1 mM FeSO₄

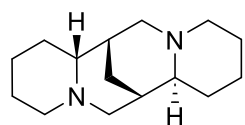
50 mM TES pH 7.5,
 10% vol toluene,
 1% vol DMSO

$[M-H_2+H]^+$
 233.2018

	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



Discovered Reaction 177. Substrate **371** + NHI_308 = desaturation



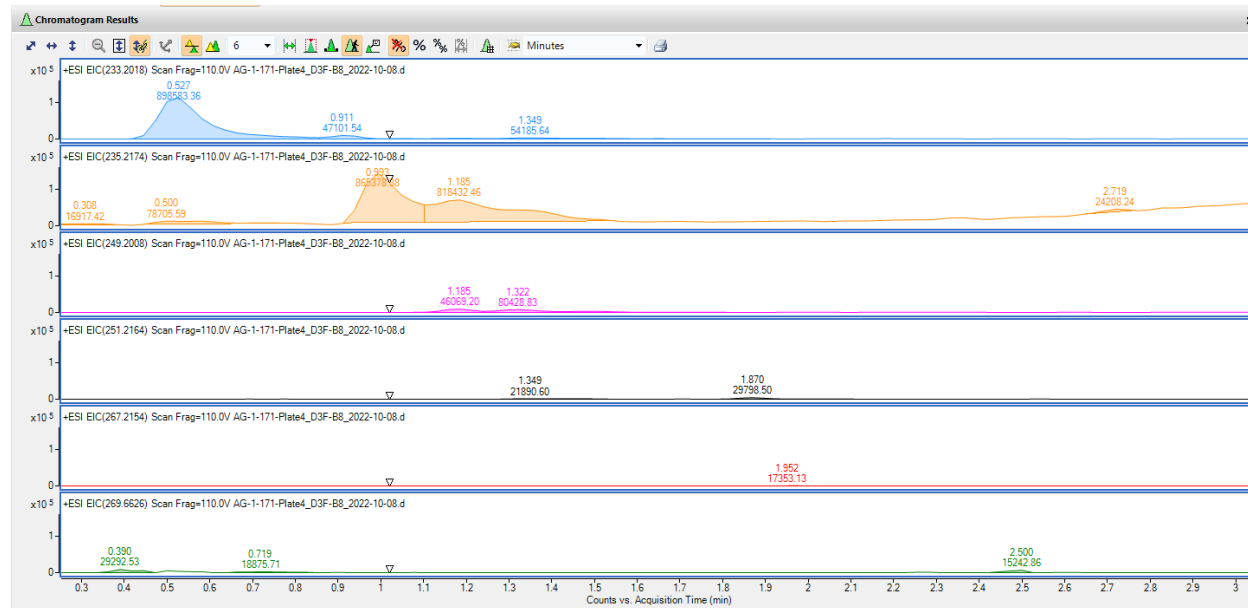
371, sparteine
[M+H]⁺ = 235.2174

NHI_308 40% vol whole cell
2 mM α-KG, 1 mM NaAsc
0.1 mM FeSO₄

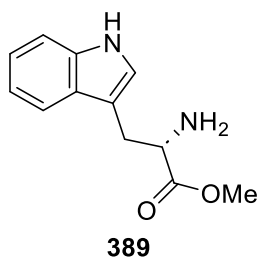
50 mM TES pH 7.5,
10% vol toluene,
1% vol DMSO

[M-H₂+H]⁺
233.2018

	Neutral	Positive	Negative
desaturation	232.1939	233.2018	231.1861
substrate	234.2096	235.2174	233.2018
oxidation/desaturation	248.1929	249.2008	247.1851
hydroxylation	250.2086	251.2164	249.2008
dihydroxylation	266.2076	267.2154	265.1998
chlorination	268.6548	269.6626	267.6469



Discovered Reaction 178. Substrate_389 + NHI_177 = hydroxylation



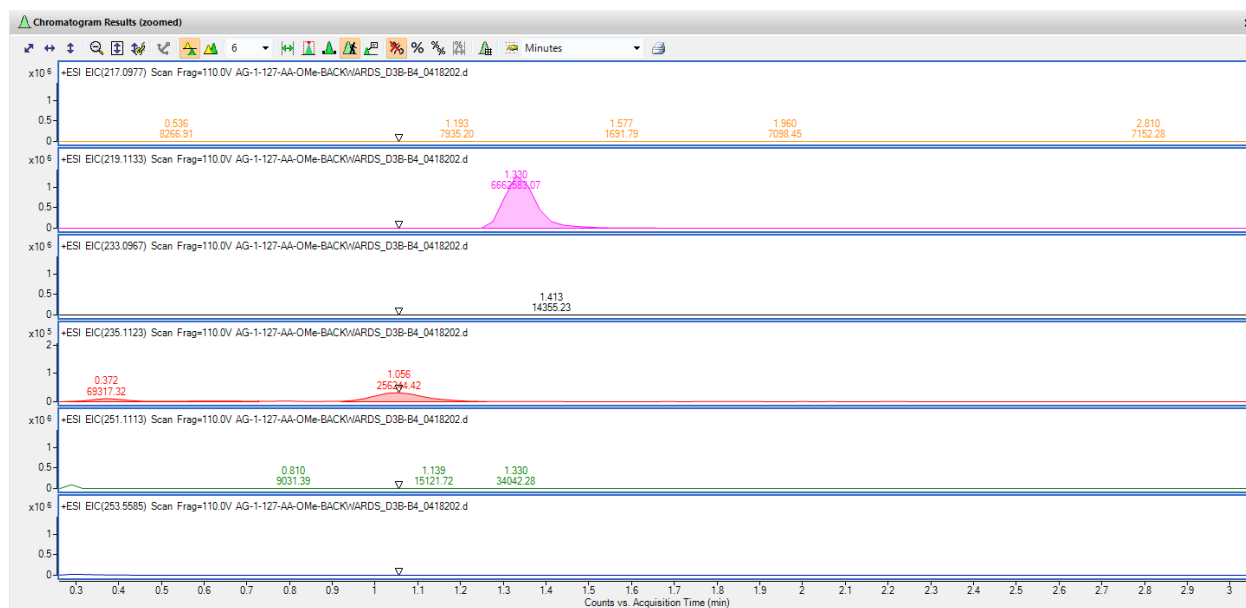
$[M+H]^+ = 219.1133$

NHI_177 40% vol whole cell
2 mM α -KG, 1 mM NaAsc
0.1 mM FeSO₄

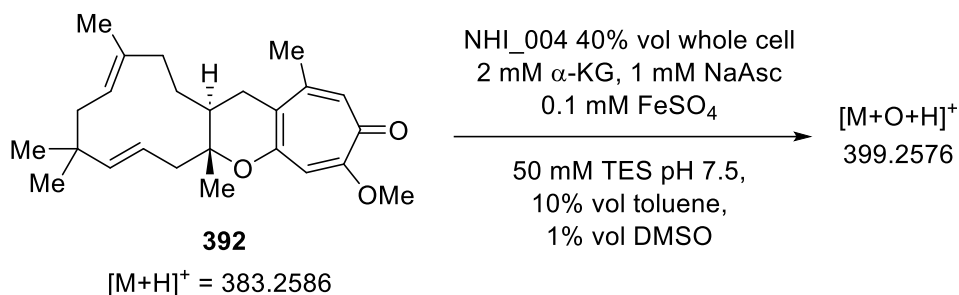
50 mM TES pH 7.5,
10% vol toluene,
1% vol DMSO

$[M+O+H]^+$
235.1123

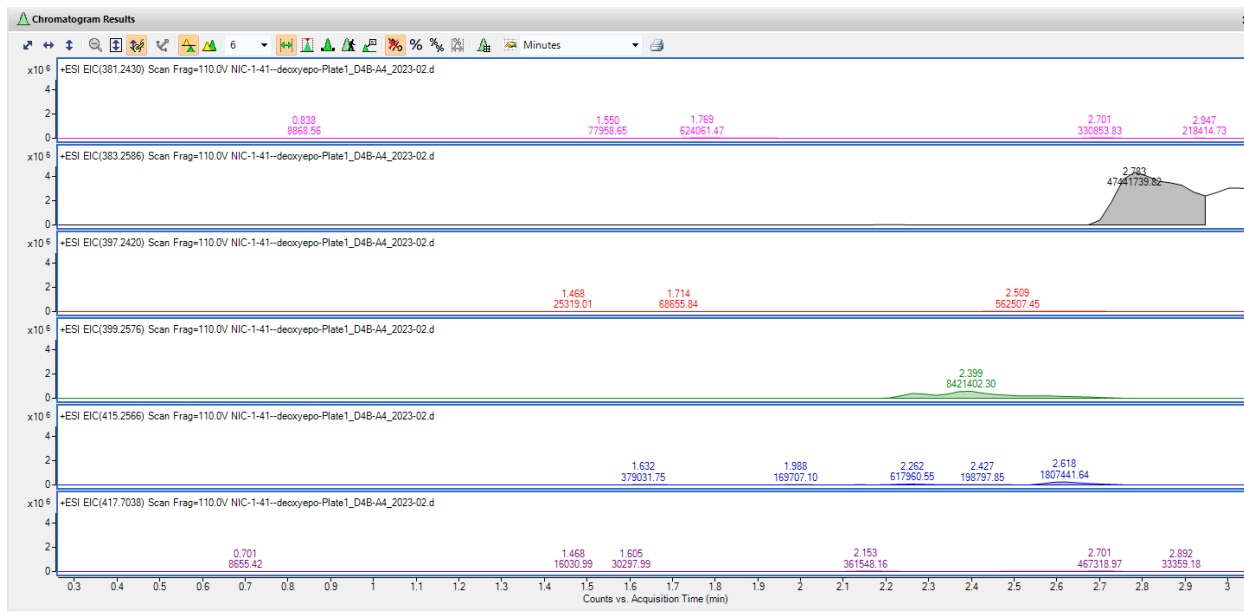
	Neutral	Positive	Negative
desaturation	216.0898	217.0977	215.0820
substrate	218.1055	219.1133	217.0977
oxidation/desaturation	232.0888	233.0967	231.0810
hydroxylation	234.1045	235.1123	233.0967
dihydroxylation	250.1035	251.1113	249.0957
chlorination	252.5507	253.5585	251.5428



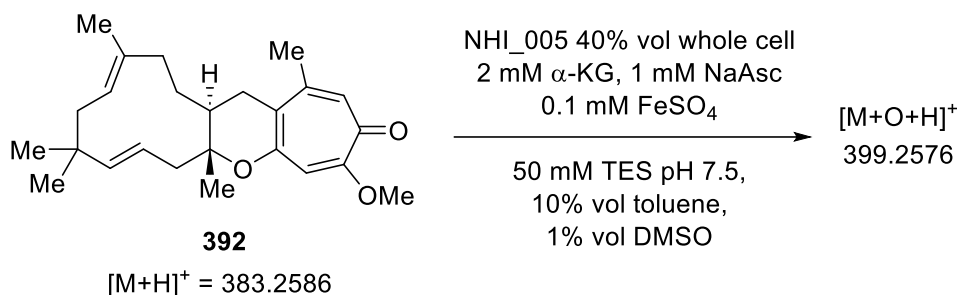
Discovered Reaction 179. Substrate_392 + NHI_004 = hydroxylation



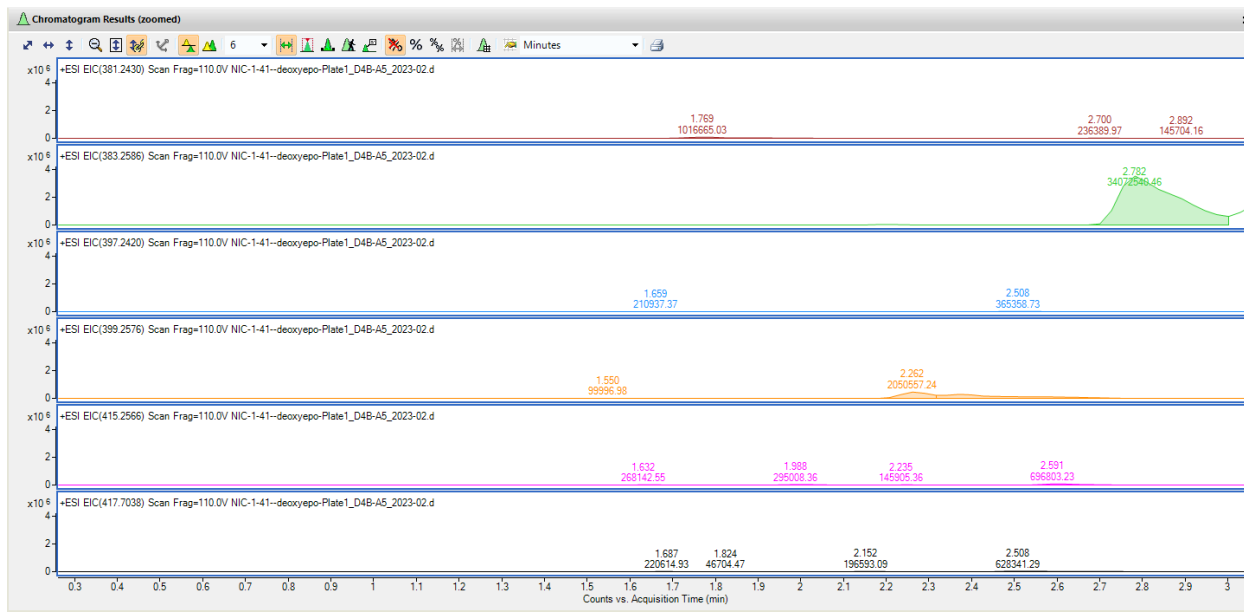
	Neutral	Positive	Negative
desaturation	380.2351	381.2430	379.2273
substrate	382.2508	383.2586	381.2430
oxidation/desaturation	396.2341	397.2420	395.2263
hydroxylation	398.2498	399.2576	397.2420
dihydroxylation	414.2488	415.2566	413.2410
chlorination	416.6960	417.7038	415.6881



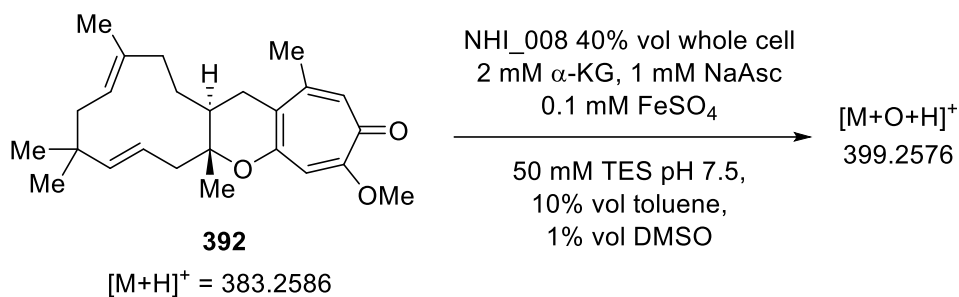
Discovered Reaction 180. Substrate_392 + NHI_005 = hydroxylation



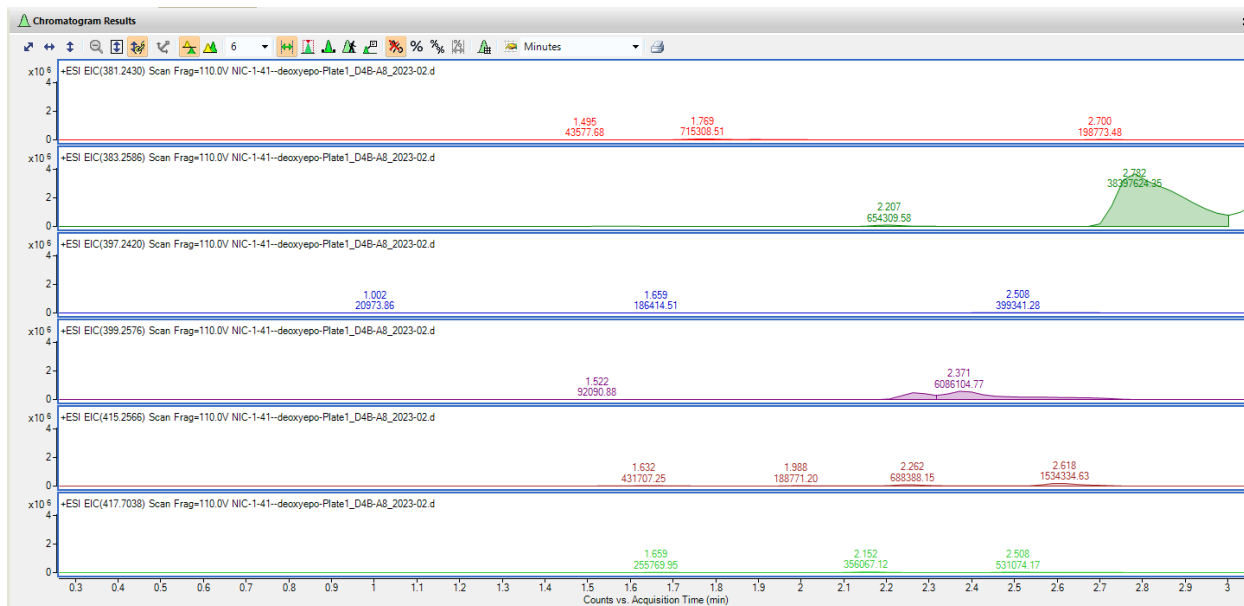
	Neutral	Positive	Negative
desaturation	380.2351	381.2430	379.2273
substrate	382.2508	383.2586	381.2430
oxidation/desaturation	396.2341	397.2420	395.2263
hydroxylation	398.2498	399.2576	397.2420
dihydroxylation	414.2488	415.2566	413.2410
chlorination	416.6960	417.7038	415.6881



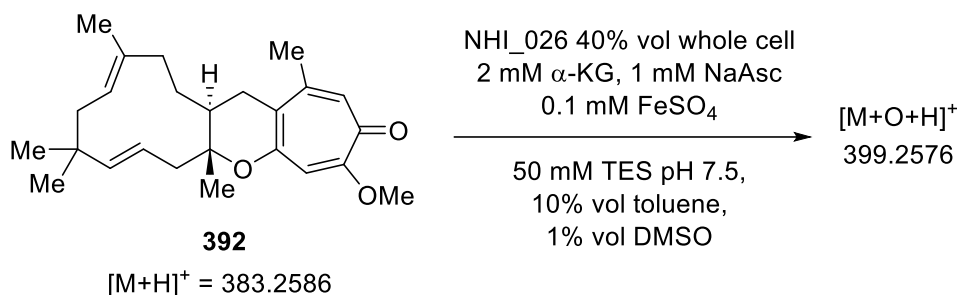
Discovered Reaction 181. Substrate **392** + NHI_008 = hydroxylation



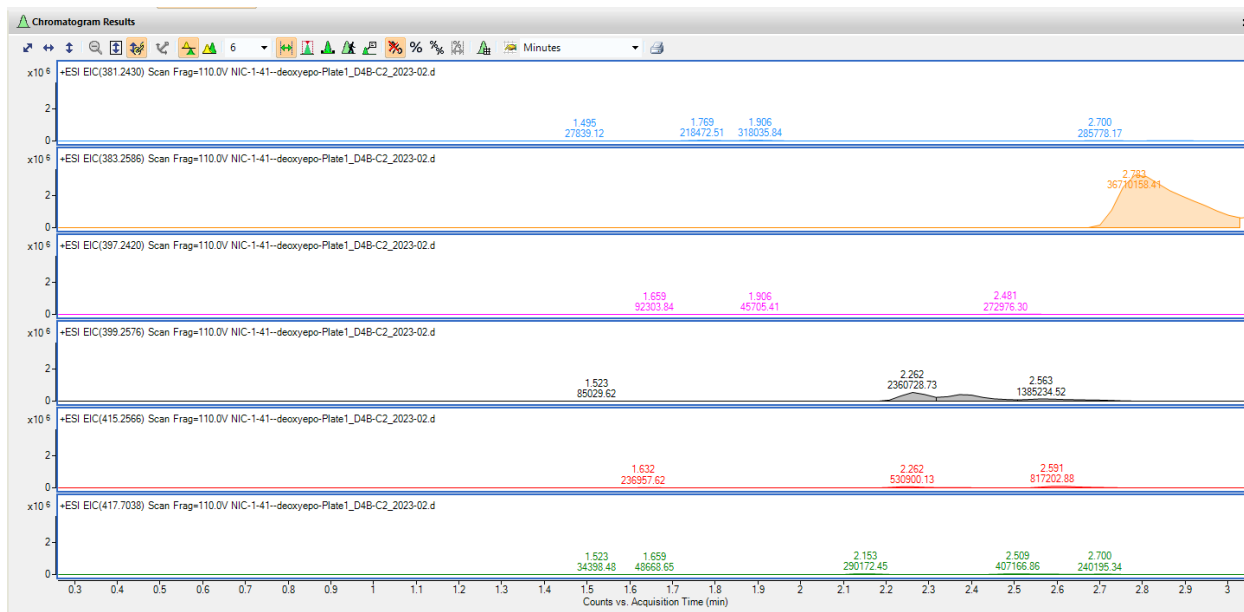
	Neutral	Positive	Negative
desaturation	380.2351	381.2430	379.2273
substrate	382.2508	383.2586	381.2430
oxidation/desaturation	396.2341	397.2420	395.2263
hydroxylation	398.2498	399.2576	397.2420
dihydroxylation	414.2488	415.2566	413.2410
chlorination	416.6960	417.7038	415.6881



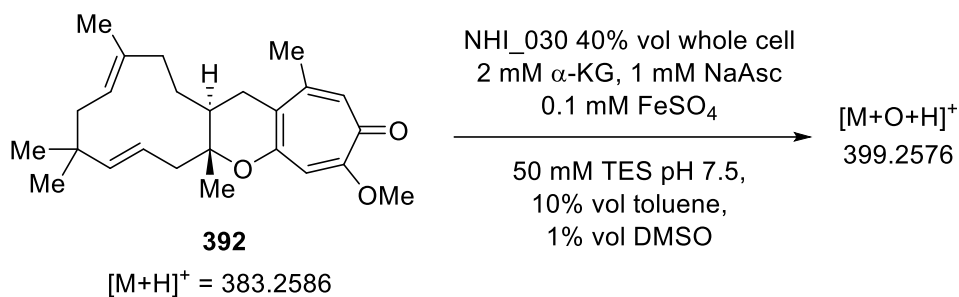
Discovered Reaction 182. Substrate_392 + NHI_026 = hydroxylation



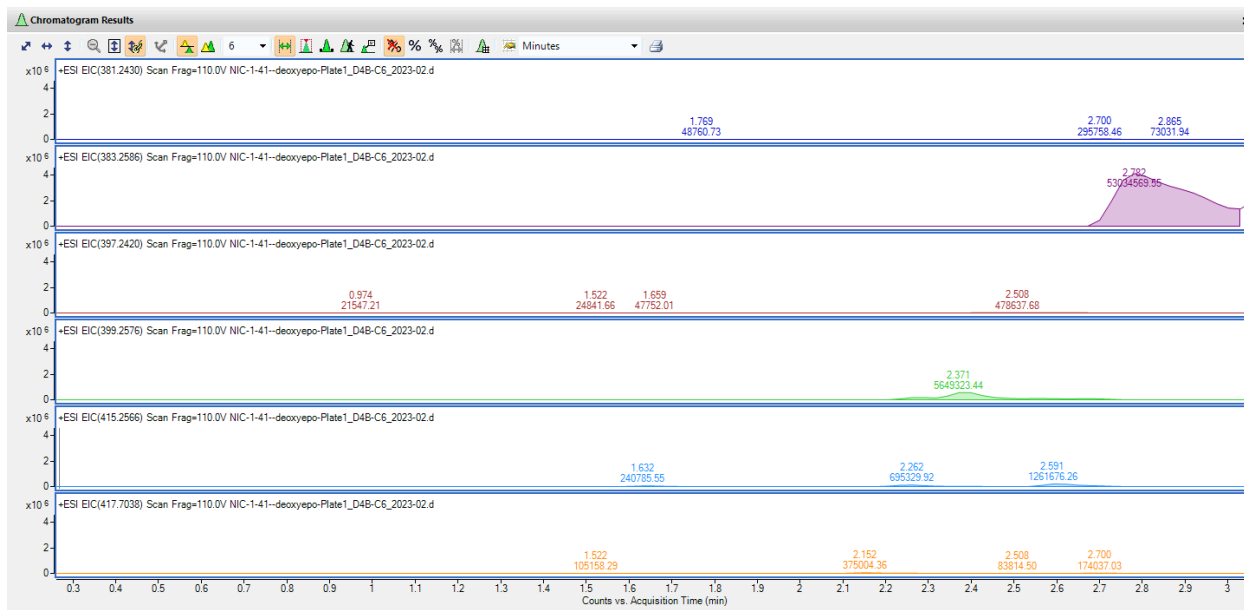
	Neutral	Positive	Negative
desaturation	380.2351	381.2430	379.2273
substrate	382.2508	383.2586	381.2430
oxidation/desaturation	396.2341	397.2420	395.2263
hydroxylation	398.2498	399.2576	397.2420
dihydroxylation	414.2488	415.2566	413.2410
chlorination	416.6960	417.7038	415.6881



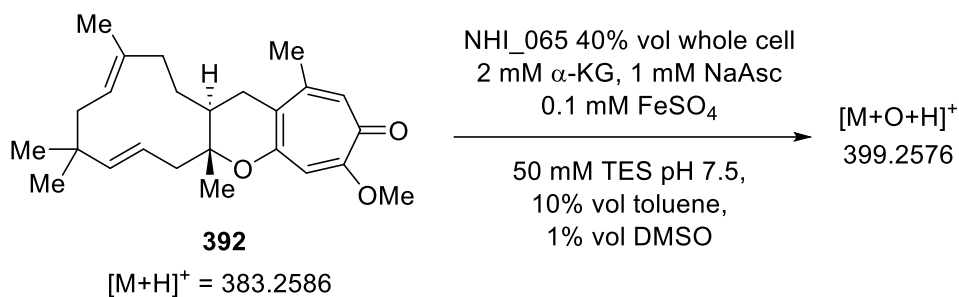
Discovered Reaction 183. Substrate_392 + NHI_030 = hydroxylation



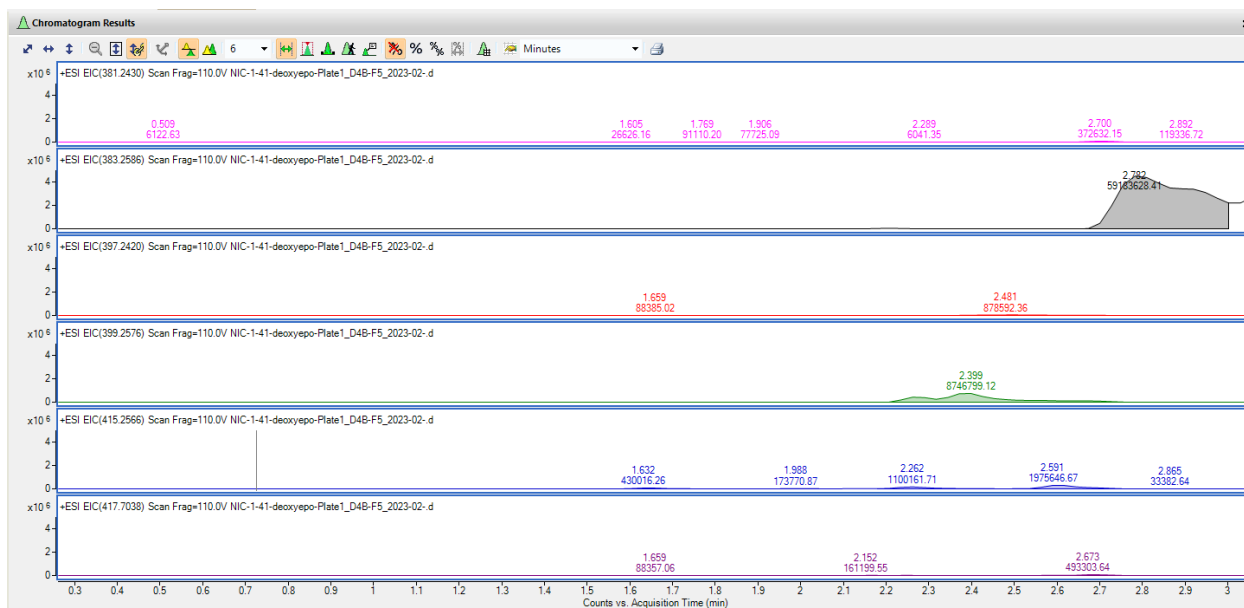
	Neutral	Positive	Negative
desaturation	380.2351	381.2430	379.2273
substrate	382.2508	383.2586	381.2430
oxidation/desaturation	396.2341	397.2420	395.2263
hydroxylation	398.2498	399.2576	397.2420
dihydroxylation	414.2488	415.2566	413.2410
chlorination	416.6960	417.7038	415.6881



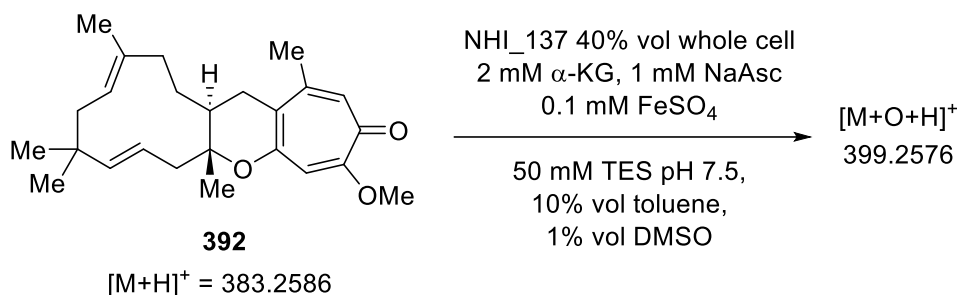
Discovered Reaction 184. Substrate_392 + NHI_065 = hydroxylation



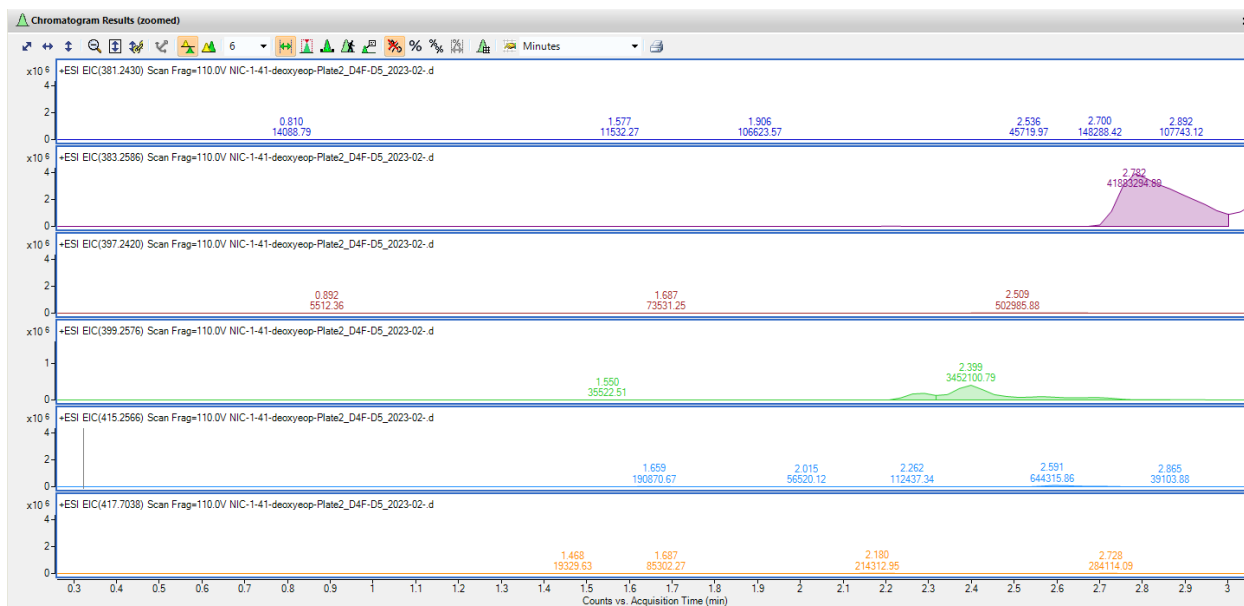
	Neutral	Positive	Negative
desaturation	380.2351	381.2430	379.2273
substrate	382.2508	383.2586	381.2430
oxidation/desaturation	396.2341	397.2420	395.2263
hydroxylation	398.2498	399.2576	397.2420
dihydroxylation	414.2488	415.2566	413.2410
chlorination	416.6960	417.7038	415.6881



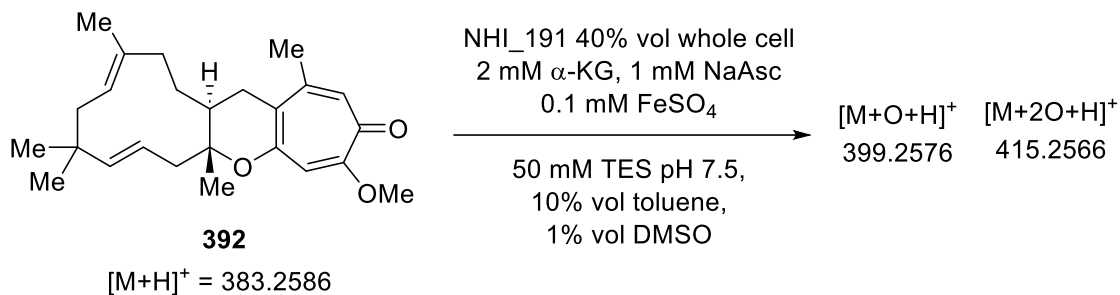
Discovered Reaction 185. Substrate_392 + NHI_137 = hydroxylation



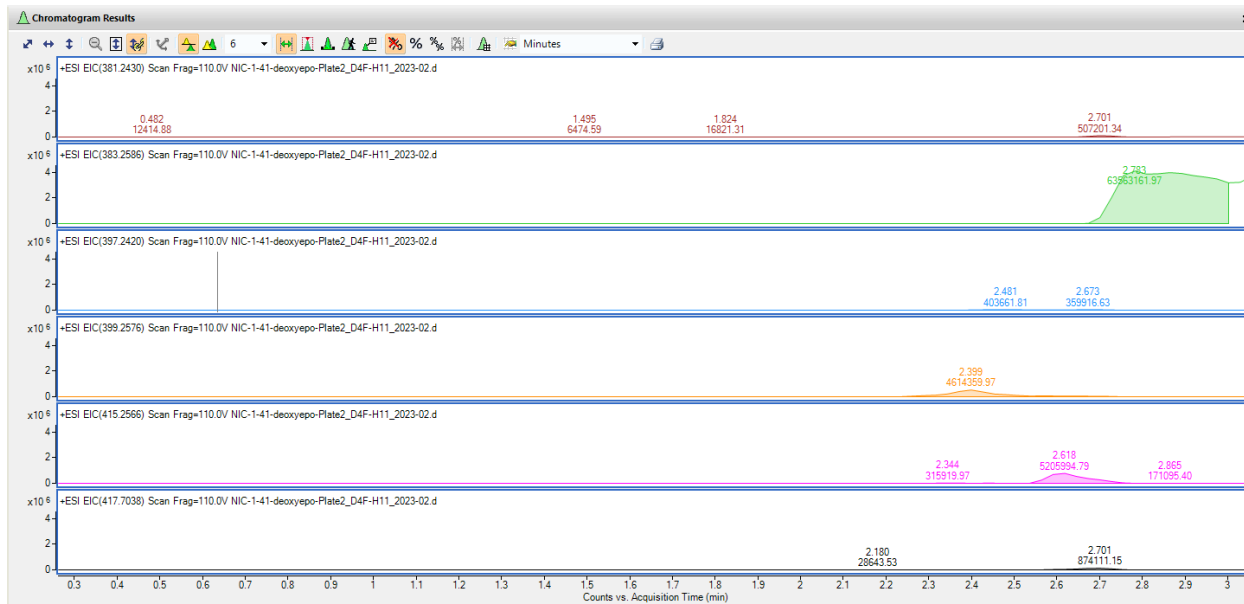
	Neutral	Positive	Negative
desaturation	380.2351	381.2430	379.2273
substrate	382.2508	383.2586	381.2430
oxidation/desaturation	396.2341	397.2420	395.2263
hydroxylation	398.2498	399.2576	397.2420
dihydroxylation	414.2488	415.2566	413.2410
chlorination	416.6960	417.7038	415.6881



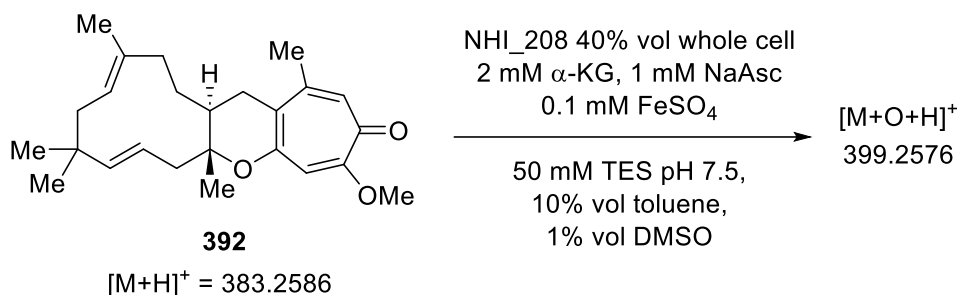
Discovered Reaction 186. Substrate_392 + NHI_191 = hydroxylation and dihydroxylation



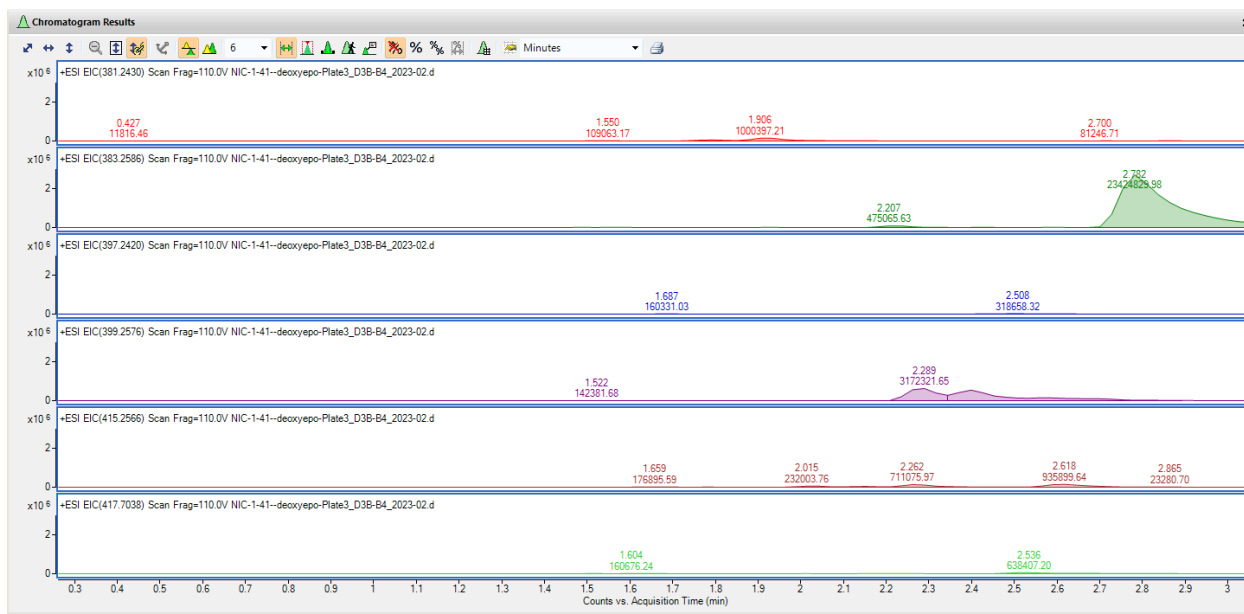
	Neutral	Positive	Negative
desaturation	380.2351	381.2430	379.2273
substrate	382.2508	383.2586	381.2430
oxidation/desaturation	396.2341	397.2420	395.2263
hydroxylation	398.2498	399.2576	397.2420
dihydroxylation	414.2488	415.2566	413.2410
chlorination	416.6960	417.7038	415.6881



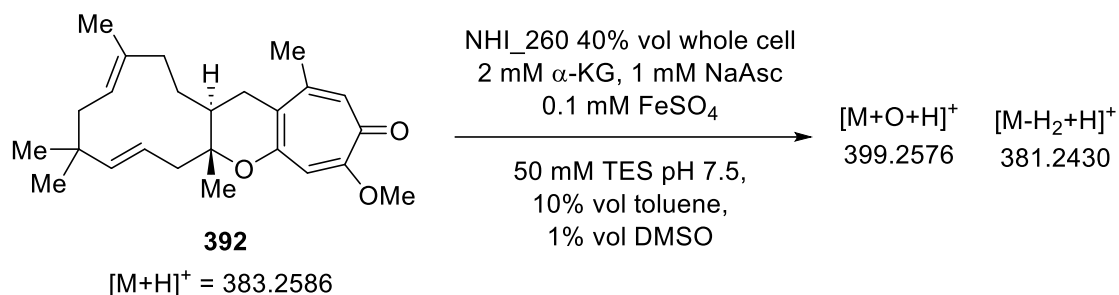
Discovered Reaction 187. Substrate_392 + NHI_208 = hydroxylation



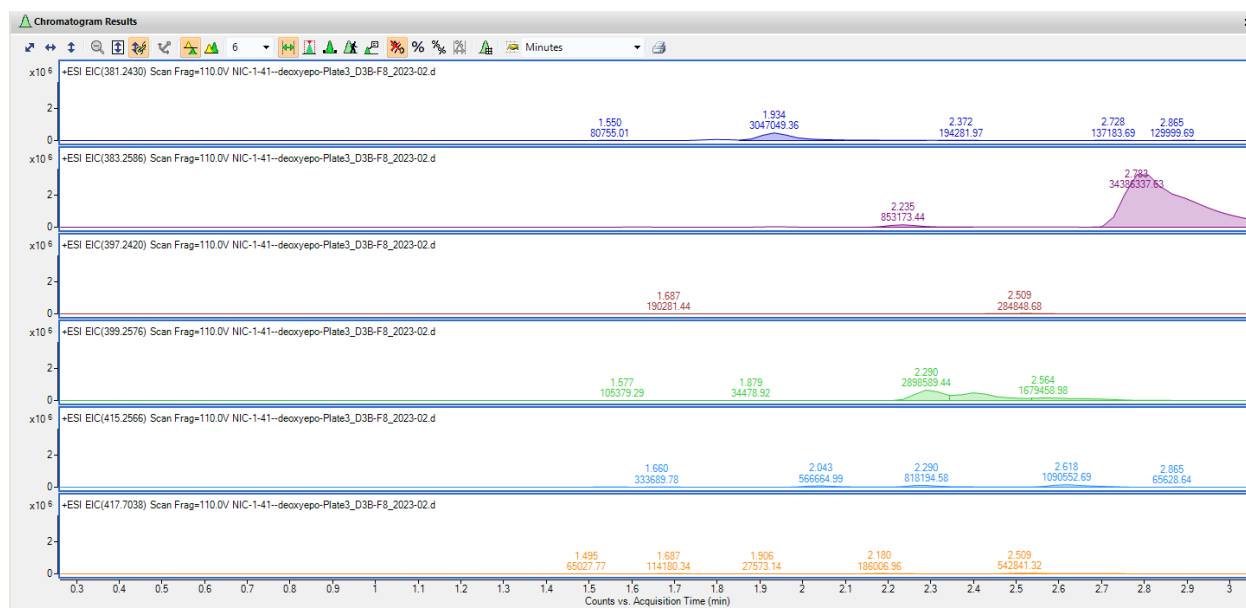
	Neutral	Positive	Negative
desaturation	380.2351	381.2430	379.2273
substrate	382.2508	383.2586	381.2430
oxidation/desaturation	396.2341	397.2420	395.2263
hydroxylation	398.2498	399.2576	397.2420
dihydroxylation	414.2488	415.2566	413.2410
chlorination	416.6960	417.7038	415.6881



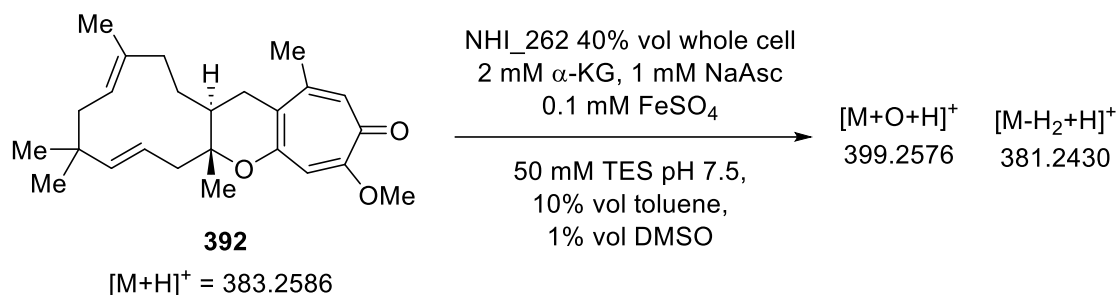
Discovered Reaction 188. Substrate **392** + NHI_260 = hydroxylation and desaturation



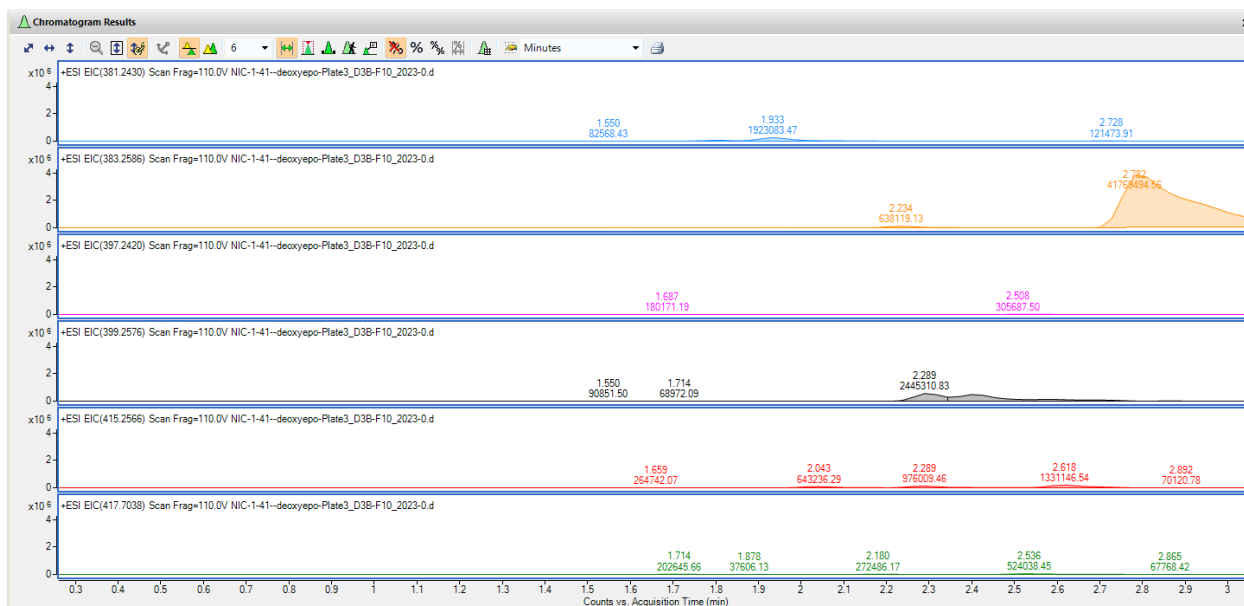
	Neutral	Positive	Negative
desaturation	380.2351	381.2430	379.2273
substrate	382.2508	383.2586	381.2430
oxidation/desaturation	396.2341	397.2420	395.2263
hydroxylation	398.2498	399.2576	397.2420
dihydroxylation	414.2488	415.2566	413.2410
chlorination	416.6960	417.7038	415.6881



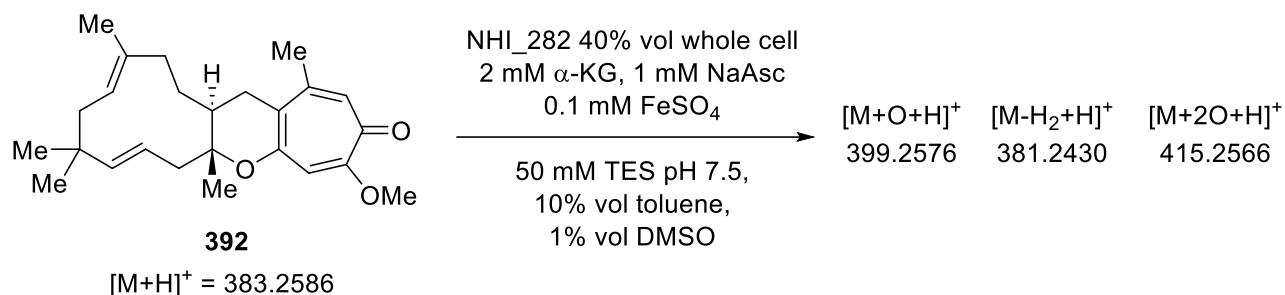
Discovered Reaction 189. Substrate_392 + NHI_262 = hydroxylation and desaturation



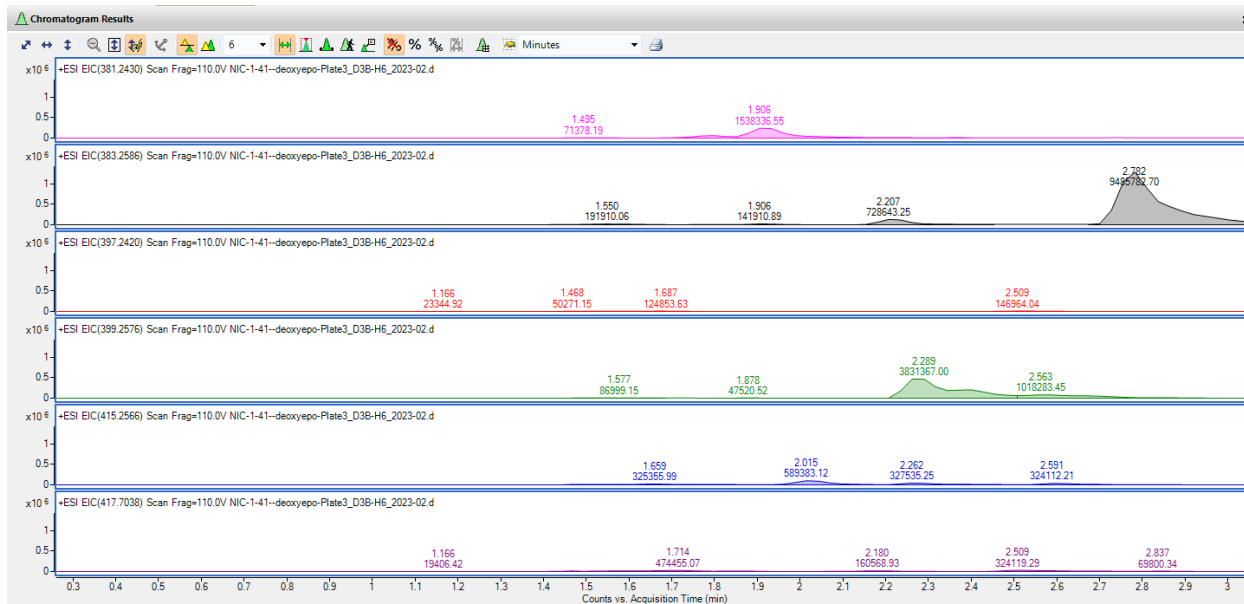
	Neutral	Positive	Negative
desaturation	380.2351	381.2430	379.2273
substrate	382.2508	383.2586	381.2430
oxidation/desaturation	396.2341	397.2420	395.2263
hydroxylation	398.2498	399.2576	397.2420
dihydroxylation	414.2488	415.2566	413.2410
chlorination	416.6960	417.7038	415.6881



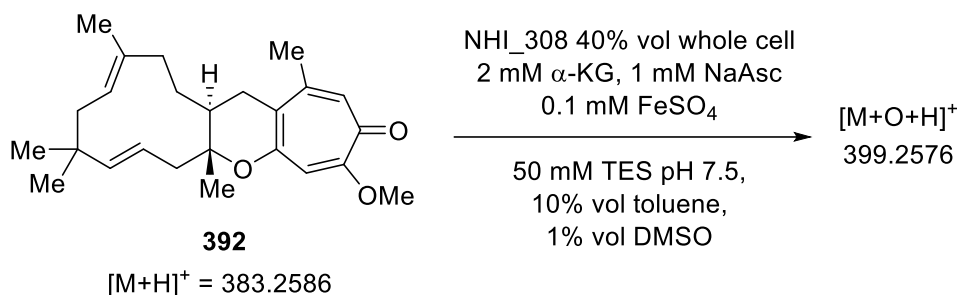
Discovered Reaction 190. Substrate_392 + NHI_282 = hydroxylation, desaturation and dihydroxylation



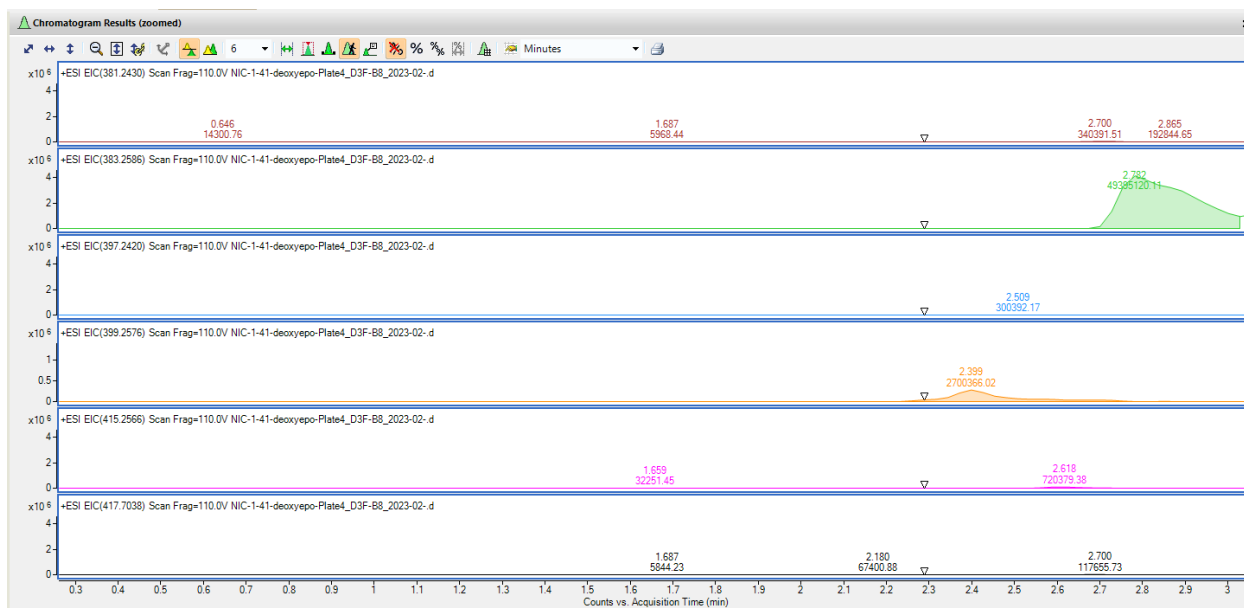
	Neutral	Positive	Negative
desaturation	380.2351	381.2430	379.2273
substrate	382.2508	383.2586	381.2430
oxidation/desaturation	396.2341	397.2420	395.2263
hydroxylation	398.2498	399.2576	397.2420
dihydroxylation	414.2488	415.2566	413.2410
chlorination	416.6960	417.7038	415.6881



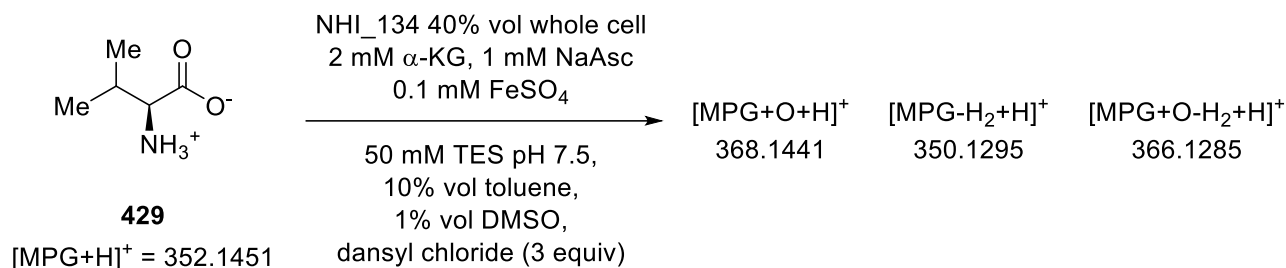
Discovered Reaction 191. Substrate_392 + NHI_308 = hydroxylation



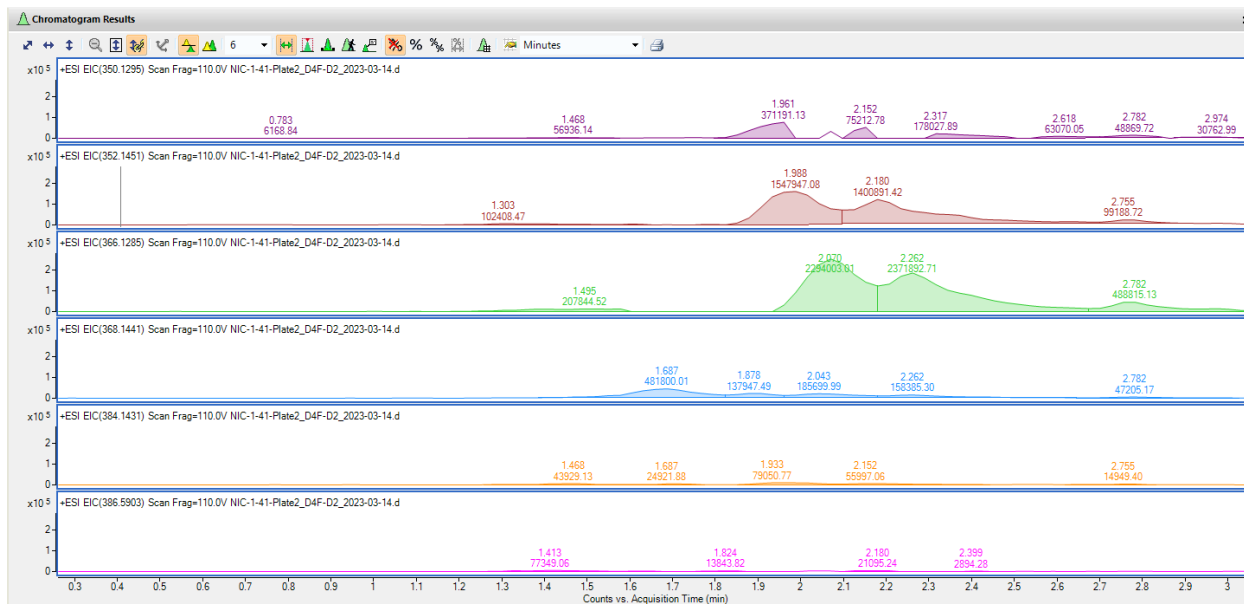
	Neutral	Positive	Negative
desaturation	380.2351	381.2430	379.2273
substrate	382.2508	383.2586	381.2430
oxidation/desaturation	396.2341	397.2420	395.2263
hydroxylation	398.2498	399.2576	397.2420
dihydroxylation	414.2488	415.2566	413.2410
chlorination	416.6960	417.7038	415.6881



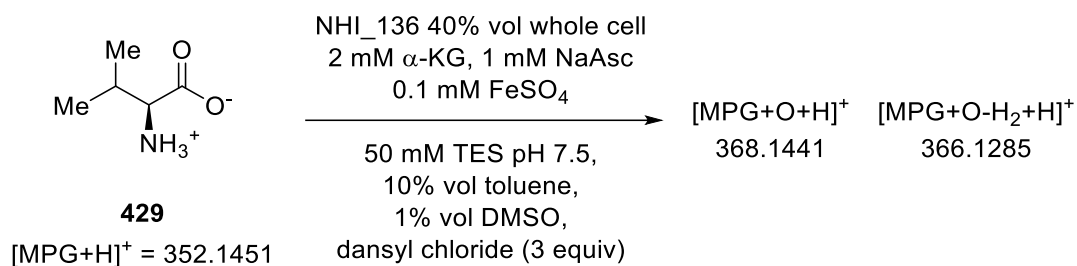
Discovered Reaction 192. Substrate_429 + NHI_134 = hydroxylation, desaturation, and oxidation/desaturation



	Neutral	Positive	Negative
desaturation	349.1216	350.1295	348.1138
substrate	351.1373	352.1451	350.1295
oxidation/desaturation	365.1206	366.1285	364.1128
hydroxylation	367.1363	368.1441	366.1285
dihydroxylation	383.1353	384.1431	382.1275
chlorination	385.5825	386.5903	384.5746



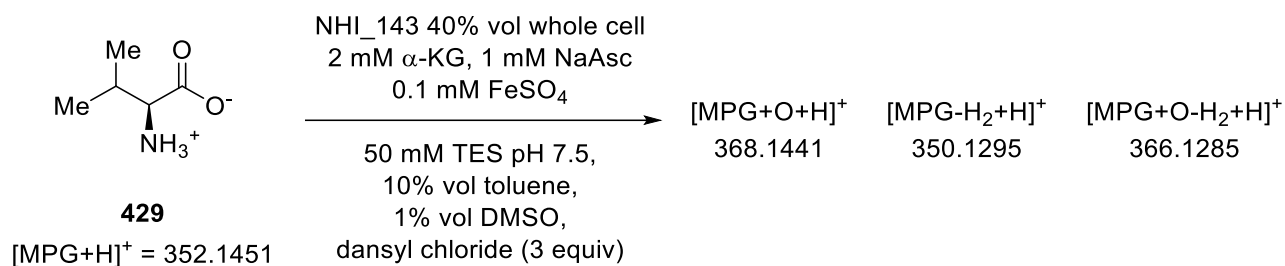
Discovered Reaction 193. Substrate_429 + NHI_136 = hydroxylation and oxidation/desaturation



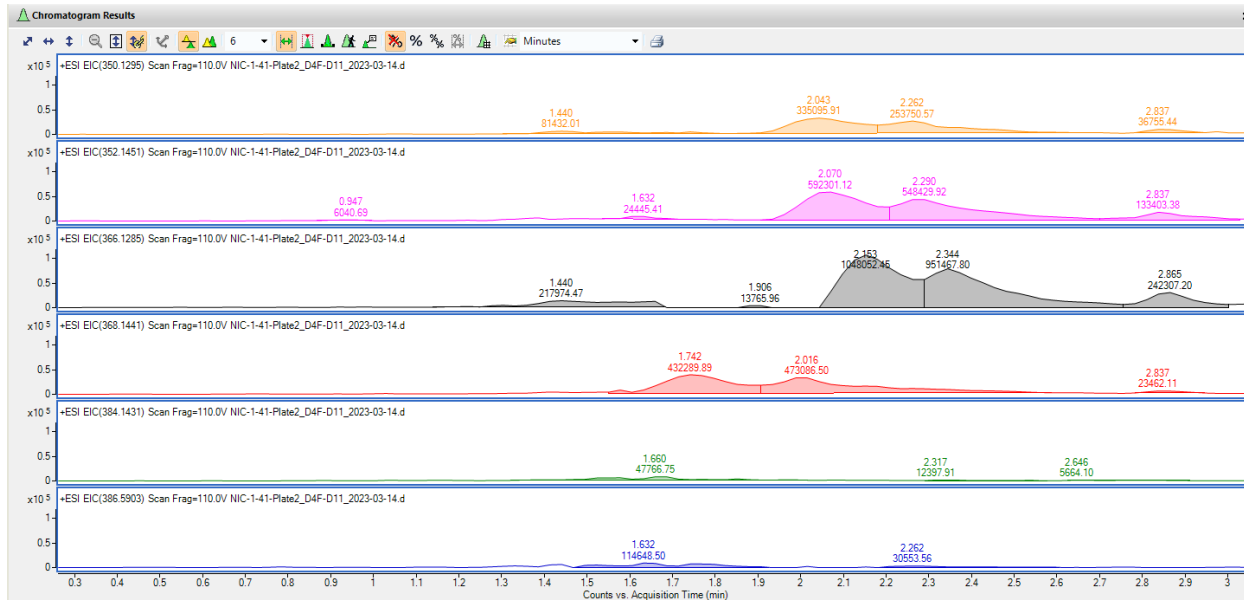
	Neutral	Positive	Negative
desaturation	349.1216	350.1295	348.1138
substrate	351.1373	352.1451	350.1295
oxidation/desaturation	365.1206	366.1285	364.1128
hydroxylation	367.1363	368.1441	366.1285
dihydroxylation	383.1353	384.1431	382.1275
chlorination	385.5825	386.5903	384.5746



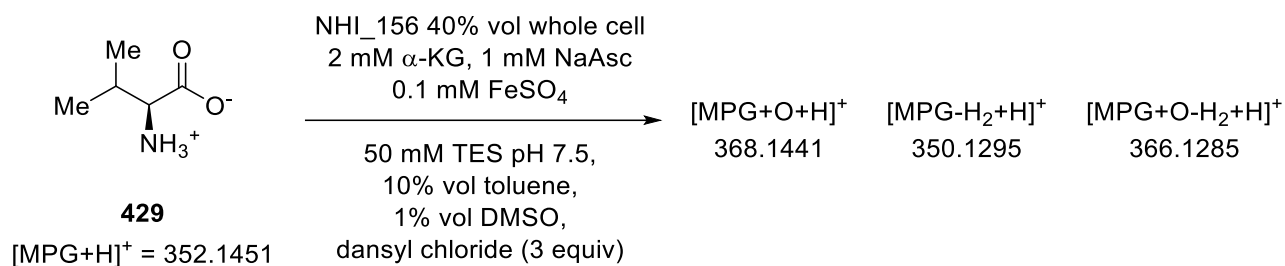
Discovered Reaction 194. Substrate_429 + NHI_143 = hydroxylation, desaturation, oxidation/desaturation



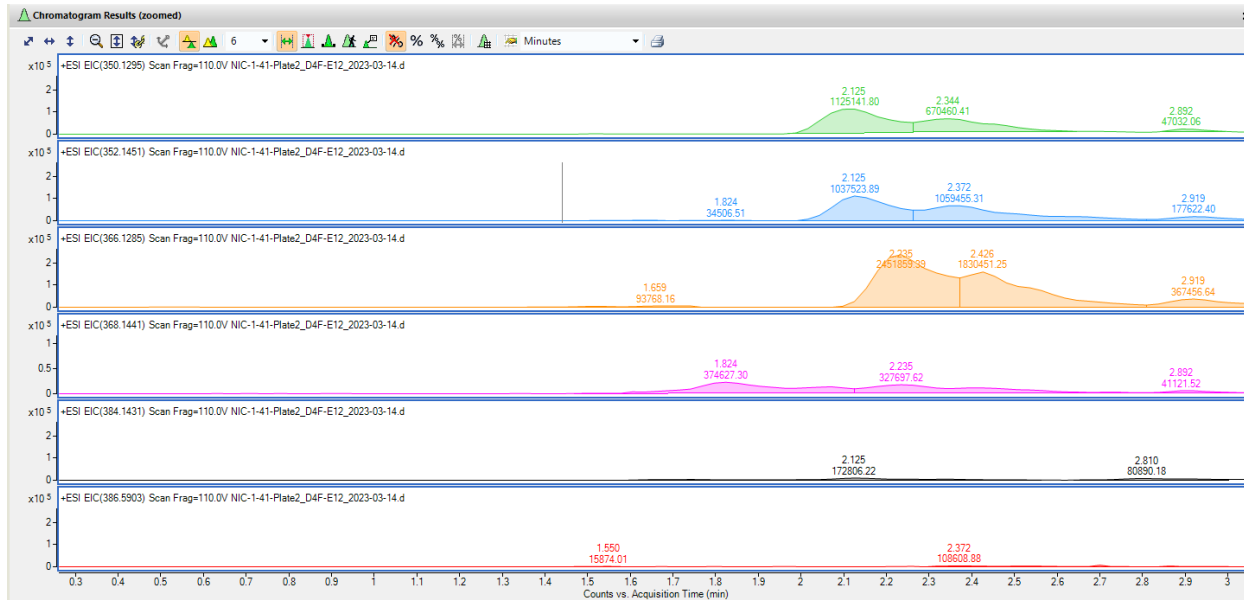
	Neutral	Positive	Negative
desaturation	349.1216	350.1295	348.1138
substrate	351.1373	352.1451	350.1295
oxidation/desaturation	365.1206	366.1285	364.1128
hydroxylation	367.1363	368.1441	366.1285
dihydroxylation	383.1353	384.1431	382.1275
chlorination	385.5825	386.5903	384.5746



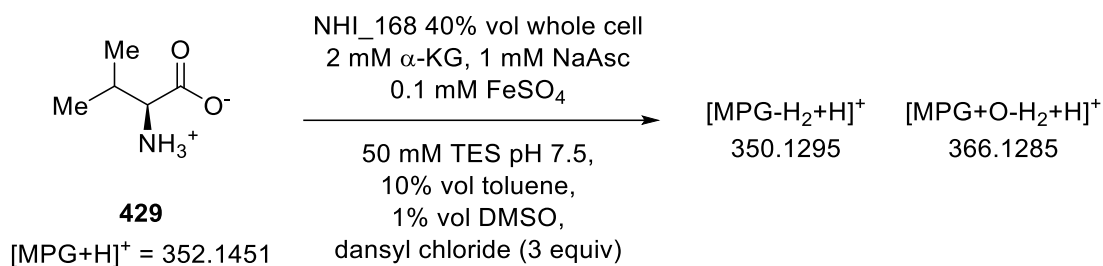
Discovered Reaction 195. Substrate_429 + NHI_156 = hydroxylation, desaturation, and oxidation/desaturation



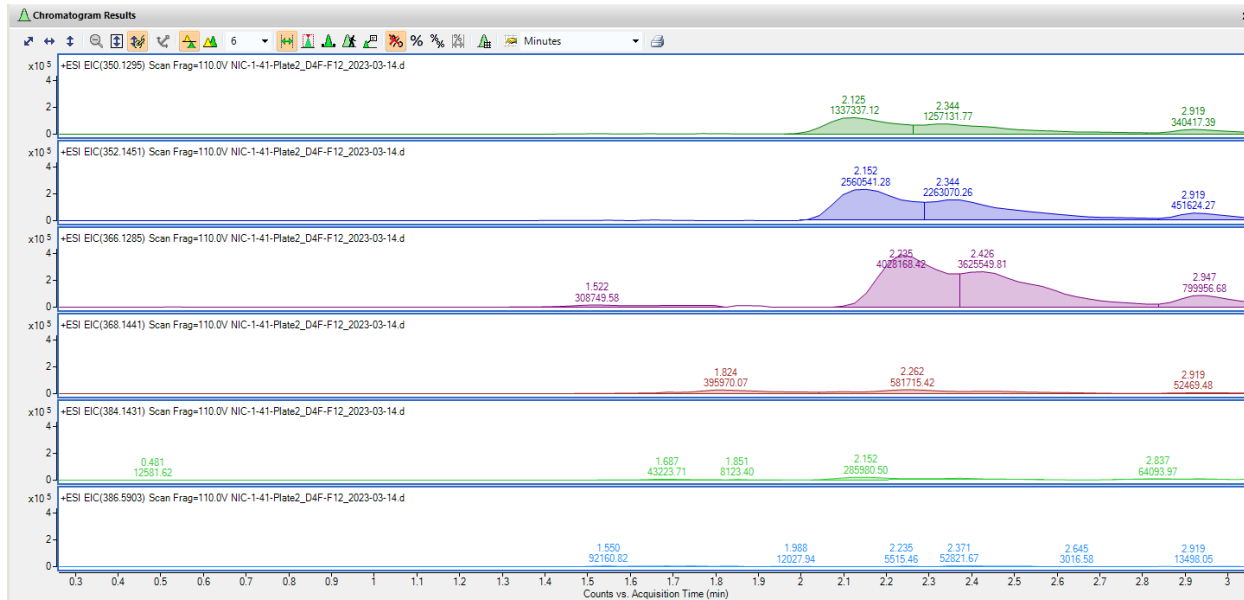
	Neutral	Positive	Negative
desaturation	349.1216	350.1295	348.1138
substrate	351.1373	352.1451	350.1295
oxidation/desaturation	365.1206	366.1285	364.1128
hydroxylation	367.1363	368.1441	366.1285
dihydroxylation	383.1353	384.1431	382.1275
chlorination	385.5825	386.5903	384.5746



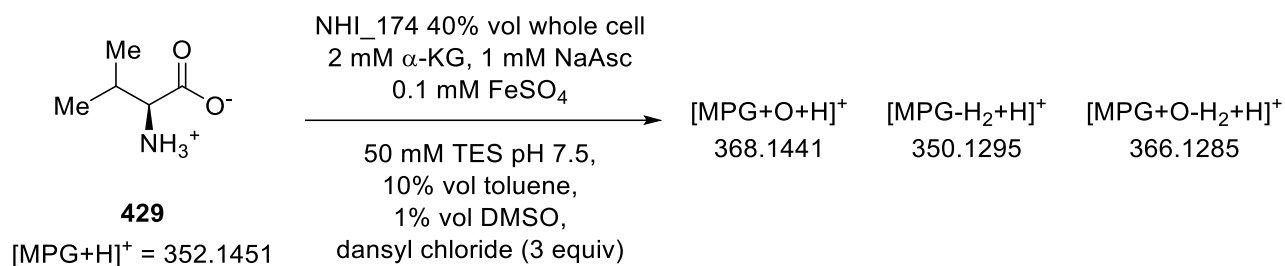
Discovered Reaction 196. Substrate_429 + NHI_168 = desaturation, and oxidation/desaturation



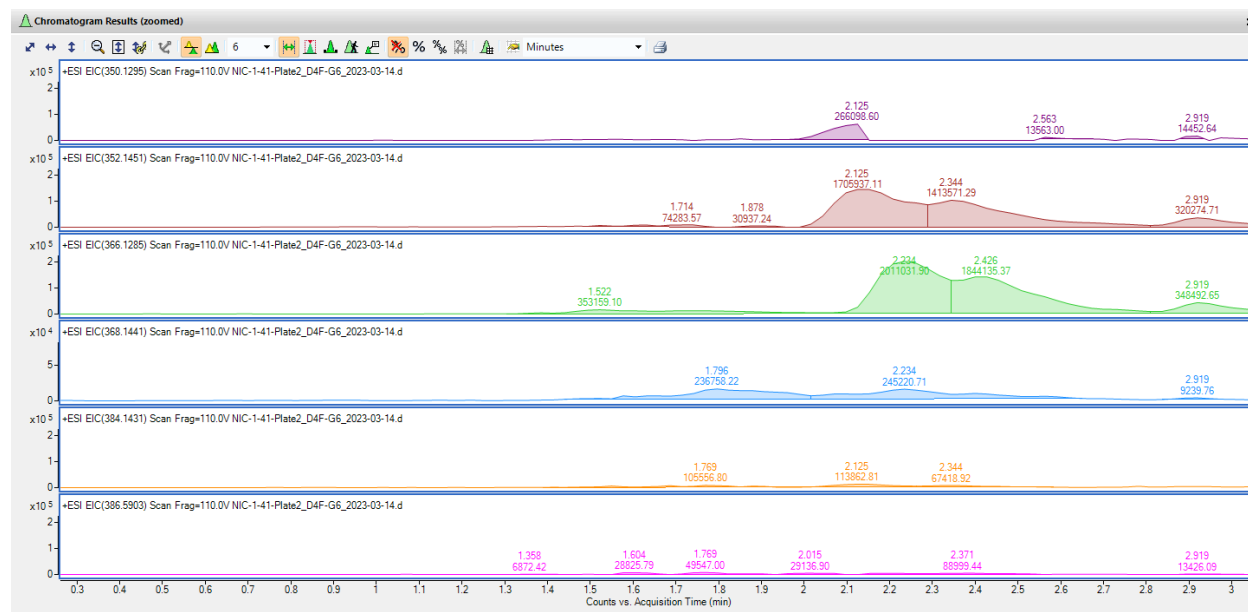
	Neutral	Positive	Negative
desaturation	349.1216	350.1295	348.1138
substrate	351.1373	352.1451	350.1295
oxidation/desaturation	365.1206	366.1285	364.1128
hydroxylation	367.1363	368.1441	366.1285
dihydroxylation	383.1353	384.1431	382.1275
chlorination	385.5825	386.5903	384.5746



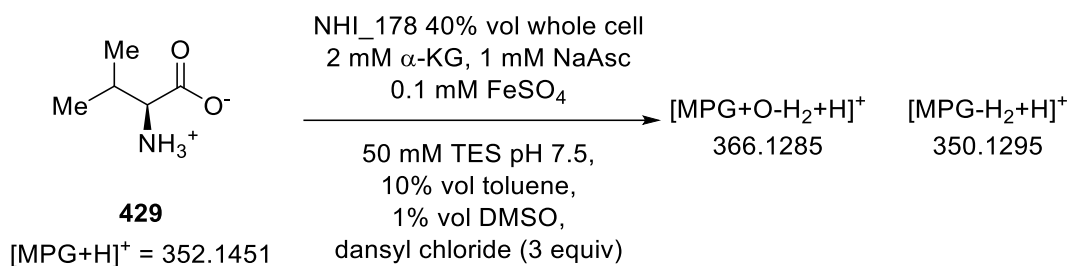
Discovered Reaction 197. Substrate_429 + NHI_174 = hydroxylation, desaturation, and oxidation/desaturation



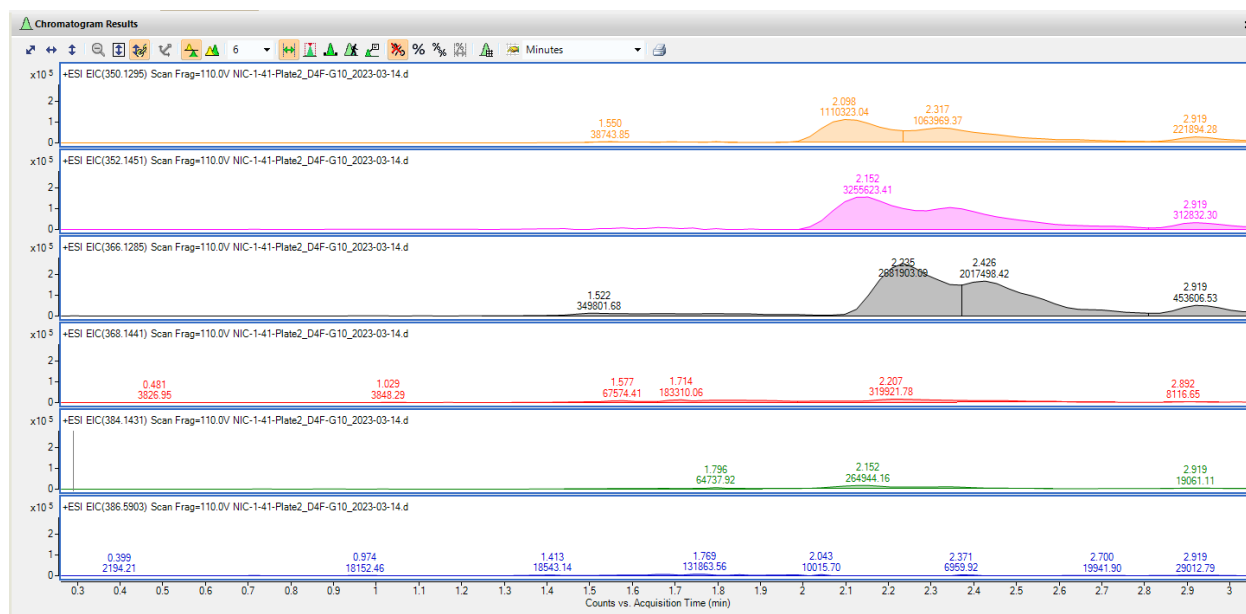
	Neutral	Positive	Negative
desaturation	349.1216	350.1295	348.1138
substrate	351.1373	352.1451	350.1295
oxidation/desaturation	365.1206	366.1285	364.1128
hydroxylation	367.1363	368.1441	366.1285
dihydroxylation	383.1353	384.1431	382.1275
chlorination	385.5825	386.5903	384.5746



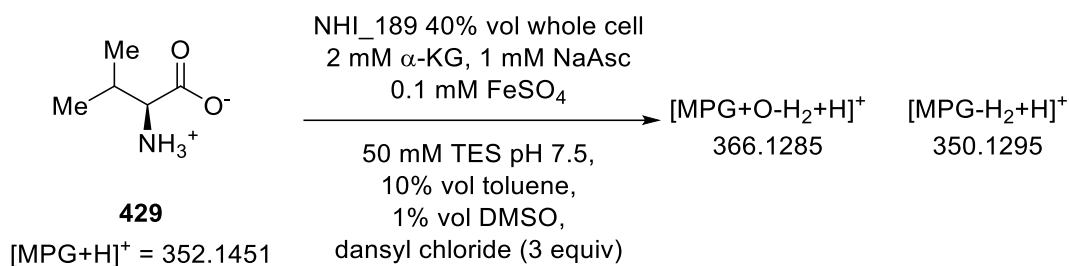
Discovered Reaction 198. Substrate_429 + NHI_178 = desaturation, and oxidation/desaturation



	Neutral	Positive	Negative
desaturation	349.1216	350.1295	348.1138
substrate	351.1373	352.1451	350.1295
oxidation/desaturation	365.1206	366.1285	364.1128
hydroxylation	367.1363	368.1441	366.1285
dihydroxylation	383.1353	384.1431	382.1275
chlorination	385.5825	386.5903	384.5746



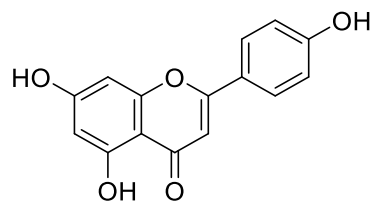
Discovered Reaction 199. Substrate_429 + NHI_189 = desaturation, and oxidation/desaturation



	Neutral	Positive	Negative
desaturation	349.1216	350.1295	348.1138
substrate	351.1373	352.1451	350.1295
oxidation/desaturation	365.1206	366.1285	364.1128
hydroxylation	367.1363	368.1441	366.1285
dihydroxylation	383.1353	384.1431	382.1275
chlorination	385.5825	386.5903	384.5746



Discovered Reaction 200. Substrate_444 + NHI_064 = hydroxylation



444

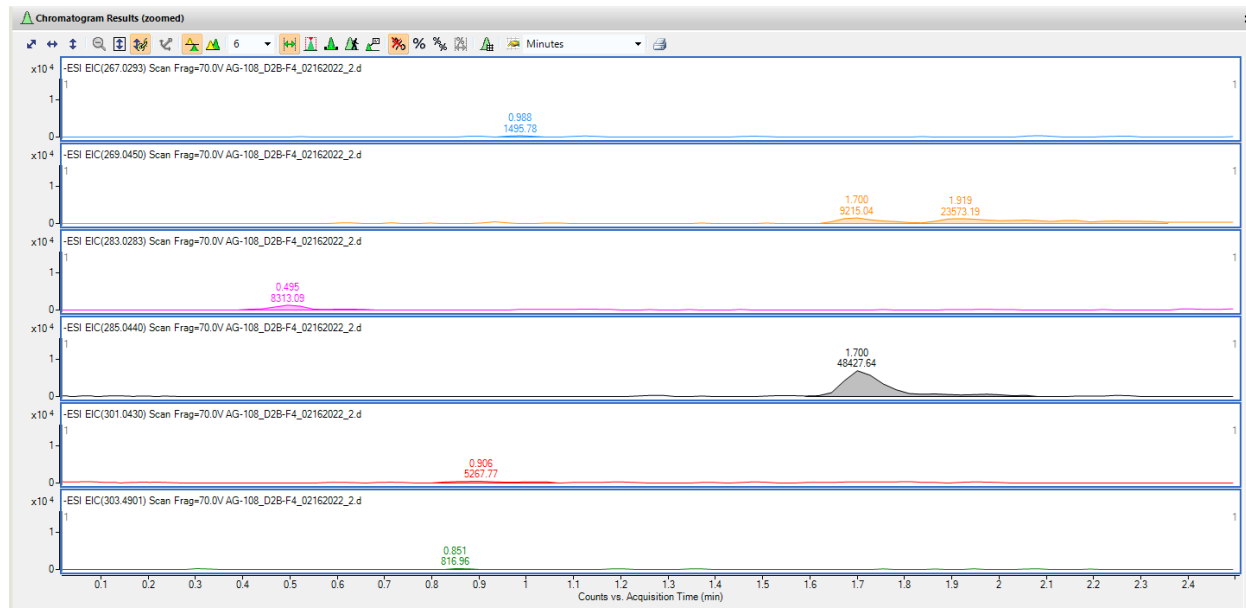
$[M-H]^- = 269.0450$

NHI_064 40% vol whole cell
2 mM α -KG, 1 mM NaAsc
0.1 mM FeSO₄

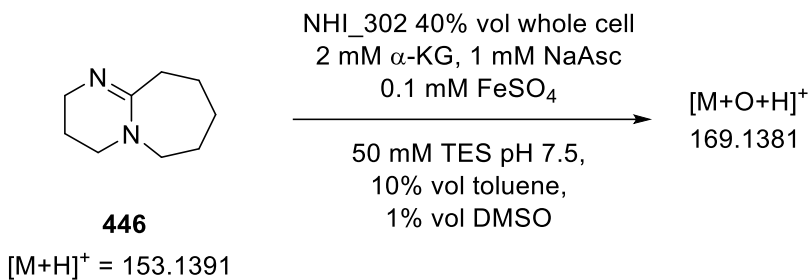
50 mM TES pH 7.5,
10% vol toluene,
1% vol DMSO

$[M+O-H]^-$
285.0440

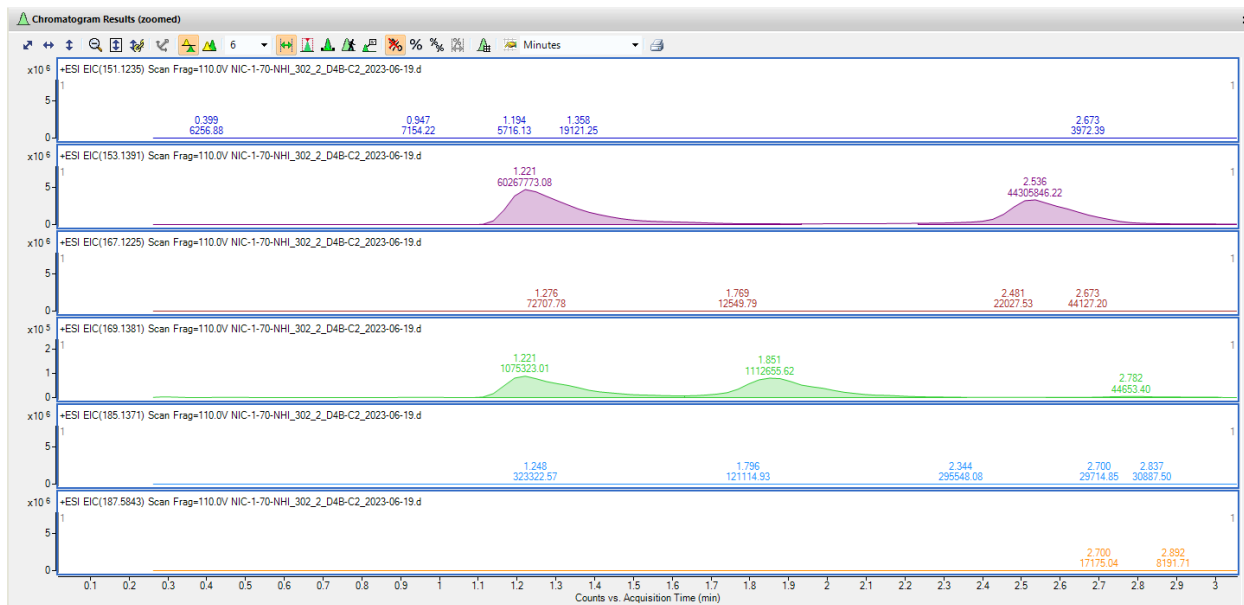
	Neutral	Positive	Negative
desaturation	268.0371	269.0450	267.0293
substrate	270.0528	271.0606	269.0450
oxidation/desaturation	284.0361	285.0440	283.0283
hydroxylation	286.0518	287.0596	285.0440
dihydroxylation	302.0508	303.0586	301.0430
chlorination	304.4980	305.5058	303.4901



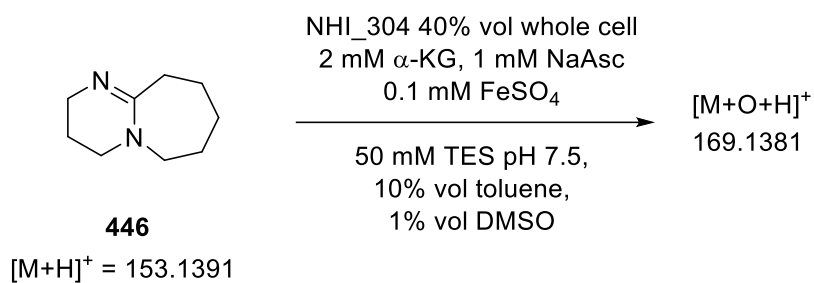
Discovered Reaction 201. Substrate_446 + NHI_302 = hydroxylation



	Neutral	Positive	Negative
desaturation	150.1156	151.1235	149.1078
substrate	152.1313	153.1391	151.1235
oxidation/desaturation	166.1146	167.1225	165.1068
hydroxylation	168.1303	169.1381	167.1225
dihydroxylation	184.1293	185.1371	183.1215
chlorination	186.5765	187.5843	185.5686



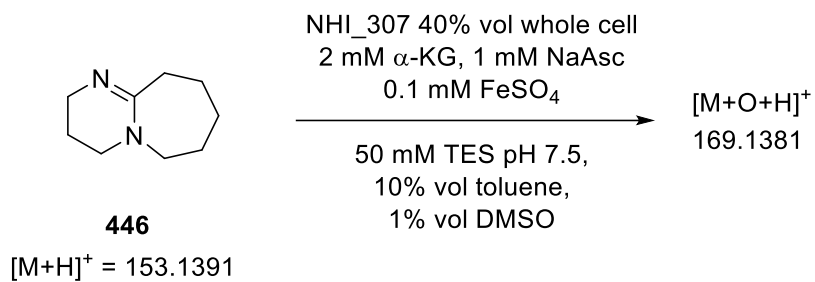
Discovered Reaction 202. Substrate_446 + NHI_304 = hydroxylation



	Neutral	Positive	Negative
desaturation	150.1156	151.1235	149.1078
substrate	152.1313	153.1391	151.1235
oxidation/desaturation	166.1146	167.1225	165.1068
hydroxylation	168.1303	169.1381	167.1225
dihydroxylation	184.1293	185.1371	183.1215
chlorination	186.5765	187.5843	185.5686



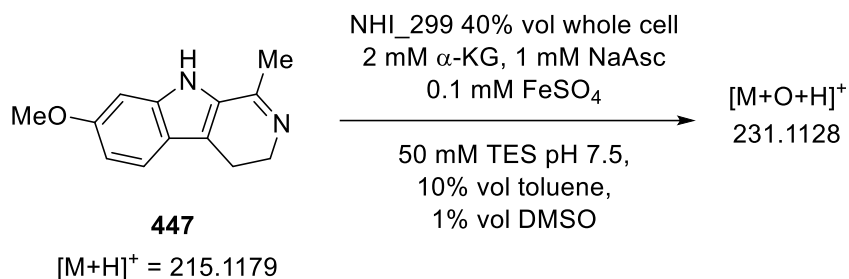
Discovered Reaction 203. Substrate **446** + NHI_307 = hydroxylation



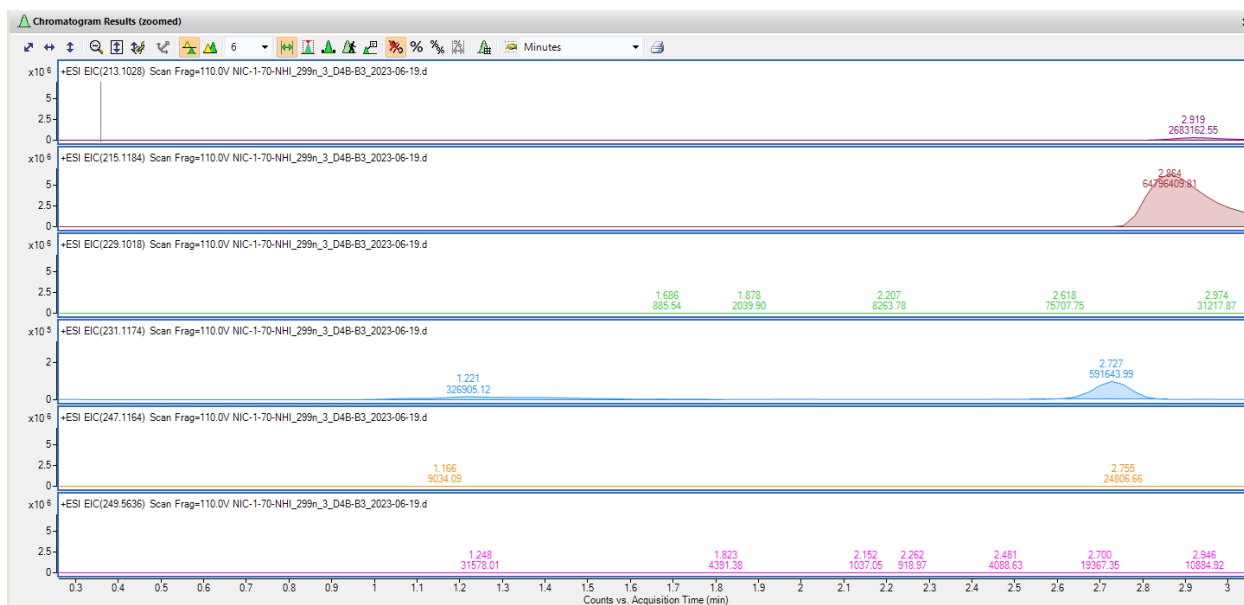
	Neutral	Positive	Negative
desaturation	150.1156	151.1235	149.1078
substrate	152.1313	153.1391	151.1235
oxidation/desaturation	166.1146	167.1225	165.1068
hydroxylation	168.1303	169.1381	167.1225
dihydroxylation	184.1293	185.1371	183.1215
chlorination	186.5765	187.5843	185.5686



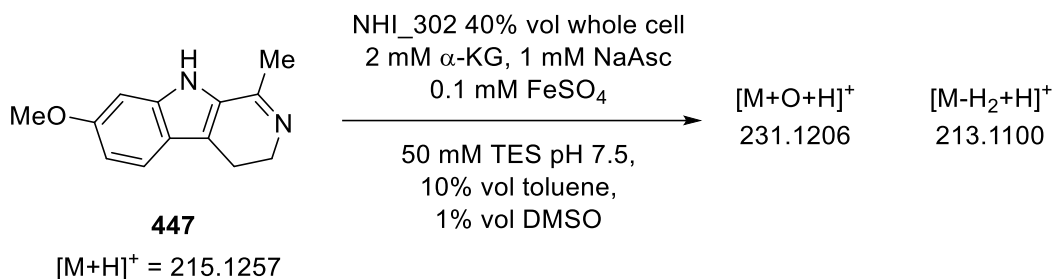
Discovered Reaction 204. Substrate_447 + NHI_299 = hydroxylation



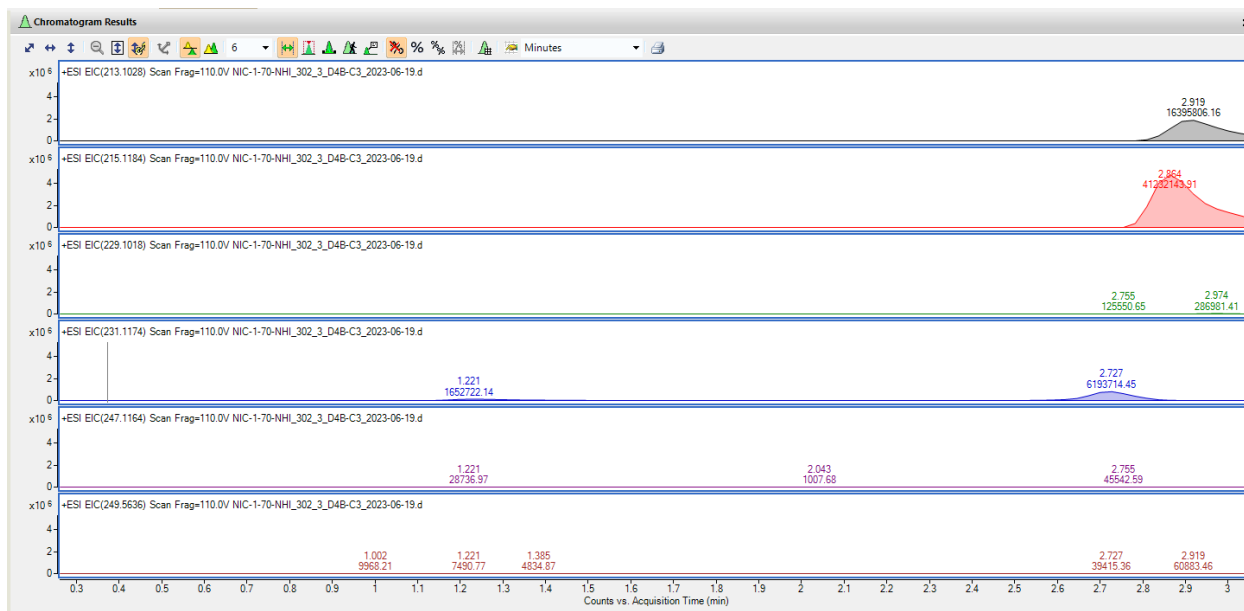
	Neutral	Positive	Negative
desaturation	212.1022	213.11007	211.0944
substrate	214.1179	215.1257	213.1101
oxidation/desaturation	228.0971	229.10497	227.0893
hydroxylation	230.1128	231.12063	229.105
dihydroxylation	246.1077	247.11553	245.0999
chlorination	248.079	249.0868	247.0711



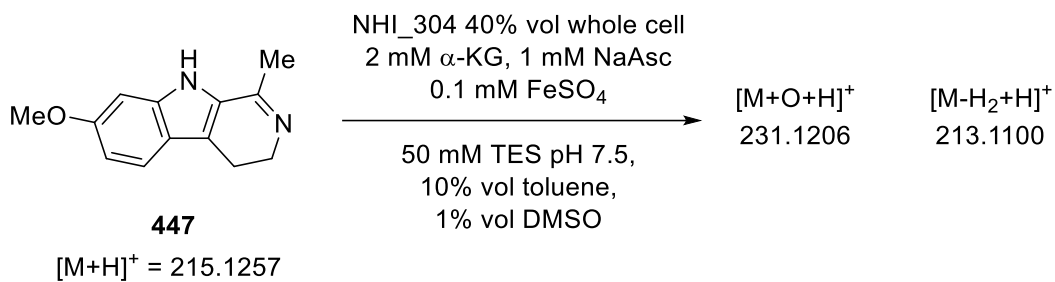
Discovered Reaction 205. Substrate **447** + NHI_302 = hydroxylation and desaturation



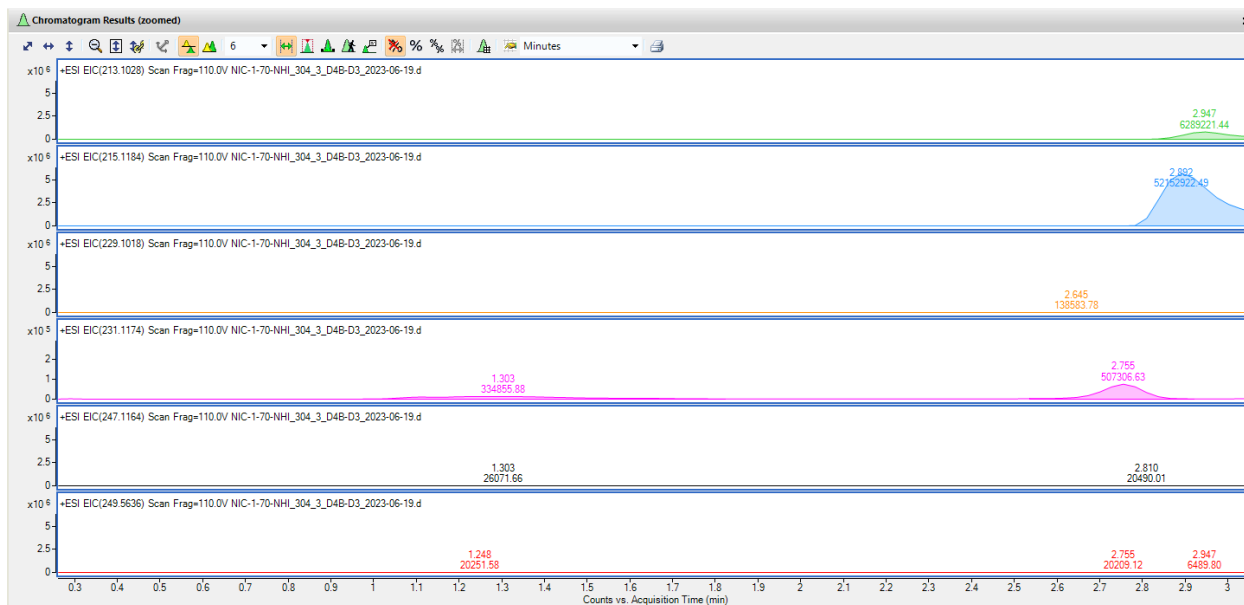
	Neutral	Positive	Negative
desaturation	212.1022	213.11007	211.0944
substrate	214.1179	215.1257	213.1101
oxidation/desaturation	228.0971	229.10497	227.0893
hydroxylation	230.1128	231.12063	229.105
dihydroxylation	246.1077	247.11553	245.0999
chlorination	248.079	249.0868	247.0711



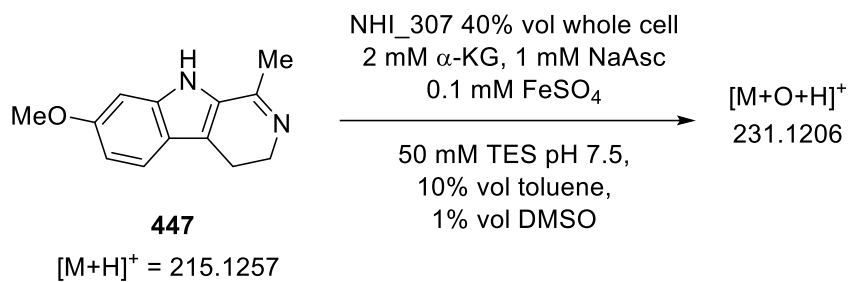
Discovered Reaction 206. Substrate **447** + NHI_304 = hydroxylation and desaturation



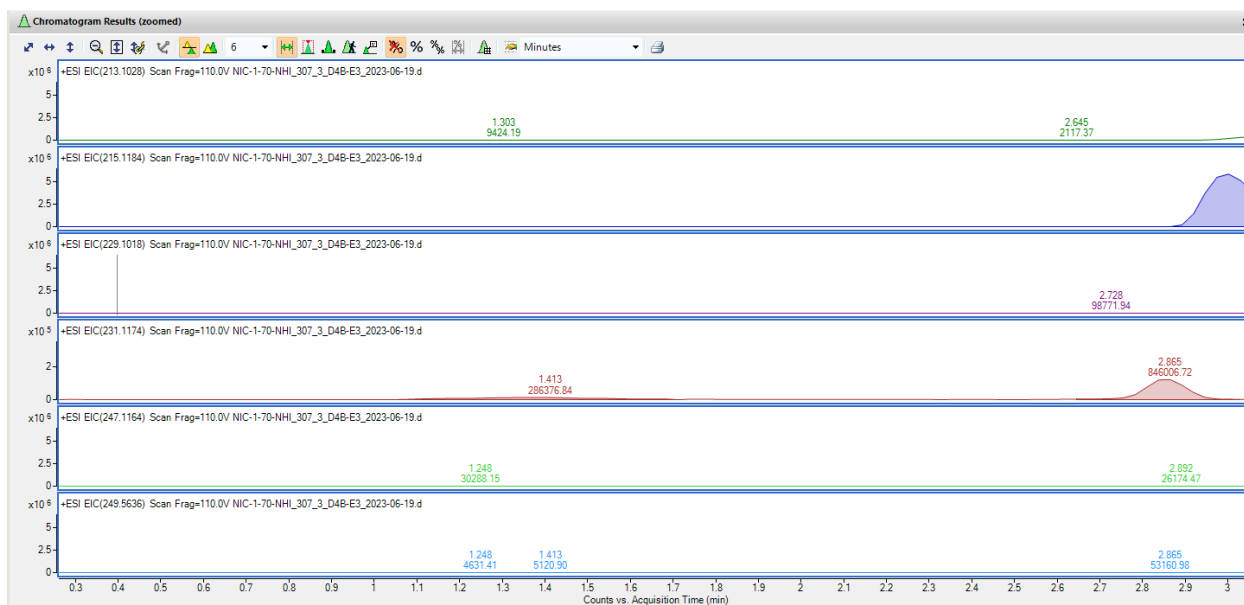
	Neutral	Positive	Negative
desaturation	212.1022	213.11007	211.0944
substrate	214.1179	215.1257	213.1101
oxidation/desaturation	228.0971	229.10497	227.0893
hydroxylation	230.1128	231.12063	229.105
dihydroxylation	246.1077	247.11553	245.0999
chlorination	248.079	249.0868	247.0711



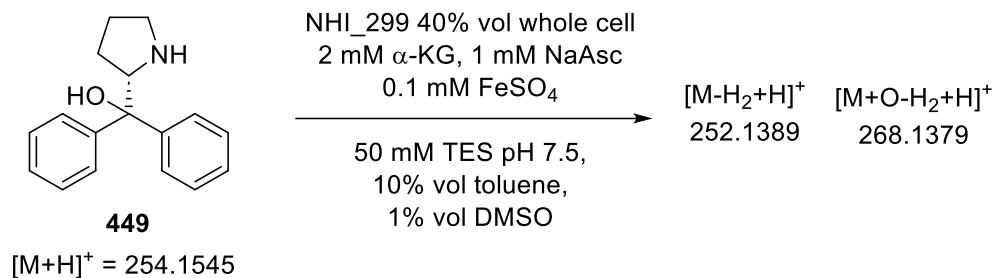
Discovered Reaction 207. Substrate **447** + NHI_307 = hydroxylation



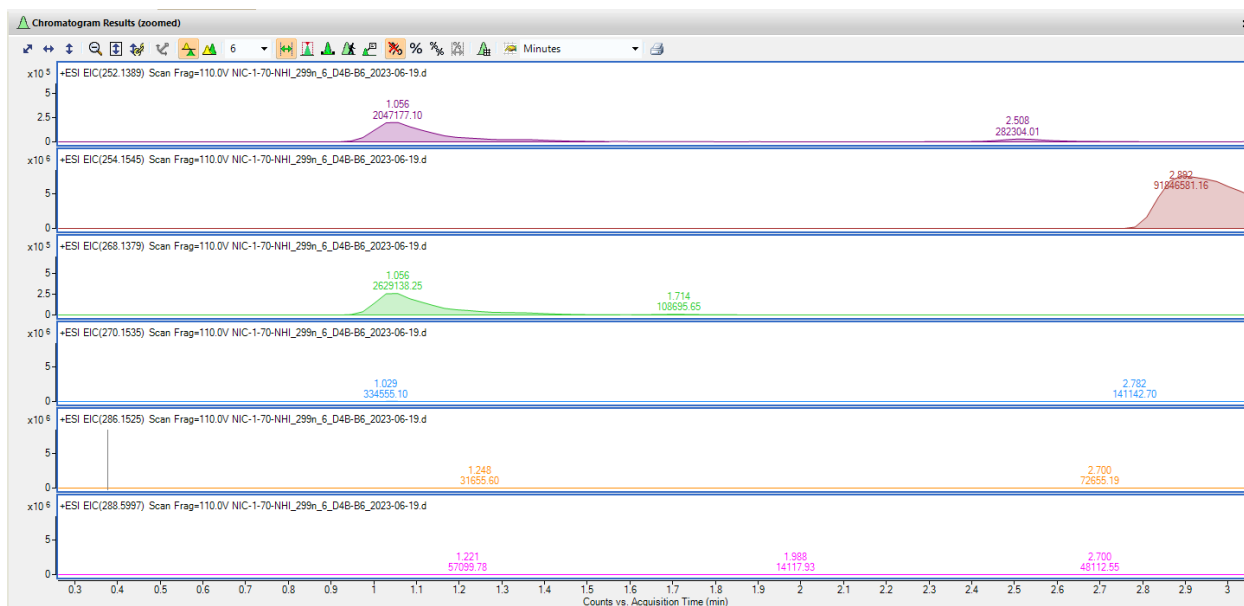
	Neutral	Positive	Negative
desaturation	212.1022	213.11007	211.0944
substrate	214.1179	215.1257	213.1101
oxidation/desaturation	228.0971	229.10497	227.0893
hydroxylation	230.1128	231.12063	229.105
dihydroxylation	246.1077	247.11553	245.0999
chlorination	248.079	249.0868	247.0711



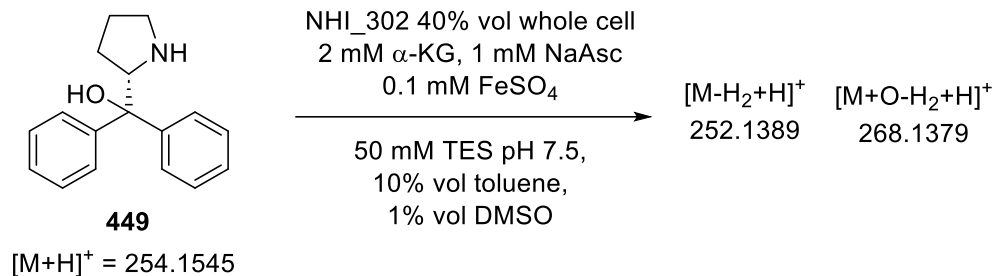
Discovered Reaction 208. Substrate_449 + NHI_299 = desaturation and oxidation/desaturation



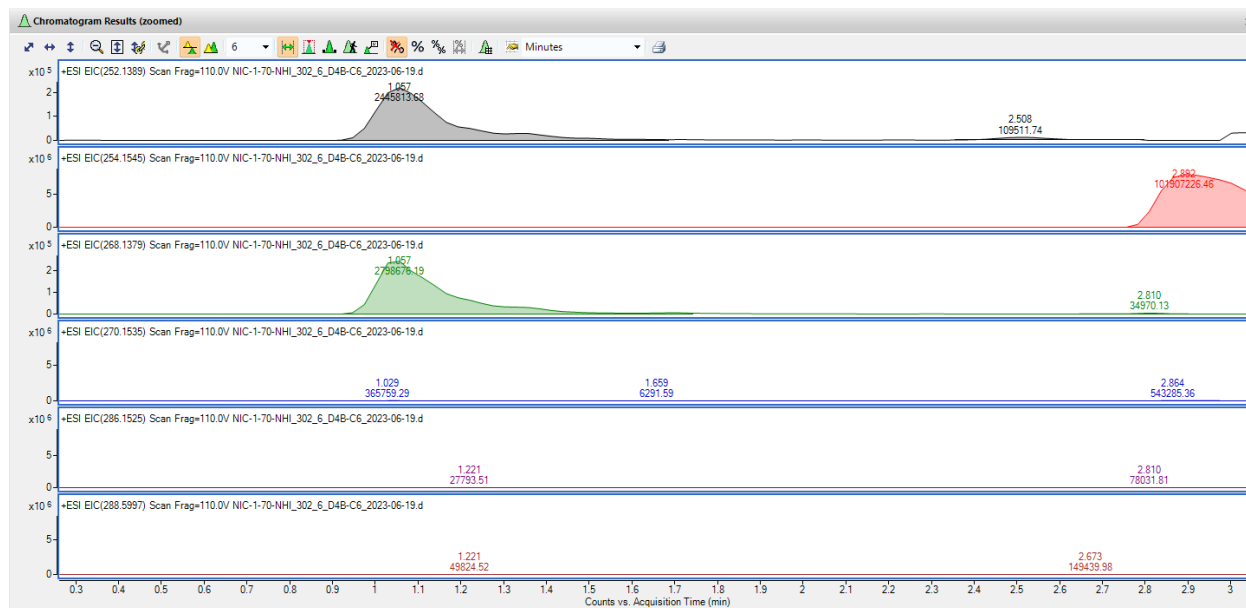
	Neutral	Positive	Negative
desaturation	251.1310	252.1389	250.1232
substrate	253.1467	254.1545	252.1389
oxidation/desaturation	267.1300	268.1379	266.1222
hydroxylation	269.1457	270.1535	268.1379
dihydroxylation	285.1447	286.1525	284.1369
chlorination	287.5919	288.5997	286.5840



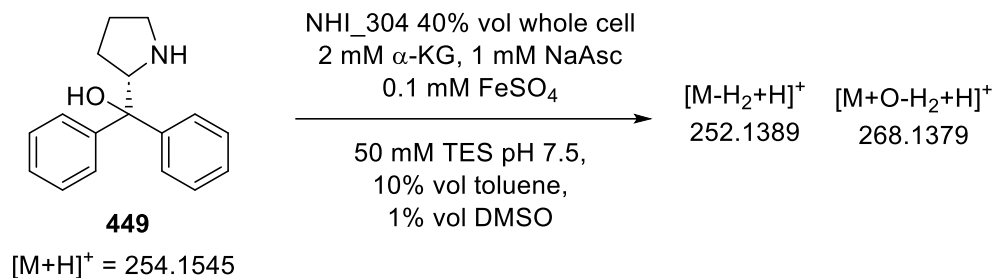
Discovered Reaction 209. Substrate **449** + NHI_302 = desaturation and oxidation/desaturation



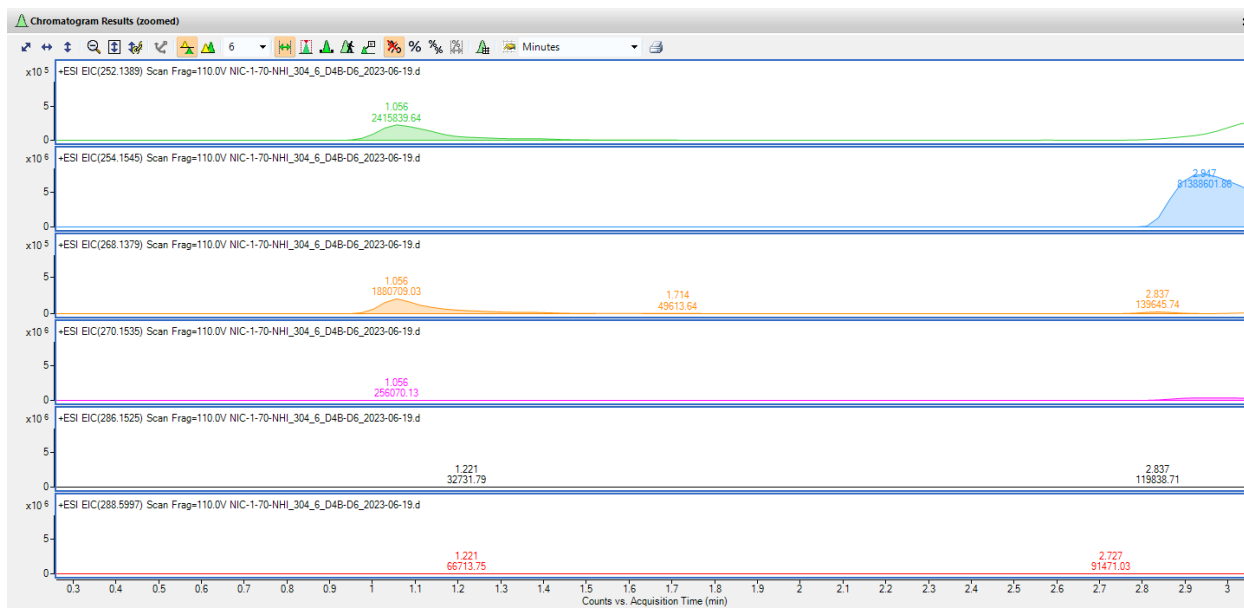
	Neutral	Positive	Negative
desaturation	251.1310	252.1389	250.1232
substrate	253.1467	254.1545	252.1389
oxidation/desaturation	267.1300	268.1379	266.1222
hydroxylation	269.1457	270.1535	268.1379
dihydroxylation	285.1447	286.1525	284.1369
chlorination	287.5919	288.5997	286.5840



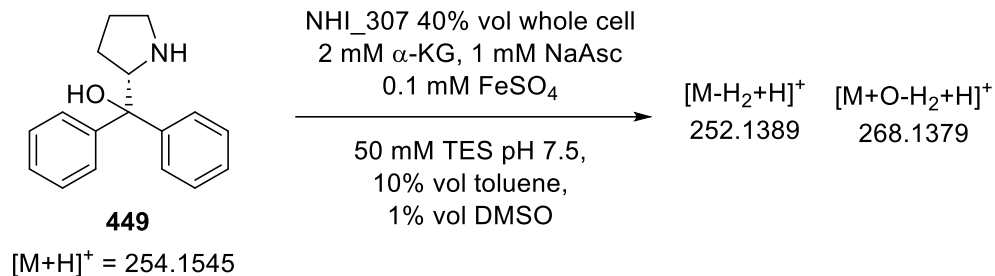
Discovered Reaction 210. Substrate_449 + NHI_304 = desaturation and oxidation/desaturation



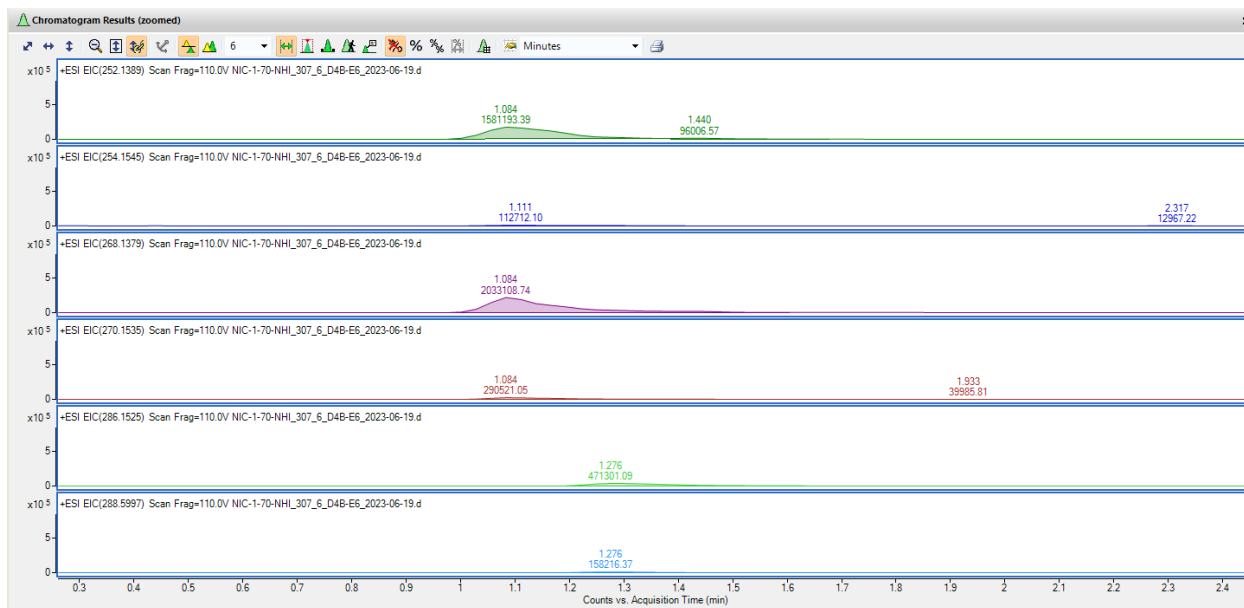
	Neutral	Positive	Negative
desaturation	251.1310	252.1389	250.1232
substrate	253.1467	254.1545	252.1389
oxidation/desaturation	267.1300	268.1379	266.1222
hydroxylation	269.1457	270.1535	268.1379
dihydroxylation	285.1447	286.1525	284.1369
chlorination	287.5919	288.5997	286.5840



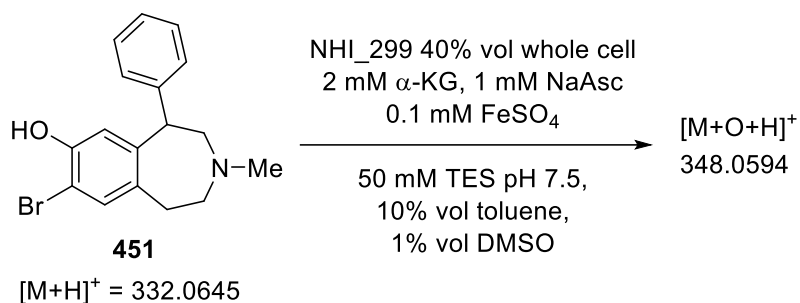
Discovered Reaction 211. Substrate **449** + NHI_307 = desaturation and oxidation/desaturation



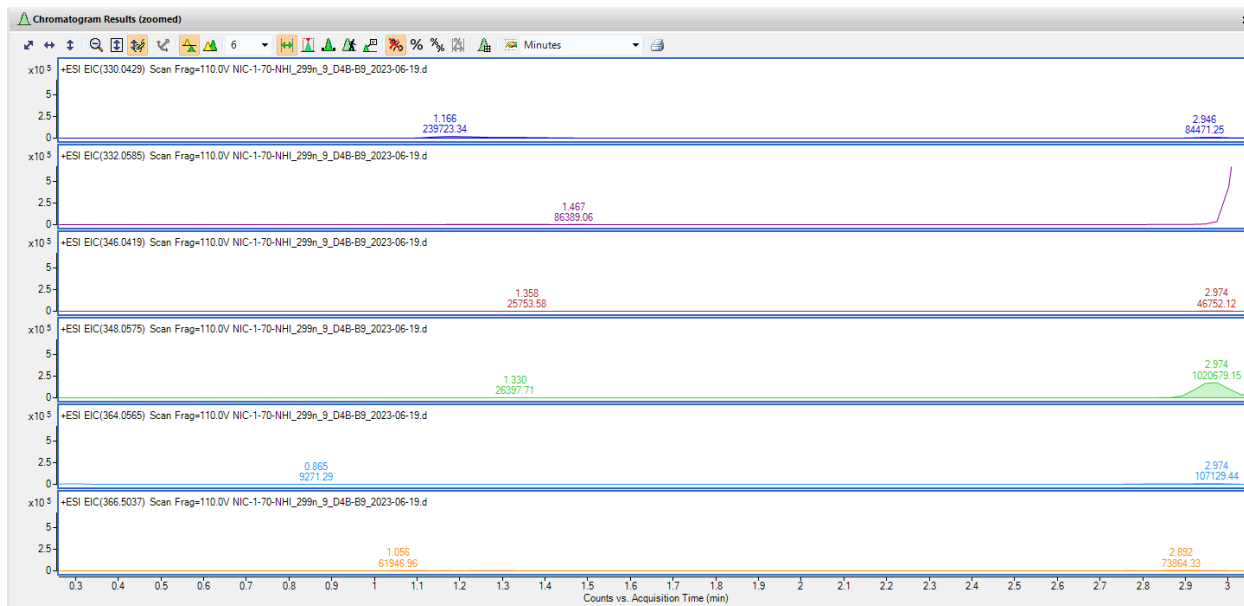
	Neutral	Positive	Negative
desaturation	251.1310	252.1389	250.1232
substrate	253.1467	254.1545	252.1389
oxidation/desaturation	267.1300	268.1379	266.1222
hydroxylation	269.1457	270.1535	268.1379
dihydroxylation	285.1447	286.1525	284.1369
chlorination	287.5919	288.5997	286.5840



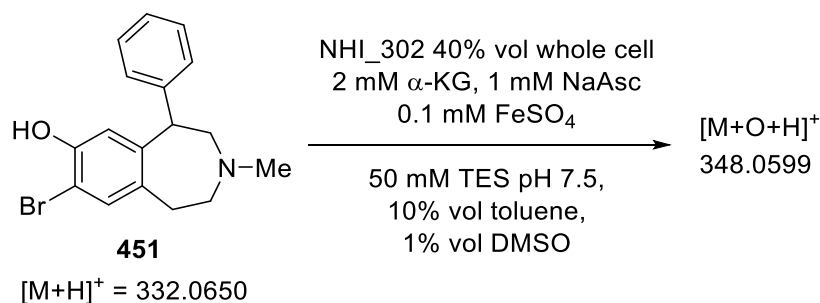
Discovered Reaction 212. Substrate_451 + NHI_299 = hydroxylation



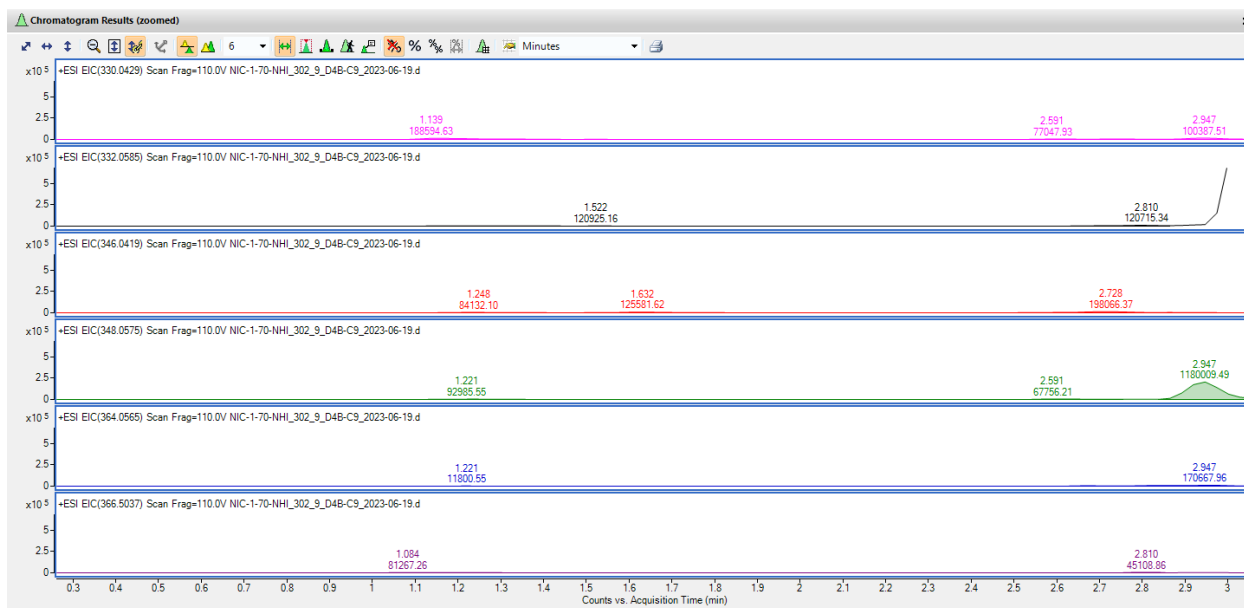
	Neutral	Positive	Negative
desaturation	329.0415	330.04937	328.0337
substrate	331.0572	332.0650	330.0494
oxidation/desaturation	345.0364	346.04427	344.0286
hydroxylation	347.0521	348.05993	346.0443
dihydroxylation	363.047	364.05483	362.0392
chlorination	365.0183	366.0261	364.0104



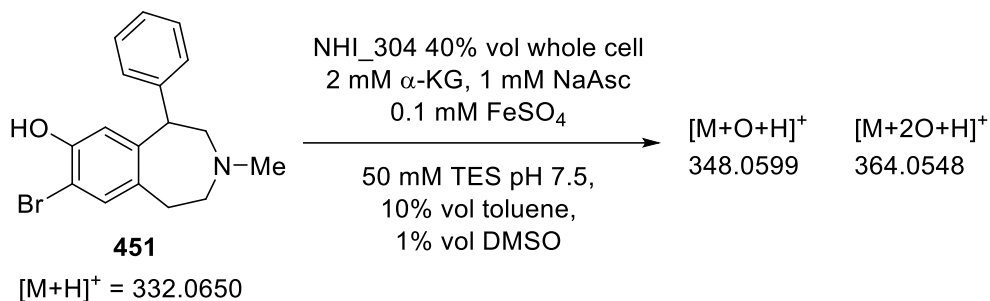
Discovered Reaction 213. Substrate_451 + NHI_302 = hydroxylation



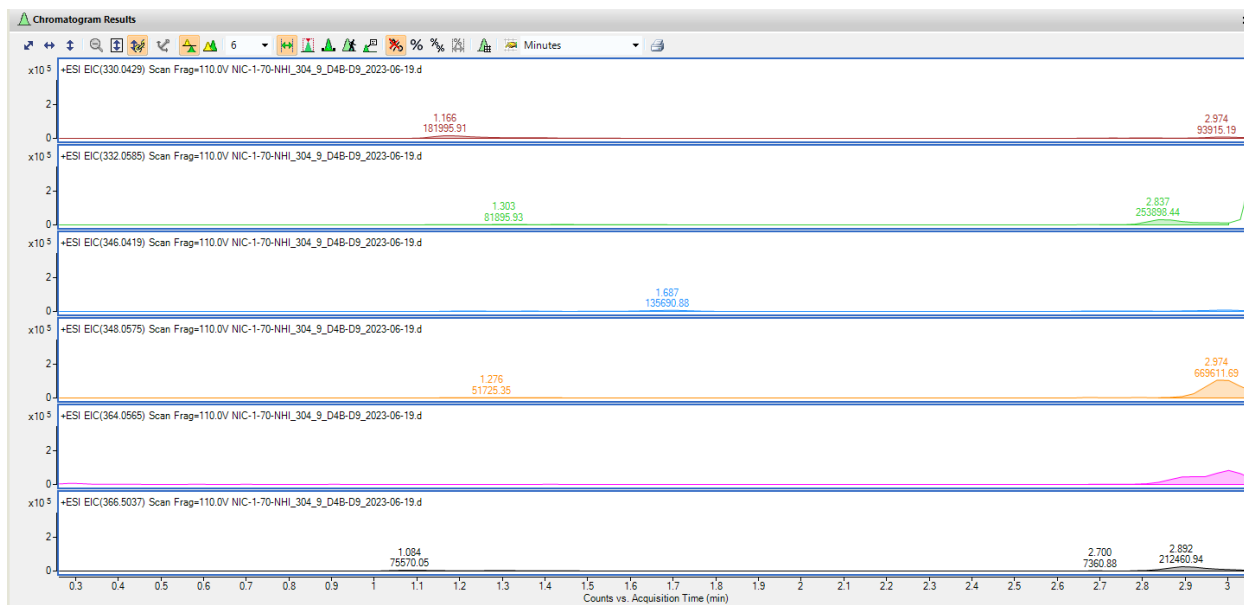
	Neutral	Positive	Negative
desaturation	329.0415	330.04937	328.0337
substrate	331.0572	332.0650	330.0494
oxidation/desaturation	345.0364	346.04427	344.0286
hydroxylation	347.0521	348.05993	346.0443
dihydroxylation	363.047	364.05483	362.0392
chlorination	365.0183	366.0261	364.0104



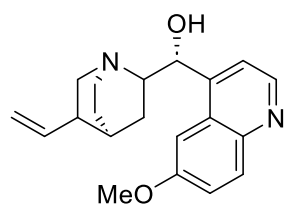
Discovered Reaction 214. Substrate_451 + NHI_304 = hydroxylation and dihydroxylation



	Neutral	Positive	Negative
desaturation	329.0415	330.04937	328.0337
substrate	331.0572	332.0650	330.0494
oxidation/desaturation	345.0364	346.04427	344.0286
hydroxylation	347.0521	348.05993	346.0443
dihydroxylation	363.047	364.05483	362.0392
chlorination	365.0183	366.0261	364.0104



Discovered Reaction 215. Substrate_453 + NHI_304 = desaturation



453

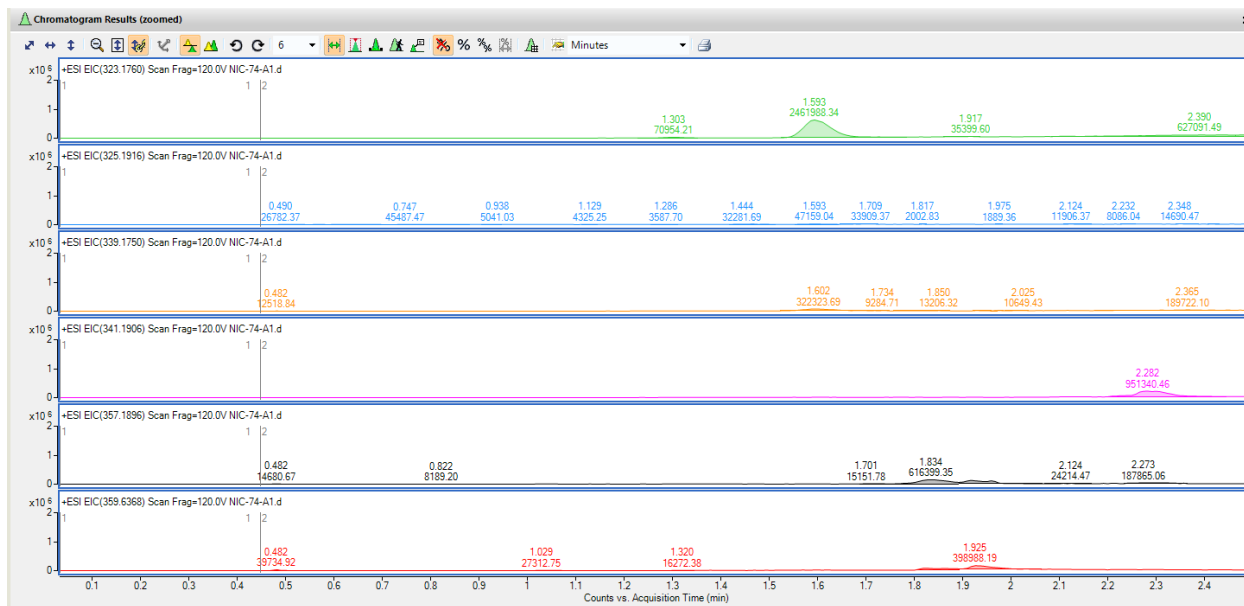
$[M+H]^+ = 325.1916$

NHI_304 40% vol whole cell
2 mM α -KG, 1 mM NaAsc
0.1 mM $FeSO_4$

50 mM TES pH 7.5,
10% vol toluene,
1% vol DMSO

$[M-H_2+H]^+$
323.1760

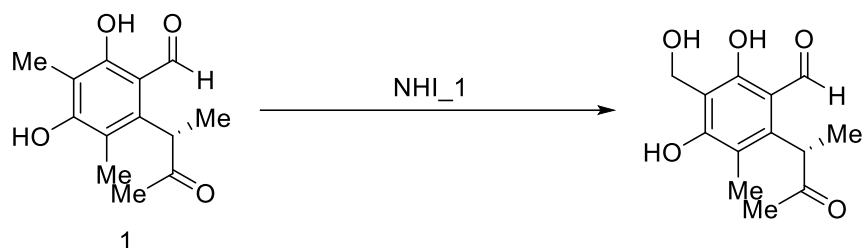
	Neutral	Positive	Negative
desaturation	322.1681	323.1760	321.1603
substrate	324.1838	325.1916	323.1760
oxidation/desaturation	338.1671	339.1750	337.1593
hydroxylation	340.1828	341.1906	339.1750
dihydroxylation	356.1818	357.1896	355.1740
chlorination	358.6290	359.6368	357.6211



12. Reactions included in database from literature

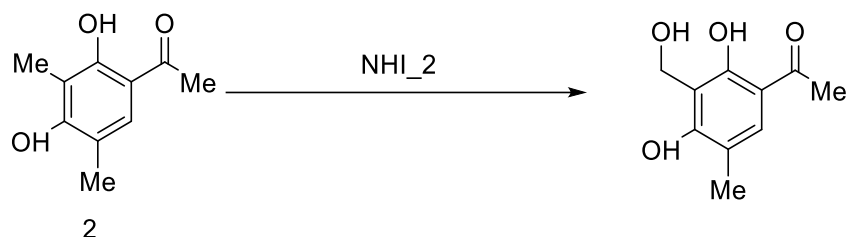
In 2023, each enzyme was searched by sequence in the UniProt database to identify all literature reports of associated reactions and the substrates and products were catalogued.

Literature Reaction 1. Substrate_001 + NHI_001 = hydroxylation



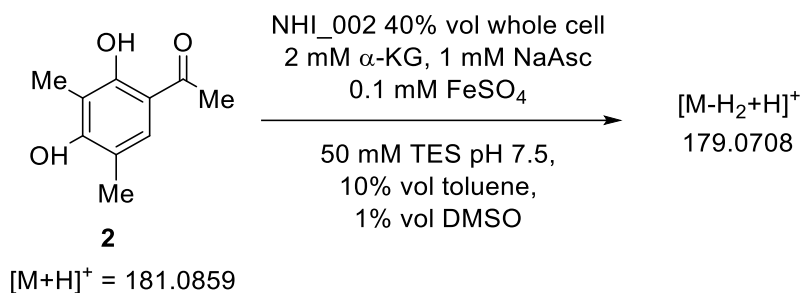
Reaction from literature¹³ – reproduction not attempted.

Literature Reaction 2. Substrate_002 + NHI_002 = desaturation



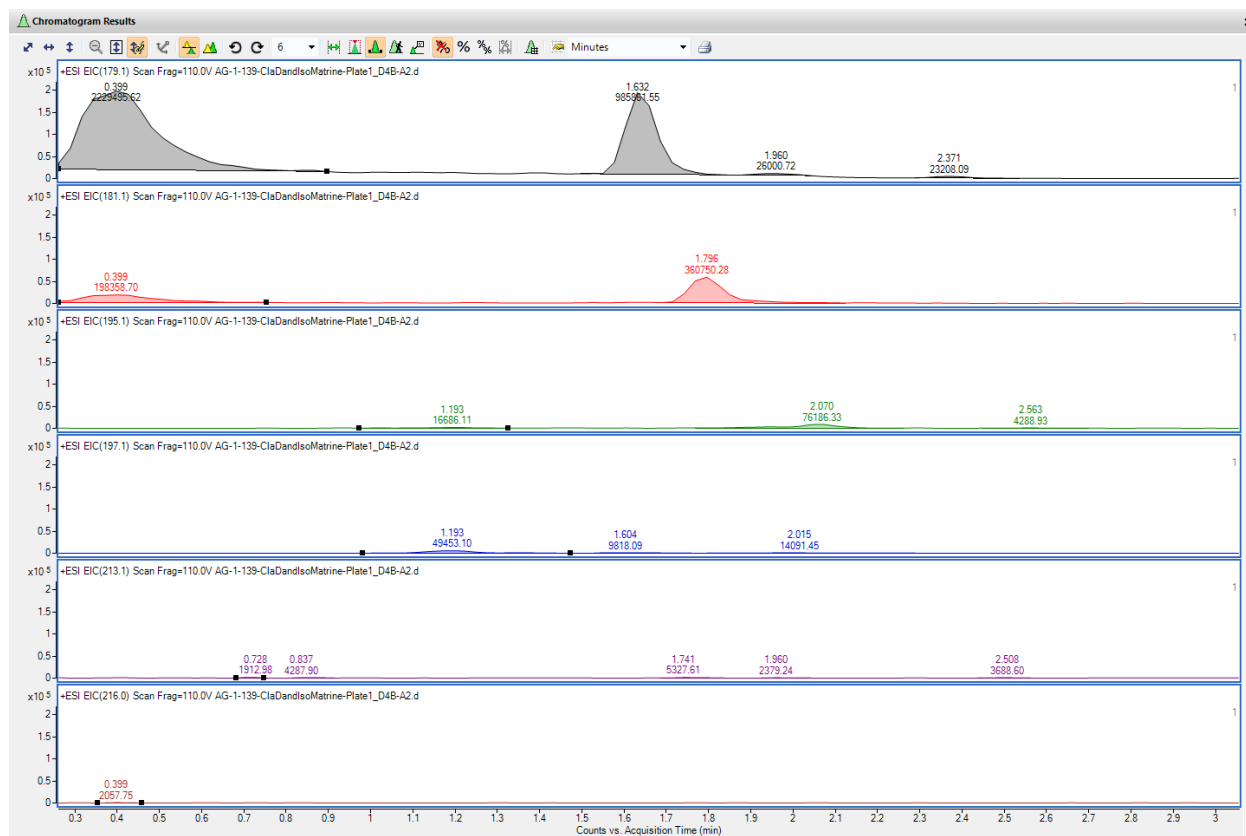
Reaction from literature¹⁴

Reaction observed: Substrate_002 + NHI_002 = desaturation

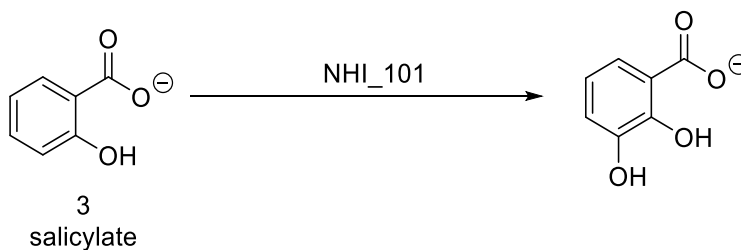


	Neutral	Positive	Negative
desaturation	178.0549	179.0628	177.0471
Substrate	180.0706	181.0784	179.0628
oxidation/desaturation	194.0499	195.0577	193.0421
hydroxylation	196.0655	197.0733	195.0577

dihydroxylation	212.0604	213.0682	211.0526
chlorination	215.0394	216.0472	214.0316



Literature Reaction 3. Substrate_003 + NHI_101 = hydroxylation

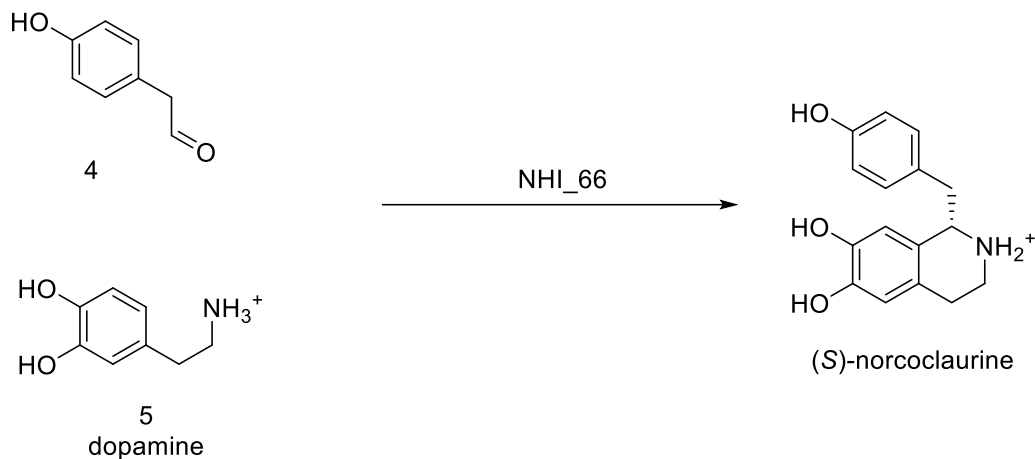


Reaction from literature¹⁵

Reaction proposed by protein similarity

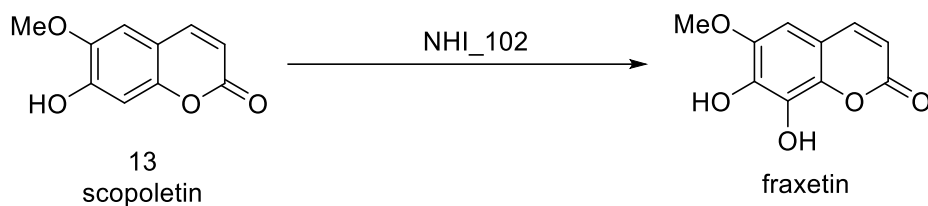
Reaction attempted, but no product formation was observed.

Literature Reaction 4. Substrate_004 + Substrate_005 + NHI_066 = carbon-carbon bond formation and condensation



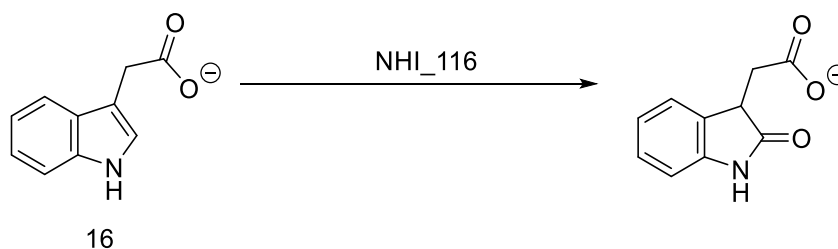
Reaction from literature¹⁶ – reproduction not attempted.

Literature Reaction 5. Substrate_013 + NHI_102 = hydroxylation



Reaction from literature¹⁷ – reproduction not attempted.

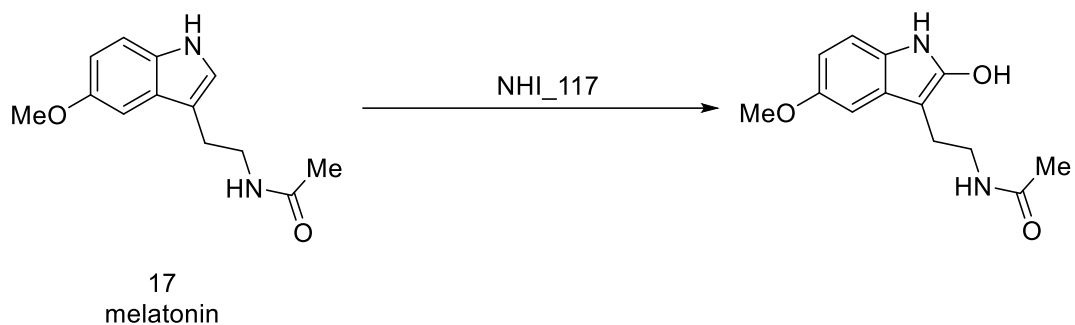
Literature Reaction 6. Substrate_016 + NHI_116 = hydroxylation and tautomerization



Reaction from literature¹⁸

Reaction attempted but no product formation was observed.

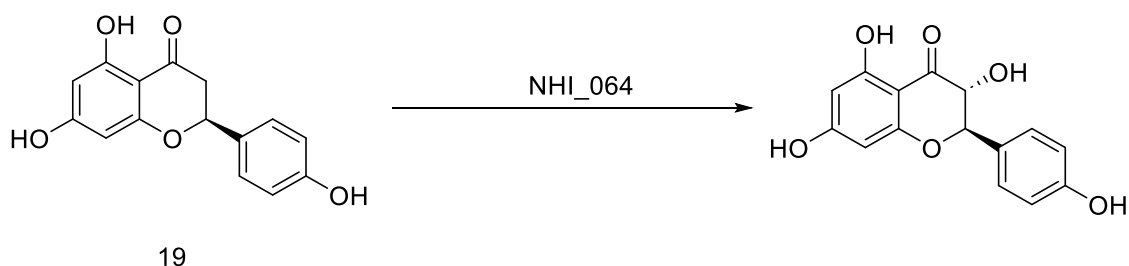
Literature Reaction 7. Substrate_017 + NHI_117 = hydroxylation



Reaction from literature¹⁹

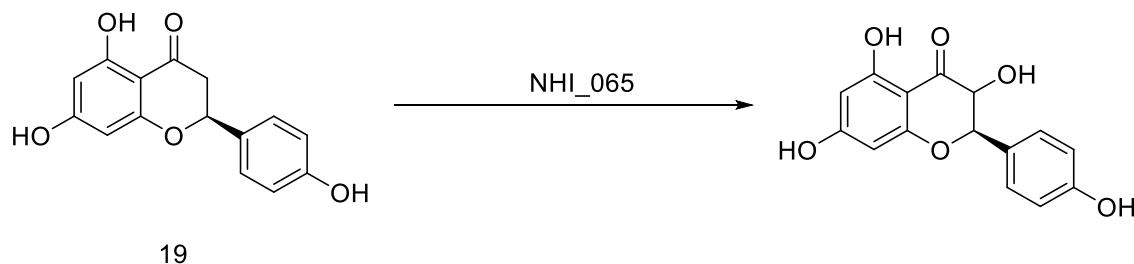
Reaction attempted but no product formation was observed.

Literature Reaction 8. Substrate_019 + NHI_064 = hydroxylation



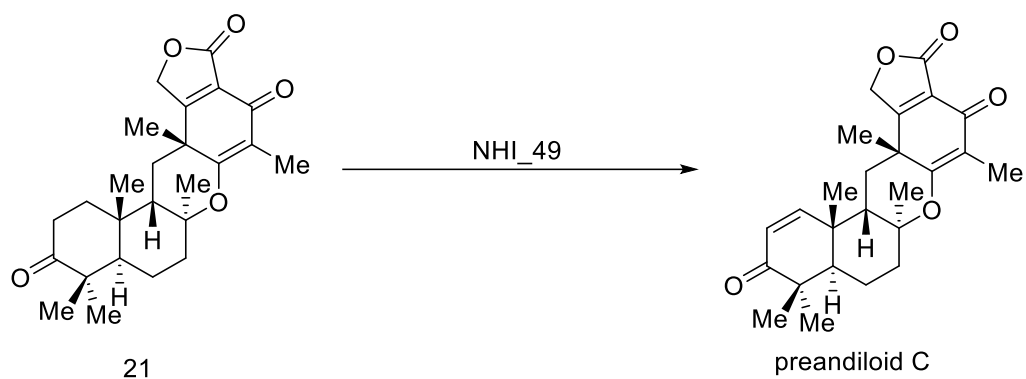
Reaction from literature²⁰ – reproduction not attempted.

Literature Reaction 9. Substrate_019 + NHI_065 = hydroxylation



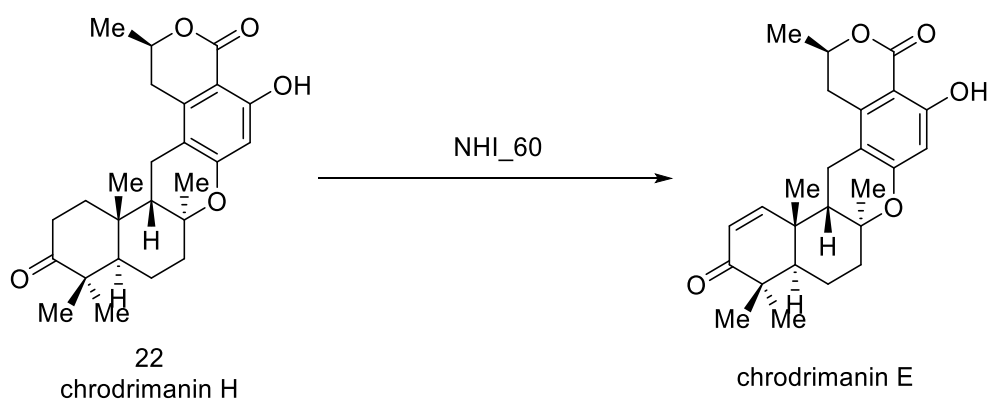
Reaction from literature²¹ – reproduction not attempted.

Literature Reaction 10. Substrate_021 + NHI_049 = desaturation



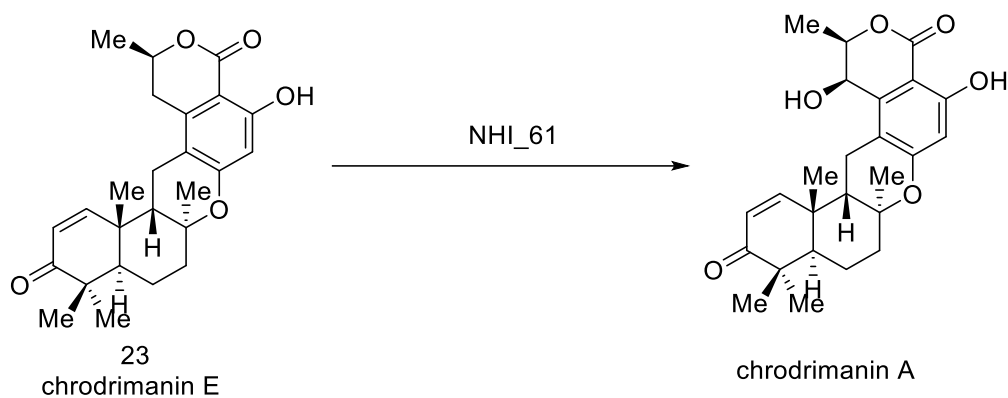
Reaction from literature²² – reproduction not attempted.

Literature Reaction 11. Substrate_022 + NHI_060 = desaturation



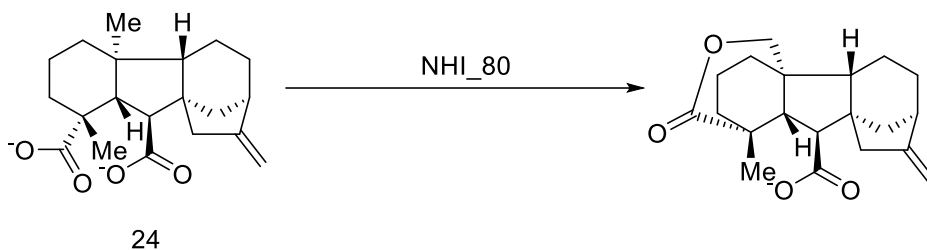
Reaction from literature²³ – reproduction not attempted.

Literature Reaction 12. Substrate_023 + NHI_061 = hydroxylation



Reaction from literature²³ – reproduction not attempted.

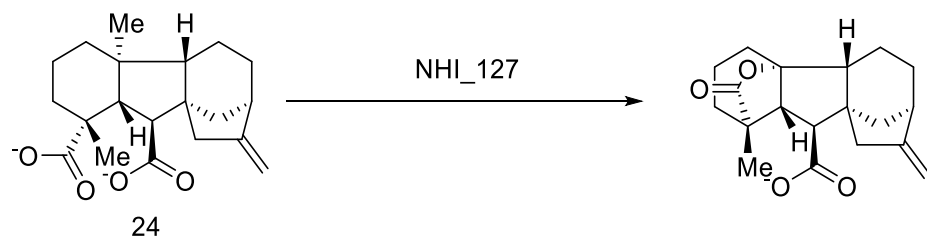
Literature Reaction 13. Substrate_024 + NHI_080 = probable hydroxylase then lactonization



Reaction from literature²⁴ – reproduction not attempted.

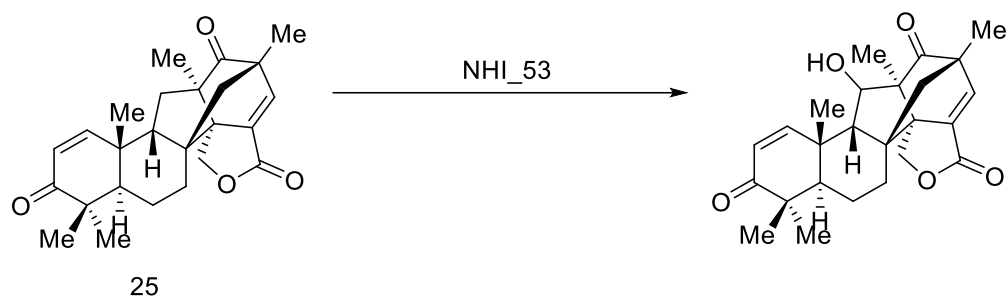
Reaction proposed by protein similarity.

Literature Reaction 14. Substrate_024 + NHI_127 = proposed activity (by similarity)



Reaction from literature²⁵ – reproduction not attempted.

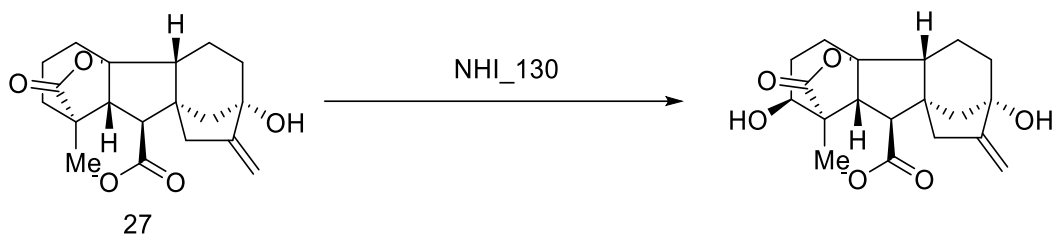
Literature Reaction 15. Substrate_025 + NHI_053 = hydroxylation



Reaction from literature²⁶ – reproduction not attempted

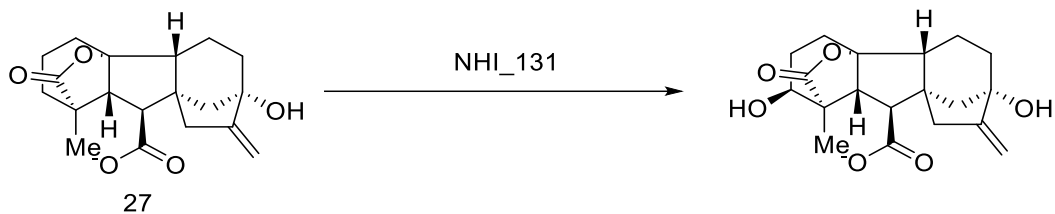
Product not characterized experimentally

Literature Reaction 16. Substrate_027 + NHI_130 = hydroxylation



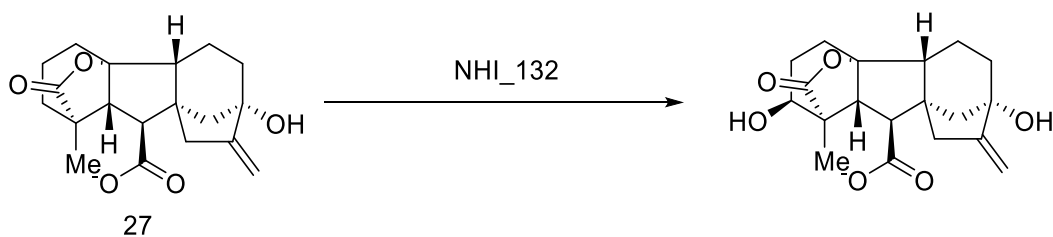
Reaction from literature²⁷ – reproduction not attempted.

Literature Reaction 17. Substrate_027 + NHI_131 = hydroxylation



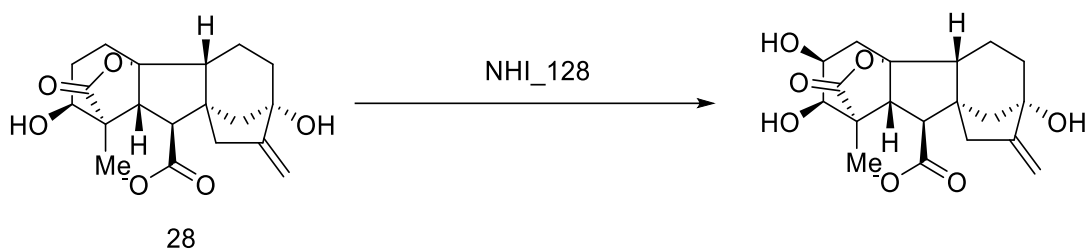
Reaction from literature²⁸ – reproduction not attempted.

Literature Reaction 18. Substrate_027 + NHI_132 = hydroxylation



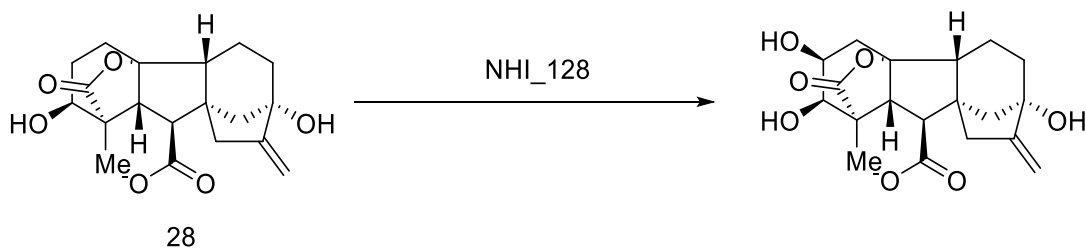
Reaction from literature²⁹ – reproduction not attempted.

Literature Reaction 19. Substrate_028 + NHI_126 = hydroxylation



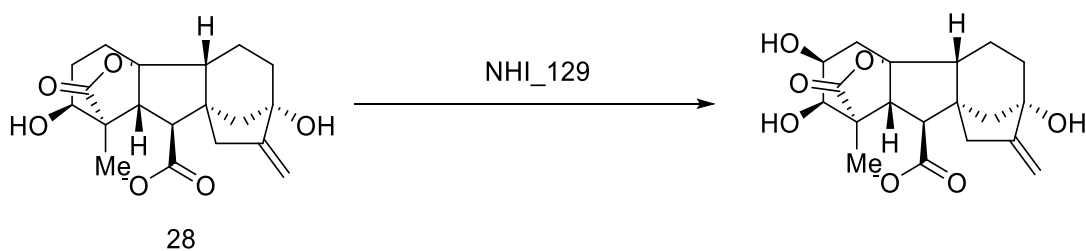
Reaction from literature³⁰ – reproduction not attempted.

Literature Reaction 20. Substrate_028 + NHI_128 = hydroxylation



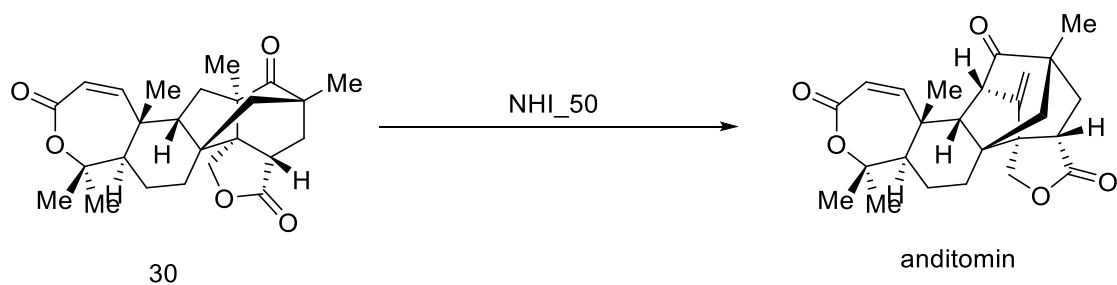
Reaction from literature³¹ – reproduction not attempted.

Literature Reaction 21. Substrate_028 + NHI_129 = hydroxylation



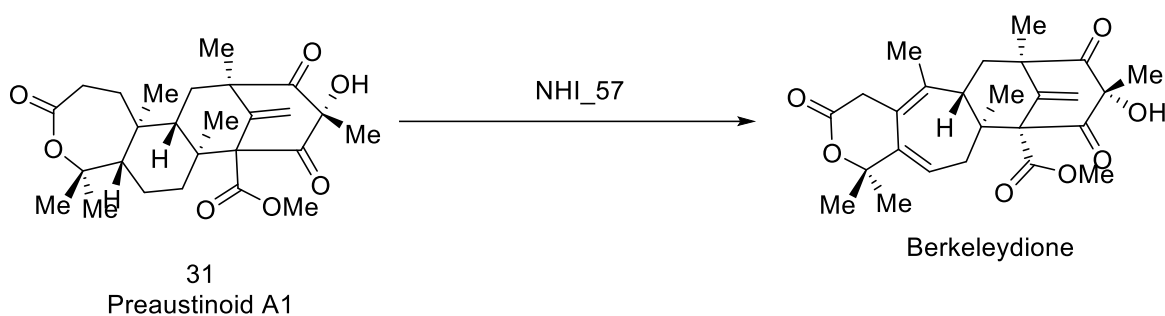
Reaction from literature³² – reproduction not attempted.

Literature Reaction 22. Substrate_030 + NHI_050 = desaturation and rearrangement



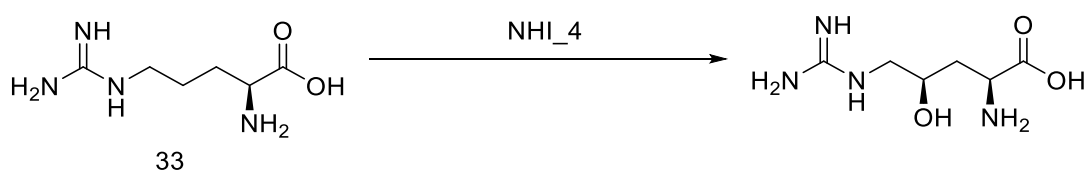
Reaction from literature³³ – reproduction not attempted

Literature Reaction 23. Substrate_031 + NHI_057 = desaturation and rearrangement



Reaction from literature³⁴ – reproduction not attempted.

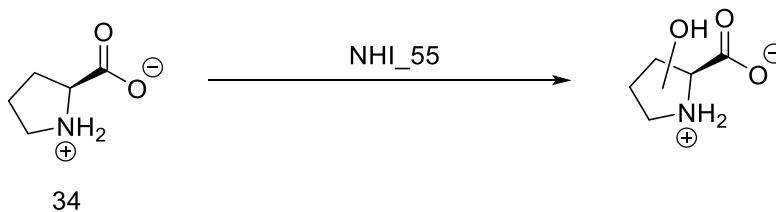
Literature Reaction 24. Substrate_033 + NHI_004 = hydroxylation



Reaction from literature³⁵

Reaction attempted but no product formation was observed.

Literature Reaction 25. Substrate_034 + NHI_055 = probable hydroxylation

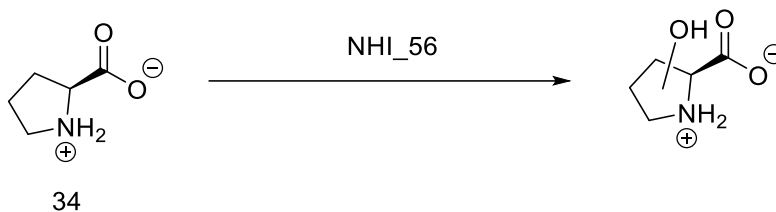


Reaction from literature³⁶

Reaction proposed by protein similarity.

Reaction attempted but no product formation was observed.

Literature Reaction 26. Substrate_034 + NHI_056 = probable hydroxylation

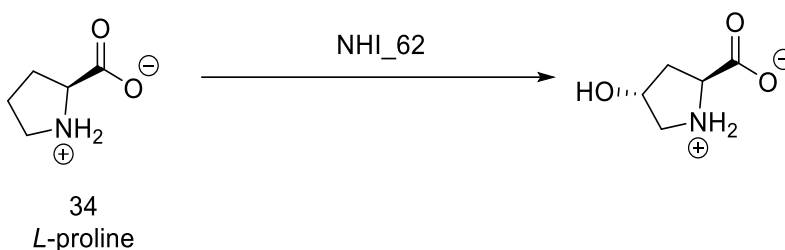


Reaction from literature³⁶

Reaction proposed by protein similarity.

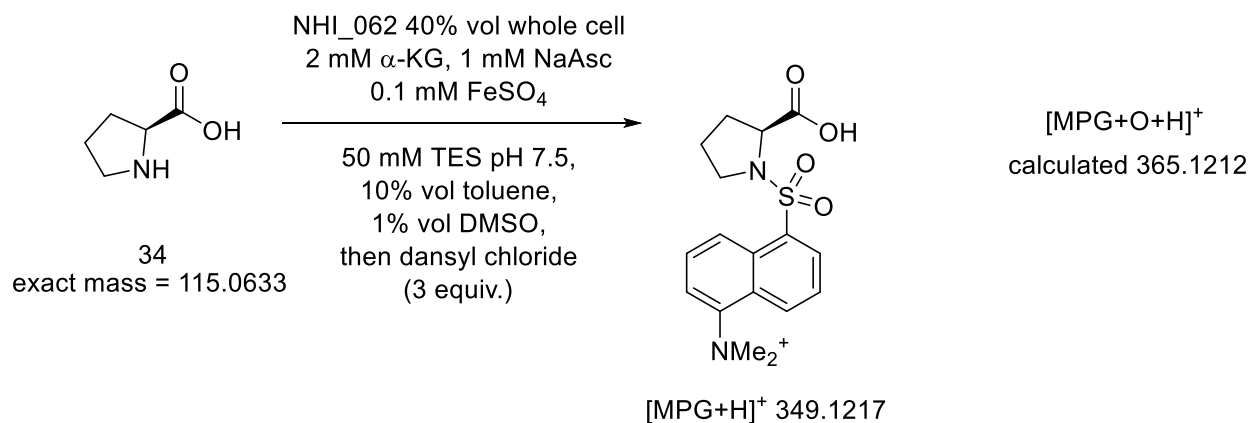
Reaction attempted but no product formation was observed.

Literature Reaction 27. Substrate_034 + NHI_062 = hydroxylation



Reaction from literature³⁷

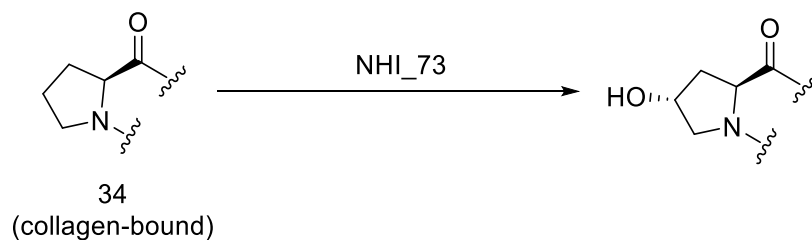
Reaction observed: Substrate_034 + NHI_062 = hydroxylation



	Neutral	Positive	Negative
Desaturation – PG	346.0987	347.1066	345.0909
Substrate – PG	348.1144	349.1222	347.1066
oxidation/desaturation - PG	362.0977	363.1056	361.0899
Hydroxylation – PG	364.1134	365.1212	363.1056
Dihydroxylation – PG	380.1124	381.1202	379.1046
Chlorination - PG	382.5596	383.5674	381.5517



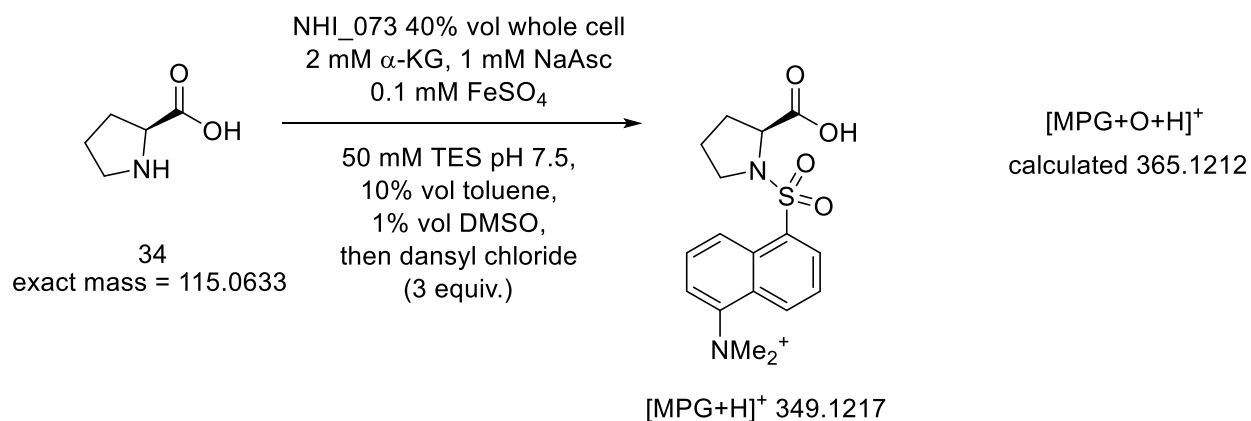
Literature Reaction 28. Substrate_034 + NHI_073 = hydroxylation



Reaction from literature³⁸

Reaction proposed by protein similarity.

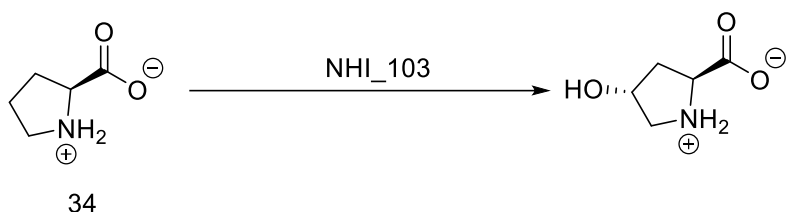
Reaction observed (discovered reaction 87): Substrate_034 + NHI_073 = hydroxylation



	Neutral	Positive	Negative
Desaturation – PG	346.0987	347.1066	345.0909
Substrate – PG	348.1144	349.1222	347.1066
oxidation/desaturation - PG	362.0977	363.1056	361.0899
Hydroxylation – PG	364.1134	365.1212	363.1056
Dihydroxylation – PG	380.1124	381.1202	379.1046
Chlorination - PG	382.5596	383.5674	381.5517

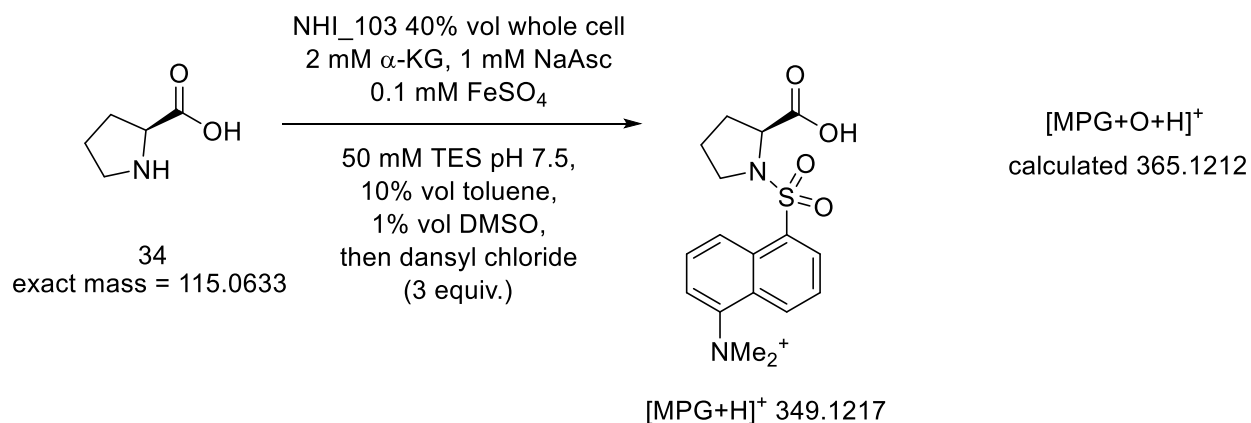


Literature Reaction 29. Substrate_034 + NHI_103 = hydroxylation

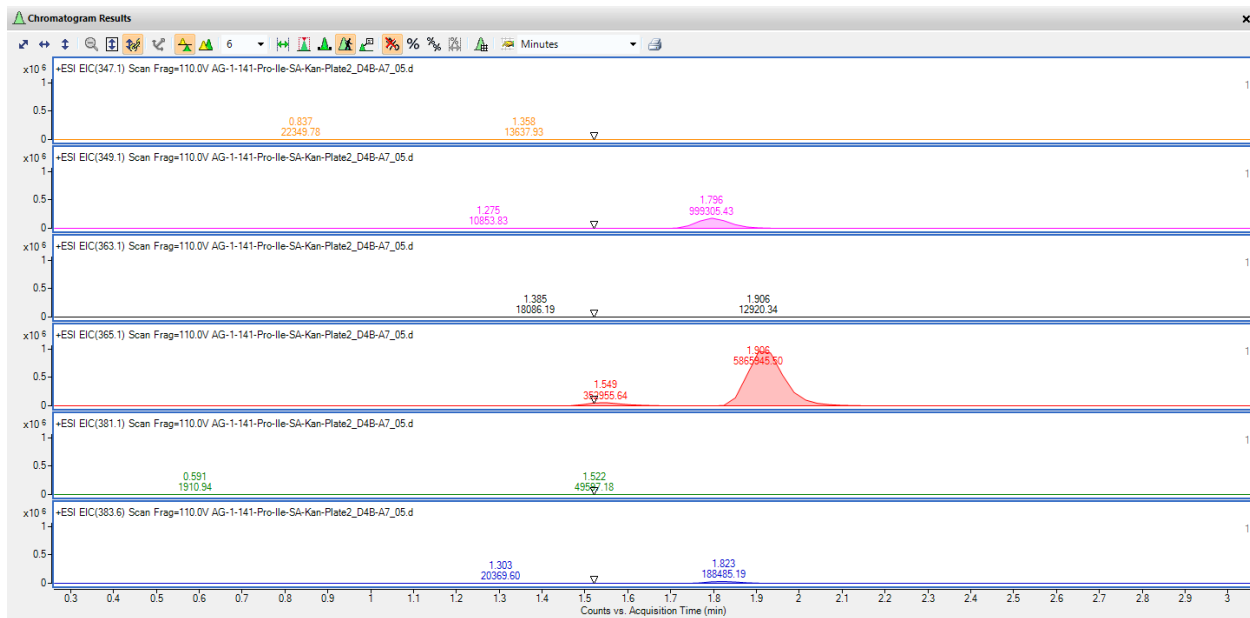


Reaction from literature³⁹

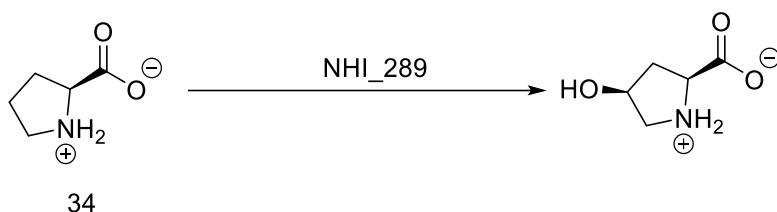
Reaction observed: Substrate_034 + NHI_103 = hydroxylation



	Neutral	Positive	Negative
Desaturation – PG	346.0987	347.1066	345.0909
Substrate – PG	348.1144	349.1222	347.1066
oxidation/desaturation - PG	362.0977	363.1056	361.0899
Hydroxylation – PG	364.1134	365.1212	363.1056
Dihydroxylation – PG	380.1124	381.1202	379.1046
Chlorination - PG	382.5596	383.5674	381.5517

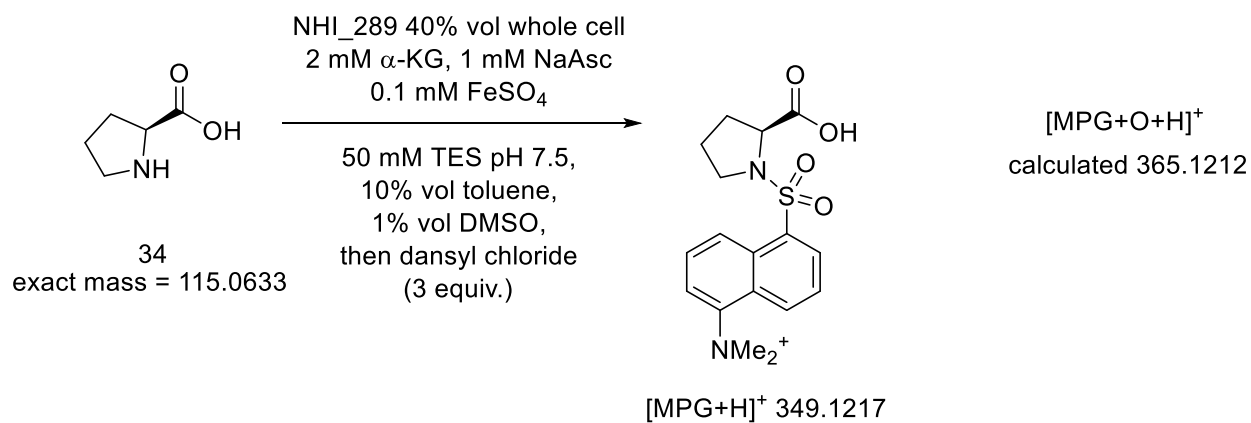


Literature Reaction 30. Substrate_034 + NHI_289 = hydroxylation

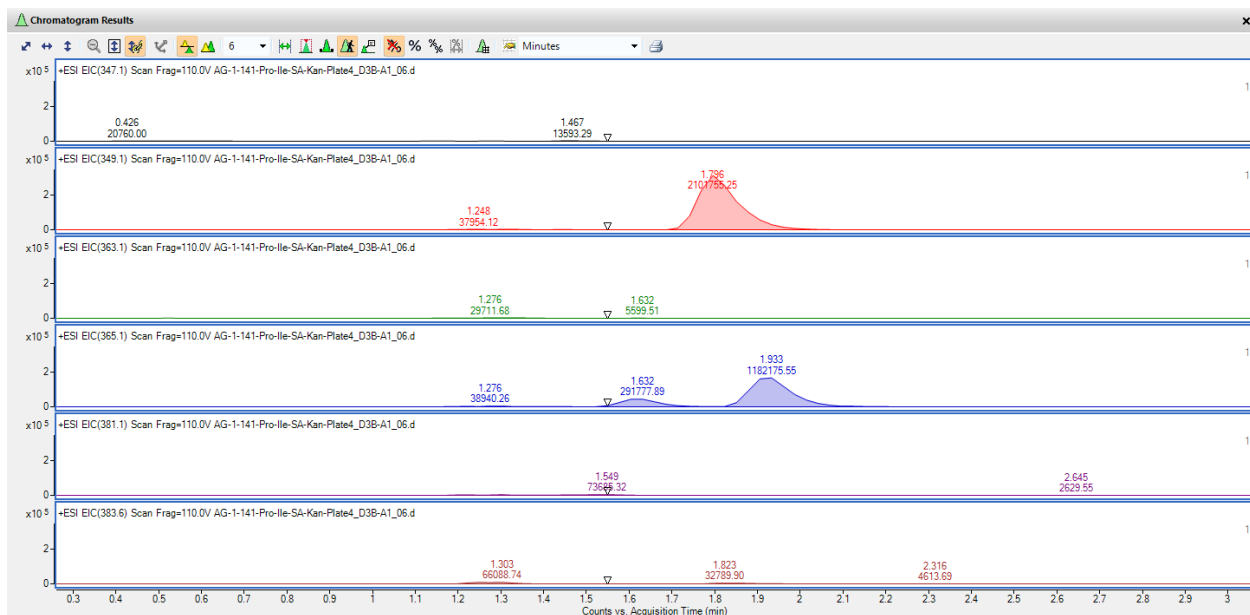


Reaction from literature⁴⁰

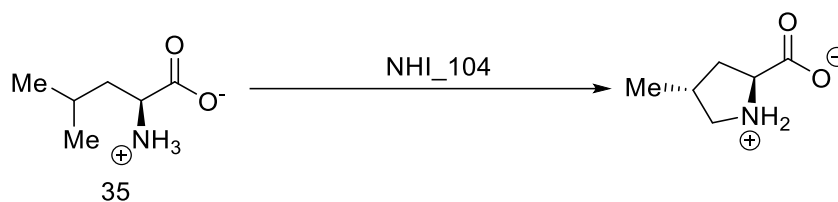
Reaction observed: Substrate_034 + NHI_289 = hydroxylation



	Neutral	Positive	Negative
Desaturation – PG	346.0987	347.1066	345.0909
Substrate – PG	348.1144	349.1222	347.1066
oxidation/desaturation - PG	362.0977	363.1056	361.0899
Hydroxylation – PG	364.1134	365.1212	363.1056
Dihydroxylation – PG	380.1124	381.1202	379.1046
Chlorination - PG	382.5596	383.5674	381.5517

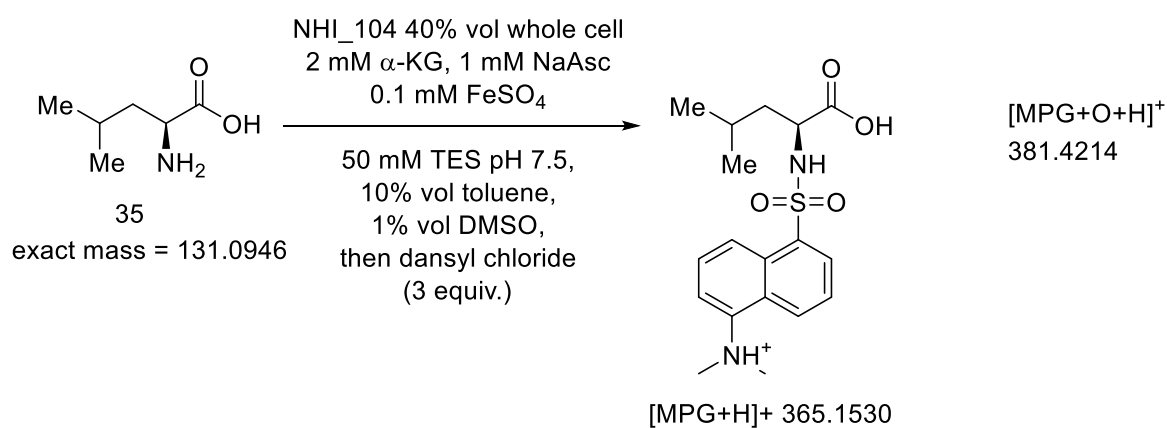


Literature Reaction 31. Substrate_035 + NHI_104 = rearrangement

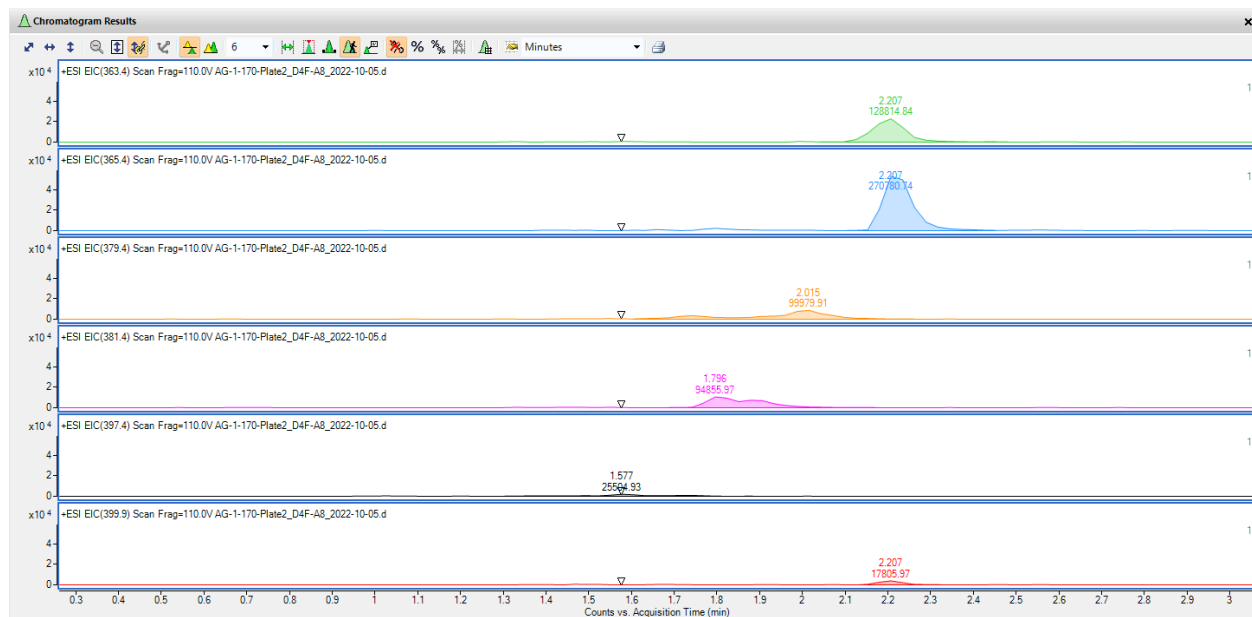


Reaction from literature⁴¹

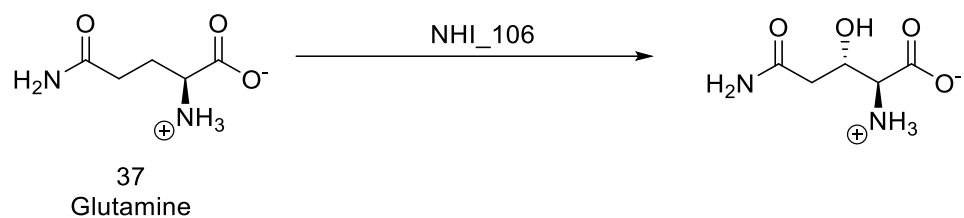
Reaction observed: Substrate_034 + NHI_104 = hydroxylation



	Neutral	Positive	Negative
Desaturation – PG	362.3988	363.4067	361.3910
Substrate – PG	364.4145	365.4223	363.4067
oxidation/desaturation - PG	378.3978	379.4057	377.3900
Hydroxylation – PG	380.4135	381.4213	379.4057
Dihydroxylation – PG	396.4125	397.4203	395.4047
Chlorination - PG	398.8597	399.8675	397.8518

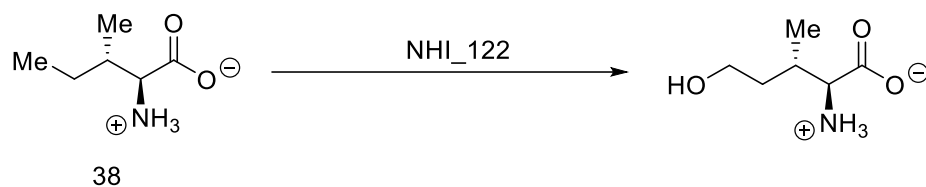


Literature Reaction 32. Substrate_037 + NHI_106 = probable hydroxylation



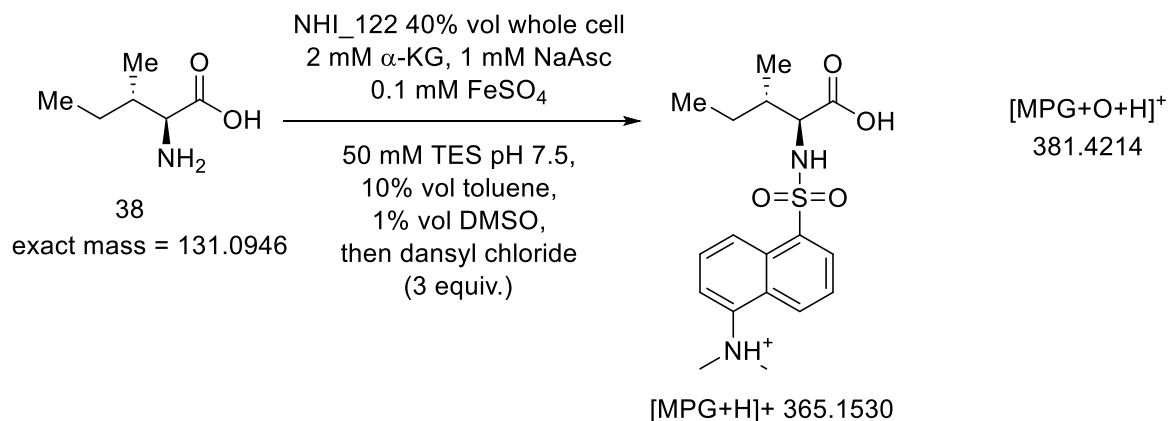
Reaction from literature⁴² – reproduction not attempted

Literature Reaction 33. Substrate_038 + NHI_122 = hydroxylation

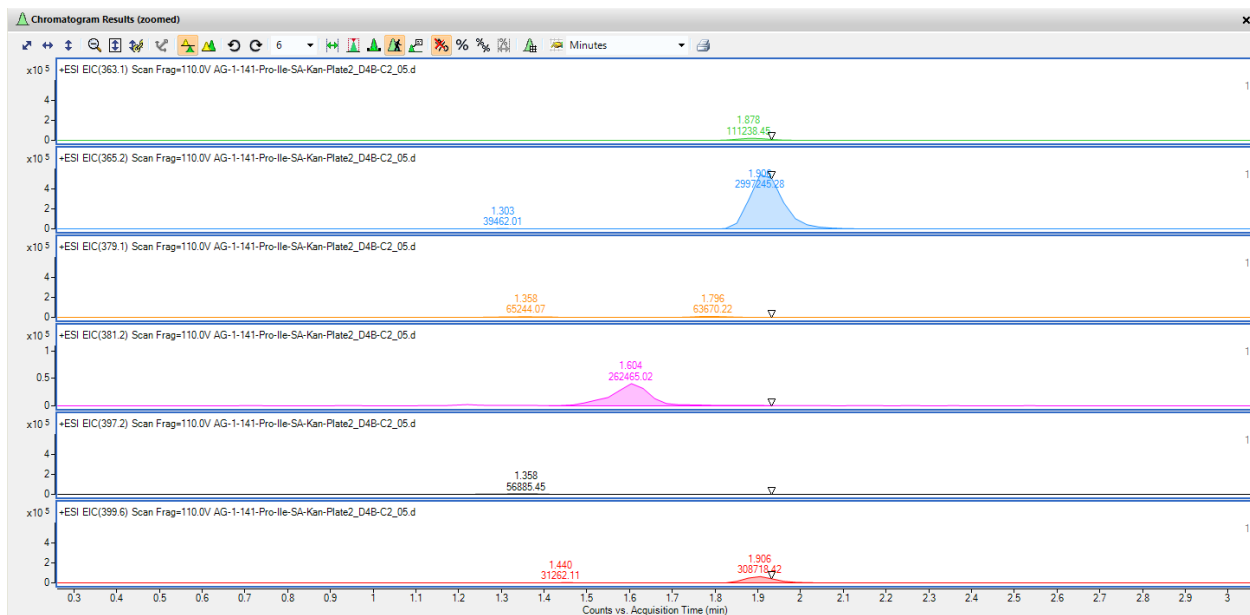


Reaction from literature⁴³

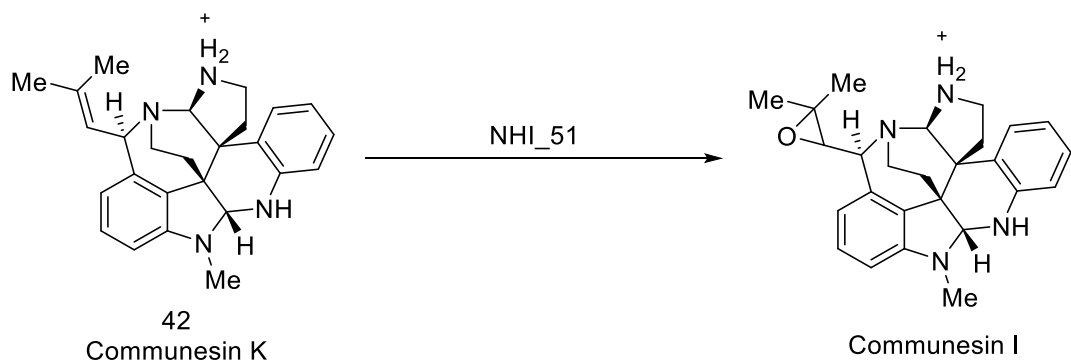
Reaction observed: Substrate_038 + NHI_122 = hydroxylation



	Neutral	Positive	Negative
Desaturation – PG	362.1300	363.1379	361.1222
Substrate – PG	364.1457	365.1535	363.1379
oxidation/desaturation - PG	378.1290	379.1369	377.1212
Hydroxylation – PG	380.1447	381.1525	379.1369
Dihydroxylation – PG	396.1437	397.1515	395.1359
Chlorination - PG	398.5909	399.5987	397.5830

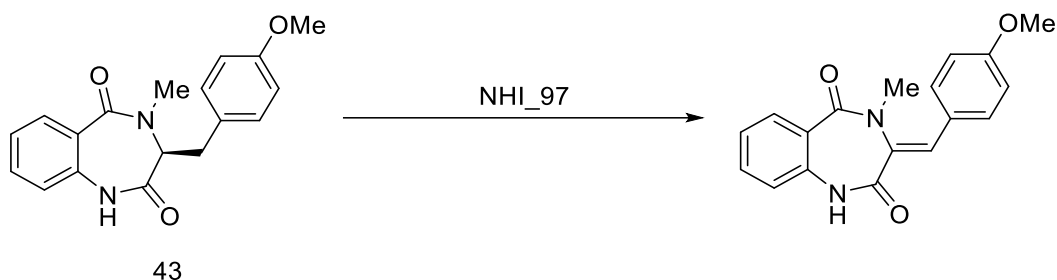


Literature Reaction 34. Substrate_042 + NHI_051 = epoxidation



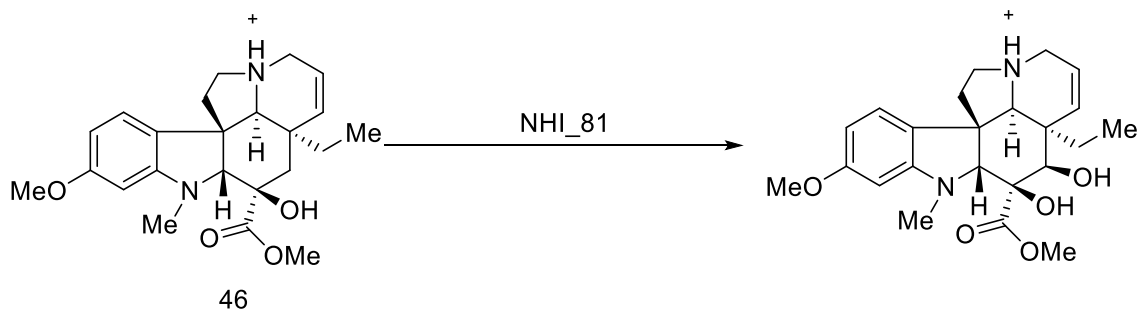
Reaction from literature⁴⁴ – reproduction not attempted.

Literature Reaction 35. Substrate_043 + NHI_097 = desaturation



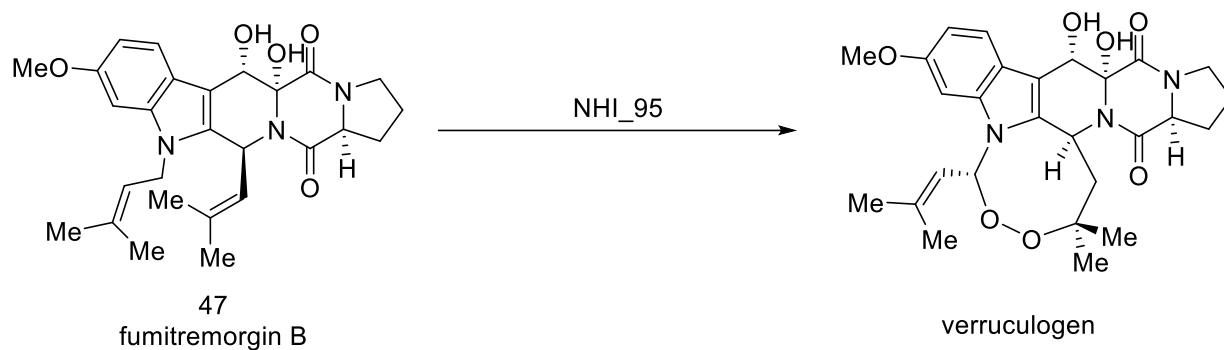
Reaction from literature⁴⁵ – reproduction not attempted.

Literature Reaction 36. Substrate_046 + NHI_081 = hydroxylation



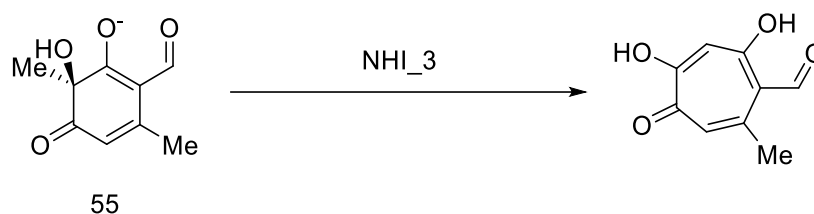
Reaction from literature⁴⁶ – reproduction not attempted.

Literature Reaction 37. Substrate_047 + NHI_095 = endoperoxidation



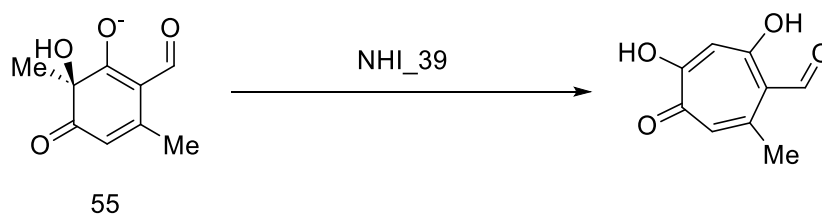
Reaction from literature⁴⁷ – reproduction not attempted.

Literature Reaction 38. Substrate_055 + NHI_003 = ring expansion (hydroxylation then rearrangement and condensation)



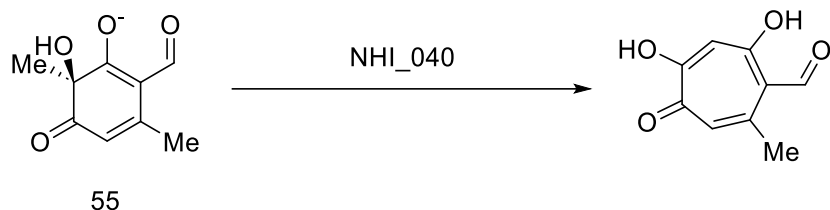
Reaction from literature⁴⁸ – Reaction not observed

Literature Reaction 39. Substrate_055 + NHI_039 = ring expansion (hydroxylation then rearrangement and condensation)



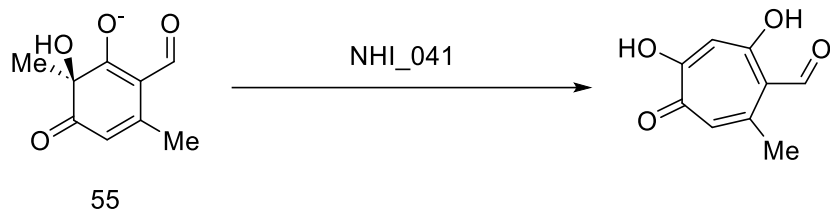
Reaction from literature⁴⁹ – Reaction not observed

Literature Reaction 40. Substrate_055 + NHI_040 = ring expansion (hydroxylation then rearrangement and condensation)



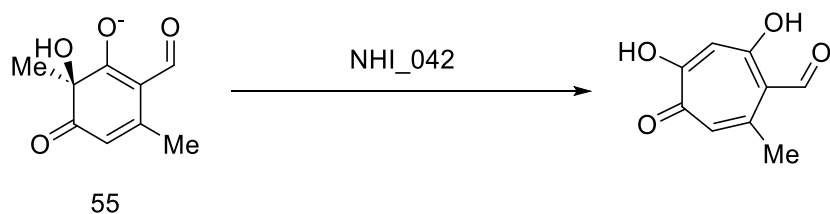
Reaction from literature⁴⁹ – Reaction not observed

Literature Reaction 41. Substrate_055 + NHI_041 = ring expansion (hydroxylation then rearrangement and condensation)



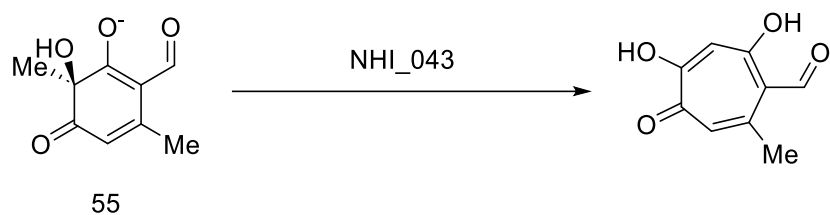
Reaction from literature⁴⁹ – Reaction not observed

Literature Reaction 42. Substrate_055 + NHI_042 = ring expansion (hydroxylation then rearrangement and condensation)



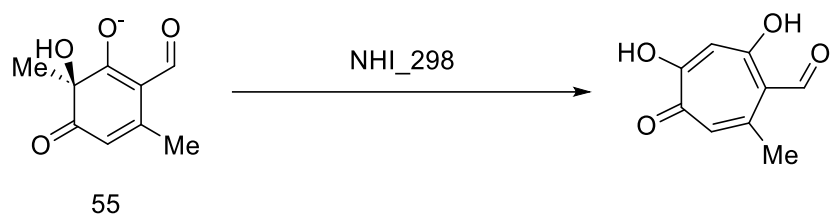
Reaction from literature⁴⁹ – Reaction not observed

Literature Reaction 43. Substrate_055 + NHI_043 = ring expansion (hydroxylation then rearrangement and condensation)



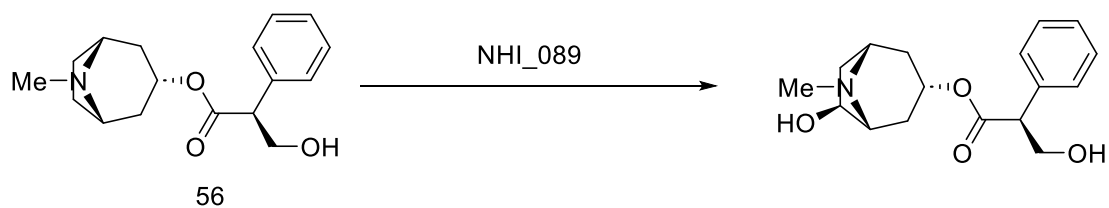
Reaction from literature⁴⁹ – Reaction not observed

Literature Reaction 44. Substrate_055 + NHI_298 = ring expansion (hydroxylation then rearrangement and condensation)



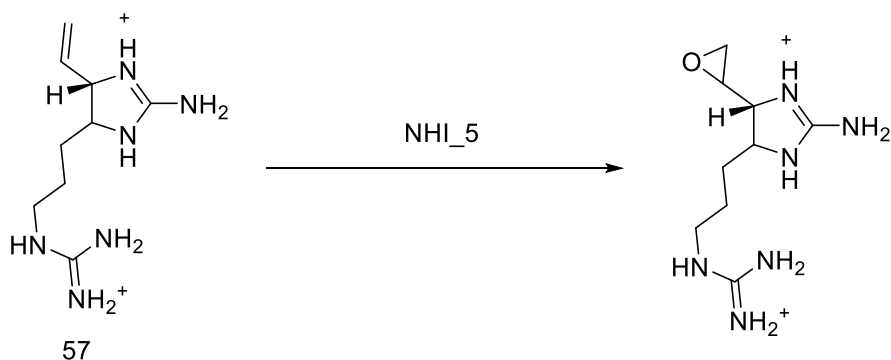
Reaction from literature⁴⁹ – Reaction not observed

Literature Reaction 45. Substrate_056 + NHI_089 = hydroxylation



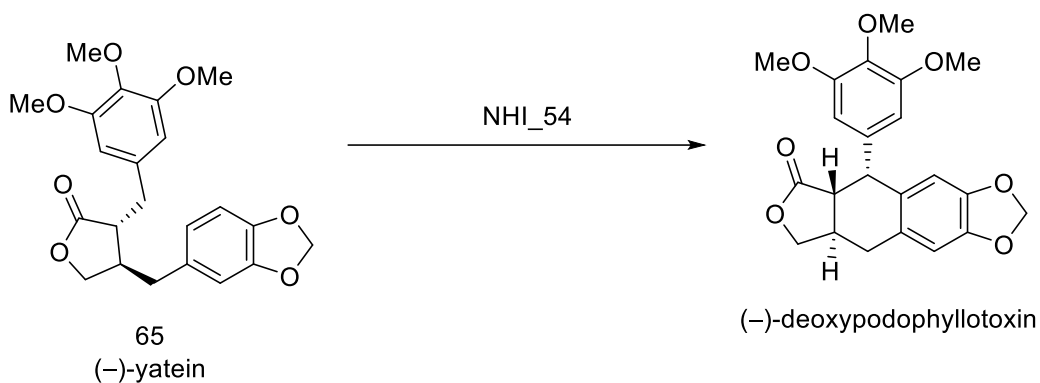
Reaction from literature⁵⁰ – reproduction not attempted

Literature Reaction 46. Substrate_057 + NHI_005 = epoxidation



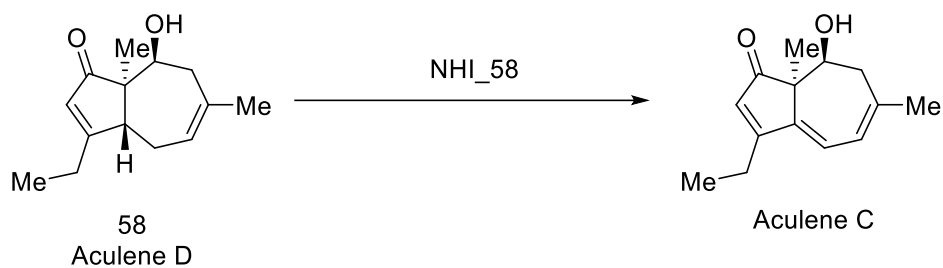
Reaction from literature⁵¹ – reproduction not attempted.

Literature Reaction 47. Substrate_065 + NHI_054 = carbon-carbon bond formation



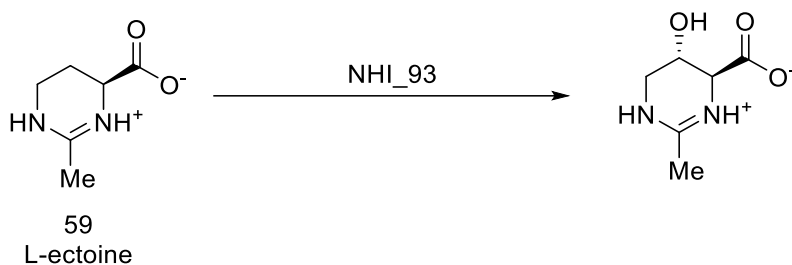
Reaction from literature⁵² – reproduction not attempted.

Literature Reaction 48. Substrate_058 + NHI_058 = desaturation



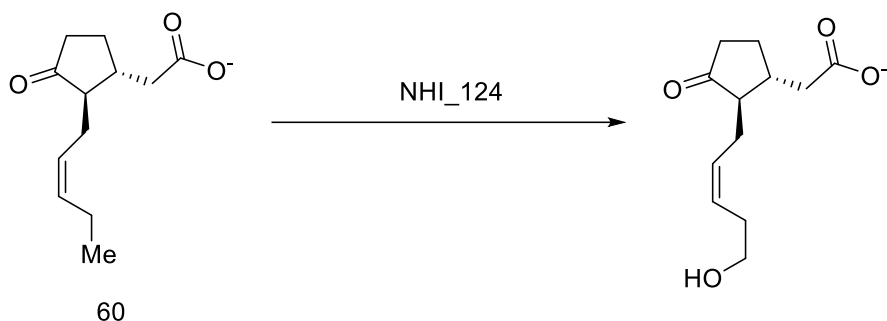
Reaction from literature⁵³ – reproduction not attempted.

Literature Reaction 49. Substrate_059 + NHI_093 = hydroxylation



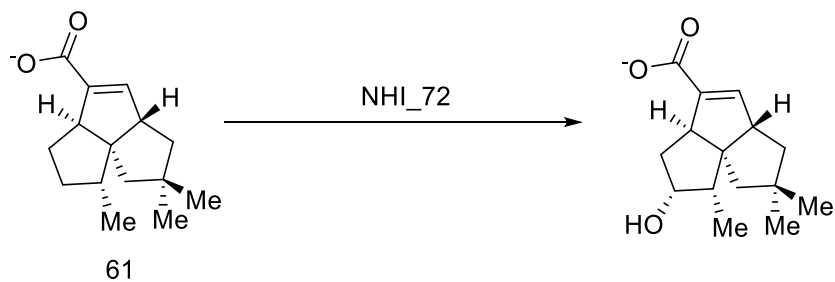
Reaction from literature⁵⁴ – reproduction not attempted.

Literature Reaction 50. Substrate_060 + NHI_124 = hydroxylation



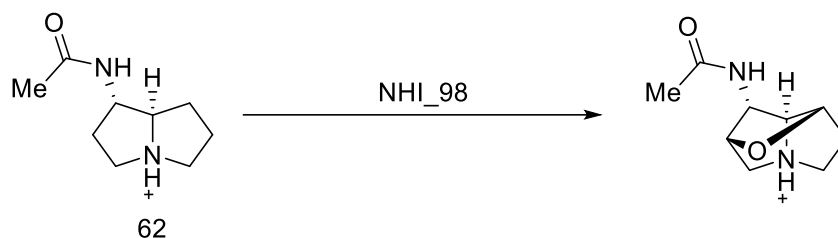
Reaction from literature⁵⁵ – reproduction not attempted.

Literature Reaction 51. Substrate_061 + NHI_072 = hydroxylation



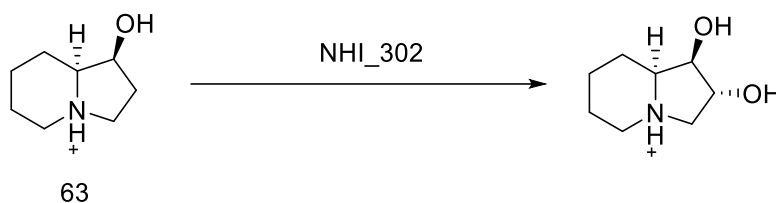
Reaction from literature⁵⁶ – reproduction not attempted

Literature Reaction 52. Substrate_062 + NHI_098 = hydroxylation, ether formation



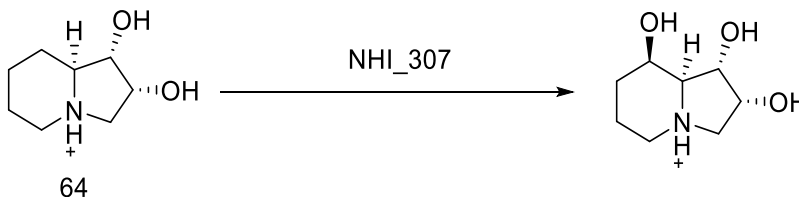
Reaction from literature⁵⁷ – reproduction not attempted.

Literature Reaction 53. Substrate_063 + NHI_302 = probable hydroxylation



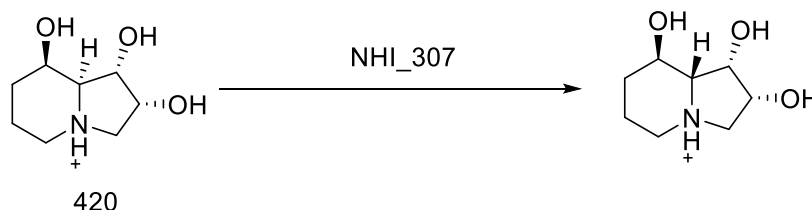
Reaction from literature⁵⁸ – reproduction not attempted.

Literature Reaction 54. Substrate_064 + NHI_307 = probable hydroxylation



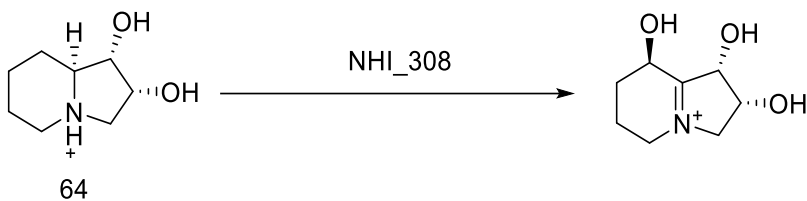
Reaction from literature⁵⁸ – reproduction not attempted.

Literature Reaction 55. Substrate_064 + NHI_307 = probable epimerization



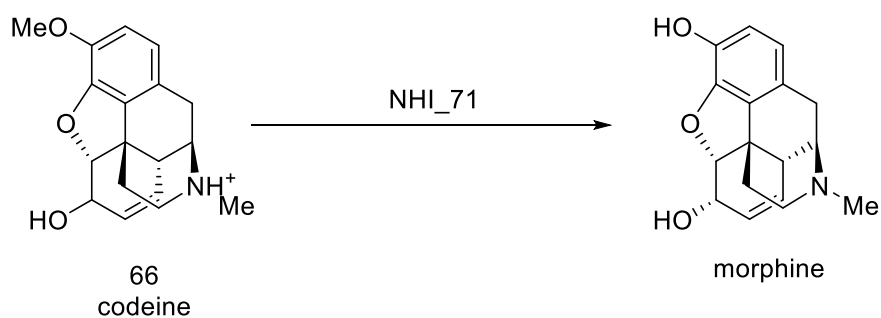
Reaction from literature⁵⁸ – reproduction not attempted.

Literature Reaction 56. Substrate_064 + NHI_308 = probable hydroxylation and desaturation



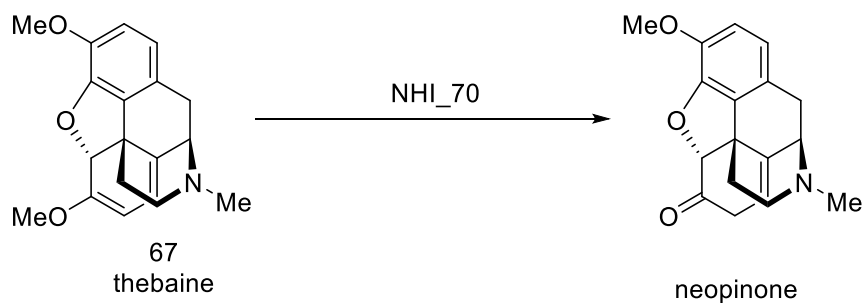
Reaction from literature⁵⁹ – reproduction not attempted.

Literature Reaction 57. Substrate_066 + NHI_071 = O-demethylation



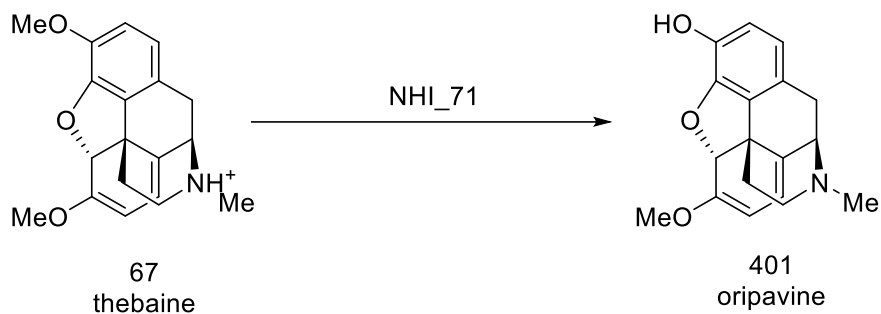
Reaction from literature⁶⁰ – reproduction not attempted

Literature Reaction 58. Substrate_067 + NHI_070 = O-demethylation and tautomerization



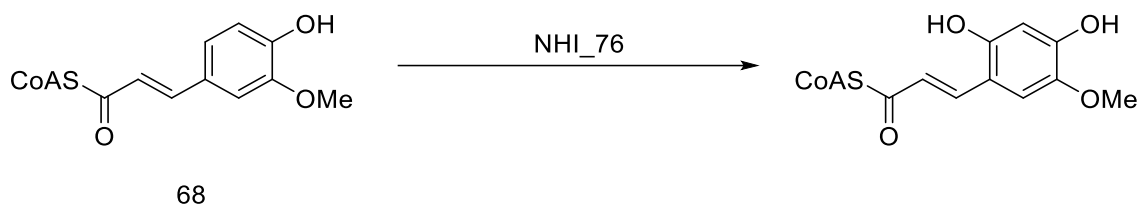
Reaction from literature⁶⁰ – reproduction not attempted

Literature Reaction 59. Substrate_067 + NHI_071 = O-demethylation



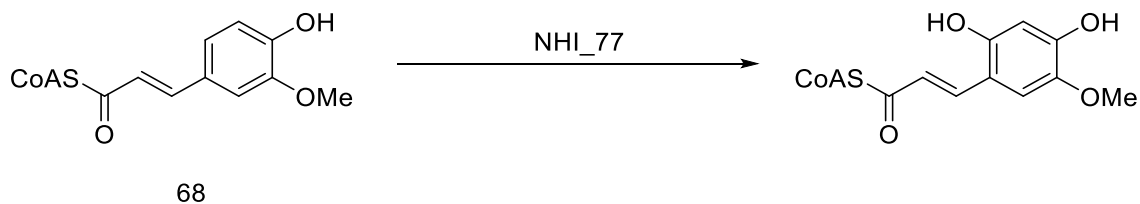
Reaction from literature⁶⁰ – reproduction not attempted

Literature Reaction 60. Substrate_068 + NHI_076 = hydroxylation



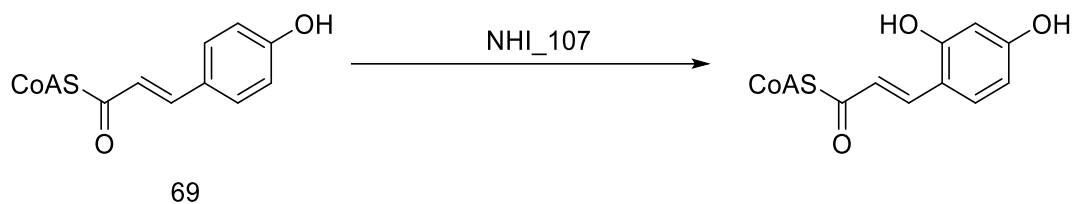
Reaction from literature⁶¹ – reproduction not attempted.

Literature Reaction 61. Substrate_068 + NHI_077 = hydroxylation



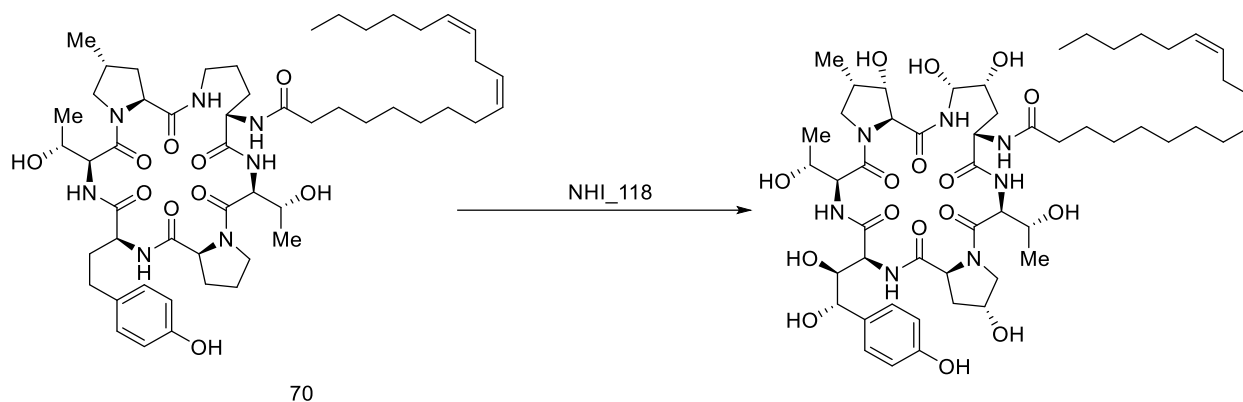
Reaction from literature⁶² – reproduction not attempted.

Literature Reaction 62. Substrate_069 + NHI_107 = hydroxylation



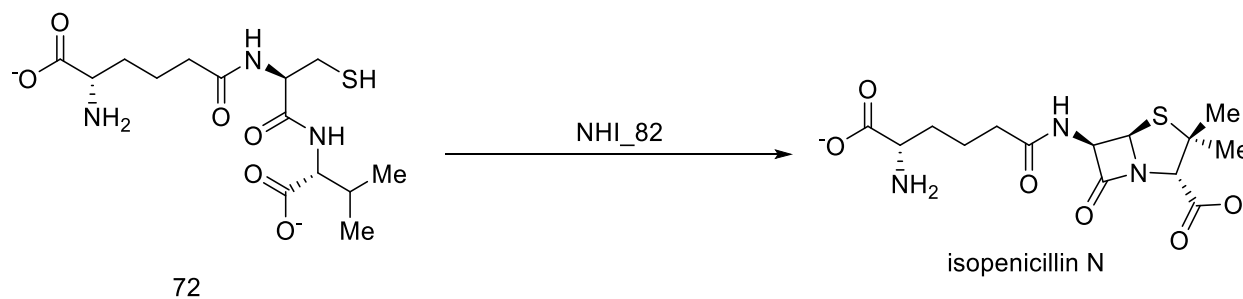
Reaction from literature⁶³ – reproduction not attempted.

Literature Reaction 63. Substrate_070 + NHI_118 = proposed hydroxylation



Reaction from literature⁶⁴ – reproduction not attempted.

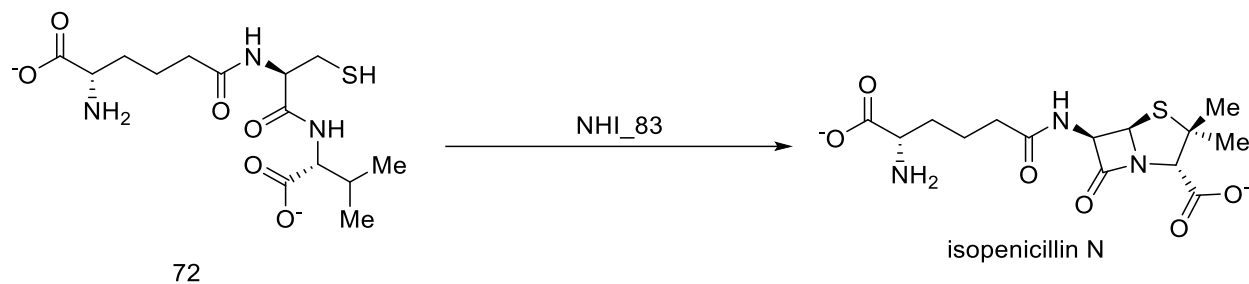
Literature Reaction 64. Substrate_072 + NHI_082 = probable desaturation (ring formation)



Reaction from literature⁶⁵ – reproduction not attempted.

Reaction proposed based on protein similarity.

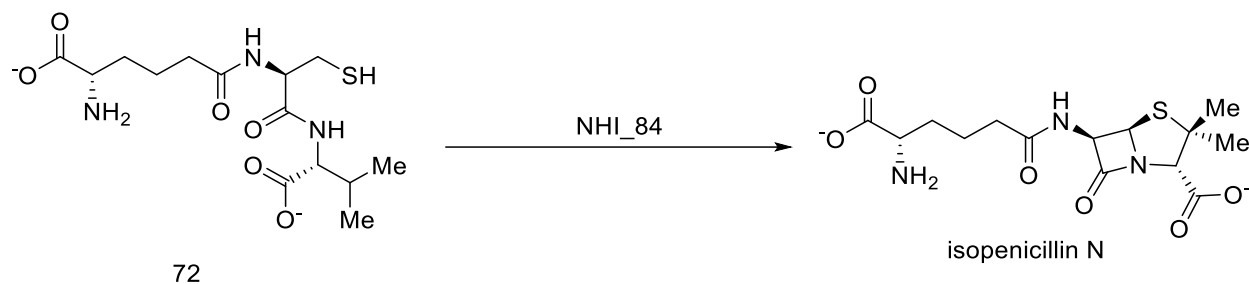
Literature Reaction 65. Substrate_072 + NHI_083 = probable desaturation (ring formation)



Reaction from literature⁶⁵ – reproduction not attempted.

Reaction proposed based on protein similarity.

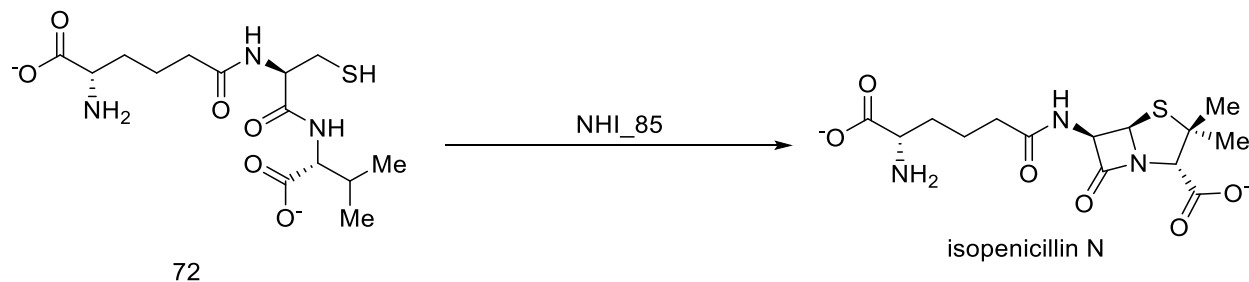
Literature Reaction 66. Substrate_072 + NHI_084 = probable desaturation (ring formation)



Reaction from literature⁶⁵ – reproduction not attempted.

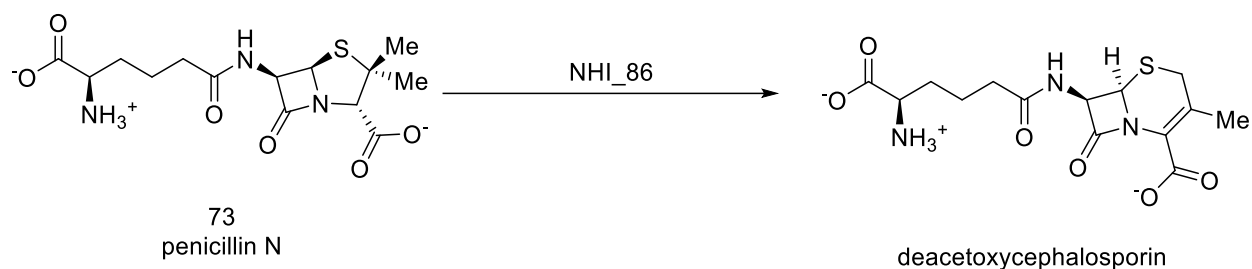
Reaction proposed based on protein similarity.

Literature Reaction 67. Substrate_072 + NHI_085 = desaturation (ring formation)



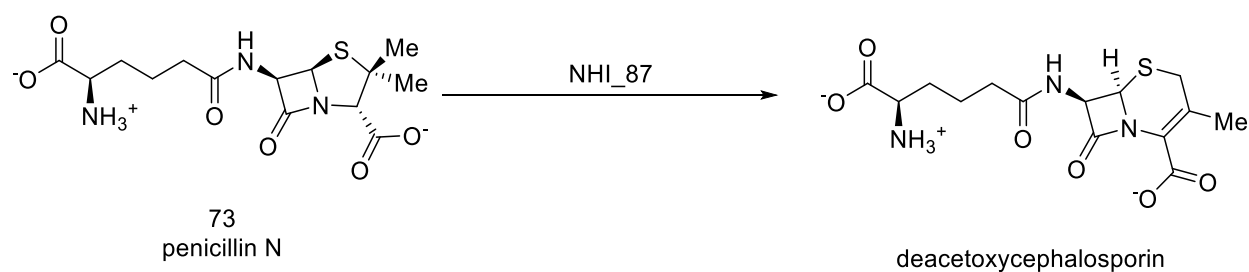
Reaction from literature⁶⁶ – reproduction not attempted.

Literature Reaction 68. Substrate_073 + NHI_086 = ring expansion and desaturation



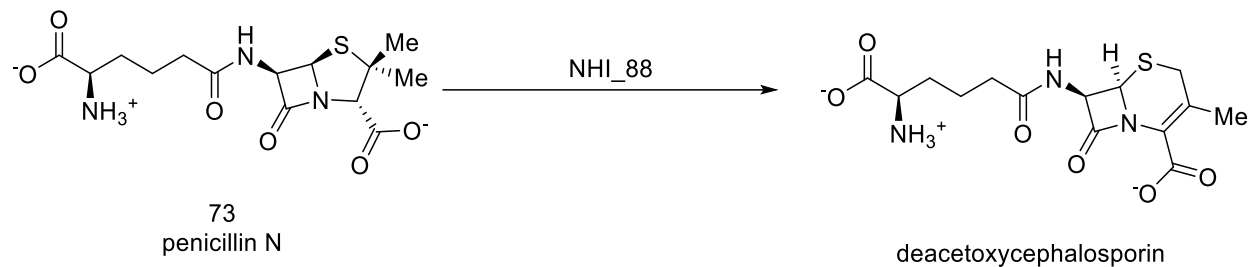
Reaction from literature⁶⁷ – reproduction not attempted.

Literature Reaction 69. Substrate_073 + NHI_087 = ring expansion and desaturation



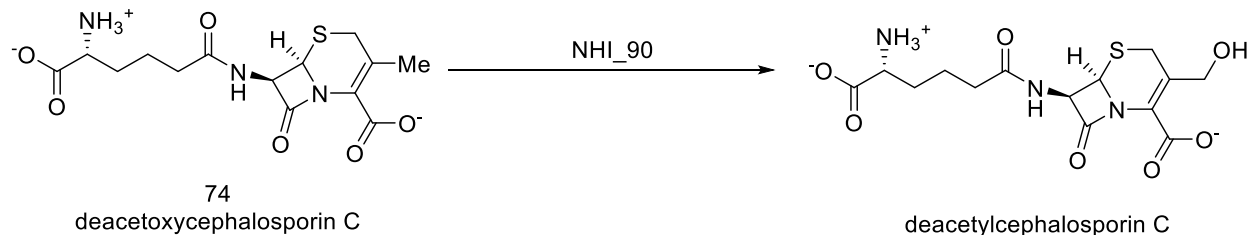
Reaction from literature⁶⁸ – reproduction not attempted.

Literature Reaction 70. Substrate_073 + NHI_088 = ring expansion and desaturation



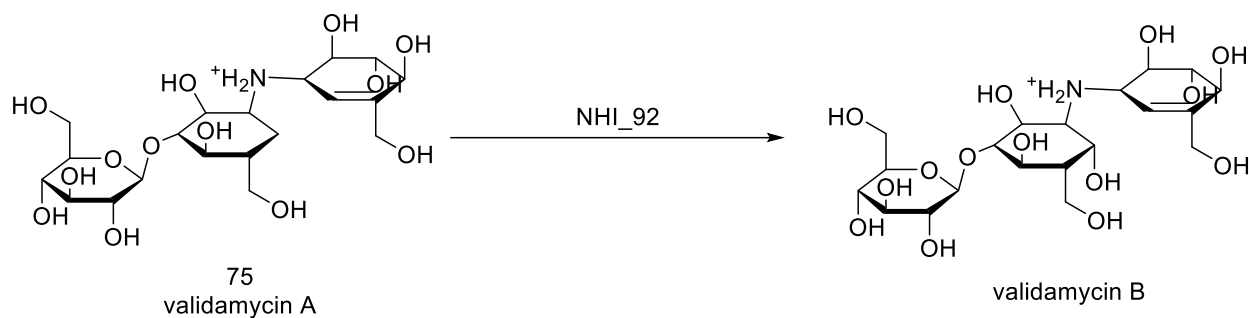
Reaction from literature⁶⁸ – reproduction not attempted.

Literature Reaction 71. Substrate_074 + NHI_090 = hydroxylation



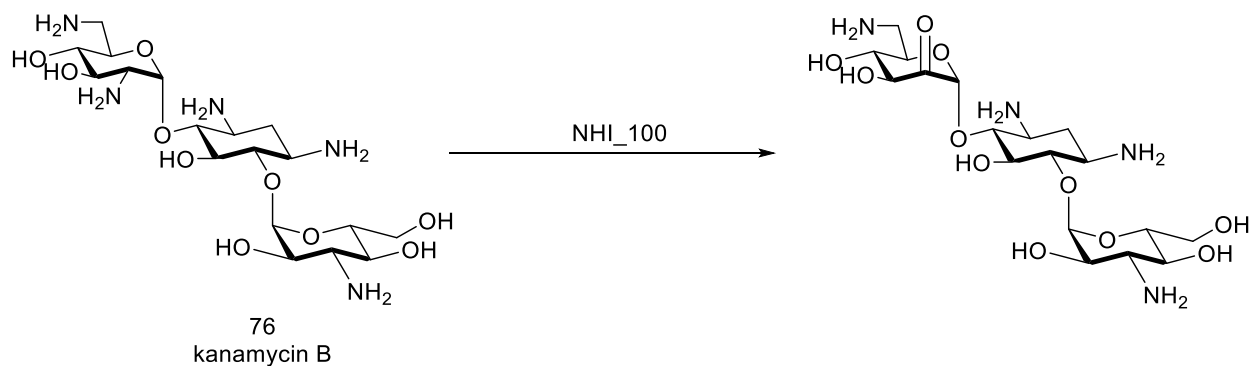
Reaction from literature⁶⁹ – reproduction not attempted.

Literature Reaction 72. Substrate_075 + NHI_092 = hydroxylation



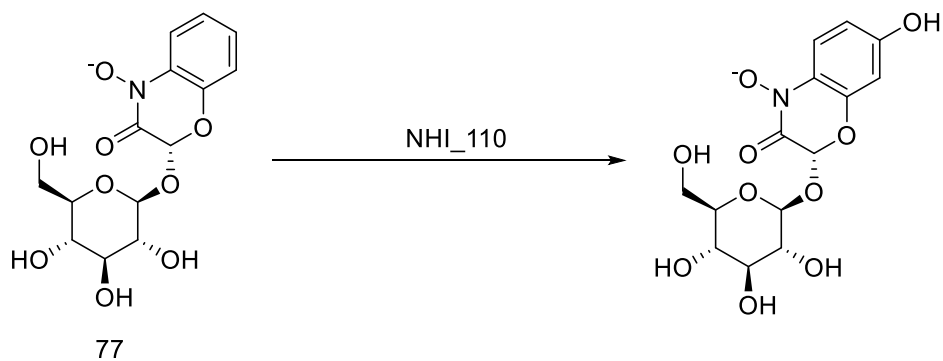
Reaction from literature⁷⁰ – reproduction not attempted.

Literature Reaction 73. Substrate_076 + NHI_100 = transamination



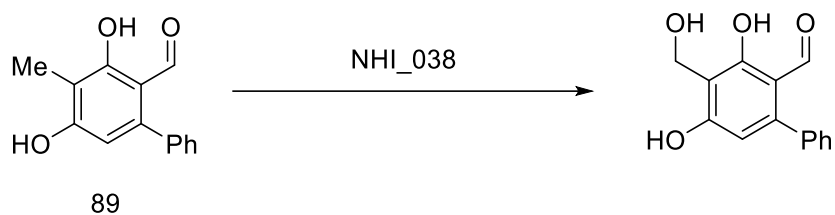
Reaction from literature⁷¹ – reproduction not attempted.

Literature Reaction 74. Substrate_077 + NHI_110 = hydroxylation



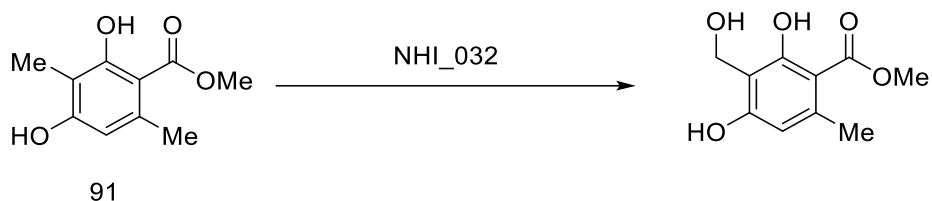
Reaction from literature⁷² – reproduction not attempted.

Literature Reaction 75. Substrate_089 + NHI_038 = hydroxylation



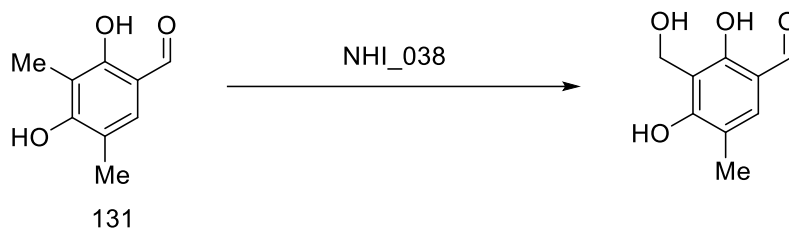
Reaction from literature⁴⁹ – reproduction not attempted

Literature Reaction 76. Substrate_091 + NHI_032 = hydroxylation



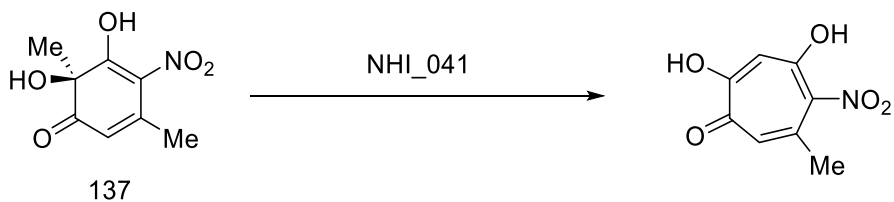
Reaction from literature⁴⁹ – reproduction not attempted

Literature Reaction 77. Substrate_131 + NHI_038 = hydroxylation



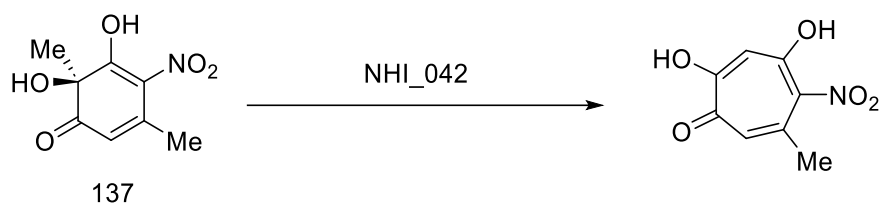
Reaction from literature⁴⁹ – reproduction not attempted

Literature Reaction 78. Substrate_137 + NHI_041 = ring expansion



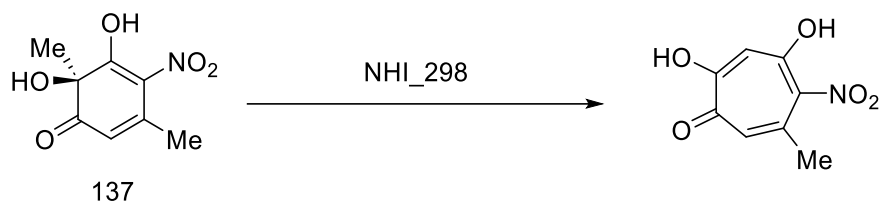
Reaction from literature⁴⁹ – reproduction not attempted

Literature Reaction 79. Substrate_137 + NHI_042 = ring expansion



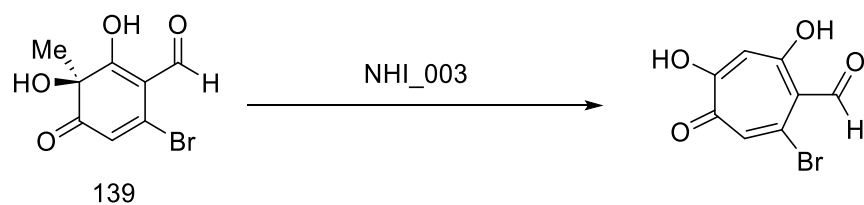
Reaction from literature⁴⁹ – reproduction not attempted

Literature Reaction 80. Substrate_137 + NHI_298 = ring expansion



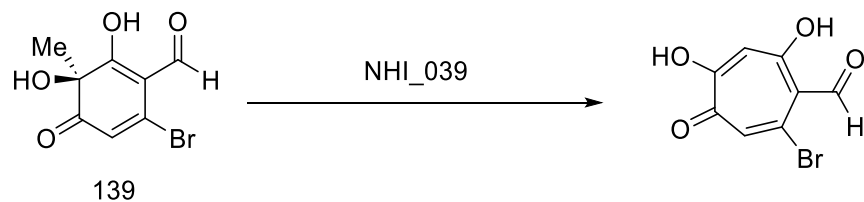
Reaction from literature⁴⁹ – reproduction not attempted

Literature Reaction 81. Substrate_139 + NHI_003 = ring expansion



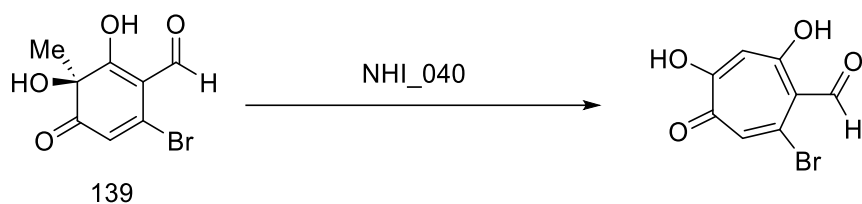
Reaction from literature⁴⁹ – reproduction not attempted

Literature Reaction 82. Substrate_139 + NHI_039 = ring expansion



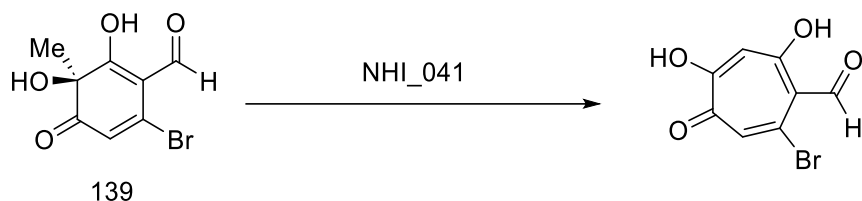
Reaction from literature⁴⁹ – reproduction not attempted

Literature Reaction 83. Substrate_139 + NHI_040 = ring expansion



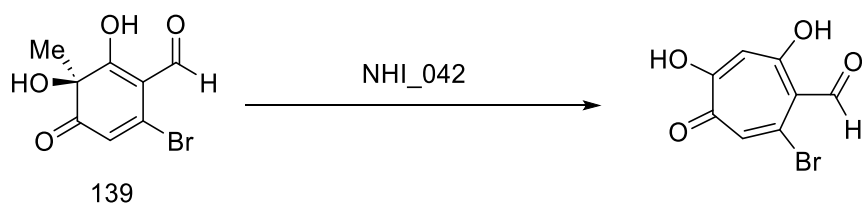
Reaction from literature⁴⁹ – reproduction not attempted

Literature Reaction 84. Substrate_139 + NHI_041 = ring expansion



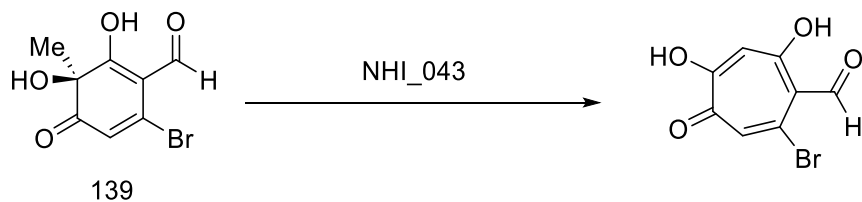
Reaction from literature⁴⁹ – reproduction not attempted

Literature Reaction 85. Substrate_139 + NHI_042 = ring expansion



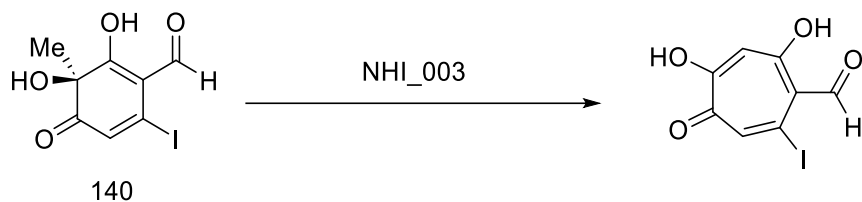
Reaction from literature⁴⁹ – reproduction not attempted

Literature Reaction 86. Substrate_139 + NHI_043 = ring expansion



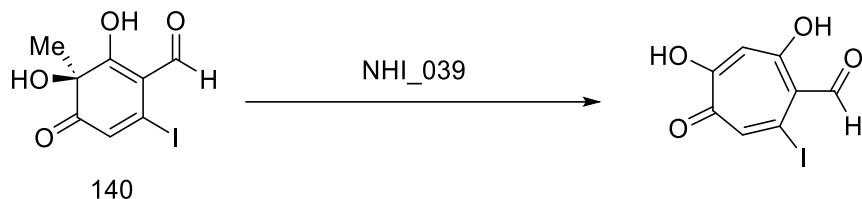
Reaction from literature⁴⁹ – reproduction not attempted

Literature Reaction 87. Substrate_140 + NHI_003 = ring expansion



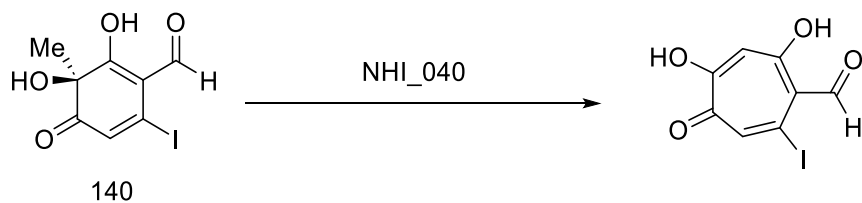
Reaction from literature search⁴⁹ – reproduction not attempted

Literature Reaction 88. Substrate_140 + NHI_039 = ring expansion



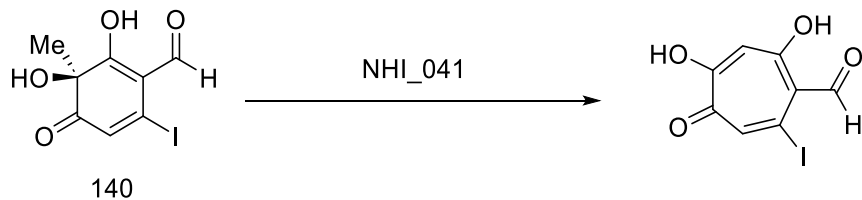
Reaction from literature⁴⁹ - reproduction not attempted

Literature Reaction 89. Substrate_140 + NHI_040 = ring expansion



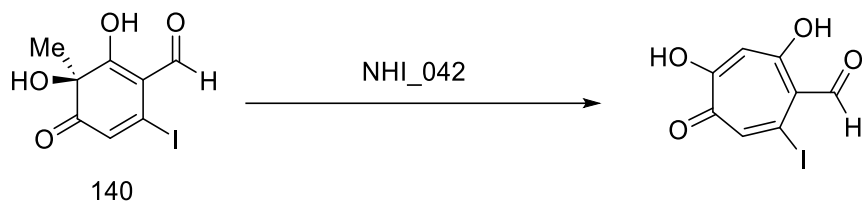
Reaction from literature⁴⁹ – reproduction not attempted

Literature Reaction 90. Substrate_140 + NHI_041 = ring expansion



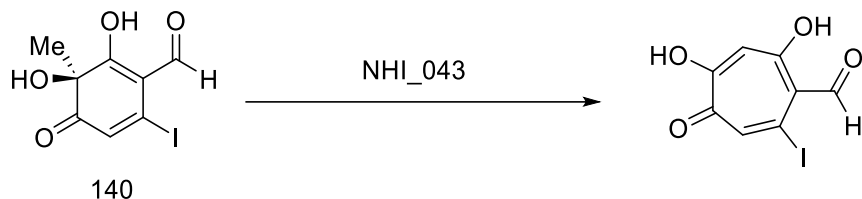
Reaction from literature⁴⁹ – reproduction not attempted

Literature Reaction 91. Substrate_140 + NHI_042 = ring expansion



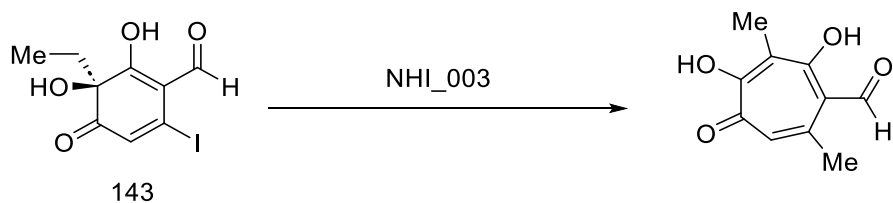
Reaction from literature⁴⁹ – reproduction not attempted

Literature Reaction 92. Substrate_140 + NHI_043 = ring expansion



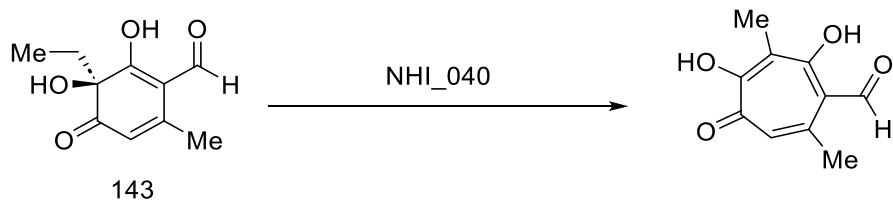
Reaction from literature⁴⁹ – reproduction not attempted

Literature Reaction 93. Substrate_143 + NHI_003 = ring expansion



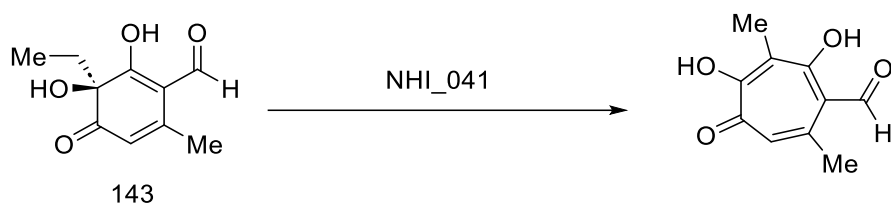
Reaction from literature⁴⁹ – reproduction not attempted

Literature Reaction 94. Substrate_143 + NHI_040 = ring expansion



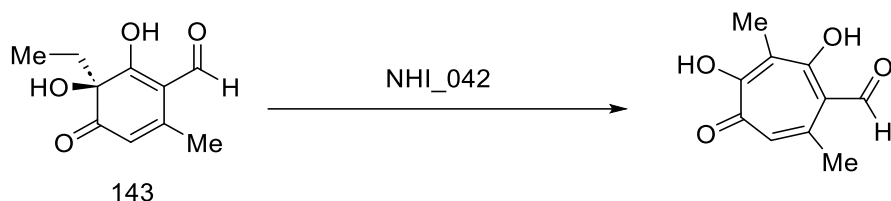
Reaction from literature⁴⁹ – reproduction not attempted

Literature Reaction 95. Substrate_143 + NHI_041 = ring expansion



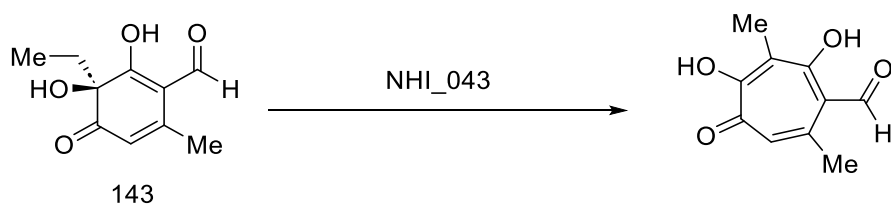
Reaction from literature⁴⁹ – reproduction not attempted

Literature Reaction 96. Substrate_143 + NHI_042 = ring expansion



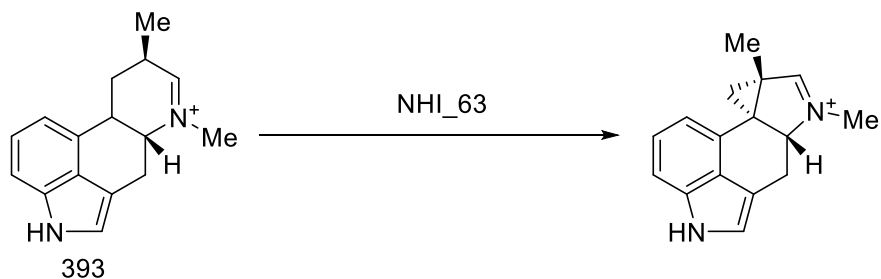
Reaction from literature⁴⁹ – reproduction not attempted

Literature Reaction 97. Substrate_143 + NHI_298 = ring expansion



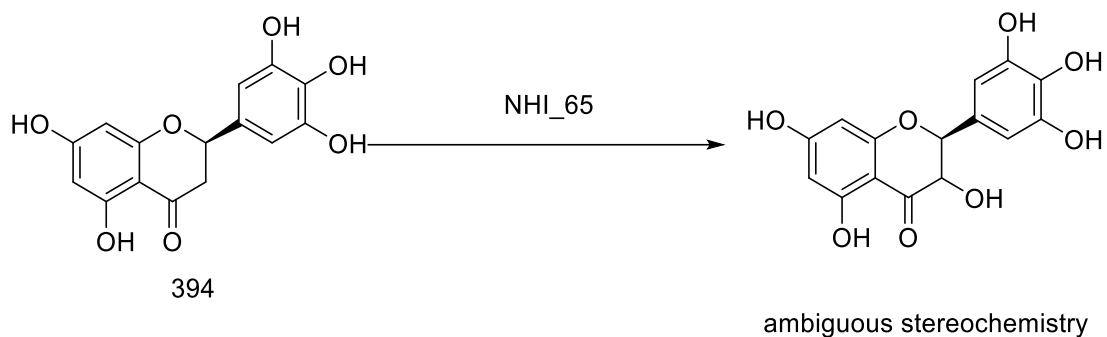
Reaction from literature⁴⁹ – reproduction not attempted

Literature Reaction 98. Substrate_393 + NHI_063 = ring contraction



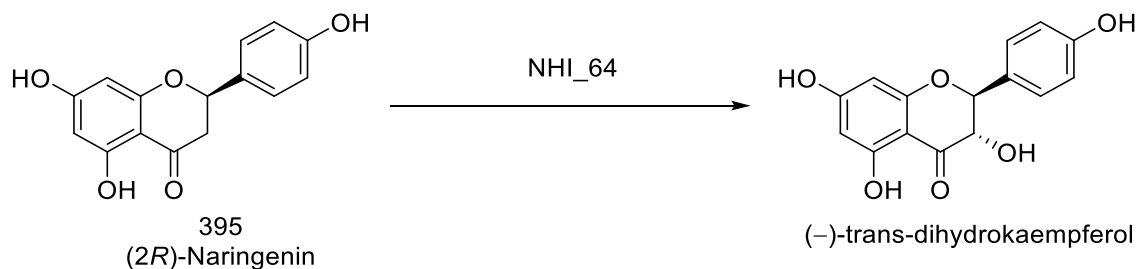
Reaction from literature⁷³ – reproduction not attempted.

Literature Reaction 99. Substrate_394 + NHI_065 = hydroxylation



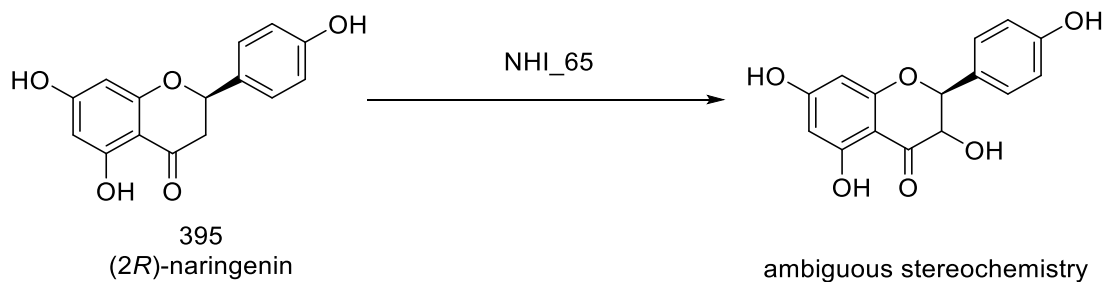
Reaction from literature²¹ – reproduction not attempted

Literature Reaction 100. Substrate_395 + NHI_064 = hydroxylation



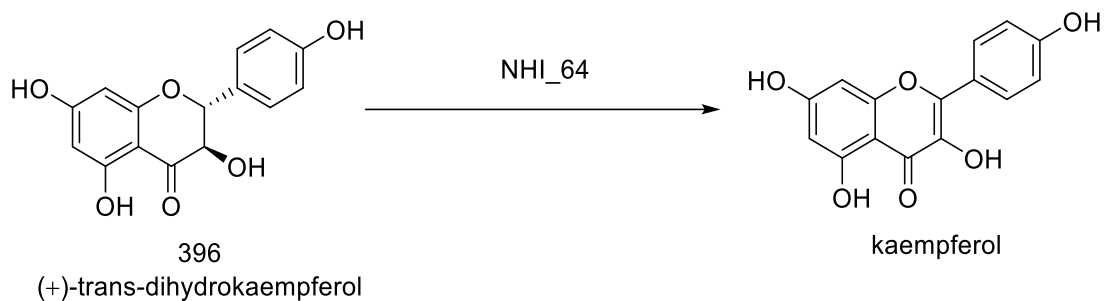
Reaction from literature⁷⁴ – reproduction not attempted

Literature Reaction 101. Substrate_395 + NHI_065 = hydroxylation



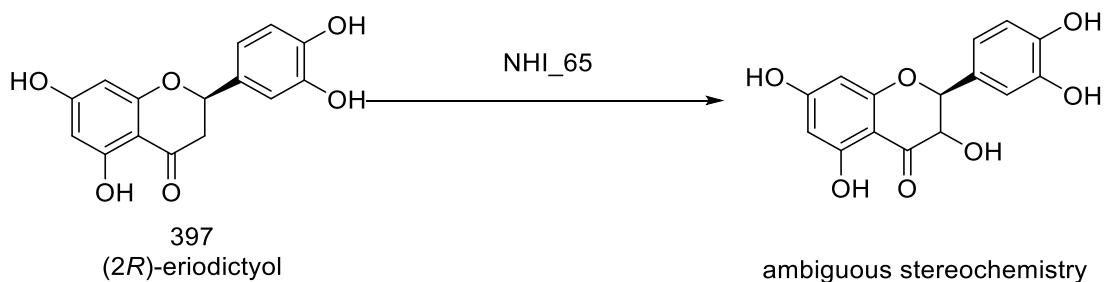
Reaction from literature²¹ – reproduction not attempted

Literature Reaction 102. Substrate_396 + NHI_064 = desaturation



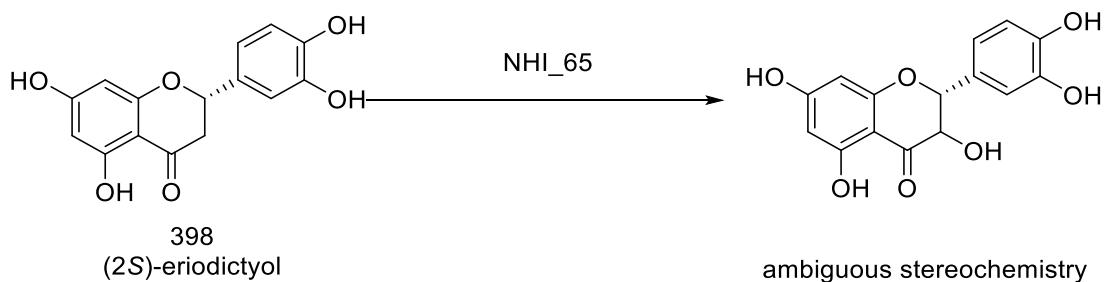
Reaction from literature⁷⁴ – reproduction not attempted

Literature Reaction 103. Substrate_397 + NHI_065 = hydroxylation



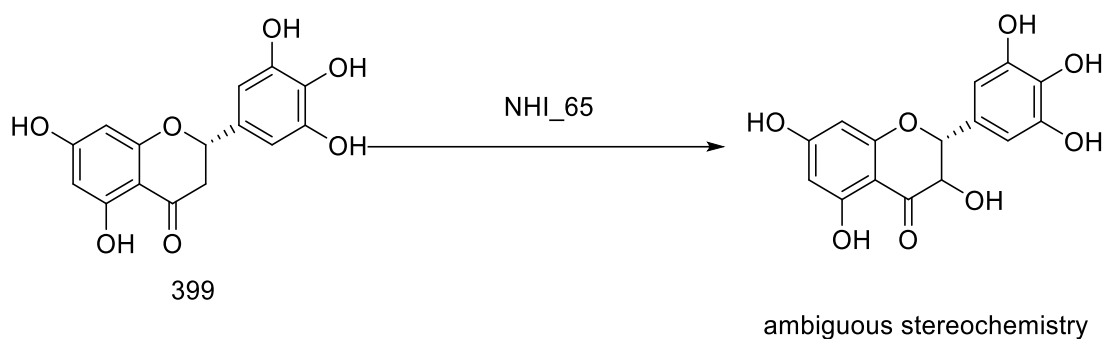
Reaction from literature²¹ – reproduction not attempted

Literature Reaction 104. Substrate_398 + NHI_065 = hydroxylation



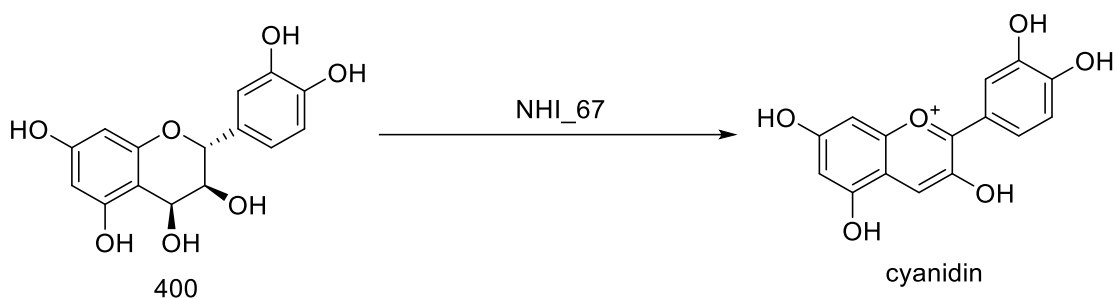
Reaction from literature²¹ – reproduction not attempted

Literature Reaction 105. Substrate_399 + NHI_065 = hydroxylation



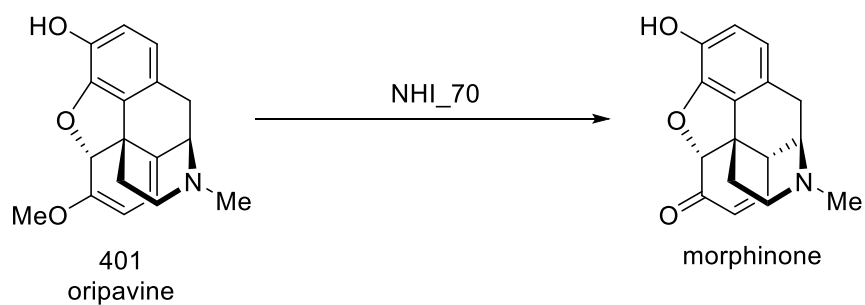
Reaction from literature²¹ – reproduction not attempted

Literature Reaction 106. Substrate_400 + NHI_067 = desaturation and condensation



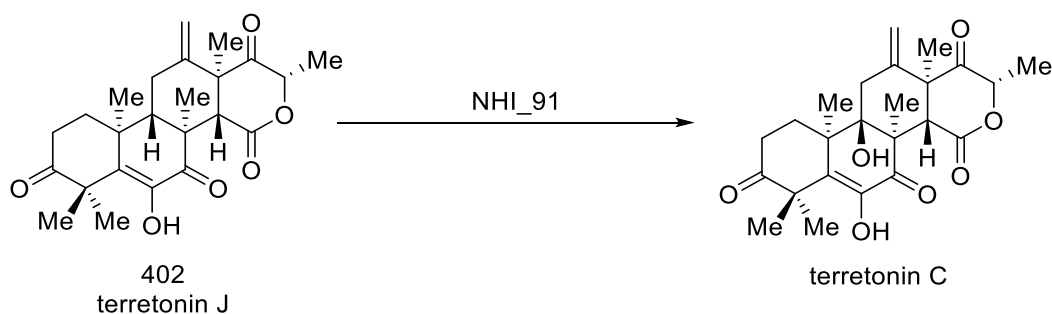
Reaction from literature⁷⁵ – reproduction not attempted.

Literature Reaction 107. Substrate_401 + NHI_070 = O-demethylation and tautomerization



Reaction from literature⁶⁰ – reproduction not attempted

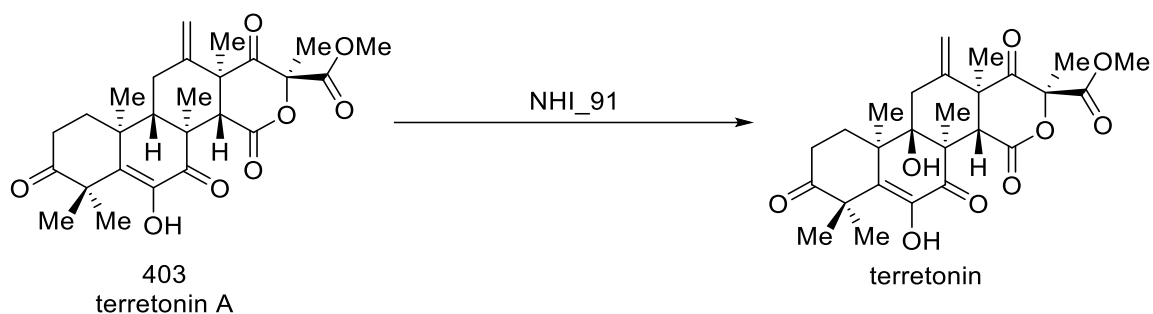
Literature Reaction 108. Substrate_402 + NHI_091 = proposed hydroxylation



Reaction from literature⁷⁶ – reproduction not attempted.

Reaction is proposed, but exact transformation hasn't been fully elucidated in biosynthetic route.

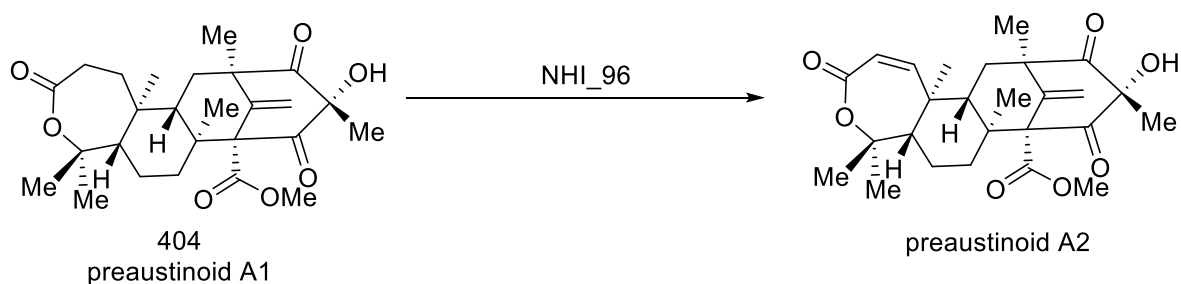
Literature Reaction 109. Substrate_403 + NHI_091 = proposed hydroxylation



Reaction from literature⁷⁶ – reproduction not attempted.

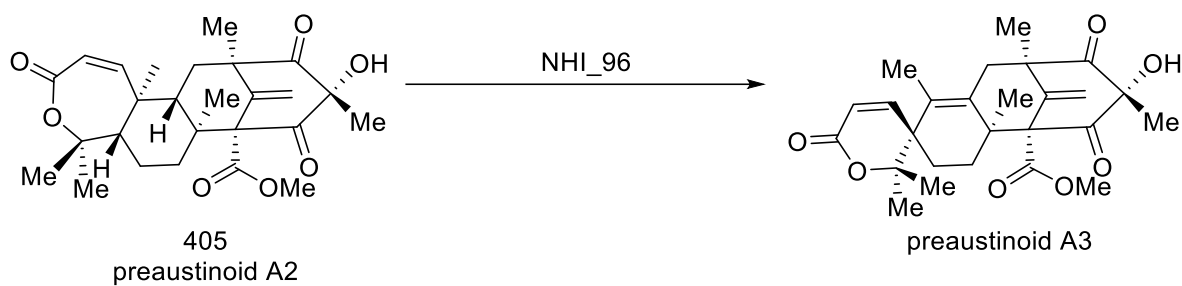
Reaction is proposed, but exact transformation hasn't been fully elucidated in biosynthetic route.

Literature Reaction 110. Substrate_404 + NHI_096 = desaturation



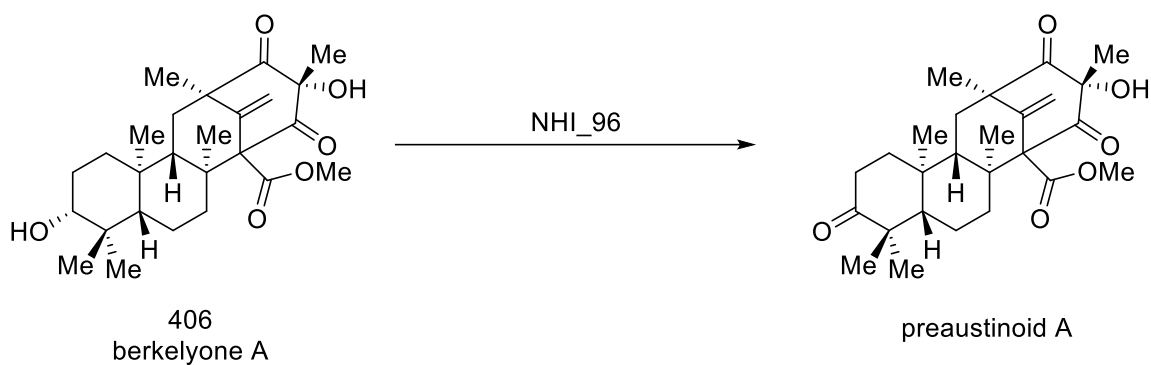
Reaction from literature⁷⁷ – reproduction not attempted.

Literature Reaction 111. Substrate_405 + NHI_096 = desaturation and rearrangement



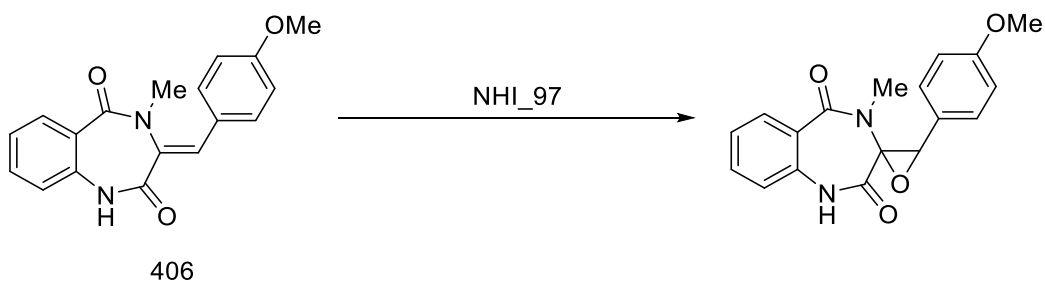
Reaction from literature⁷⁷ – reproduction not attempted.

Literature Reaction 112. Substrate_406 + NHI_096 = desaturation



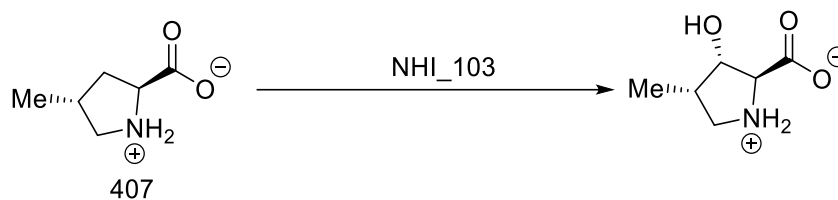
Reaction from literature⁷⁷ – reproduction not attempted.

Literature Reaction 113. Substrate_406 + NHI_097 = epoxidation



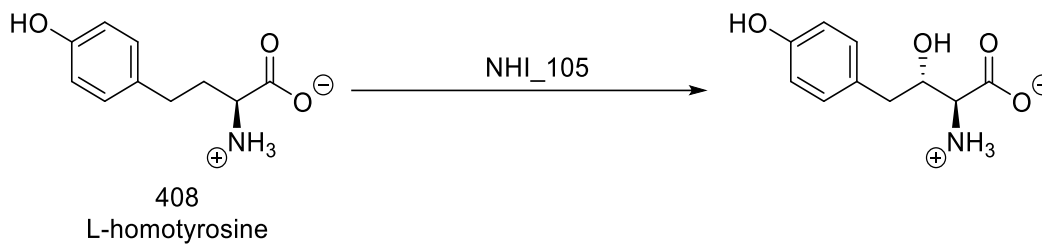
Reaction from literature⁴⁵ – reproduction not attempted.

Literature Reaction 114. Substrate_407 + NHI_103 = hydroxylation



Reaction from literature³⁹ – reproduction not attempted.

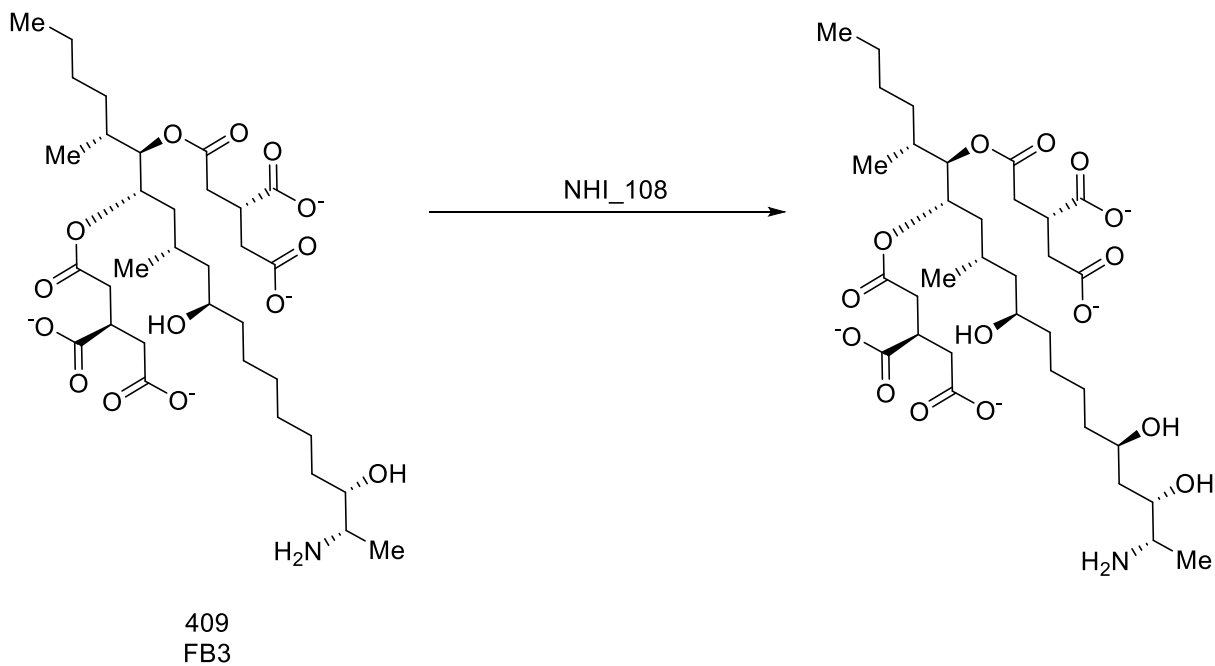
Literature Reaction 115. Substrate_408 + NHI_105 = hydroxylation



Reaction from literature⁷⁸ – reproduction not attempted.

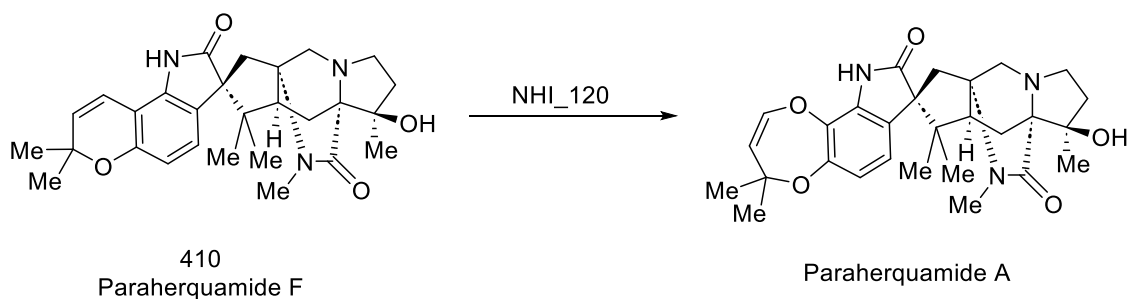
Reaction proposed in biosynthetic route.

Literature Reaction 116. Substrate_409 + NHI_108 = hydroxylation



Reaction from literature⁷⁹ – reproduction not attempted.

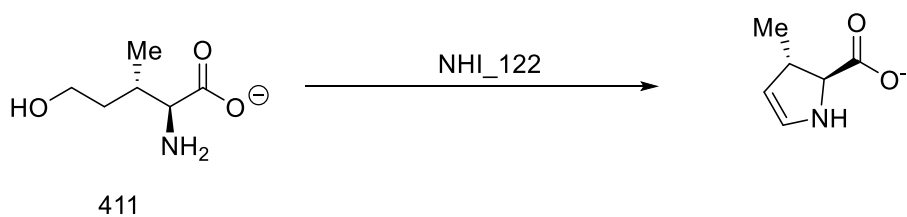
Literature Reaction 117. Substrate_410 + NHI_120 = hydroxylation



Reaction from literature⁸⁰ – reproduction not attempted.

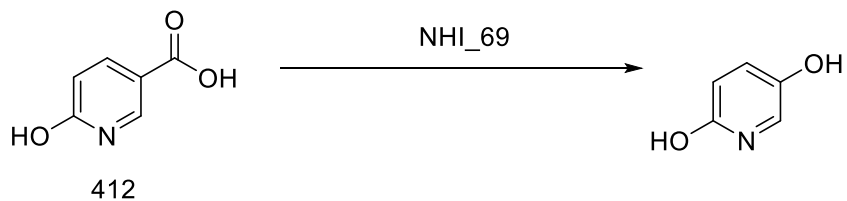
Exact substrate and product are unknown.

Literature Reaction 118. Substrate_411 + NHI_122 = oxidation, condensation and elimination



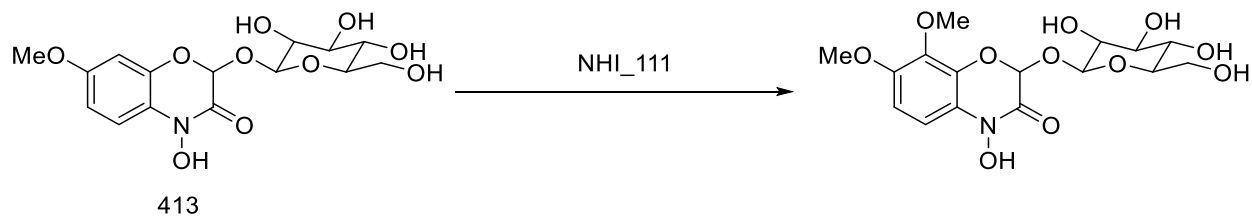
Reaction from literature⁴³ – reproduction not attempted.

Literature Reaction 119. Substrate_412 + NHI_069 = oxidative decarboxylation



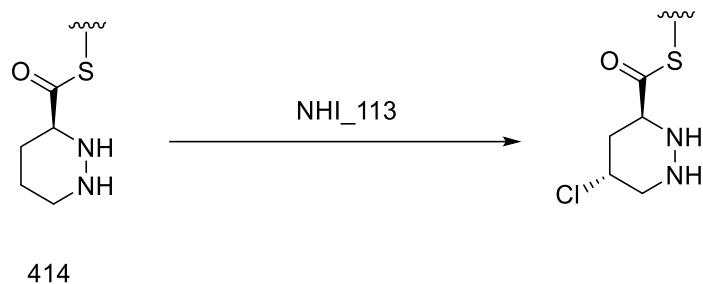
Reaction from literature^{81,82} – reproduction not attempted.

Literature Reaction 120. Substrate_413 + NHI_111 = hydroxylation and methylation



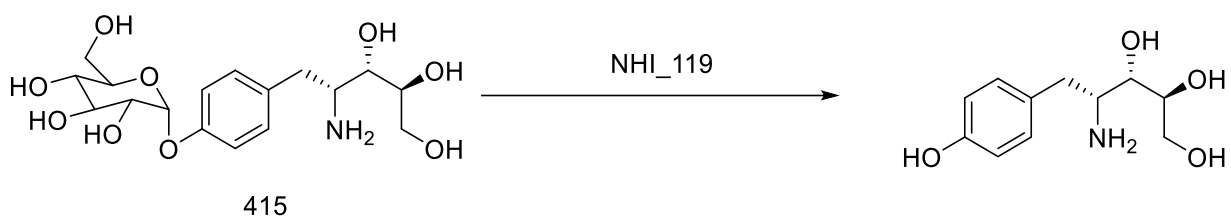
Reaction from literature⁸³ – reproduction not attempted.

Literature Reaction 121. Substrate_414 + NHI_113 = chlorination



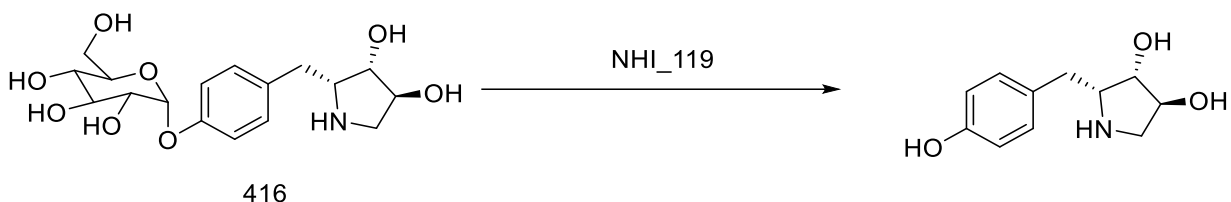
Reaction from literature⁸⁴ – reproduction not attempted.

Literature Reaction 122. Substrate_415 + NHI_119 = deglycosylation



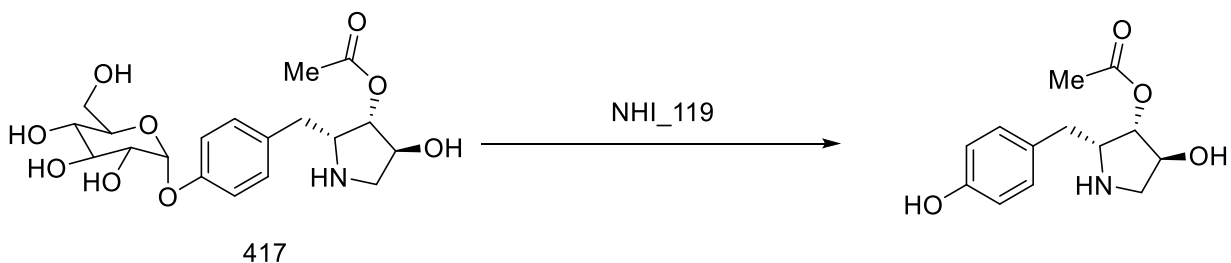
Reaction from literature⁸⁵ – reproduction not attempted.

Literature Reaction 123. Substrate_416 + NHI_119 = deglycosylation



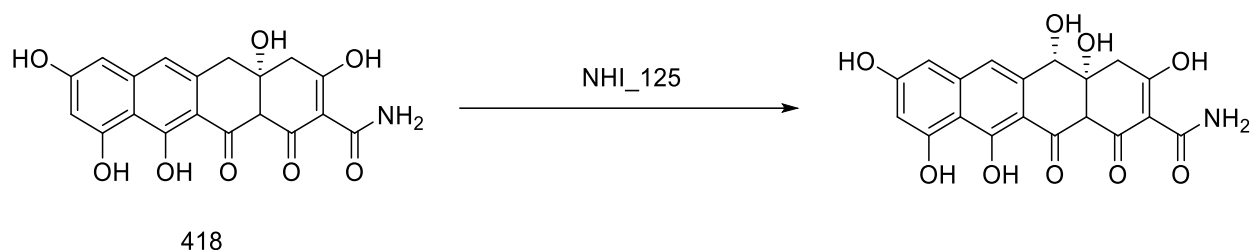
Reaction from literature⁸⁵ – reproduction not attempted.

Literature Reaction 124. Substrate_417 + NHI_119 = deglycosylation



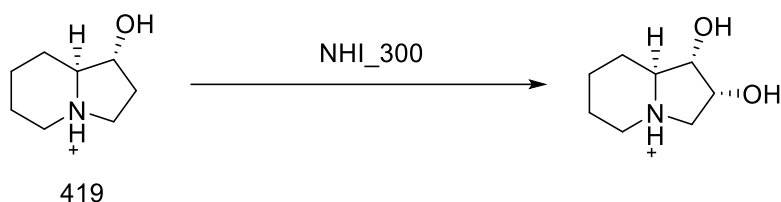
Reaction from literature⁸⁵ – reproduction not attempted.

Literature Reaction 125. Substrate_418 + NHI_125 = hydroxylation



Reaction from literature⁸⁶ – reproduction not attempted.

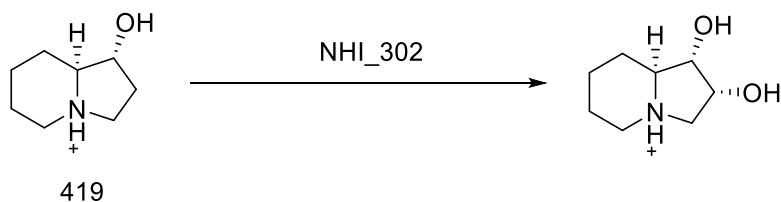
Literature Reaction 126. Substrate_419 + NHI_300 = hydroxylation



Reaction from literature⁵⁹ – reproduction not attempted.

Proposed by protein similarity

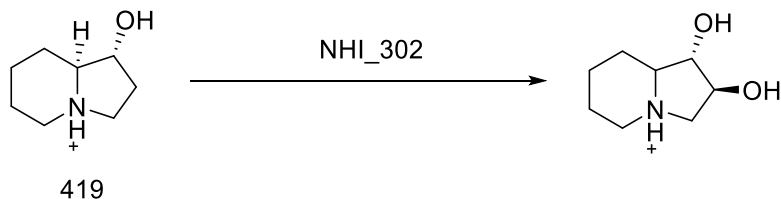
Literature Reaction 127. Substrate_419 + NHI_302 = hydroxylation



Reaction from literature⁵⁸ – reproduction not attempted.

Proposed by protein similarity

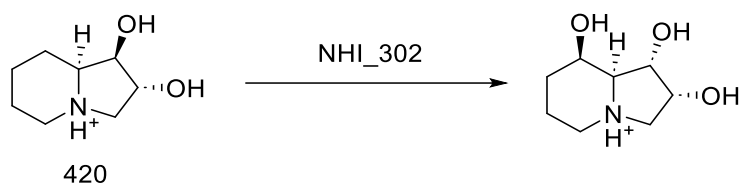
Literature Reaction 128. Substrate_419 + NHI_302 = hydroxylation



Reaction from literature⁵⁸ – reproduction not attempted.

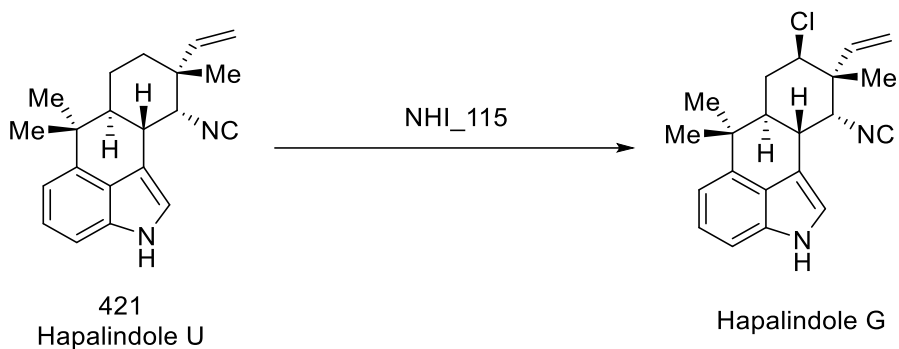
Proposed by protein similarity

Literature Reaction 129. Substrate_420 + NHI_307 = hydroxylation



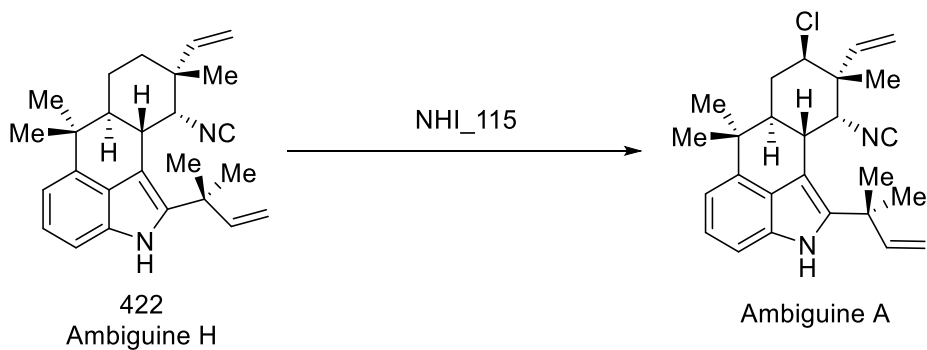
Reaction from literature⁵⁸ – reproduction not attempted.

Literature Reaction 130. Substrate_421 + NHI_115 = proposed chlorination



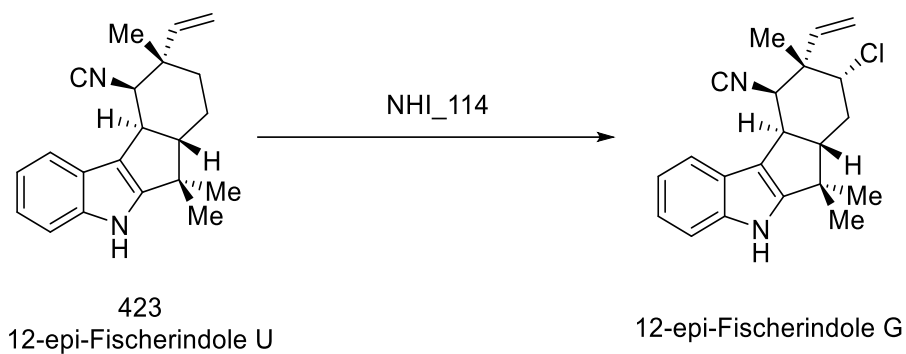
Reaction from literature⁸⁷ – reproduction not attempted.

Literature Reaction 131. Substrate_422 + NHI_115 = proposed chlorination



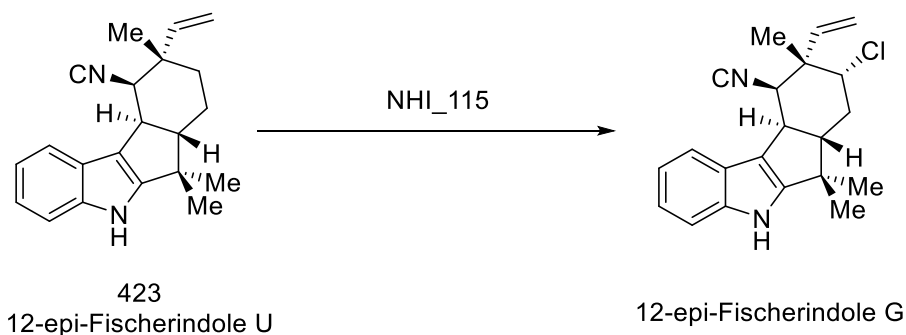
Reaction from literature⁸⁷ – reproduction not attempted.

Literature Reaction 132. Substrate_423 + NHI_114 = chlorination



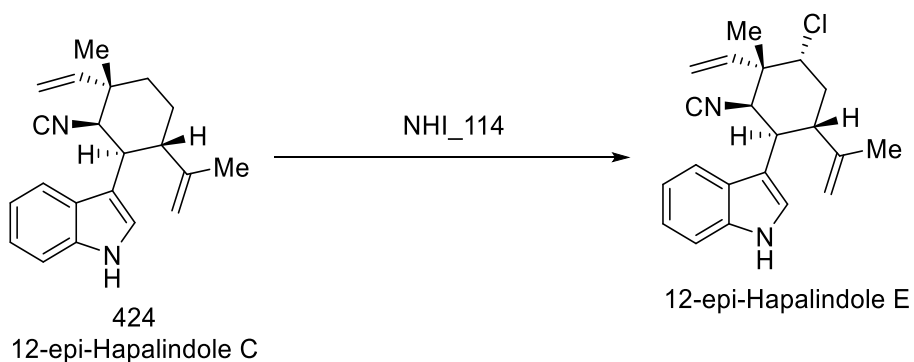
Reaction from literature⁸⁸ – reproduction not attempted.

Literature Reaction 133. Substrate_423 + NHI_115 = chlorination



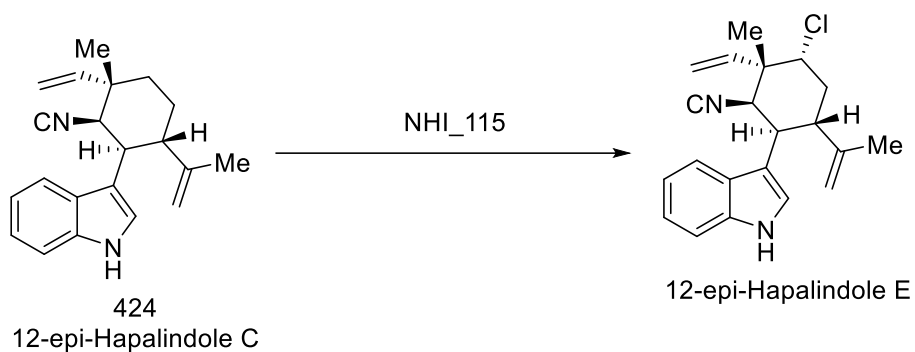
Reaction from literature⁸⁸ – reproduction not attempted.

Literature Reaction 134. Substrate_424 + NHI_114 = chlorination



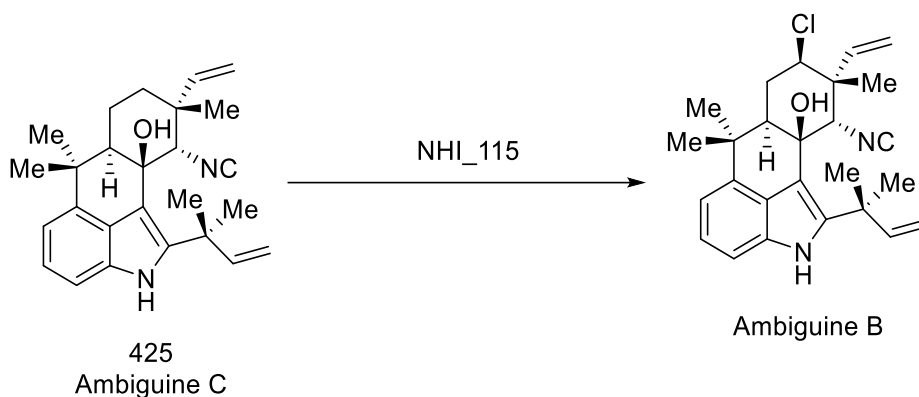
Reaction from literature⁸⁸ – reproduction not attempted.

Literature Reaction 135. Substrate_424 + NHI_115 = chlorination



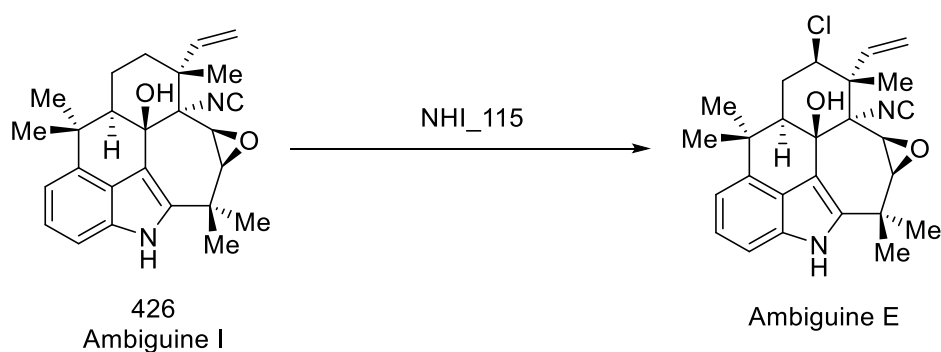
Reaction from literature⁸⁸ – reproduction not attempted.

Literature Reaction 136. Substrate_425 + NHI_115 = chlorination



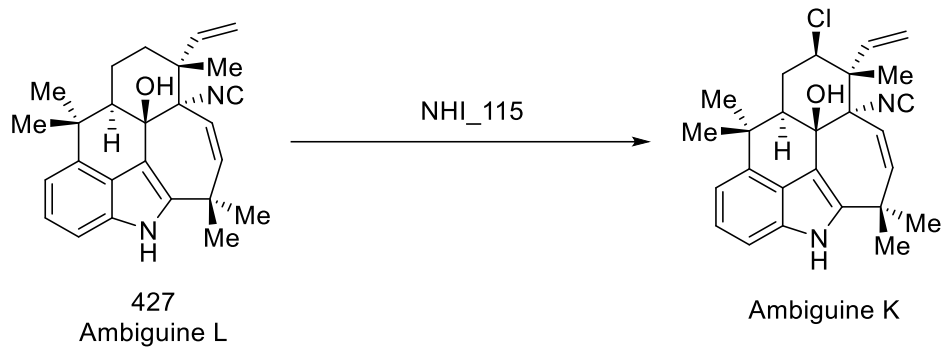
Reaction from literature⁸⁸ – reproduction not attempted.

Literature Reaction 137. Substrate_426 + NHI_115 = chlorination



Reaction from literature⁸⁸ – reproduction not attempted.

Literature Reaction 138. Substrate_427 + NHI_115 = chlorination



Reaction from literature⁸⁸ – reproduction not attempted.

13. Summary of reactions in BioCatSet1 database

Supplemental Table S3. Reaction Table. Substrate number corresponds to ID in substrate table (Supplemental Table S5). Enzyme number corresponds to ID in enzyme table (Supplemental Table S3). Reaction type referred to as hydroxylation (OH), desaturation (Desat), a combination of the two (OH/Desat) and rearrangement (RAR). Reaction source is identified with a T in either literature, observed, or both. The division of the data is signified as a T in either Train or Test and corresponds to the assignment of the substrate.

Rxn ID	Substrate	Enzyme	Reaction Type	Literature	Observed	Train	Test
1	002	001	Desat		T	T	
2	002	005	Desat		T	T	
3	002	006	OH		T	T	
4	002	015	OH		T	T	
5	002	018	Desat		T	T	
6	002	019	OH		T	T	
7	002	020	Desat		T	T	
8	002	022	OH		T	T	
9	002	024	OH		T	T	
10	002	025	Desat		T	T	
11	002	028	OH		T	T	
12	002	123	OH		T	T	
13	002	311	Desat		T	T	
14	002	313	Desat		T	T	
15	007	088	OH		T		T
16	008	001	OH		T		T
17	008	002	OH		T		T
18	008	005	OH		T		T
19	008	007	OH		T		T
20	008	008	OH		T		T
21	008	010	OH		T		T
22	008	011	OH		T		T
23	008	012	OH		T		T
24	008	015	OH		T		T
25	008	016	OH		T		T
26	008	017	OH		T		T
27	008	018	OH		T		T
28	008	020	OH		T		T
29	008	021	OH		T		T
30	008	022	OH		T		T
31	008	026	OH		T		T
32	008	027	OH		T		T
33	008	028	OH		T		T
34	008	029	OH		T		T
35	008	030	OH		T		T
36	008	031	OH		T		T

37	008	032	OH	T	T
38	008	033	OH	T	T
39	008	034	OH	T	T
40	008	038	OH	T	T
41	008	050	OH	T	T
42	008	055	OH	T	T
43	008	073	OH	T	T
44	008	087	OH	T	T
45	008	110	OH	T	T
46	008	123	OH	T	T
47	010	002	Desat	T	T
48	010	013	OH	T	T
49	010	014	OH	T	T
50	010	018	OH/Desat	T	T
51	010	019	OH/Desat	T	T
52	010	021	OH/Desat	T	T
53	010	022	OH/Desat	T	T
54	010	023	OH/Desat	T	T
55	010	024	Desat	T	T
56	010	025	OH/Desat	T	T
57	010	029	OH	T	T
58	010	038	OH	T	T
59	010	041	OH	T	T
60	010	044	OH	T	T
61	010	045	OH	T	T
62	010	046	OH	T	T
63	010	123	OH	T	T
64	010	168	OH	T	T
65	010	193	OH	T	T
66	016	052	OH	T	T
67	016	171	OH	T	T
68	016	274	OH	T	T
69	020	070	OH	T	T
70	020	107	OH	T	T
71	020	123	OH	T	T
72	020	130	OH	T	T
73	020	300	OH	T	T
74	020	311	OH	T	T
75	029	091	Desat	T	T
76	029	095	Desat	T	T
77	029	219	Desat	T	T
78	033	083	Desat	T	T
79	034	057	OH	T	T
80	034	059	OH	T	T
81	034	060	OH	T	T
82	034	061	OH	T	T
83	034	064	OH	T	T
84	034	065	OH	T	T
85	034	069	OH	T	T
86	034	070	OH	T	T
87	034	073	OH	T	T

88	034	076	OH	T	T
89	034	078	OH	T	T
90	034	079	OH	T	T
91	034	084	Desat	T	T
92	034	141	OH	T	T
93	034	288	OH	T	T
94	034	289	OH	T	T
95	035	078	OH	T	T
96	035	079	RAR	T	T
97	035	288	RAR	T	T
98	035	289	RAR	T	T
99	038	079	OH	T	T
100	038	104	Desat	T	T
101	048	006	OH	T	T
102	048	007	OH	T	T
103	048	009	OH	T	T
104	048	010	OH	T	T
105	048	011	OH	T	T
106	048	058	OH/Desat	T	T
107	048	142	OH/Desat	T	T
108	048	299	OH/Desat	T	T
109	048	300	Desat	T	T
110	048	302	Desat	T	T
111	049	058	OH/Desat	T	T
112	049	142	Desat	T	T
113	049	299	Desat	T	T
114	049	302	Desat	T	T
115	049	303	Desat	T	T
116	049	304	Desat	T	T
117	051	110	Desat	T	T
118	051	123	RAR	T	T
119	055	082	OH	T	T
120	055	092	OH	T	T
121	078	052	OH	T	T
122	078	057	OH	T	T
123	078	058	OH	T	T
124	078	091	OH	T	T
125	078	096	OH	T	T
126	078	192	OH	T	T
127	078	274	OH	T	T
128	079	054	OH	T	T
129	079	057	OH	T	T
130	079	108	OH	T	T
131	079	130	OH	T	T
132	079	249	OH	T	T
133	079	299	OH	T	T
134	079	302	OH	T	T
135	079	310	OH	T	T
136	081	142	Desat	T	T
137	081	299	OH/Desat	T	T
138	081	302	OH/Desat	T	T

139	081	303	Desat	T		T
140	081	304	OH/Desat	T		T
141	081	307	Desat	T		T
142	081	308	Desat	T		T
143	083	009	OH	T	T	
144	083	010	OH	T	T	
145	083	041	OH	T	T	
146	083	192	OH	T	T	
147	189	005	OH	T	T	
148	234	123	OH	T		T
149	234	130	OH	T		T
150	234	202	OH	T		T
151	341	309	OH	T		T
152	355	058	OH	T	T	
153	355	091	Desat	T	T	
154	355	131	Desat	T	T	
155	355	142	Desat	T	T	
156	355	299	OH	T	T	
157	355	302	OH	T	T	
158	355	303	Desat	T	T	
159	355	304	OH/Desat	T	T	
160	355	307	OH/Desat	T	T	
161	355	308	OH/Desat	T	T	
162	357	177	OH	T		T
163	359	072	OH	T		T
164	359	196	OH	T		T
165	359	197	OH	T		T
166	371	057	Desat	T	T	
167	371	058	Desat	T	T	
168	371	108	OH	T	T	
169	371	142	OH	T	T	
170	371	207	OH/Desat	T	T	
171	371	232	OH/Desat	T	T	
172	371	299	OH	T	T	
173	371	302	Desat	T	T	
174	371	304	OH/Desat	T	T	
175	371	305	Desat	T	T	
176	371	306	OH	T	T	
177	371	307	Desat	T	T	
178	371	308	Desat	T	T	
179	389	177	OH	T		T
180	392	004	OH	T	T	
181	392	005	OH	T	T	
182	392	008	OH	T	T	
183	392	026	OH	T	T	
184	392	030	OH	T	T	
185	392	065	OH	T	T	
186	392	137	OH	T	T	
187	392	191	OH	T	T	
188	392	208	OH	T	T	
189	392	260	OH/Desat	T	T	

190	392	262	OH/Desat		T	T	
191	392	282	OH/Desat		T	T	
192	392	308	OH		T	T	
193	429	134	OH/Desat		T		T
194	429	136	OH/Desat		T		T
195	429	143	OH		T		T
196	429	156	OH/Desat		T		T
197	429	168	OH/Desat		T		T
198	429	174	OH/Desat		T		T
199	429	178	OH/Desat		T		T
200	429	189	OH/Desat		T		T
201	444	064	OH		T		T
202	446	302	OH		T	T	
203	446	304	OH		T	T	
204	446	307	OH		T	T	
205	447	299	OH		T	T	
206	447	302	OH/Desat		T	T	
207	447	304	OH/Desat		T	T	
208	447	307	OH		T	T	
209	449	299	OH/Desat		T		T
210	449	302	OH/Desat		T		T
211	449	304	OH/Desat		T		T
212	449	307	OH/Desat		T		T
213	451	299	OH		T	T	
214	451	302	OH		T	T	
215	451	304	OH		T	T	
216	453	304	Desat		T		T
217	001	001	OH	T			T
218	002	002	OH	T		T	
219	003	101	OH	T			T
220	004	066	C-C Bond Formation	T			T
221	005	066	C-C Bond Formation	T		T	
222	013	102	OH	T		T	
223	016	116	OH	T			T
224	017	117	OH	T			T
225	019	064		T			T
226	019	065		T			T
227	021	049	Desat	T		T	
228	022	060	Desat	T		T	
229	023	061	OH	T			T
230	024	080	OH	T		T	
231	024	127		T		T	
232	025	053	OH	T			T
233	027	130	OH	T			T
234	027	131	OH	T			T
235	027	132	OH	T			T
236	028	126	OH	T		T	
237	028	128	OH	T		T	
238	028	129	OH	T		T	

239	030	050	Desat	T		T
240	031	057	Desat	T		T
241	033	004	OH	T	T	
242	034	055	OH	T		T
243	034	056	OH	T		T
244	034	062	OH	T		T
245	034	073	OH	T		T
246	034	103	OH	T		T
247	034	289	OH	T		T
248	035	104	RAR	T	T	
249	037	106	OH	T		T
250	038	122	OH	T	T	
251	042	051		T	T	
252	043	097	Desat	T		T
253	046	081	OH	T		T
254	047	095		T		T
255	055	003	Desat	T	T	
256	055	039	Desat	T	T	
257	055	040	Desat	T	T	
258	055	041	Desat	T	T	
259	055	042	Desat	T	T	
260	055	043	Desat	T	T	
261	055	298	Desat	T	T	
262	056	089		T		T
263	057	005	Epoxidation	T		T
264	065	054	C-C Bond Formation	T	T	
265	058	058	Desat	T		T
266	059	093	OH	T	T	
267	060	124	OH	T		T
268	061	072	OH	T		T
269	062	098	OH	T	T	
270	063	302	OH	T	T	
271	064	307	OH	T		T
272	064	307		T		T
273	064	308	OH	T		T
274	066	071	O- demethylation	T	T	
275	067	070	O- demethylation	T		T
276	067	071	O- demethylation	T		T
277	068	076	OH	T	T	
278	068	077	OH	T	T	
279	069	107	OH	T	T	
280	070	118	OH	T		T
281	072	082	Desat	T		T
282	072	083	Desat	T		T
283	072	084	Desat	T		T
284	072	085	Desat	T		T
285	073	086	Desat	T	T	

286	073	087	Desat	T	T	
287	073	088	Desat	T	T	
288	074	090	OH	T		T
289	075	092	OH	T		T
290	076	100	Transamination	T		
291	077	110	OH	T		T
292	089	038	OH	T	T	
293	091	032	OH	T	T	
294	131	038	OH	T	T	
295	137	041	Desat	T	T	
296	137	042	Desat	T	T	
297	137	298	Desat	T	T	
298	139	003	Desat	T	T	
299	139	039	Desat	T	T	
300	139	040	Desat	T	T	
301	139	041	Desat	T	T	
302	139	042	Desat	T	T	
303	139	043	Desat	T	T	
304	140	003	Desat	T		T
305	140	039	Desat	T		T
306	140	040	Desat	T		T
307	140	041	Desat	T		T
308	140	042	Desat	T		T
309	140	043	Desat	T		T
310	143	003	Desat	T		T
311	143	040	Desat	T		T
312	143	041	Desat	T		T
313	143	042	Desat	T		T
314	143	298	Desat	T		T
315	393	063		T	T	
316	394	065	OH	T		T
317	395	064	OH	T	T	
318	395	065	OH	T	T	
319	396	064	Desat	T		T
320	397	065	OH	T	T	
321	398	065	OH	T		T
322	399	065	OH	T	T	
323	400	067	Desat	T		T
324	401	070	O-demethylation	T		T
325	402	091	OH	T	T	
326	403	091	OH	T	T	
327	404	098	Desat	T		T
328	405	096	Desat	T	T	
329	406	096	Desat	T		T
330	406	097	Epoxidation	T		T
331	407	103	OH	T		T
332	408	105	OH	T		T
333	409	108	OH	T		T
334	410	120	OH	T	T	
335	411	122	OH	T		T

336	412	069		T		T
337	413	111	OH	T		T
338	414	113	Chlorination	T		T
339	415	119		T	T	
340	416	119		T		T
341	417	119		T	T	
342	418	125	OH	T	T	
343	419	300	OH	T	T	
344	419	302	OH	T	T	
345	419	302	OH	T	T	
346	420	307		T		T
347	421	115	Chlorination	T	T	
348	422	115	Chlorination	T		T
349	423	114	Chlorination	T		T
350	423	115	Chlorination	T		T
351	424	114	Chlorination	T	T	
352	424	115	Chlorination	T	T	
353	425	115	Chlorination	T	T	
354	426	115	Chlorination	T	T	
355	427	115	Chlorination	T	T	

14. Summary of enzymes in aKGLib1

Supplemental Table S4. Summary of all enzymes in aKGLib1. The repository refers to the source for the sequence, UniProt, Joint Genome Institute (JGI) and ancestral reconstruction (ASR). Accession ID is for the UniProt database, if available. Annotation score as identified on UniProt, if there is no UniProt entry for an enzyme, it is deemed a 1. Enzyme name is common name if well reported in biosynthetic literature. Organism for all enzymes listed, when naturally occurring. Outcome of the SDS-PAGE assay for overexpression. Activity reported in literature, T = true, F = not found in literature. The native function for the enzyme is annotated as hydroxylation (OH), desaturation (desat), rearrangement (RAR), epimerization (epim), others, or if the native function is not reported (NR). Native reaction (rxn) tested signifies if the exact reaction in literature was attempted in our high-throughput workflow. 0 = reaction not tested (due to lack of access to known substrate), 1 = reaction tested, but not observed, 2 = reaction tested and some product formation was observed, although it may not align with the annotated native function. Discovered reaction is noted as a T (true) or F (false) if the enzyme was observed to be compatible with any substrate beyond that previously reported in the literature. The discovered function annotated as hydroxylation (OH), desaturation (Desat), rearrangement (RAR), or no reaction was discovered (ND).

Enzyme ID	Repository	Accession ID	Annotation Score X/5	Enzyme Name	Organism	Expressed	Activity Reported in Literature	Native Function	Native Rxn Tested	Discovered Rxn	Discovered Function
1	UniProt	A0A159BP93	3	CitB	<i>Monascus ruber</i> (Mold)	Yes	T	OH	0	T	OH/Desat
2	UniProt	A0A481WNL2	4	ClaD	<i>Penicillium crustosum</i> (Blue mold fungus)	Yes	T	OH	2	T	OH/Desat
3	UniProt	B8M9K5	3	TropC	<i>Talaromyces stipitatus</i>	Yes	T	Ring expansion	0	F	ND
4	UniProt	Q6WZB0	4	VioC	<i>Streptomyces vinaceus</i>		T	OH	0	T	OH
5	UniProt	C3RVQ1	1	SxtS	<i>Microseira wollei</i>		T	Epoxidation	0	T	OH/Desat
6	UniProt	A0A0A2K1M1	1		<i>Penicillium expansum</i> (Blue mold rot fungus)	Yes	F	NR	NR	T	OH
7	UniProt	A0A364L2J7	1		<i>Talaromyces amestolkiae</i>	Yes	F	NR	NR	T	OH
8	UniProt	A0A384JB0J	2		<i>Botryotinia fuckeliana</i> (strain B05.10) (Noble rot fungus) (Botrytis cinerea)	Yes	F	NR	NR	T	OH/Desat
9	UniProt	A0A1L7X7S5	1		<i>Phialocephala subalpina</i>	Yes	F	NR	NR	T	OH
10	UniProt	A0A178EYA2	1		<i>Trichophyton rubrum</i> (Athlete's foot fungus) (Epidermophyton rubrum)	Yes	F	NR	NR	T	OH
11	UniProt	A0A2J6SBY6	1		<i>Hyaloscypha variabilis</i> (strain UAMH 11265 / GT02V1 / F) (Meliniomyces variabilis)	Yes	F	NR	NR	T	OH
12	UniProt	A0A2J6SF42	1		<i>Hyaloscypha bicolor</i> E	Yes	F	NR	NR	T	OH

13	JGI		1		Yes	F	NR	NR	T	OH
14	JGI		1		Yes	F	NR	NR	T	OH
15	JGI / UniProt	V5FKX9	1	Byssoschlamys spectabilis (strain No. 5 / NBR C 109023) (Paecilomyces variotii)	Yes	F	NR	NR	T	OH
16	JGI		1		Yes	F	NR	NR	T	OH
17	JGI		1		Yes	F	NR	NR	T	OH
18	UniProt	A0A3D8Q Q42	1	Coleophoma cylindrospora	Yes	F	NR	NR	T	OH/Desat
19	UniProt	A0A059JC A6	1	Trichophyton interdigitale (strain MR816)	Yes	F	NR	NR	T	OH/Desat
20	UniProt	A0A1R3R SN7	1	Aspergillus carbonarius (strain ITEM 5010)	Yes	F	NR	NR	T	OH/Desat
21	UniProt	E4V420	1	Arthroderma gypseum (strain ATCC MYA-4604 / CBS 118893) (Microsporum gypseum)	Yes	F	NR	NR	T	OH/Desat
22	UniProt	A0A8E0QJ 37	1	Aspergillus udagawae	Yes	F	NR	NR	T	OH/Desat
23	UniProt	D4B497	1	Arthroderma benthamiae (strain ATCC MYA-4681 / CBS 112371) (Trichophyton mentagrophytes)	Yes	F	NR	NR	T	OH/Desat
24	UniProt	A0A0U1LT B7	1	Talaromyces islandicus (Penicillium islandicum)	Yes	F	NR	NR	T	OH/Desat
25	JGI		1		Yes	F	NR	NR	T	OH/Desat
26	JGI / UniProt	A0A8H4N5 01	1	Botryosphaeria dothidea	Yes	F	NR	NR	T	OH
27	JGI		1		Yes	F	NR	NR	T	OH
28	JGI		1		Yes	F	NR	NR	T	OH
29	UniProt	A0A194V8 V1	1	Valsa mali var. pyri (nom. inval.)	Yes	F	NR	NR	T	OH
30	UniProt	A0A194U MQ8	1	Valsa mali var. pyri (nom. inval.)	Yes	F	NR	NR	T	OH
31	UniProt	G4NB73	1	Pyricularia oryzae (strain 70-15 / ATCC MYA-4617 / FGSC 8958) (Rice blast fungus) (Magnaporthe oryzae)	Yes	F	NR	NR	T	OH
32	JGI		1		Yes	T	OH	0	T	OH
33	JGI		1		Yes	F	NR	NR	T	OH
34	JGI		1		Yes	F	NR	NR	T	OH
35	JGI / UniProt	A0A2T4AE B8	1	Trichoderma harzianum CBS 226.95	Yes	F	NR	NR	F	ND
36	JGI		1		Yes	F	NR	NR	F	ND
37	JGI		1		Yes	F	NR	NR	F	ND
38	JGI		1		Yes	T	OH	0	T	OH/Desat
39	JGI / UniProt	A0A4Z0YN I3	1	Xylaria hypoxylon	Yes	T	Ring expansion	0	F	ND
40	JGI / UniProt	Q5BG04	2	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) (Aspergillus nidulans)	Yes	T	Ring expansion	0	F	ND
41	JGI		1		Yes	T	Ring expansion	0	T	OH/Desat
42	JGI	A0A0L0N2 H4	1	Tolypocladium ophioglossoides (strain CBS 100239) (Golden-thread cordyceps) (Elaphocordyceps ophioglossoides)	Yes	T	Ring expansion	0	F	ND
43	JGI	A0A0L0NH 81	1	Tolypocladium ophioglossoides (strain CBS 100239) (Golden-thread cordyceps) (Elaphocordyceps ophioglossoides)	Yes	T	Ring expansion	0	F	ND
44	genbank		1		Yes	F	NR	NR	T	OH

45	genbank		1			Yes	F	NR	NR	T	OH
46	PATRIC		1			Yes	F	NR	NR	T	OH/Desat
47	PATRIC		1			Yes	F	NR	NR	F	ND
48	PATRIC		1			Yes	F	NR	NR	F	ND
49	UniProt	A0A097ZP D5	3	AndA	<i>Aspergillus stellatus</i>	Yes	T	Desat	0	F	ND
50	UniProt	A0A097ZP D9	3	AndF	<i>Aspergillus stellatus</i>	Yes	T	Desat/RAR	0	T	OH
51	UniProt	A0A0A2JY K3	3	CnsJ	<i>Penicillium expansum</i>	No	T	Epoxidatio n	0	F	ND
52	UniProt	A0A6J4CV F6	1	SptA	<i>Aspergillus sp.</i>	Yes	F	NR	NR	T	OH
53	UniProt	A0A6J4CX 17	1	SptF	<i>Aspergillus sp.</i>	Yes	T	OH	0	F	ND
54	UniProt	A0A0N9H Q36	4	Phex308 48 (2- ODD)	<i>Sinopodophyllum hexandrum</i>	Yes	T	C-C Formation	0	T	OH
55	UniProt	A0A166YZ Y4	3	PpzD	<i>Metarhizium rileyi RCEF 4871</i>	Yes	T	OH	1	T	OH
56	UniProt	A0A166YZ Y9	3	PpzC	<i>Metarhizium rileyi RCEF 4871</i>	Yes	T	OH	1	F	ND
57	UniProt	A0A1E1FF L0	5	PrhA	<i>Penicillium brasilianum</i>	Yes	T	Desat/RAR	0	T	OH
58	UniProt	A0A1L9W UX8	3	AneA	<i>Aspergillus aculeatus ATCC 16872</i>	Yes	T	Desat	0	T	OH/Desat
59	UniProt	A0A2Z5TI R0	2	HimG	<i>Aspergillus japonicus</i>	Yes	F	NR	NR	T	OH
60	UniProt	A0A3G9H 185	3	CdmA	<i>Talaromyces verruculosus</i>	No	T	Desat	0	T	OH
61	UniProt	A0A3G9G R23	3	CdmD	<i>Talaromyces verruculosus</i>	Yes	T	OH	0	T	OH
62	UniProt	A0A411L0 30	3	BuaE	<i>Aspergillus burnettii</i>	No	T	OH	2	F	ND
63	UniProt	G8GV69	3	EasH	<i>Claviceps purpurea 20.1</i>	Yes	T	Ring contraction	0	F	ND
64	UniProt	Q8ZWQ9	4	FLS	<i>Citrus unshiu</i>	Yes	T	OH	0	T	OH
65	UniProt	A0A4D6Q 9B0	3	F3H	<i>Crocasmia x crocasmiflora</i>	Yes	T	OH	NR	T	OH
66	UniProt	A2A1A0	4	NCS1	<i>Coptis japonica</i>	Yes	T	C-C Formation	0	F	ND
67	UniProt	A2WQ39	3	LDO1	<i>Oryza sativa Japonica group</i>	No	T	Desaturati on	0	F	ND
68	UniProt	Q67VR7	3	LDO2	<i>Oryza sativa Japonica group</i>	Yes	F	NR	NR	F	ND
69	UniProt	C8VK14	3	HxnY	<i>Aspergillus nidulans FGSC A4</i>	No	T	NR	0	T	OH
70	UniProt	D4N500	5	T6ODM	<i>Papaver somniferum</i>	Yes	T	Demethyla tion	0	T	OH
71	UniProt	D4N502	5	CODM	<i>Papaver somniferum</i>	Yes	T	Demethyla tion	0	F	ND
72	UniProt	E3VWI4	3	PntH	<i>Streptomyces arenae</i>	Yes	T	OH	0	T	OH
73	UniProt	F4ILF8	4	prolyl-4- hydroxyl ase 13	<i>Arabidopsis thaliana</i>	Yes	T	OH	2	F	ND
74	UniProt	F4KAS1	2	FLS4	<i>Arabidopsis thaliana</i>	Yes	F	NR	NR	F	ND
75	UniProt	F4K7D5	2	FLS6	<i>Arabidopsis thaliana</i>	No	F	NR	NR	F	ND
76	UniProt	G9M9M1	4	F6'H1	<i>Ipomoea batatas</i>	Yes	T	OH	0	T	OH
77	UniProt	G9M9M4	5	F6'H2	<i>Ipomoea batatas</i>	Yes	T	OH	0	F	ND
78	UniProt	K0DZA0	3	HtyE	<i>Aspergillus rugulosus</i>	Yes	F	NR	NR	T	OH/RAR
79	UniProt	A0A140G9 36	1	AniF	<i>Aspergillus nidulans NRRL 8112</i>	Yes	F	NR	NR	T	OH/RAR
80	UniProt	P93771	5	GA20ox 1-A-D	<i>Oryza sativa Japonica</i>	No	T	OH	0	F	ND
81	UniProt	O04847	4	D4H	<i>Catharanthus roseus</i>	Yes	T	OH	0	F	ND
82	UniProt	P08703	4	PcbC	<i>Penicillium chrysogenum</i>	Yes	T	Ring Formation	0	T	Ring expansion
83	UniProt	P27744	3	PcbC	<i>Amycolatopsis lactamdurans</i>	Yes	T	Ring Formation	0	T	Desat
84	UniProt	Q48739	3	PcbC	<i>Lysobacter lactamgenus</i>	Yes	T	Ring Formation	0	T	Desat
85	UniProt	P05326	5	IpnA	<i>Aspergillus nidulans FGSC A4</i>	Yes	T	Ring Formation	0	F	ND
86	UniProt	P11935	4	CefEF	<i>Acremonium chrysogenum</i>	Yes	T	Ring expansion / Desat	0	F	ND
87	UniProt	P18548	3	CefE	<i>Steptomyces clavuligerus</i>	Yes	T	Ring expansion / Desat	0	T	OH
88	UniProt	Q03047	3	CefE	<i>Amycolatopsis lactamdurans</i>	Yes	T	Ring expansion / Desat	0	T	OH

89	UniProt	P24397	4	H6H	<i>Hyoscyamus niger</i>	Yes	T	NR	NR	F	ND
90	UniProt	P42220	4	CeIF	<i>Streptomyces clavuligerus</i>	Yes	T	OH	0	F	ND
91	UniProt	Q0C8A0	3	Trt7	<i>Aspergillus terreus</i> NIH2624	No	T	OH	0	T	OH/Desat
92	UniProt	Q15JG7	4	VldW	<i>Streptomyces hygroscopicus</i> subsp. <i>limoneus</i>	Yes	T	OH	0	T	Ring expansion
93	UniProt	Q2TDY4	5	EctD	<i>Virgibacillus salexigens</i>	Yes	T	OH	0	F	ND
94	UniProt	K0BAV0	2	EctD homolog	<i>Candidatus Nitrospumilus sediminis</i>	Yes	F	NR	NR	F	ND
95	UniProt	Q4WAW9	4	FtmOx1	<i>Aspergillus fumigatus</i> Af293	Yes	T	Peroxi-dation	0	T	Desat
96	UniProt	Q5AR34	5	AusE	<i>Aspergillus nidulans</i> FGSC A4	Yes	T	Desat/RAR	NR	T	OH
97	UniProt	Q5AR53	4	AsqJ	<i>Aspergillus nidulans</i> FGSC A4	Yes	T	Desat / Epoxidation	0	F	ND
98	UniProt	Q5MNH6	3	LolO 1/2	<i>Epichloe uncinata</i>	Yes	T	OH / Ring Formation	0	F	ND
99	UniProt	Q5MNH9	3	LolE 1/2	<i>Epichloe uncinata</i> (Endophyte fungus) (Neotyphodium uncinatum)		F	NR	NR	F	ND
100	UniProt	Q5MNH9	3	KanJ	<i>Epichloe uncinata</i>	Yes	T	Transamination	1	F	ND
101	UniProt	Q6L732	3	Downy Mildew Resistance	<i>Streptomyces kanamyceticus</i>	Yes	T	OH	1	F	ND
102	UniProt	Q9FLV0	5	scopoletin-8-hydroxylase	<i>Arabidopsis thaliana</i>	Yes	T	OH	0	F	ND
103	UniProt	Q9LE86	5	GloF (GLOXY 2)	<i>Arabidopsis thaliana</i>	No	T	OH		F	ND
104	UniProt	S3D784	3	GloC (GLOXY 4)	<i>Glarea lozoyensis</i> ATCC 20868	Yes	T	RAR		T	OH
105	UniProt	S3D9F9	4	GloM (GLOXY 1)	<i>Glarea lozoyensis</i> ATCC 20868	Yes	T	OH	0	F	ND
106	UniProt	S3DB70	3	GloE (GLOXY 3)	<i>Glarea lozoyensis</i> ATCC 20868	Yes	T	OH		F	ND
107	UniProt	S3E7Q2	3	Diox4	<i>Glarea lozoyensis</i> ATCC 20868	No	T	OH	0	T	OH
108	UniProt	W5QJZ5	5	Fum3p	<i>Ruta graveolens</i>	Yes	T	OH	0	T	OH
109	UniProt	W7LKX6	3	PODA	<i>Fusarium verticillioides</i> 7600	Yes	F	NR	NR	F	ND
110	UniProt	D4N501	4	BX6	<i>Papaver somniferum</i>	Yes	T	OH	0	T	OH/RAR
111	UniProt	Q84TC2	5	BX13	<i>Zea mays</i>	No	T	OH	0	F	ND
112	UniProt	B6TBU1	1	HPPD	<i>Zea mays</i>	No	F	NR	NR	F	ND
113	UniProt	F4IDP2	2	KthP	<i>Arabidopsis thaliana</i>	Yes	T	Cl	0	F	ND
114	UniProt		1	WelO5	<i>Kutzneria</i> sp. 744	Yes	T	Cl	0	F	ND
115	UniProt	AJJ28572	1	AmbO5	<i>Hapalosiphon welwitschii</i> UTEX B 1830	Yes	T	Cl	0	F	ND
116	UniProt	Q01IX6	2	DAO	<i>Fischerella ambigua</i> UTEX 1903	No	T	OH	0	F	ND
117	UniProt	Q6Z244	4	M2H	<i>Oryza sativa Indica</i> group	Yes	T	OH	0	F	ND
118	UniProt	K0E678	3	EcdG	<i>Oryza sativa Japonica</i> group	Yes	T	OH	0	F	ND
119	UniProt	A0A140G934	1	AniG	<i>Aspergillus rugulosus</i>	Yes	T	NR	0	F	ND
120	UniProt	L0E2Q1	3	PhqC	<i>Aspergillus nidulans</i> NRRL 8112	Yes	T	OH	0	F	ND
121	UniProt	B8NI22	3	ImqE	<i>Penicillium fellutanum</i>	No	F	NR	NR	F	ND
122	UniProt	A0A411KUQ7	3	UcsF	<i>Aspergillus flavus</i> NRRL3357	Yes	T	OH	2	F	ND
123	UniProt	Q7LL04	2		<i>Schizosaccharomyces pombe</i>	Yes	F	NR	NR	T	OH
124	UniProt	O80449	5	ANS (JOX4)	<i>Arabidopsis thaliana</i>	No	T	OH	0	F	ND
125	UniProt	D7PHZ1	3	VrtI	<i>Penicillium aethiopicum</i>	No	T	OH	0	F	ND
126	UniProt	Q8S0S6	4	GA2ox3	<i>Oryza sativa Japonica</i> group	No	T	OH	0	F	ND
127	UniProt	Q4PT02	4	GA2ox5	<i>Arabidopsis thaliana</i>	Yes	T	NR	0	F	ND
128	UniProt	Q9SQ80	4	GA2ox1	<i>Pisum sativum</i>	No	T	OH	0	F	ND
129	UniProt	Q8LEA2	4	GA2ox1-2	<i>Arabidopsis thaliana</i>	No	T	OH	0	F	ND

130	UniProt	Q3I411	4	GA3ox2-1	<i>Triticum aestivum</i>	No	T	OH	0	T	OH
131	UniProt	O24648	5		<i>Pisum sativum</i>	No	T	OH	0	T	OH
132	UniProt	Q6AT12	4	GA3ox1	<i>Oryza sativa Japonica group</i>	No	T	OH	0	F	ND
133	UniProt	A0A517QI98	1		<i>Thalassoglobus polymorphus</i>	Yes	F	NR	NR	F	ND
134	UniProt	A0A111VWG0	1		<i>Chitinophaga sp. CF118</i>	Yes	F	NR	NR	T	OH
135	UniProt	Q5XGE0	3		<i>Xenopus tropicalis</i>	No	F	NR	NR	F	ND
136	UniProt	A0A3A9XB12	1		<i>Aquimarina sp. AD1</i>	Yes	F	NR	NR	T	OH
137	UniProt	W6RL34	1		<i>Pseudomonas pseudoalcaligenes CECT 5344</i>	Yes	F	NR	NR	T	OH
138	UniProt	A0A151GP07	1		<i>Drechmeria coniospora</i>	Yes	F	NR	NR	F	ND
139	UniProt	A0A1Q9AX96	1		<i>Xaviernesmea oryzae</i>	Yes	F	NR	NR	F	ND
140	UniProt	A0A366QSL8	1		<i>Fusarium coffeatum</i>	Yes	F	NR	NR	F	ND
141	UniProt	A0A2E3YBW8	1		<i>Gemmatimonadetes bacterium</i>	Yes	F	NR	NR	T	OH
142	UniProt	W9Y7Q8	1		<i>Capronia coronata CBS 617.96</i>	Yes	F	NR	NR	T	OH/Desat
143	UniProt	A0A0W0Z044	2		<i>Legionella shakespearei</i>	Yes	F	NR	NR	T	OH
144	UniProt	A0A1H5STF5	1		<i>Actinacidiphila yanglinensis</i>	Yes	F	NR	NR	F	ND
145	UniProt	A0A6G9AYH6	1		<i>Spirosoma aureum</i>	Yes	F	NR	NR	F	ND
146	UniProt	A0A524Q650	1		<i>Xanthomonadales bacterium</i>	No	F	NR	NR	F	ND
147	UniProt	W9YUG9	2		<i>Capronia epimyces CBS 606.96</i>	Yes	F	NR	NR	F	ND
148	UniProt	UPI00015F68DC	1		<i>Chlamydomonas reinhardtii</i>	No	F	NR	NR	F	ND
149	UniProt	UPI000896EC1F	1		<i>Amycolatopsis xylanica</i>	Yes	F	NR	NR	F	ND
150	UniProt	UPI0011012F4F	1		<i>Rhodofomes roseus</i>	Yes	F	NR	NR	F	ND
151	UniProt	UPI0000D8657E	1		<i>Coccidioides immitis RS</i>	No	F	NR	NR	F	ND
152	UniProt	UPI0003E10C4B	1		<i>Amborella trichopoda</i>	No	F	NR	NR	F	ND
153	UniProt	UPI0009CF6755	1		<i>Penicillium solatum</i>	No	F	NR	NR	F	ND
154	UniProt		1			No	F	NR	NR	F	ND
155	UniProt	A0A2E2FNU9	1		<i>Crocinitomicaceae bacterium</i>	Yes	F	NR	NR	F	ND
156	UniProt	A0A2D5KDL4	1		<i>Flavobacteriales bacterium</i>	Yes	F	NR	NR	T	OH
157	UniProt	A0A345QVE9	1		<i>Sulfitobacter sp. SK012</i>	Yes	F	NR	NR	F	ND
158	UniProt	A0A0C5AE62	1		<i>Cyanophage P-TIM40</i>	Yes	F	NR	NR	F	ND
159	UniProt	A0A2E6I4K1	1		<i>Gemmatimonadetes bacterium</i>	Yes	F	NR	NR	F	ND
160	UniProt	A0A5N9AZG9	1		<i>SAR202 cluster bacterium</i>	Yes	F	NR	NR	F	ND
161	UniProt	UPI0005EA34B6	1		<i>Vibrio crassostreae</i>	No	F	NR	NR	F	ND
162	UniProt	UPI001410A5DA	1		<i>Actinobacteria bacterium</i>	No	F	NR	NR	F	ND
163	UniProt	UPI0005A38E5A	1		<i>Pisolithus tinctorius Marx 270</i>	No	F	NR	NR	F	ND
164	UniProt	UPI0004E09BF2	1		<i>Synechococcus sp. KORDI-100</i>	Yes	F	NR	NR	F	ND
165	UniProt	UPI000E0BBE3	1		<i>Malaciobacter mytili LMG 24559</i>	Yes	F	NR	NR	F	ND
166	UniProt	UPI00121E53B8	1		<i>Chloroflexi bacterium</i>	Yes	F	NR	NR	F	ND
167	UniProt	UPI000F20B1A3	1		<i>Nitrospirae bacterium</i>	Yes	F	NR	NR	F	ND
168	UniProt	UPI0009809D14	1		<i>Castor canadensis</i>	No	F	NR	NR	T	OH
169	UniProt	UPI0007021EE0	1		<i>Pedobacter sp.</i>	Yes	F	NR	NR	F	ND
170	UniProt		1			No	F	NR	NR	F	ND
171	UniProt	UPI0006245174	1		<i>Pseudomonas sp. CCOS 191</i>	Yes	F	NR	NR	T	OH
172	UniProt	A0A0C2ZJU0	1		<i>Sulfurovum sp. PC08-66</i>	Yes	F	NR	NR	F	ND
173	UniProt	A0A139GVU7	1		<i>Pseudocercospora eumusae</i>	No	F	NR	NR	F	ND

174	UniProt	A0A6A5X5 T5	1	<i>Aaosphaeria arxii</i> CBS 175.79	Yes	F	NR	NR	T	OH
175	UniProt	A0A2E9M EH1	1	<i>Gemmatimonadetes</i> <i>bacterium</i>	No	F	NR	NR	F	ND
176	UniProt	A0A2E1P Q50	1	<i>Gammaproteobacteri</i> <i>a bacterium</i>	Yes	F	NR	NR	F	ND
177	UniProt	A0A0F7LT 18	1	<i>Photorhabdus</i> <i>thracensis</i>	Yes	F	NR	NR	T	OH
178	UniProt	A0A6G0W 9P8	1	<i>Aphanomyces</i> <i>euteiches</i>	Yes	F	NR	NR	T	OH
179	UniProt	A0A4Q7IS 82	1	<i>Pseudoalteromonas</i> <i>phenolica</i>	Yes	F	NR	NR	F	ND
180	UniProt	A0A191ZI N0	1	<i>Halothiobacillus</i> sp. LS2	Yes	F	NR	NR	F	ND
181	UniProt	A0A409YN Q7	1	<i>Panaeolus</i> <i>cyaneus</i>	Yes	F	NR	NR	F	ND
182	UniProt	NR65644. 1	1	<i>Actinomyces</i> <i>mexicana</i>	No	F	NR	NR	F	ND
183	UniProt	A0A0F4YT 51	2	<i>Rasamsonia</i> <i>emersonii</i> CBS 393.64	Yes	F	NR	NR	F	ND
184	UniProt	B2J7U7	1	<i>Nostoc punctiforme</i>	No	F	NR	NR	F	ND
185	UniProt	A0A3B8M KP2	1	<i>Candidatus</i> <i>Latescibacteria</i> <i>bacterium</i>	Yes	F	NR	NR	F	ND
186	UniProt	A0A409VI Y3	1	<i>Panaeolus</i> <i>cyaneus</i>	Yes	F	NR	NR	F	ND
187	UniProt	A0A3B8R2 H9	1	<i>Gammaproteobacteri</i> <i>a bacterium</i>	Yes	F	NR	NR	F	ND
188	UniProt	W9CV72	1	<i>Sclerotinia borealis</i> F-4128	Yes	F	NR	NR	F	ND
189	UniProt	UPI0003D 1BCC0	1	<i>Candidatus</i> <i>Pelagibacter ubique</i> HIMB083	Yes	F	NR	NR	T	OH
190	UniProt	UPI000381 2D2E	1	<i>Amycolatopsis alba</i> DSM 44262	Yes	F	NR	NR	F	ND
191	UniProt	UPI000F6 9A703	1	<i>Paenibacillus</i> <i>baekrodamisoli</i>	Yes	F	NR	NR	T	OH
192	UniProt	UPI00139 CCC18	1	<i>Nodularia</i> sp. (in: Bacteria)	Yes	F	NR	NR	T	OH
193	UniProt	UPI000DF EA68F	1	<i>Pseudomonas</i> <i>mendocina</i>	Yes	F	NR	NR	T	OH
194	UniProt	UPI00029 CB7B3	1	<i>Rhodococcus</i> <i>opacus</i>	Yes	F	NR	NR	F	ND
195	UniProt	UPI001465 27FB	1	<i>Paraburkholderia</i> <i>humilis</i>	Yes	F	NR	NR	F	ND
196	UniProt	UPI000D3 FC885	1	<i>Alphaproteobacteria</i> <i>bacterium</i> MarineAlpha5_Bin7	Yes	F	NR	NR	T	OH
197	UniProt	UPI001295 71DE	1	<i>Streptomyces</i> <i>jumonjinensis</i>	Yes	F	NR	NR	T	OH
198	UniProt	UPI001084 27B7	1	<i>Leptospira meyeri</i>	Yes	F	NR	NR	F	ND
199	UniProt	UPI00072 B98D6	1	<i>Candidatus</i> <i>Nitrospira nitrificans</i>	Yes	F	NR	NR	F	ND
200	UniProt	UPI000891 AC76	1	<i>Rhizobiales</i> <i>bacterium</i> GAS113	Yes	F	NR	NR	F	ND
201	UniProt	UPI001193 7DEF	1	<i>Auriculariopsis ampla</i>	Yes	F	NR	NR	F	ND
202	UniProt	UPI000C5 71DF5	1	<i>Candidatus</i> <i>Woesearchaeota</i> <i>archaeon</i>	Yes	F	NR	NR	T	OH
203	UniProt	UPI000503 79AD	1	<i>Sphingobium</i> sp. ba1	Yes	F	NR	NR	F	ND
204	UniProt	UPI000917 8082	1	<i>Marisediminitalia</i> <i>aggregata</i>	Yes	F	NR	NR	F	ND
205	UniProt	UPI00092 C9754	1	<i>Sphingobacteriales</i> <i>bacterium</i> 50-39	Yes	F	NR	NR	F	ND
206	UniProt	UPI00087 A7A88	1	<i>Afipia</i> sp. GAS231	Yes	F	NR	NR	F	ND
207	UniProt	UPI000285 82EE	1	<i>uncultured bacterium</i>	Yes	F	NR	NR	T	OH/Desat
208	UniProt	UPI000E3 72CD9	1	<i>Aspergillus</i> <i>mulundensis</i>		F	NR	NR	T	OH
209	UniProt	UPI000C5 D262B	1	<i>Gemmatimonadacea</i> <i>e bacterium</i>	No	F	NR	NR	F	ND
210	UniProt	UPI000C9 1F8B1	1	<i>Gemmatimonadetes</i> <i>bacterium</i>	Yes	F	NR	NR	F	ND
211	UniProt	UPI00028 D3A0F	1	<i>Trypanosoma cruzi</i> <i>marinkellei</i>	Yes	F	NR	NR	F	ND
212	UniProt	UPI000B6 0B5D7	1	<i>Raphidiopsis curvata</i> NIES-932	Yes	F	NR	NR	F	ND
213	UniProt	UPI000B6 3BE34	1	<i>Macleaya cordata</i>	No	F	NR	NR	F	ND
214	UniProt	UPI000887 0AE8	1	<i>Brevundimonas</i> sp. 374	Yes	F	NR	NR	F	ND
215	UniProt	UPI0009F 07C43	1	<i>Achlya hypogyna</i>	No	F	NR	NR	F	ND
216	UniProt	UPI000CE A0075	1	<i>Cuspidothrix</i> <i>issatschenkoi</i> CHARLIE-1	Yes	F	NR	NR	F	ND

217	UniProt	UPI000C9 5D4FF	1	<i>Gemmatimonadetes bacterium</i>	Yes	F	NR	NR	F	ND
218	UniProt	UPI000C6 3C870	1	<i>Acidimicrobiaceae bacterium</i>	Yes	F	NR	NR	F	ND
219	UniProt	UPI0013A DE792	1	<i>Acidimicrobiia bacterium</i>	Yes	F	NR	NR	T	Desat
220	UniProt	UPI0013B 1657E	1	<i>Massarina eburnea CBS 473.64</i>	No	F	NR	NR	F	ND
221	UniProt	UPI000C3 AC804	1	<i>Planctomycetaceae bacterium</i>	Yes	F	NR	NR	F	ND
222	UniProt	UPI00143 ECFAB	1	<i>Streptomyces sp. RPA4-5</i>	No	F	NR	NR	F	ND
223	UniProt	UPI000EE A119A	1	<i>Candidatus Poribacteria bacterium</i>	Yes	F	NR	NR	F	ND
224	UniProt	UPI00140 DC67F	1	<i>Diaphorobacter sp. HDW4A</i>	Yes	F	NR	NR	F	ND
225	UniProt	UPI000DC F6863	1	<i>Lysobacter sp. N42</i>	Yes	F	NR	NR	F	ND
226	UniProt	UPI000D9 1C86C	1	<i>Acidobacteria bacterium</i>	Yes	F	NR	NR	F	ND
227	UniProt	UPI000B5 7535E	1	<i>Ostreococcus tauri</i>	No	F	NR	NR	F	ND
228	UniProt	UPI000C0 B36EF	1	<i>Planctomycetaceae bacterium</i>	Yes	F	NR	NR	F	ND
229	UniProt	UPI001293 5DA4	1	<i>Streptomyces fegopyri</i>	No	F	NR	NR	F	ND
230	UniProt	A0A6G2J MV6	1	<i>Gemmatimonadetes bacterium</i>	Yes	F	NR	NR	F	ND
231	UniProt	A0A1V9ZY 10	1	<i>Thraustotheca clavata</i>	No	F	NR	NR	F	ND
232	UniProt	A0A2T5JG 62	1	<i>Mucilaginibacter yxingensis</i>	Yes	F	NR	NR	T	OH/Desat
233	UniProt	UPI000C9 623A7	1	<i>Gammaproteobacteri a bacterium</i>	Yes	F	NR	NR	F	ND
234	UniProt	UPI000964 7D65	1	<i>Nitrospirae bacterium 13_2_20CM_2_61_4</i>	Yes	F	NR	NR	F	ND
235	UniProt	UPI00006 E6E63	1	<i>gamma proteobacterium HTCC2207</i>	Yes	F	NR	NR	F	ND
236	UniProt	UPI000E7 2DC2A	1	<i>Coralococcus sp. H22C18031201</i>	Yes	F	NR	NR	F	ND
237	UniProt	UPI000037 C631	1	<i>Cupriavidus metallidurans</i>	Yes	F	NR	NR	F	ND
238	UniProt	UPI000F7 A4E1E	1	<i>Streptomyces sp. WAC05858</i>	No	F	NR	NR	F	ND
239	UniProt	UPI001136 7EBA	1	<i>Hortaea thailandica</i>	No	F	NR	NR	F	ND
240	UniProt	UPI0010A CC555	1	<i>Ferrimonas sp. IMCC35002</i>	Yes	F	NR	NR	F	ND
241	UniProt	UPI000960 AFD5	1	<i>Cyanobacteria bacterium 13_1_20CM_4_61_6</i>	Yes	F	NR	NR	F	ND
242	UniProt	UPI000D4 83B19	1	<i>Bacteroidetes bacterium</i>	Yes	F	NR	NR	F	ND
243	UniProt	UPI0009F 0C221	1	<i>Achlya hypogyna</i>	Yes	F	NR	NR	F	ND
244	UniProt	UPI001775 75D6	1	<i>Gammaproteobacteri a bacterium</i>	Yes	F	NR	NR	F	ND
245	UniProt	UPI000296 6AF3	1	<i>Solanum tuberosum</i>	No	F	NR	NR	F	ND
246	UniProt	UPI001208 B377	1	<i>OM182 bacterium</i>	Yes	F	NR	NR	F	ND
247	UniProt	UPI0010A DD044	1	<i>Polyangium sp. SDU3-1</i>	Yes	F	NR	NR	F	ND
248	UniProt	UPI000461 74BB	1	<i>Tilletiaria anomala UBC 951</i>	Yes	F	NR	NR	F	ND
249	UniProt	UPI000C9 78002	1	<i>Ponticaulis sp.</i>	Yes	F	NR	NR	T	OH
250	UniProt	UPI000C4 01849	1	<i>Nitrospinae bacterium</i>	Yes	F	NR	NR	F	ND
251	UniProt	UPI0013C 053B1	1	<i>Streptomyces sp. SID11233</i>	Yes	F	NR	NR	F	ND
252	UniProt	UPI0008E 185C7	1	<i>Enterovibrio norvegicus DSM 15893</i>	Yes	F	NR	NR	F	ND
253	UniProt	UPI0008E B8589	1	<i>Variovorax sp. PDC80</i>	Yes	F	NR	NR	F	ND
254	UniProt	UPI00049 B9835	1	<i>Saprolegnia parasitica CBS 223.65</i>	No	F	NR	NR	F	ND
255	UniProt	UPI000E3 A8C3E	1	<i>Verrucomicrobia bacterium</i>	Yes	F	NR	NR	F	ND
256	UniProt	UPI0013C CFCED	1	<i>Symploca sp. SIO3C6</i>	Yes	F	NR	NR	F	ND
257	UniProt	UPI001380 80CB	1	<i>Gemmatimonadetes bacterium</i>	No	F	NR	NR	F	ND
258	UniProt	UPI0012C B1408	1	<i>Lasiodiplodia theobromae</i>	Yes	F	NR	NR	F	ND
259	UniProt	A0A6G2J MV6	1	<i>Gemmatimonadetes bacterium</i>	Yes	F	NR	NR	F	ND
260	UniProt	N8YF47	1	<i>Acinetobacter guillouiae</i>	No	F	NR	NR	T	OH/Desat

261	UniProt	A0A1A6A C64	1		<i>Kwoniella dejecticola</i> CBS 10117	No	F	NR	NR	F	ND
262	UniProt	A0A257HL X6	1		<i>Alphaproteobacteria</i> <i>bacterium</i> PA1	Yes	F	NR	NR	T	OH/Desat
263	UniProt	A0A150W CQ9	1		<i>Bdellovibrio</i> <i>bacteriovorus</i>	Yes	F	NR	NR	F	ND
264	UniProt	A0A6P6BJ G2	1		<i>Durio zibethinus</i>	No	F	NR	NR	F	ND
265	UniProt	B3KTF4	1		<i>Homo sapiens</i>	No	F	NR	NR	F	ND
266	UniProt	Q6N063-2	4		<i>Homo sapiens</i>	Yes	F	NR	NR	F	ND
267	UniProt	A0A1Q4A EE8	1		<i>Mesorhizobium</i> sp. 65-26	Yes	F	NR	NR	F	ND
268	UniProt	UPI000069 06CA	1		<i>Synechococcus</i> sp. RS9917	Yes	F	NR	NR	F	ND
269	UniProt	UPI0002A 00A83	1		<i>Calothrix parietina</i>	Yes	F	NR	NR	F	ND
270	UniProt	UPI000740 8FAF	1		<i>Burkholderia cepacia</i> JBK9	Yes	F	NR	NR	F	ND
271	UniProt	UPI000227 714E	1		<i>Sphingobium</i> sp. SYK-6	Yes	F	NR	NR	F	ND
272	UniProt	UPI000457 EAEF	1		<i>Eucalyptus grandis</i>	No	F	NR	NR	F	ND
273	UniProt	UPI0009D 1DCFE	1		<i>Rhodanobacter</i> sp. B05	Yes	F	NR	NR	F	ND
274	UniProt	UPI0000E 2A4D0	1		<i>Aspergillus terreus</i> NIH2624	Yes	F	NR	NR	T	OH
275	UniProt	UPI0000D7 DEBDF	1		<i>Candidatus</i> <i>Moanabacter tarae</i>	Yes	F	NR	NR	F	ND
276	UniProt	UPI00029 EF329	1		<i>Cyanobium gracile</i> PCC 6307	Yes	F	NR	NR	F	ND
277	UniProt	UPI00072 F5426	1		<i>Lacimicrobium</i> <i>alkaliphilum</i>	Yes	F	NR	NR	F	ND
278	UniProt	UPI000803 C8F7	1		<i>Micromonospora</i> <i>krabiensis</i>	Yes	F	NR	NR	F	ND
279	UniProt	UPI0006B E9C50	1		<i>Spinacia oleracea</i>	Yes	F	NR	NR	F	ND
280	UniProt	UPI000813 23D9	1		<i>Pseudoalteromonas</i> <i>luteoviolacea</i>	Yes	F	NR	NR	F	ND
281	UniProt	UPI00080 D6E20	1		<i>Kwoniella</i> <i>mangroviensis</i> CBS 10435	Yes	F	NR	NR	F	ND
282	UniProt	UPI0007B D8335	1		<i>Sistotremastrum</i> <i>niveocreum</i> HHB9708	Yes	F	NR	NR	T	OH/Desat
283	UniProt	UPI000B7 56545	1		<i>Gamma</i> proteobacteri <i>a bacterium</i> TMED34	Yes	F	NR	NR	F	ND
284	UniProt	UPI0005C 0F588	1		<i>Cladophialophora</i> <i>bantiana</i> CBS 173.52	Yes	F	NR	NR	F	ND
285	UniProt	UPI000A2 EAD49	1		<i>Hortaea werneckii</i> EXF-2000	No	F	NR	NR	F	ND
286	UniProt	UPI00080 CBF60	1		<i>Kwoniella</i> <i>heveanensis</i> CBS 569	No	F	NR	NR	F	ND
287	UniProt	UPI00090 B02F2	1		<i>Bradyrhizobium</i> <i>erythrophlei</i>	Yes	F	NR	NR	F	ND
288	UniProt	UPI00000 C93C6	1		<i>Mesorhizobium</i> <i>japonicum</i>	Yes	F	NR	NR	T	OH
289	UniProt	Q989T9	1		<i>Mesorhizobium</i> <i>japonicum</i>	No	T	OH	2	T	OH
290	UniProt	A0A067S9 04	1		<i>Galerina marginata</i> CBS 339.88	Yes	F	NR	NR	F	ND
291	UniProt	A0A0N7JH R7	1		<i>Caulobacter henricii</i>	No	F	NR	NR	F	ND
292	UniProt	A0A225AK 31	1		<i>Talaromyces</i> <i>atroroseus</i>	Yes	F	NR	NR	F	ND
293	UniProt	A0A6A1V G40	2		<i>Morella rubra</i>	No	F	NR	NR	F	ND
294	UniProt	A0A171KV R8	2		<i>Kerstesia gyiorum</i>	Yes	F	NR	NR	F	ND
295	UniProt	A0A5J5C0 82	2		<i>Nyssa sinensis</i>	Yes	F	NR	NR	F	ND
296	UniProt	A0A1H4ZS 08	2		<i>Beijerinckia</i> sp. 28- YEA-48	Yes	F	NR	NR	F	ND
297	UniProt	M2N2R9	1		<i>Baudoinia</i> <i>panamericana</i> UAMH 10762	No	F	NR	NR	F	ND
298	UniProt	UPI000A1 4E4A5	1	XenC / Asl3	<i>Mycobacterium</i> <i>parmense</i>	Yes	T	Desat	2	F	ND
299	UniProt	A0A4Z0Z1 K1	1	SwnH2 (X.hyp)	<i>Xylaria hypoxylon</i>	No	F	NR	0	T	OH/Desat
300	UniProt	D4AU30	3	SwnH2 (T.ben)	<i>Arthroderma</i> <i>benhamiae</i>	Yes	T	OH	0	T	Desat
301	UniProt	A0A2Z2EX E9	1	SwnH2 (A.oxy)	<i>Alternaria oxytropis</i>	No	F	NR	0	F	ND
302	UniProt	E9F8M4	3	SwnH2 (M.rob)	<i>Metarhizium robertsii</i>	Yes	T	OH	0	T	OH/Desat
303	UniProt	A0A0D2B7 G0	1	SwnH1 (E.spin)	<i>Exophiala spinifera</i>	Yes	F	NR	0	T	OH/Desat
304	UniProt	A0A1W2T WF6	1	SwnH2 (R.nec)	<i>Rosellinia necatrix</i>	Yes	F	NR	0	T	OH/Desat

305	UniProt	A0A4Z0YV N9	1	SwnH1 (X.hyp)	Xylaria hypoxylon	Yes	F	NR	0	T	OH
306	UniProt	A0A2Z2EX F3	1	SwnH1 (A.oxy)	Alternaria oxytropis	Yes	F	NR	0	T	OH
307	UniProt	E9F8L9	3	SwnH1 (M.rob)	Metarhizium robertsii	Yes	T	OH/Epim	0	T	OH/Desat
308	UniProt	D4AU26	3	SwnH1 (T.ben)	Arthroderma benhamiae	Yes	T	OH/Desat	0	T	OH
309	ASR		1	ANC1		Yes	F	NR	NR	T	OH
310	ASR		1	ANC2		Yes	F	NR	NR	T	OH
311	ASR		1	ANC3		Yes	F	NR	NR	T	OH/Desat
312	ASR		1	ANC4		Yes	F	NR	NR	F	ND
313	ASR		1	ANC5			F	NR	NR	T	Desat
314	ASR		1	ANC6		Yes	F	NR	NR	F	ND

15. Alignment score percent (AS%)

Calculations

To quantify the relationship between all of the enzymes in our library, the 314 enzymes were extracted from the larger (~27,000 sequences) SSN maintaining the lowest possible alignment score of 50. All edges and associated alignment scores were extrapolated from the SSN and used to generate a dataset of similarities for all enzymes in the library, with alignment scores 5–210 representing percent identity of 19–99%. The fully identical percent of 100 was calculated as a self-referential alignment score = 215. With 215 set as the maximum alignment score, all alignment scores were converted to alignment score percents (AS %), in which $AS \% = \text{alignment score} / \text{maximum alignment score}$. This conversion allowed us to represent an SSN as collections of AS %, in which all enzymes with edges alignment score values greater than 5 were represented.

Supplemental Table S5. Alignment score percents. Node 1 and node 2 are corresponding to nodes in the aKGLib1 SSN and nodes are aligned with enzyme IDs in Supplemental Table S3. The AS% is calculated as described above, derived from the alignment score associated with the edge in the SSN. All nodes were additionally self-referenced with AS% of 100.

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
1	1	100.00%		44	38	7.44%		108	52	13.95%
1	6	80.93%		44	98	6.98%		108	63	13.02%
1	7	66.05%		44	121	6.98%		108	49	12.56%
1	8	64.19%		44	43	6.98%		108	306	11.16%
1	309	60.00%		44	83	6.51%		108	59	10.23%
1	12	53.95%		44	84	6.51%		108	305	9.77%
1	18	53.02%		44	106	6.51%		108	308	9.77%
1	24	48.84%		44	67	6.05%		108	307	9.77%
1	2	47.91%		44	82	6.05%		108	300	8.37%
1	15	47.91%		44	54	6.05%		108	304	8.37%
1	22	47.91%		44	33	6.05%		108	302	8.37%
1	11	45.12%		44	125	6.05%		108	51	7.91%
1	28	43.26%		44	88	5.58%		108	299	7.44%
1	29	43.26%		44	86	5.58%		108	303	6.98%
1	25	42.79%		44	119	5.58%		108	301	6.51%
1	26	42.79%		44	116	5.58%		108	193	4.65%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
1	9	42.33%		44	85	5.12%		108	224	4.19%
1	17	41.86%		44	68	5.12%		108	242	3.72%
1	30	41.86%		44	105	5.12%		108	99	3.72%
1	13	41.40%		44	118	4.65%		108	156	3.26%
1	16	40.93%		45	45	100.00%		109	109	100.00%
1	27	40.93%		45	28	20.47%		109	70	87.91%
1	10	40.47%		45	296	20.00%		109	71	74.88%
1	20	40.47%		45	22	19.07%		109	66	35.35%
1	21	40.47%		45	18	19.07%		109	124	32.09%
1	14	40.00%		45	11	19.07%		109	101	24.19%
1	23	40.00%		45	309	18.60%		109	131	22.79%
1	19	39.53%		45	16	18.60%		109	64	22.33%
1	37	33.49%		45	9	18.14%		109	76	22.33%
1	31	33.49%		45	2	18.14%		109	65	21.86%
1	310	31.16%		45	1	18.14%		109	107	20.47%
1	311	30.70%		45	20	18.14%		109	80	20.00%
1	312	29.77%		45	25	18.14%		109	293	20.00%
1	41	29.77%		45	6	17.67%		109	295	20.00%
1	34	29.30%		45	47	17.21%		109	77	19.53%
1	40	28.84%		45	56	17.21%		109	117	19.53%
1	35	28.84%		45	46	17.21%		109	130	19.07%
1	313	28.84%		45	8	16.74%		109	67	18.60%
1	39	27.44%		45	69	16.74%		109	111	18.60%
1	314	27.44%		45	294	16.74%		109	127	18.60%
1	38	27.44%		45	7	16.28%		109	102	18.60%
1	43	26.98%		45	48	16.28%		109	81	18.14%
1	69	26.98%		45	37	16.28%		109	89	17.67%
1	3	26.51%		45	310	16.28%		109	68	16.74%
1	298	26.51%		45	109	15.81%		109	129	16.74%
1	36	26.51%		45	24	15.81%		109	45	15.81%
1	32	26.05%		45	30	15.81%		109	128	15.35%
1	42	25.12%		45	27	15.81%		109	27	14.42%
1	33	24.19%		45	29	15.81%		109	30	14.42%
1	153	20.47%		45	31	15.35%		109	110	14.42%
1	45	18.14%		45	15	15.35%		109	126	14.42%
1	296	18.14%		45	259	15.35%		109	294	14.42%
1	294	17.67%		45	40	14.88%		109	309	14.42%
1	48	14.88%		45	26	14.88%		109	9	13.95%
1	71	13.95%		45	311	14.88%		109	25	13.95%
1	70	13.49%		45	129	14.88%		109	11	13.49%
1	109	13.02%		45	297	14.88%		109	74	13.49%
1	129	13.02%		45	44	14.42%		109	132	13.49%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
1	259	13.02%		45	66	13.95%		109	1	13.02%
1	128	12.09%		45	77	13.95%		109	15	13.02%
1	44	12.09%		45	76	13.95%		109	20	13.02%
1	46	12.09%		45	101	13.95%		109	75	13.02%
1	47	11.63%		45	17	13.95%		109	16	12.56%
1	79	11.63%		45	153	13.95%		109	22	12.56%
1	124	11.63%		45	71	13.49%		109	31	12.56%
1	77	11.63%		45	70	13.49%		109	35	12.56%
1	297	11.16%		45	3	13.49%		109	6	12.09%
1	104	11.16%		45	131	13.49%		109	18	12.09%
1	127	11.16%		45	124	13.49%		109	28	12.09%
1	293	11.16%		45	23	13.49%		109	296	12.09%
1	56	11.16%		45	42	13.49%		109	3	11.63%
1	102	10.70%		45	10	13.02%		109	7	11.63%
1	295	10.70%		45	102	13.02%		109	8	11.63%
1	76	10.70%		45	107	13.02%		109	34	11.63%
1	92	10.70%		45	312	13.02%		109	37	11.63%
1	131	10.70%		45	313	13.02%		109	310	11.63%
1	66	10.23%		45	12	13.02%		109	311	11.63%
1	103	10.23%		45	14	13.02%		109	2	11.16%
1	62	10.23%		45	39	13.02%		109	69	11.16%
1	78	10.23%		45	293	13.02%		109	153	11.16%
1	89	10.23%		45	117	13.02%		109	29	10.70%
1	101	9.77%		45	65	12.56%		109	41	10.70%
1	65	9.77%		45	298	12.56%		109	116	10.70%
1	55	9.77%		45	32	12.56%		109	13	10.23%
1	121	9.30%		45	33	12.56%		109	24	10.23%
1	81	9.30%		45	35	12.56%		109	39	10.23%
1	107	9.30%		45	41	12.56%		109	40	10.23%
1	117	9.30%		45	34	12.56%		109	48	10.23%
1	82	9.30%		45	89	12.09%		109	313	10.23%
1	126	8.84%		45	19	12.09%		109	314	10.23%
1	64	8.84%		45	68	11.63%		109	10	9.77%
1	68	8.84%		45	80	11.63%		109	14	9.77%
1	143	8.84%		45	67	11.63%		109	17	9.77%
1	98	8.37%		45	92	11.63%		109	19	9.77%
1	83	8.37%		45	43	11.63%		109	23	9.77%
1	85	8.37%		45	128	11.63%		109	26	9.77%
1	67	8.37%		45	13	11.63%		109	38	9.77%
1	132	8.37%		45	55	11.16%		109	47	9.77%
1	122	7.91%		45	21	11.16%		109	56	9.77%
1	80	7.91%		45	130	11.16%		109	312	9.77%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
1	110	7.91%		45	314	11.16%		109	21	9.30%
1	111	7.91%		45	79	10.70%		109	298	9.30%
1	125	7.44%		45	62	10.70%		109	12	8.84%
1	54	7.44%		45	36	10.70%		109	42	8.84%
1	116	7.44%		45	127	10.70%		109	43	8.84%
1	84	6.98%		45	38	10.70%		109	46	8.84%
1	75	6.98%		45	78	10.23%		109	62	8.84%
1	105	6.98%		45	83	10.23%		109	92	8.84%
1	130	6.98%		45	84	10.23%		109	32	8.84%
1	120	6.51%		45	126	10.23%		109	36	8.37%
1	74	6.51%		45	64	9.77%		109	44	8.37%
1	88	5.12%		45	82	9.30%		109	121	8.37%
1	86	5.12%		45	103	9.30%		109	259	7.91%
1	118	5.12%		45	104	9.30%		109	104	7.91%
1	119	5.12%		45	85	8.84%		109	143	7.44%
1	106	4.65%		45	111	8.84%		109	33	6.51%
1	174	4.19%		45	132	8.84%		109	84	6.51%
1	90	3.72%		45	116	8.84%		109	106	6.51%
2	2	100.00%		45	143	8.37%		109	297	6.05%
2	22	64.65%		45	295	7.91%		109	103	6.05%
2	18	60.47%		45	110	7.91%		109	55	5.58%
2	7	49.30%		45	81	7.44%		109	79	5.58%
2	8	49.30%		45	121	7.44%		109	83	5.58%
2	309	48.84%		45	125	7.44%		109	122	5.58%
2	1	47.91%		45	75	6.98%		109	125	5.58%
2	6	46.98%		45	98	6.98%		109	78	5.12%
2	15	41.40%		45	122	6.98%		109	82	5.12%
2	24	40.47%		45	120	6.98%		109	98	5.12%
2	29	39.53%		45	54	6.51%		109	54	4.65%
2	12	38.60%		45	106	6.51%		109	105	4.65%
2	25	37.67%		45	119	6.51%		109	88	4.19%
2	9	36.74%		45	118	6.05%		109	119	4.19%
2	28	36.74%		45	74	5.58%		109	251	4.19%
2	16	36.28%		45	105	5.12%		109	86	3.72%
2	20	36.28%		45	90	4.65%		109	118	3.72%
2	21	34.42%		45	86	4.65%		109	238	3.72%
2	11	33.95%		45	87	4.19%		109	245	3.72%
2	17	33.49%		45	88	3.72%		110	110	100.00%
2	13	33.02%		45	251	3.72%		110	111	73.49%
2	26	33.02%		46	46	100.00%		110	295	38.60%
2	23	33.02%		46	9	17.67%		110	81	35.81%
2	10	32.56%		46	45	17.21%		110	107	21.40%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
2	27	32.56%		46	31	16.74%		110	101	20.47%
2	14	32.09%		46	30	16.28%		110	102	19.07%
2	30	32.09%		46	28	16.28%		110	77	18.60%
2	19	32.09%		46	11	15.81%		110	124	18.60%
2	37	30.23%		46	20	15.81%		110	76	17.21%
2	31	29.77%		46	310	15.81%		110	65	14.88%
2	69	28.84%		46	309	15.35%		110	71	14.42%
2	310	25.58%		46	311	15.35%		110	109	14.42%
2	40	24.65%		46	26	14.88%		110	70	13.02%
2	39	24.19%		46	39	14.88%		110	89	12.56%
2	311	24.19%		46	312	14.88%		110	80	12.56%
2	35	23.72%		46	37	14.42%		110	67	12.56%
2	312	23.72%		46	7	13.49%		110	293	12.56%
2	313	23.26%		46	298	13.49%		110	64	12.09%
2	3	22.79%		46	25	13.49%		110	66	11.63%
2	314	22.79%		46	40	13.49%		110	131	11.63%
2	34	22.79%		46	294	13.49%		110	117	11.63%
2	42	22.33%		46	48	13.02%		110	48	11.63%
2	38	22.33%		46	27	13.02%		110	129	11.16%
2	32	21.86%		46	6	12.56%		110	311	11.16%
2	41	21.86%		46	16	12.56%		110	130	11.16%
2	43	21.86%		46	3	12.09%		110	127	10.70%
2	298	21.40%		46	1	12.09%		110	44	10.70%
2	36	20.47%		46	69	12.09%		110	294	10.70%
2	33	19.07%		46	17	12.09%		110	309	10.23%
2	45	18.14%		46	15	12.09%		110	68	10.23%
2	153	17.67%		46	35	12.09%		110	128	9.77%
2	294	17.67%		46	153	12.09%		110	312	9.77%
2	296	16.28%		46	42	12.09%		110	30	9.77%
2	48	13.49%		46	8	11.63%		110	314	9.77%
2	259	13.02%		46	12	11.63%		110	26	9.77%
2	47	12.09%		46	32	11.63%		110	25	9.30%
2	56	11.63%		46	314	11.63%		110	313	9.30%
2	70	11.63%		46	36	11.63%		110	15	9.30%
2	71	11.63%		46	24	11.63%		110	27	9.30%
2	109	11.16%		46	43	11.63%		110	74	9.30%
2	62	11.16%		46	34	11.63%		110	259	9.30%
2	44	10.70%		46	259	11.63%		110	132	9.30%
2	107	10.70%		46	18	11.16%		110	56	8.84%
2	76	10.23%		46	38	11.16%		110	11	8.84%
2	46	10.23%		46	22	11.16%		110	40	8.84%
2	124	10.23%		46	313	11.16%		110	38	8.84%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
2	83	9.77%		46	41	11.16%		110	126	8.84%
2	128	9.77%		46	296	11.16%		110	69	8.84%
2	129	9.77%		46	293	10.70%		110	7	8.37%
2	55	9.77%		46	29	10.70%		110	6	8.37%
2	297	9.77%		46	80	10.23%		110	41	8.37%
2	295	9.30%		46	2	10.23%		110	39	8.37%
2	77	9.30%		46	47	10.23%		110	310	8.37%
2	111	9.30%		46	127	10.23%		110	8	8.37%
2	122	8.84%		46	10	9.77%		110	31	8.37%
2	293	8.84%		46	23	9.77%		110	296	8.37%
2	127	8.84%		46	13	9.77%		110	42	8.37%
2	130	8.84%		46	76	9.30%		110	17	8.37%
2	101	8.37%		46	124	9.30%		110	9	7.91%
2	67	8.37%		46	33	9.30%		110	16	7.91%
2	65	8.37%		46	14	9.30%		110	298	7.91%
2	117	8.37%		46	19	9.30%		110	18	7.91%
2	102	8.37%		46	109	8.84%		110	36	7.91%
2	92	8.37%		46	21	8.84%		110	19	7.91%
2	132	8.37%		46	70	8.37%		110	12	7.91%
2	131	7.91%		46	77	7.91%		110	20	7.91%
2	68	7.91%		46	75	7.91%		110	1	7.91%
2	80	7.91%		46	92	7.91%		110	45	7.91%
2	125	7.91%		46	101	7.91%		110	35	7.91%
2	81	7.44%		46	44	7.91%		110	3	7.91%
2	89	7.44%		46	66	7.44%		110	37	7.91%
2	66	7.44%		46	65	7.44%		110	32	7.91%
2	64	7.44%		46	56	7.44%		110	14	7.44%
2	110	7.44%		46	129	7.44%		110	23	7.44%
2	79	7.44%		46	295	7.44%		110	10	7.44%
2	103	7.44%		46	297	7.44%		110	22	7.44%
2	104	7.44%		46	104	7.44%		110	28	7.44%
2	84	6.98%		46	102	7.44%		110	2	7.44%
2	78	6.98%		46	71	6.98%		110	153	7.44%
2	143	6.98%		46	78	6.98%		110	297	7.44%
2	85	6.51%		46	62	6.98%		110	21	6.98%
2	82	6.51%		46	107	6.98%		110	24	6.98%
2	121	6.51%		46	89	6.51%		110	43	6.98%
2	126	6.51%		46	83	6.51%		110	92	6.98%
2	75	6.05%		46	81	6.51%		110	75	6.51%
2	98	6.05%		46	82	6.51%		110	121	6.05%
2	74	5.58%		46	55	6.51%		110	29	6.05%
2	106	5.58%		46	117	6.51%		110	34	6.05%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
2	88	4.65%		46	143	6.51%		110	46	6.05%
2	120	4.65%		46	111	6.51%		110	62	6.05%
2	116	4.65%		46	103	6.51%		110	143	6.05%
2	86	4.19%		46	132	6.51%		110	79	6.05%
2	90	3.72%		46	84	6.05%		110	116	6.05%
2	87	3.72%		46	74	6.05%		110	78	6.05%
2	118	3.72%		46	64	6.05%		110	13	6.05%
2	119	3.72%		46	110	6.05%		110	47	5.58%
2	174	3.72%		46	125	6.05%		110	125	5.58%
3	3	100.00%		46	79	5.58%		110	98	5.12%
3	310	68.37%		46	128	5.58%		110	33	5.12%
3	311	60.93%		46	106	5.58%		110	55	5.12%
3	312	59.07%		46	121	5.58%		110	106	5.12%
3	313	58.14%		46	126	5.58%		110	103	5.12%
3	43	54.88%		46	130	5.58%		110	122	4.65%
3	34	53.49%		46	98	5.12%		110	105	4.65%
3	41	53.02%		46	54	4.65%		110	119	3.72%
3	314	53.02%		46	116	4.65%		110	88	3.26%
3	35	52.56%		46	88	4.19%		110	120	3.26%
3	32	51.16%		46	131	4.19%		110	118	3.26%
3	298	50.70%		46	87	3.72%		110	104	3.26%
3	40	49.77%		46	120	3.72%		111	111	100.00%
3	38	49.77%		46	174	3.26%		111	110	73.49%
3	39	49.77%		47	47	100.00%		111	295	40.00%
3	36	48.37%		47	296	18.60%		111	81	36.28%
3	42	43.72%		47	45	17.21%		111	101	23.72%
3	37	40.93%		47	69	16.28%		111	107	23.72%
3	33	40.00%		47	309	16.28%		111	102	21.86%
3	309	32.09%		47	39	16.28%		111	77	21.40%
3	11	31.16%		47	25	16.28%		111	76	20.93%
3	9	30.23%		47	311	15.81%		111	124	20.00%
3	28	30.23%		47	312	15.81%		111	109	18.60%
3	25	29.77%		47	20	15.35%		111	70	18.14%
3	20	29.77%		47	310	14.88%		111	65	17.21%
3	27	29.77%		47	3	14.42%		111	89	15.81%
3	24	29.30%		47	40	14.42%		111	131	14.88%
3	15	28.84%		47	28	14.42%		111	293	14.88%
3	31	28.37%		47	31	14.42%		111	64	14.42%
3	6	27.44%		47	11	14.42%		111	71	14.42%
3	30	27.44%		47	43	14.42%		111	66	13.95%
3	17	26.98%		47	8	13.95%		111	67	13.95%
3	7	26.51%		47	32	13.95%		111	80	13.95%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
3	16	26.51%		47	15	13.95%		111	117	13.49%
3	1	26.51%		47	298	13.95%		111	68	12.56%
3	8	26.05%		47	314	13.95%		111	130	12.09%
3	153	26.05%		47	38	13.95%		111	127	11.63%
3	21	24.65%		47	56	13.49%		111	294	11.63%
3	18	24.65%		47	9	13.49%		111	48	11.16%
3	26	24.65%		47	313	13.49%		111	56	10.70%
3	10	23.72%		47	36	13.49%		111	129	10.70%
3	19	23.72%		47	42	13.49%		111	311	10.70%
3	14	23.72%		47	6	13.02%		111	74	10.70%
3	23	23.72%		47	153	13.02%		111	153	10.70%
3	13	23.26%		47	16	13.02%		111	309	10.70%
3	22	23.26%		47	294	13.02%		111	27	10.70%
3	2	22.79%		47	7	12.56%		111	69	10.70%
3	12	22.79%		47	293	12.56%		111	44	10.23%
3	69	22.33%		47	24	12.56%		111	132	10.23%
3	29	21.40%		47	13	12.56%		111	128	9.77%
3	296	18.14%		47	2	12.09%		111	40	9.77%
3	294	17.21%		47	124	12.09%		111	30	9.77%
3	47	14.42%		47	30	12.09%		111	9	9.77%
3	92	14.42%		47	89	11.63%		111	26	9.77%
3	259	14.42%		47	1	11.63%		111	17	9.77%
3	45	13.49%		47	80	11.63%		111	259	9.77%
3	71	13.02%		47	10	11.63%		111	18	9.30%
3	297	13.02%		47	48	11.63%		111	312	9.30%
3	76	13.02%		47	92	11.63%		111	25	9.30%
3	46	12.09%		47	37	11.63%		111	15	9.30%
3	48	12.09%		47	35	11.63%		111	313	9.30%
3	109	11.63%		47	21	11.63%		111	310	9.30%
3	77	11.16%		47	23	11.63%		111	7	9.30%
3	124	10.70%		47	127	11.63%		111	2	9.30%
3	70	10.70%		47	41	11.63%		111	296	9.30%
3	122	10.70%		47	14	11.63%		111	21	8.84%
3	129	10.70%		47	297	11.63%		111	45	8.84%
3	66	10.23%		47	259	11.63%		111	19	8.84%
3	103	10.23%		47	62	11.16%		111	16	8.84%
3	117	10.23%		47	83	11.16%		111	75	8.84%
3	65	9.77%		47	26	11.16%		111	11	8.84%
3	128	9.77%		47	19	11.16%		111	35	8.84%
3	101	9.30%		47	27	11.16%		111	6	8.84%
3	62	9.30%		47	76	10.70%		111	13	8.37%
3	107	9.30%		47	33	10.70%		111	24	8.37%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
3	102	9.30%		47	18	10.70%		111	41	8.37%
3	44	9.30%		47	12	10.70%		111	314	8.37%
3	55	8.84%		47	44	10.70%		111	42	8.37%
3	81	8.84%		47	128	10.23%		111	39	8.37%
3	132	8.84%		47	129	10.23%		111	3	8.37%
3	293	8.84%		47	101	10.23%		111	31	8.37%
3	83	8.37%		47	22	10.23%		111	37	8.37%
3	98	8.37%		47	46	10.23%		111	8	8.37%
3	79	8.37%		47	71	9.77%		111	23	7.91%
3	111	8.37%		47	64	9.77%		111	10	7.91%
3	80	8.37%		47	66	9.77%		111	14	7.91%
3	104	8.37%		47	131	9.77%		111	298	7.91%
3	67	7.91%		47	29	9.77%		111	47	7.91%
3	68	7.91%		47	34	9.77%		111	12	7.91%
3	84	7.91%		47	109	9.77%		111	22	7.91%
3	64	7.91%		47	107	9.77%		111	43	7.91%
3	110	7.91%		47	75	9.30%		111	1	7.91%
3	82	7.44%		47	55	9.30%		111	116	7.91%
3	89	7.44%		47	74	9.30%		111	92	7.91%
3	75	7.44%		47	65	9.30%		111	126	7.91%
3	127	7.44%		47	81	9.30%		111	297	7.91%
3	121	7.44%		47	295	9.30%		111	28	7.44%
3	130	7.44%		47	130	9.30%		111	38	7.44%
3	74	6.98%		47	17	9.30%		111	36	7.44%
3	126	6.98%		47	77	8.84%		111	79	7.44%
3	131	6.98%		47	70	8.84%		111	32	7.44%
3	56	6.51%		47	117	8.84%		111	121	6.98%
3	78	6.51%		47	82	8.37%		111	62	6.98%
3	295	6.51%		47	84	7.91%		111	78	6.98%
3	125	6.51%		47	78	7.91%		111	103	6.98%
3	85	6.05%		47	85	7.91%		111	29	6.51%
3	143	6.05%		47	122	7.91%		111	34	6.51%
3	120	5.58%		47	104	7.91%		111	46	6.51%
3	54	5.58%		47	111	7.91%		111	20	6.05%
3	106	5.58%		47	102	7.91%		111	143	6.05%
3	116	5.58%		47	79	7.44%		111	125	6.05%
3	105	4.19%		47	126	7.44%		111	82	5.12%
4	4	100.00%		47	132	7.44%		111	33	5.12%
5	5	100.00%		47	103	7.44%		111	122	5.12%
5	205	5.58%		47	67	6.98%		111	55	5.12%
6	6	100.00%		47	68	6.98%		111	106	5.12%
6	1	80.93%		47	143	6.98%		111	105	4.65%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
6	7	66.51%		47	120	6.51%		111	98	4.19%
6	8	63.72%		47	106	6.51%		111	86	4.19%
6	309	59.07%		47	98	6.05%		111	251	3.72%
6	12	53.95%		47	121	5.58%		111	120	3.26%
6	18	53.49%		47	110	5.58%		111	88	3.26%
6	24	49.30%		47	116	5.58%		111	119	3.26%
6	22	47.91%		47	125	5.12%		112	112	100.00%
6	15	47.44%		47	54	4.65%		113	113	100.00%
6	2	46.98%		47	88	4.65%		113	146	7.44%
6	11	44.65%		47	105	4.19%		113	93	5.12%
6	28	43.72%		47	119	3.72%		113	154	5.12%
6	29	42.79%		47	86	3.26%		113	162	3.72%
6	26	42.79%		47	118	3.26%		113	267	3.26%
6	25	42.33%		47	270	3.26%		113	255	3.26%
6	30	41.86%		48	48	100.00%		114	114	100.00%
6	13	41.40%		48	259	32.09%		114	115	65.12%
6	17	41.40%		48	309	18.60%		114	171	3.72%
6	9	40.93%		48	28	18.14%		115	115	100.00%
6	20	40.93%		48	15	16.74%		115	114	65.12%
6	14	40.00%		48	296	16.74%		115	171	4.19%
6	10	39.53%		48	9	16.28%		116	116	100.00%
6	21	39.53%		48	45	16.28%		116	124	11.63%
6	16	39.53%		48	7	15.81%		116	80	11.63%
6	27	39.53%		48	69	15.81%		116	70	11.16%
6	23	39.53%		48	22	15.81%		116	293	11.16%
6	19	38.60%		48	31	15.81%		116	127	10.70%
6	31	33.02%		48	8	15.35%		116	101	10.70%
6	37	33.02%		48	16	15.35%		116	109	10.70%
6	310	30.23%		48	11	15.35%		116	81	10.23%
6	311	30.23%		48	41	15.35%		116	65	10.23%
6	41	29.30%		48	294	15.35%		116	54	10.23%
6	312	28.84%		48	20	15.35%		116	131	10.23%
6	40	28.37%		48	35	15.35%		116	27	10.23%
6	35	28.37%		48	30	15.35%		116	16	10.23%
6	34	28.37%		48	25	15.35%		116	7	10.23%
6	313	27.91%		48	6	14.88%		116	71	9.77%
6	3	27.44%		48	1	14.88%		116	309	9.77%
6	39	27.44%		48	24	14.88%		116	117	9.77%
6	43	26.51%		48	27	14.88%		116	130	9.77%
6	298	26.51%		48	13	14.88%		116	66	9.77%
6	314	26.51%		48	10	14.42%		116	295	9.77%
6	69	26.51%		48	21	14.42%		116	9	9.30%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
6	36	26.05%		48	14	14.42%		116	129	9.30%
6	38	26.05%		48	23	14.42%		116	69	9.30%
6	32	25.58%		48	18	14.42%		116	64	9.30%
6	42	24.65%		48	37	14.42%		116	28	9.30%
6	33	23.26%		48	19	13.95%		116	92	9.30%
6	153	20.93%		48	311	13.95%		116	89	8.84%
6	296	19.53%		48	40	13.95%		116	76	8.84%
6	294	18.60%		48	2	13.49%		116	30	8.84%
6	45	17.67%		48	32	13.49%		116	26	8.84%
6	48	14.88%		48	26	13.49%		116	45	8.84%
6	71	13.02%		48	312	13.49%		116	8	8.84%
6	47	13.02%		48	310	13.49%		116	21	8.84%
6	44	12.56%		48	39	13.49%		116	107	8.37%
6	46	12.56%		48	17	13.02%		116	128	7.91%
6	259	12.56%		48	124	13.02%		116	62	7.91%
6	109	12.09%		48	298	13.02%		116	11	7.91%
6	129	12.09%		48	44	13.02%		116	12	7.91%
6	70	12.09%		48	34	13.02%		116	17	7.91%
6	124	11.63%		48	46	13.02%		116	296	7.91%
6	128	11.63%		48	314	13.02%		116	32	7.91%
6	56	11.63%		48	3	12.09%		116	15	7.91%
6	79	11.63%		48	12	12.09%		116	111	7.91%
6	66	11.16%		48	36	12.09%		116	102	7.91%
6	102	11.16%		48	313	12.09%		116	153	7.44%
6	76	11.16%		48	153	11.63%		116	19	7.44%
6	104	11.16%		48	47	11.63%		116	312	7.44%
6	297	11.16%		48	110	11.63%		116	14	7.44%
6	77	11.16%		48	42	11.63%		116	23	7.44%
6	127	10.70%		48	38	11.63%		116	10	7.44%
6	293	10.70%		48	104	11.63%		116	40	7.44%
6	131	10.70%		48	65	11.16%		116	77	7.44%
6	101	10.23%		48	92	11.16%		116	310	7.44%
6	65	10.23%		48	111	11.16%		116	311	7.44%
6	55	10.23%		48	43	11.16%		116	6	7.44%
6	103	10.23%		48	56	10.70%		116	1	7.44%
6	89	10.23%		48	29	10.70%		116	24	6.98%
6	295	10.23%		48	128	10.70%		116	298	6.98%
6	62	10.23%		48	33	10.70%		116	25	6.98%
6	92	10.23%		48	64	10.23%		116	13	6.98%
6	107	9.77%		48	71	10.23%		116	29	6.98%
6	64	9.77%		48	79	10.23%		116	22	6.98%
6	82	9.77%		48	102	10.23%		116	294	6.98%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
6	78	9.77%		48	109	10.23%		116	43	6.98%
6	121	9.30%		48	78	9.77%		116	313	6.51%
6	67	9.30%		48	101	9.77%		116	18	6.51%
6	68	9.30%		48	89	9.30%		116	48	6.51%
6	132	9.30%		48	70	9.30%		116	20	6.51%
6	98	8.84%		48	67	9.30%		116	55	6.51%
6	81	8.84%		48	107	9.30%		116	34	6.51%
6	117	8.84%		48	293	9.30%		116	314	6.05%
6	85	8.84%		48	130	9.30%		116	41	6.05%
6	111	8.84%		48	55	8.84%		116	31	6.05%
6	122	8.37%		48	76	8.84%		116	39	6.05%
6	110	8.37%		48	77	8.84%		116	132	6.05%
6	74	8.37%		48	121	8.84%		116	259	6.05%
6	75	7.91%		48	129	8.84%		116	125	6.05%
6	80	7.91%		48	117	8.84%		116	37	6.05%
6	83	7.91%		48	131	8.84%		116	110	6.05%
6	130	7.91%		48	103	8.84%		116	36	5.58%
6	143	7.91%		48	297	8.84%		116	56	5.58%
6	125	7.44%		48	81	8.37%		116	38	5.58%
6	54	7.44%		48	66	8.37%		116	126	5.58%
6	126	7.44%		48	68	8.37%		116	47	5.58%
6	116	7.44%		48	80	8.37%		116	35	5.58%
6	120	6.51%		48	62	8.37%		116	3	5.58%
6	105	6.51%		48	295	8.37%		116	44	5.58%
6	84	6.51%		48	120	8.37%		116	42	5.58%
6	119	5.12%		48	127	7.91%		116	74	5.12%
6	118	5.12%		48	132	7.91%		116	67	5.12%
6	90	4.65%		48	82	7.44%		116	75	5.12%
6	88	4.65%		48	122	7.44%		116	33	5.12%
6	86	4.65%		48	143	6.98%		116	79	5.12%
6	106	4.19%		48	98	6.51%		116	297	5.12%
6	174	4.19%		48	83	6.51%		116	106	5.12%
6	138	3.72%		48	126	6.51%		116	103	5.12%
6	87	3.26%		48	116	6.51%		116	104	5.12%
7	7	100.00%		48	119	6.05%		116	2	4.65%
7	6	66.51%		48	106	6.05%		116	46	4.65%
7	1	66.05%		48	125	6.05%		116	120	4.65%
7	8	65.58%		48	74	5.58%		116	78	4.65%
7	309	59.53%		48	84	5.58%		116	213	4.19%
7	12	57.21%		48	118	5.58%		116	68	4.19%
7	22	52.56%		48	105	5.58%		116	86	4.19%
7	18	52.09%		48	85	5.12%		116	98	4.19%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
7	15	50.23%		48	54	5.12%		116	122	3.72%
7	24	49.77%		48	75	5.12%		116	121	3.72%
7	2	49.30%		48	90	4.65%		117	117	100.00%
7	25	44.65%		48	238	3.72%		117	64	23.26%
7	28	44.19%		48	270	3.26%		117	101	20.47%
7	9	43.72%		49	49	100.00%		117	124	20.00%
7	17	42.79%		49	52	78.14%		117	70	19.53%
7	11	42.33%		49	142	24.65%		117	109	19.53%
7	26	42.33%		49	91	24.19%		117	71	19.07%
7	29	41.86%		49	60	22.79%		117	89	18.14%
7	16	41.40%		49	61	22.33%		117	66	17.67%
7	27	40.47%		49	58	20.93%		117	76	17.21%
7	13	40.00%		49	53	20.93%		117	295	17.21%
7	30	39.53%		49	50	19.53%		117	67	17.21%
7	20	39.53%		49	95	15.81%		117	107	16.74%
7	23	39.53%		49	57	15.35%		117	81	16.28%
7	10	39.07%		49	97	13.95%		117	77	16.28%
7	21	39.07%		49	96	13.95%		117	80	16.28%
7	14	38.60%		49	63	12.56%		117	65	16.28%
7	19	38.14%		49	108	12.56%		117	68	16.28%
7	31	36.28%		49	306	6.05%		117	74	15.81%
7	37	33.02%		49	305	5.58%		117	102	15.81%
7	310	29.77%		49	308	5.12%		117	131	15.35%
7	312	29.77%		49	307	4.65%		117	126	15.35%
7	69	29.30%		49	303	4.65%		117	128	14.88%
7	311	29.30%		49	301	3.72%		117	129	14.88%
7	313	28.84%		50	50	100.00%		117	293	14.42%
7	40	28.84%		50	53	77.67%		117	75	14.42%
7	35	27.91%		50	61	37.21%		117	309	13.95%
7	39	27.91%		50	60	36.28%		117	130	13.95%
7	43	27.44%		50	91	32.56%		117	25	13.95%
7	34	27.44%		50	142	25.12%		117	127	13.49%
7	38	27.44%		50	58	22.33%		117	111	13.49%
7	41	27.44%		50	52	21.40%		117	19	13.02%
7	298	26.98%		50	49	19.53%		117	45	13.02%
7	314	26.98%		50	97	19.07%		117	21	12.56%
7	3	26.51%		50	95	18.14%		117	13	12.56%
7	32	26.05%		50	57	16.28%		117	132	12.56%
7	36	25.58%		50	108	15.35%		117	30	12.56%
7	42	22.33%		50	96	14.88%		117	14	12.09%
7	33	22.33%		50	63	14.88%		117	23	12.09%
7	153	22.33%		50	306	10.23%		117	28	12.09%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
7	296	20.47%		50	51	9.77%		117	9	12.09%
7	294	18.14%		50	59	9.30%		117	10	11.63%
7	45	16.28%		50	307	9.30%		117	26	11.63%
7	48	15.81%		50	308	8.84%		117	16	11.63%
7	71	13.49%		50	305	8.37%		117	110	11.63%
7	46	13.49%		50	304	7.91%		117	69	11.16%
7	259	13.02%		50	300	7.44%		117	11	11.16%
7	70	12.56%		50	301	7.44%		117	17	11.16%
7	295	12.56%		50	303	6.98%		117	27	10.70%
7	124	12.56%		50	302	6.98%		117	37	10.70%
7	47	12.56%		50	299	5.58%		117	15	10.23%
7	129	12.09%		50	100	4.65%		117	294	10.23%
7	128	12.09%		50	229	4.19%		117	310	10.23%
7	92	12.09%		50	246	3.72%		117	3	10.23%
7	127	12.09%		50	99	3.26%		117	20	10.23%
7	44	12.09%		50	285	3.26%		117	7	9.77%
7	109	11.63%		50	194	3.26%		117	24	9.77%
7	76	11.16%		50	248	3.26%		117	116	9.77%
7	297	11.16%		51	51	100.00%		117	18	9.30%
7	131	11.16%		51	59	18.14%		117	22	9.30%
7	293	11.16%		51	306	15.35%		117	1	9.30%
7	56	10.70%		51	303	14.88%		117	83	9.30%
7	62	10.70%		51	307	13.02%		117	259	9.30%
7	79	10.70%		51	308	13.02%		117	47	8.84%
7	77	10.23%		51	300	13.02%		117	6	8.84%
7	89	10.23%		51	305	11.63%		117	29	8.84%
7	55	10.23%		51	301	11.63%		117	48	8.84%
7	116	10.23%		51	60	11.16%		117	56	8.84%
7	117	9.77%		51	304	11.16%		117	296	8.84%
7	101	9.77%		51	302	10.70%		117	153	8.84%
7	107	9.77%		51	299	10.70%		117	44	8.37%
7	130	9.77%		51	53	9.77%		117	312	8.37%
7	65	9.77%		51	50	9.77%		117	8	8.37%
7	102	9.77%		51	91	8.84%		117	31	8.37%
7	104	9.77%		51	58	8.37%		117	35	8.37%
7	121	9.30%		51	96	7.91%		117	2	8.37%
7	64	9.30%		51	108	7.91%		117	62	8.37%
7	66	9.30%		51	57	7.44%		117	38	7.91%
7	103	9.30%		51	95	6.98%		117	98	7.91%
7	111	9.30%		51	61	6.51%		117	311	7.91%
7	78	9.30%		51	142	6.51%		117	42	7.91%
7	122	8.84%		51	63	4.65%		117	40	7.91%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
7	81	8.84%		51	97	4.19%		117	12	7.44%
7	67	8.37%		51	193	3.26%		117	39	7.44%
7	110	8.37%		52	52	100.00%		117	92	7.44%
7	132	8.37%		52	49	78.14%		117	298	7.44%
7	83	8.37%		52	91	26.51%		117	32	7.44%
7	68	7.91%		52	142	25.58%		117	313	6.98%
7	80	7.91%		52	60	25.12%		117	314	6.98%
7	143	7.91%		52	61	23.72%		117	82	6.98%
7	85	7.44%		52	53	22.79%		117	43	6.98%
7	125	7.44%		52	58	22.33%		117	36	6.98%
7	126	7.44%		52	50	21.40%		117	54	6.98%
7	75	6.98%		52	95	17.21%		117	46	6.51%
7	74	6.98%		52	57	16.74%		117	79	6.51%
7	98	6.98%		52	97	15.35%		117	55	6.05%
7	82	6.98%		52	96	15.35%		117	34	6.05%
7	84	6.51%		52	63	14.42%		117	121	5.58%
7	105	6.05%		52	108	13.95%		117	78	5.58%
7	88	5.58%		52	306	7.44%		117	103	5.58%
7	120	5.58%		52	305	6.51%		117	106	5.58%
7	54	5.58%		52	307	6.05%		117	84	5.12%
7	90	5.58%		52	308	6.05%		117	85	5.12%
7	106	5.12%		52	303	6.05%		117	122	5.12%
7	86	4.65%		52	59	5.12%		117	125	5.12%
7	119	4.65%		52	304	5.12%		117	297	5.12%
7	118	4.65%		52	300	4.65%		117	41	4.65%
7	87	3.72%		52	301	4.65%		117	143	4.65%
7	174	3.26%		52	302	4.65%		117	86	4.19%
8	8	100.00%		52	100	3.72%		117	119	4.19%
8	7	65.58%		53	53	100.00%		117	238	4.19%
8	1	64.19%		53	50	77.67%		117	120	3.72%
8	6	63.72%		53	61	37.21%		117	251	3.72%
8	309	59.07%		53	60	36.74%		117	88	3.26%
8	12	56.28%		53	91	33.02%		118	118	100.00%
8	22	54.42%		53	142	25.12%		118	119	90.70%
8	18	52.09%		53	58	23.72%		118	105	48.84%
8	15	49.30%		53	52	22.79%		118	106	16.74%
8	2	49.30%		53	49	20.93%		118	125	11.16%
8	24	47.91%		53	97	19.07%		118	297	7.91%
8	25	43.72%		53	95	18.60%		118	26	6.51%
8	28	42.79%		53	57	16.74%		118	78	6.51%
8	29	42.79%		53	96	15.81%		118	15	6.51%
8	21	42.79%		53	63	15.35%		118	309	6.51%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
8	23	42.33%		53	108	15.35%		118	27	6.05%
8	10	41.86%		53	51	9.77%		118	79	6.05%
8	13	41.86%		53	59	8.84%		118	45	6.05%
8	11	41.86%		53	307	8.37%		118	12	6.05%
8	9	41.40%		53	308	8.37%		118	24	6.05%
8	17	41.40%		53	306	8.37%		118	30	6.05%
8	14	41.40%		53	304	8.37%		118	9	5.58%
8	16	41.40%		53	305	7.44%		118	48	5.58%
8	19	40.93%		53	301	7.44%		118	18	5.58%
8	26	40.93%		53	300	7.44%		118	22	5.58%
8	20	38.60%		53	302	7.44%		118	20	5.58%
8	30	38.60%		53	299	6.05%		118	17	5.58%
8	27	38.60%		53	303	5.58%		118	310	5.12%
8	31	33.02%		53	100	4.19%		118	29	5.12%
8	37	32.56%		53	229	4.19%		118	1	5.12%
8	310	30.70%		53	99	3.72%		118	25	5.12%
8	311	30.23%		53	285	3.26%		118	16	5.12%
8	312	29.30%		54	54	100.00%		118	69	5.12%
8	313	28.84%		54	116	10.23%		118	8	5.12%
8	35	28.37%		54	131	8.37%		118	6	5.12%
8	40	27.91%		54	293	7.91%		118	37	5.12%
8	34	27.91%		54	69	7.44%		118	311	4.65%
8	314	27.91%		54	1	7.44%		118	41	4.65%
8	41	27.91%		54	6	7.44%		118	312	4.65%
8	69	27.44%		54	80	7.44%		118	76	4.65%
8	39	27.44%		54	101	7.44%		118	7	4.65%
8	298	27.44%		54	11	7.44%		118	44	4.65%
8	38	27.44%		54	309	7.44%		118	28	4.65%
8	43	26.98%		54	24	6.98%		118	11	4.65%
8	36	26.05%		54	132	6.98%		118	35	4.65%
8	3	26.05%		54	28	6.98%		118	70	4.19%
8	32	24.65%		54	311	6.98%		118	103	4.19%
8	42	24.19%		54	20	6.98%		118	101	4.19%
8	33	22.79%		54	124	6.98%		118	36	3.72%
8	153	20.93%		54	27	6.98%		118	55	3.72%
8	296	19.53%		54	117	6.98%		118	124	3.72%
8	294	17.21%		54	9	6.51%		118	65	3.72%
8	45	16.74%		54	8	6.51%		118	122	3.72%
8	48	15.35%		54	26	6.51%		118	296	3.72%
8	47	13.95%		54	37	6.51%		118	64	3.72%
8	56	13.49%		54	153	6.51%		118	130	3.72%
8	71	12.56%		54	45	6.51%		118	2	3.72%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
8	70	12.56%		54	64	6.05%		118	31	3.72%
8	259	12.09%		54	65	6.05%		118	67	3.72%
8	109	11.63%		54	66	6.05%		118	107	3.72%
8	128	11.63%		54	35	6.05%		118	109	3.72%
8	46	11.63%		54	296	6.05%		118	102	3.72%
8	129	10.70%		54	44	6.05%		118	71	3.26%
8	295	10.70%		54	92	5.58%		118	77	3.26%
8	131	10.70%		54	7	5.58%		118	47	3.26%
8	293	10.23%		54	3	5.58%		118	293	3.26%
8	92	10.23%		54	71	5.58%		118	14	3.26%
8	44	9.77%		54	107	5.58%		118	23	3.26%
8	297	9.77%		54	15	5.58%		118	10	3.26%
8	62	9.77%		54	310	5.58%		118	13	3.26%
8	132	9.77%		54	31	5.58%		118	21	3.26%
8	101	9.30%		54	313	5.58%		118	89	3.26%
8	65	9.30%		54	127	5.58%		118	110	3.26%
8	81	9.30%		54	74	5.12%		119	119	100.00%
8	89	9.30%		54	70	5.12%		119	118	90.70%
8	124	9.30%		54	84	5.12%		119	105	48.37%
8	130	9.30%		54	48	5.12%		119	106	15.81%
8	76	8.84%		54	18	5.12%		119	125	11.63%
8	127	8.84%		54	42	5.12%		119	297	7.44%
8	79	8.84%		54	25	5.12%		119	26	6.98%
8	55	8.84%		54	29	5.12%		119	79	6.98%
8	116	8.84%		54	30	5.12%		119	45	6.51%
8	117	8.37%		54	19	5.12%		119	78	6.51%
8	75	8.37%		54	76	4.65%		119	48	6.05%
8	122	8.37%		54	75	4.65%		119	311	6.05%
8	110	8.37%		54	83	4.65%		119	12	6.05%
8	111	8.37%		54	62	4.65%		119	15	6.05%
8	143	8.37%		54	17	4.65%		119	309	6.05%
8	107	7.91%		54	128	4.65%		119	30	6.05%
8	77	7.91%		54	47	4.65%		119	27	6.05%
8	105	7.91%		54	40	4.65%		119	9	5.58%
8	103	7.91%		54	130	4.65%		119	28	5.58%
8	78	7.91%		54	312	4.65%		119	44	5.58%
8	102	7.91%		54	109	4.65%		119	18	5.58%
8	104	7.91%		54	129	4.65%		119	298	5.58%
8	66	7.44%		54	46	4.65%		119	69	5.58%
8	67	7.44%		54	314	4.19%		119	29	5.58%
8	83	7.44%		54	126	4.19%		119	24	5.58%
8	80	7.44%		54	102	4.19%		119	17	5.58%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
8	74	7.44%		54	55	3.72%		119	20	5.58%
8	125	7.44%		54	77	3.72%		119	36	5.12%
8	98	7.44%		54	43	3.72%		119	41	5.12%
8	64	7.44%		54	104	3.72%		119	43	5.12%
8	68	6.98%		54	297	3.72%		119	310	5.12%
8	126	6.98%		54	82	3.26%		119	313	5.12%
8	82	6.51%		54	295	2.79%		119	314	5.12%
8	85	6.51%		55	55	100.00%		119	22	5.12%
8	54	6.51%		55	62	43.26%		119	312	5.12%
8	121	6.05%		55	103	41.86%		119	8	5.12%
8	84	5.58%		55	79	41.40%		119	1	5.12%
8	90	5.12%		55	78	40.47%		119	25	5.12%
8	119	5.12%		55	121	31.16%		119	16	5.12%
8	118	5.12%		55	104	30.23%		119	35	5.12%
8	120	4.65%		55	120	29.77%		119	6	5.12%
8	88	4.65%		55	122	27.44%		119	40	5.12%
8	106	4.65%		55	27	13.02%		119	7	4.65%
8	87	4.19%		55	9	12.56%		119	11	4.65%
8	86	4.19%		55	26	12.56%		119	37	4.65%
8	174	4.19%		55	25	12.56%		119	103	4.65%
9	9	100.00%		55	69	12.09%		119	64	4.19%
9	11	67.91%		55	44	12.09%		119	34	4.19%
9	309	51.16%		55	309	12.09%		119	55	4.19%
9	27	49.30%		55	28	11.63%		119	71	4.19%
9	30	49.30%		55	11	11.63%		119	70	4.19%
9	25	46.98%		55	98	11.16%		119	130	4.19%
9	26	46.98%		55	45	11.16%		119	76	4.19%
9	17	46.51%		55	17	11.16%		119	296	4.19%
9	24	44.19%		55	24	10.70%		119	107	4.19%
9	7	43.72%		55	37	10.70%		119	117	4.19%
9	15	43.26%		55	22	10.70%		119	101	4.19%
9	31	43.26%		55	65	10.23%		119	109	4.19%
9	37	42.33%		55	6	10.23%		119	102	4.19%
9	1	42.33%		55	92	10.23%		119	124	3.72%
9	28	41.86%		55	7	10.23%		119	89	3.72%
9	8	41.40%		55	296	10.23%		119	65	3.72%
9	6	40.93%		55	15	10.23%		119	122	3.72%
9	16	40.93%		55	311	10.23%		119	2	3.72%
9	20	40.00%		55	30	10.23%		119	39	3.72%
9	22	39.53%		55	129	10.23%		119	47	3.72%
9	18	38.60%		55	20	10.23%		119	13	3.72%
9	2	36.74%		55	13	10.23%		119	67	3.72%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
9	12	36.28%		55	64	9.77%		119	10	3.72%
9	10	34.88%		55	2	9.77%		119	14	3.72%
9	14	34.88%		55	1	9.77%		119	42	3.72%
9	13	34.42%		55	29	9.77%		119	21	3.72%
9	23	34.42%		55	314	9.77%		119	23	3.72%
9	29	34.42%		55	312	9.77%		119	31	3.72%
9	19	34.42%		55	19	9.77%		119	110	3.72%
9	21	33.95%		55	77	9.30%		119	129	3.26%
9	310	33.95%		55	10	9.30%		119	77	3.26%
9	69	33.02%		55	47	9.30%		119	293	3.26%
9	311	31.63%		55	294	9.30%		119	62	3.26%
9	40	31.16%		55	102	9.30%		119	259	3.26%
9	312	30.70%		55	21	9.30%		119	19	3.26%
9	3	30.23%		55	14	9.30%		119	68	3.26%
9	313	29.77%		55	12	9.30%		119	132	3.26%
9	35	29.77%		55	3	8.84%		119	111	3.26%
9	34	29.30%		55	8	8.84%		120	120	100.00%
9	41	29.30%		55	297	8.84%		120	104	40.47%
9	39	29.30%		55	313	8.84%		120	121	38.14%
9	314	28.84%		55	48	8.84%		120	55	29.77%
9	32	28.37%		55	310	8.84%		120	62	29.77%
9	43	28.37%		55	35	8.84%		120	122	29.30%
9	38	27.44%		55	298	8.84%		120	103	26.98%
9	298	25.58%		55	38	8.84%		120	79	26.51%
9	42	24.65%		55	23	8.84%		120	78	26.05%
9	153	24.65%		55	31	8.84%		120	98	10.23%
9	36	24.19%		55	56	8.37%		120	11	9.30%
9	296	23.26%		55	76	8.37%		120	296	9.30%
9	33	23.26%		55	293	8.37%		120	28	9.30%
9	294	20.00%		55	107	8.37%		120	102	9.30%
9	45	18.14%		55	39	8.37%		120	24	8.84%
9	46	17.67%		55	36	8.37%		120	124	8.84%
9	48	16.28%		55	18	8.37%		120	20	8.84%
9	76	15.35%		55	126	8.37%		120	44	8.84%
9	77	14.88%		55	128	7.91%		120	64	8.37%
9	107	14.88%		55	41	7.91%		120	48	8.37%
9	56	14.88%		55	16	7.91%		120	9	7.91%
9	293	14.88%		55	81	7.44%		120	25	7.91%
9	71	14.88%		55	40	7.44%		120	30	7.91%
9	62	14.88%		55	42	7.44%		120	37	7.44%
9	109	13.95%		55	101	7.44%		120	309	7.44%
9	259	13.95%		55	43	7.44%		120	31	7.44%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
9	47	13.49%		55	124	7.44%		120	16	6.98%
9	297	13.49%		55	153	7.44%		120	27	6.98%
9	65	13.02%		55	67	6.98%		120	293	6.98%
9	44	13.02%		55	68	6.98%		120	69	6.98%
9	78	13.02%		55	295	6.98%		120	45	6.98%
9	70	13.02%		55	34	6.98%		120	77	6.51%
9	79	13.02%		55	66	6.51%		120	47	6.51%
9	101	12.56%		55	259	6.51%		120	26	6.51%
9	124	12.56%		55	46	6.51%		120	56	6.51%
9	55	12.56%		55	32	6.51%		120	1	6.51%
9	103	12.56%		55	130	6.51%		120	6	6.51%
9	89	12.09%		55	116	6.51%		120	15	6.51%
9	117	12.09%		55	83	6.05%		120	294	6.51%
9	80	12.09%		55	75	6.05%		120	76	6.05%
9	64	12.09%		55	117	6.05%		120	126	6.05%
9	127	11.63%		55	127	6.05%		120	313	6.05%
9	104	11.63%		55	143	6.05%		120	17	6.05%
9	98	11.16%		55	71	5.58%		120	92	6.05%
9	92	11.16%		55	74	5.58%		120	18	6.05%
9	131	11.16%		55	89	5.58%		120	13	6.05%
9	66	10.70%		55	70	5.58%		120	81	6.05%
9	295	10.70%		55	109	5.58%		120	101	6.05%
9	129	10.70%		55	131	5.12%		120	3	5.58%
9	102	10.23%		55	111	5.12%		120	311	5.58%
9	121	10.23%		55	33	5.12%		120	14	5.58%
9	83	9.77%		55	125	5.12%		120	7	5.58%
9	130	9.77%		55	110	5.12%		120	19	5.58%
9	111	9.77%		55	84	4.65%		120	84	5.58%
9	128	9.77%		55	82	4.65%		120	68	5.58%
9	81	9.77%		55	80	4.65%		120	295	5.58%
9	85	9.30%		55	132	4.65%		120	129	5.58%
9	116	9.30%		55	88	4.19%		120	67	5.58%
9	125	9.30%		55	86	4.19%		120	12	5.58%
9	75	9.30%		55	119	4.19%		120	10	5.58%
9	82	8.84%		55	87	3.72%		120	88	5.58%
9	132	8.84%		55	85	3.72%		120	297	5.58%
9	122	8.37%		55	54	3.72%		120	131	5.12%
9	126	8.37%		55	118	3.72%		120	65	5.12%
9	143	8.37%		55	105	3.72%		120	128	5.12%
9	120	7.91%		55	174	3.26%		120	312	5.12%
9	110	7.91%		56	56	100.00%		120	22	5.12%
9	74	7.44%		56	69	20.93%		120	80	5.12%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
9	67	7.44%		56	45	17.21%		120	43	4.65%
9	84	7.44%		56	9	14.88%		120	310	4.65%
9	68	6.98%		56	296	14.42%		120	8	4.65%
9	105	6.98%		56	8	13.49%		120	41	4.65%
9	106	6.98%		56	47	13.49%		120	2	4.65%
9	54	6.51%		56	11	13.49%		120	23	4.65%
9	119	5.58%		56	28	13.49%		120	127	4.65%
9	118	5.58%		56	309	13.02%		120	314	4.65%
9	86	4.65%		56	20	13.02%		120	85	4.65%
9	264	3.26%		56	294	13.02%		120	130	4.65%
10	10	100.00%		56	2	11.63%		120	107	4.65%
10	14	99.53%		56	6	11.63%		120	116	4.65%
10	23	99.53%		56	40	11.63%		120	83	4.19%
10	19	96.74%		56	26	11.63%		120	35	4.19%
10	21	90.70%		56	35	11.63%		120	66	4.19%
10	13	84.19%		56	27	11.63%		120	89	4.19%
10	309	47.44%		56	25	11.63%		120	153	4.19%
10	15	45.12%		56	30	11.63%		120	21	4.19%
10	8	41.86%		56	37	11.63%		120	34	4.19%
10	24	41.40%		56	15	11.63%		120	82	4.19%
10	25	40.47%		56	16	11.63%		120	40	4.19%
10	1	40.47%		56	77	11.16%		120	86	4.19%
10	16	39.53%		56	1	11.16%		120	46	3.72%
10	6	39.53%		56	17	11.16%		120	32	3.72%
10	7	39.07%		56	29	11.16%		120	117	3.72%
10	20	36.28%		56	297	11.16%		120	90	3.26%
10	11	36.28%		56	39	11.16%		120	132	3.26%
10	9	34.88%		56	83	10.70%		120	111	3.26%
10	18	34.42%		56	7	10.70%		120	110	3.26%
10	30	33.95%		56	102	10.70%		121	121	100.00%
10	12	33.95%		56	311	10.70%		121	104	40.00%
10	29	33.02%		56	111	10.70%		121	120	38.14%
10	26	33.02%		56	31	10.70%		121	55	31.16%
10	22	33.02%		56	48	10.70%		121	103	31.16%
10	17	32.56%		56	153	10.70%		121	62	30.70%
10	2	32.56%		56	92	10.23%		121	79	30.23%
10	27	31.63%		56	79	10.23%		121	78	29.30%
10	28	31.63%		56	71	10.23%		121	122	27.44%
10	31	27.91%		56	18	10.23%		121	11	11.16%
10	37	25.58%		56	81	9.77%		121	124	11.16%
10	310	25.12%		56	98	9.77%		121	9	10.23%
10	311	24.65%		56	62	9.77%		121	30	10.23%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
10	69	24.19%		56	70	9.77%		121	98	9.77%
10	3	23.72%		56	107	9.77%		121	28	9.77%
10	312	23.26%		56	313	9.77%		121	25	9.77%
10	39	23.26%		56	101	9.77%		121	20	9.77%
10	35	22.79%		56	41	9.77%		121	69	9.77%
10	43	22.79%		56	312	9.77%		121	309	9.77%
10	313	22.33%		56	109	9.77%		121	1	9.30%
10	40	22.33%		56	34	9.77%		121	6	9.30%
10	41	22.33%		56	44	9.77%		121	27	9.30%
10	314	22.33%		56	314	9.77%		121	7	9.30%
10	38	21.86%		56	293	9.77%		121	296	9.30%
10	298	21.86%		56	259	9.77%		121	71	9.30%
10	32	21.40%		56	82	9.30%		121	26	9.30%
10	34	21.40%		56	78	9.30%		121	294	9.30%
10	36	20.00%		56	43	9.30%		121	64	8.84%
10	42	19.07%		56	310	9.30%		121	48	8.84%
10	153	17.67%		56	24	9.30%		121	16	8.84%
10	33	16.74%		56	103	9.30%		121	313	8.37%
10	296	15.81%		56	126	9.30%		121	129	8.37%
10	48	14.42%		56	42	9.30%		121	40	8.37%
10	294	14.42%		56	21	9.30%		121	297	8.37%
10	45	13.02%		56	76	8.84%		121	17	8.37%
10	71	12.09%		56	110	8.84%		121	102	8.37%
10	117	11.63%		56	104	8.84%		121	109	8.37%
10	101	11.63%		56	295	8.84%		121	293	7.91%
10	47	11.63%		56	117	8.84%		121	70	7.91%
10	124	11.63%		56	22	8.84%		121	312	7.91%
10	70	10.23%		56	38	8.84%		121	10	7.91%
10	89	10.23%		56	12	8.84%		121	14	7.91%
10	92	10.23%		56	85	8.37%		121	311	7.91%
10	259	10.23%		56	10	8.37%		121	101	7.91%
10	66	10.23%		56	55	8.37%		121	81	7.44%
10	109	9.77%		56	36	8.37%		121	43	7.44%
10	128	9.77%		56	19	8.37%		121	128	7.44%
10	132	9.77%		56	23	8.37%		121	19	7.44%
10	44	9.77%		56	13	8.37%		121	37	7.44%
10	129	9.77%		56	80	7.91%		121	45	7.44%
10	46	9.77%		56	84	7.91%		121	3	7.44%
10	65	9.77%		56	33	7.91%		121	31	7.44%
10	104	9.77%		56	298	7.91%		121	15	7.44%
10	297	9.77%		56	14	7.91%		121	23	7.44%
10	62	9.30%		56	64	7.44%		121	24	7.44%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
10	293	9.30%		56	67	7.44%		121	18	7.44%
10	127	9.30%		56	68	7.44%		121	76	6.98%
10	131	9.30%		56	129	7.44%		121	295	6.98%
10	55	9.30%		56	46	7.44%		121	298	6.98%
10	67	8.84%		56	127	7.44%		121	34	6.98%
10	295	8.84%		56	124	7.44%		121	310	6.98%
10	77	8.84%		56	32	7.44%		121	35	6.98%
10	107	8.37%		56	131	7.44%		121	44	6.98%
10	64	8.37%		56	65	6.98%		121	13	6.98%
10	80	8.37%		56	66	6.98%		121	65	6.98%
10	76	8.37%		56	128	6.98%		121	127	6.98%
10	130	8.37%		56	143	6.98%		121	92	6.98%
10	56	8.37%		56	89	6.51%		121	111	6.98%
10	111	7.91%		56	3	6.51%		121	77	6.51%
10	79	7.91%		56	120	6.51%		121	36	6.51%
10	78	7.91%		56	132	6.05%		121	67	6.51%
10	121	7.91%		56	75	5.58%		121	85	6.51%
10	102	7.91%		56	122	5.58%		121	66	6.51%
10	110	7.44%		56	116	5.58%		121	21	6.51%
10	116	7.44%		56	130	5.58%		121	22	6.51%
10	81	6.98%		56	121	5.12%		121	41	6.51%
10	68	6.98%		56	74	4.65%		121	2	6.51%
10	122	6.98%		56	125	4.19%		121	32	6.51%
10	143	6.98%		57	57	100.00%		121	88	6.05%
10	75	6.05%		57	96	67.91%		121	82	6.05%
10	103	6.05%		57	58	25.58%		121	8	6.05%
10	82	6.05%		57	142	23.72%		121	110	6.05%
10	98	6.05%		57	108	23.72%		121	83	5.58%
10	74	5.58%		57	91	20.47%		121	68	5.58%
10	125	5.58%		57	61	17.21%		121	131	5.58%
10	83	5.58%		57	60	17.21%		121	47	5.58%
10	120	5.58%		57	53	16.74%		121	39	5.58%
10	126	5.12%		57	52	16.74%		121	314	5.58%
10	105	5.12%		57	50	16.28%		121	126	5.58%
10	85	5.12%		57	49	15.35%		121	38	5.58%
10	106	4.65%		57	95	14.88%		121	153	5.58%
10	86	4.65%		57	97	14.88%		121	80	5.58%
10	84	4.19%		57	63	14.42%		121	46	5.58%
10	90	4.19%		57	308	13.02%		121	12	5.58%
10	88	3.72%		57	306	13.02%		121	107	5.58%
10	119	3.72%		57	305	11.63%		121	117	5.58%
10	118	3.26%		57	307	11.16%		121	56	5.12%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
11	11	100.00%		57	303	10.70%		121	89	5.12%
11	9	67.91%		57	59	10.23%		121	84	5.12%
11	309	51.63%		57	304	9.77%		121	29	5.12%
11	30	48.37%		57	300	9.30%		121	132	5.12%
11	25	46.98%		57	302	9.30%		121	130	4.19%
11	27	46.51%		57	299	8.84%		121	33	4.19%
11	26	45.12%		57	301	7.91%		121	143	3.72%
11	1	45.12%		57	51	7.44%		121	116	3.72%
11	6	44.65%		57	229	4.65%		122	122	100.00%
11	24	43.72%		58	58	100.00%		122	104	30.23%
11	17	43.26%		58	142	39.07%		122	120	29.30%
11	7	42.33%		58	60	26.51%		122	55	27.44%
11	8	41.86%		58	57	25.58%		122	121	27.44%
11	15	41.40%		58	91	25.12%		122	78	23.72%
11	28	41.40%		58	61	25.12%		122	79	23.26%
11	20	41.40%		58	97	23.72%		122	62	22.79%
11	37	40.47%		58	96	23.72%		122	103	22.33%
11	31	40.00%		58	53	23.72%		122	312	10.70%
11	16	39.53%		58	108	22.79%		122	3	10.70%
11	18	38.14%		58	63	22.33%		122	311	10.70%
11	13	37.67%		58	50	22.33%		122	27	10.23%
11	22	37.21%		58	52	22.33%		122	313	10.23%
11	23	36.74%		58	49	20.93%		122	310	10.23%
11	19	36.28%		58	95	20.00%		122	43	9.77%
11	10	36.28%		58	59	10.70%		122	28	9.77%
11	12	36.28%		58	303	10.23%		122	298	9.77%
11	14	36.28%		58	307	9.77%		122	15	9.30%
11	21	35.35%		58	306	9.30%		122	309	9.30%
11	310	35.35%		58	308	8.84%		122	31	9.30%
11	2	33.95%		58	305	8.84%		122	36	9.30%
11	311	33.95%		58	300	8.37%		122	2	8.84%
11	29	32.56%		58	51	8.37%		122	7	8.84%
11	34	32.56%		58	302	7.91%		122	25	8.84%
11	69	32.09%		58	301	7.44%		122	296	8.84%
11	312	32.09%		58	304	7.44%		122	44	8.84%
11	40	31.63%		58	299	6.51%		122	9	8.37%
11	3	31.16%		58	156	3.72%		122	17	8.37%
11	35	31.16%		58	224	3.72%		122	40	8.37%
11	41	30.70%		58	255	3.26%		122	129	8.37%
11	39	30.70%		58	193	3.26%		122	24	8.37%
11	313	30.23%		59	59	100.00%		122	6	8.37%
11	32	29.30%		59	51	18.14%		122	11	8.37%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
11	314	29.30%		59	306	13.49%		122	8	8.37%
11	43	27.91%		59	301	13.02%		122	314	8.37%
11	38	27.91%		59	308	12.56%		122	47	7.91%
11	42	26.98%		59	305	12.09%		122	29	7.91%
11	298	26.51%		59	304	11.63%		122	26	7.91%
11	36	25.58%		59	300	11.63%		122	69	7.91%
11	33	24.65%		59	307	11.63%		122	23	7.91%
11	296	24.65%		59	302	11.63%		122	20	7.91%
11	153	24.19%		59	303	11.16%		122	1	7.91%
11	294	20.47%		59	142	11.16%		122	30	7.91%
11	45	19.07%		59	58	10.70%		122	294	7.91%
11	46	15.81%		59	108	10.23%		122	41	7.91%
11	48	15.35%		59	57	10.23%		122	38	7.91%
11	71	14.88%		59	299	9.77%		122	64	7.44%
11	47	14.42%		59	91	9.30%		122	128	7.44%
11	77	14.42%		59	50	9.30%		122	89	7.44%
11	259	14.42%		59	60	8.84%		122	48	7.44%
11	56	13.49%		59	53	8.84%		122	35	7.44%
11	109	13.49%		59	96	7.91%		122	19	7.44%
11	107	13.49%		59	97	7.91%		122	14	7.44%
11	76	13.02%		59	61	5.58%		122	21	7.44%
11	62	13.02%		59	52	5.12%		122	37	7.44%
11	124	13.02%		59	95	4.19%		122	32	7.44%
11	44	12.56%		59	224	3.26%		122	92	6.98%
11	78	12.56%		59	205	3.26%		122	45	6.98%
11	85	12.56%		60	60	100.00%		122	22	6.98%
11	79	12.09%		60	61	37.67%		122	12	6.98%
11	70	12.09%		60	91	36.74%		122	10	6.98%
11	65	12.09%		60	53	36.74%		122	16	6.98%
11	82	11.63%		60	50	36.28%		122	39	6.98%
11	55	11.63%		60	58	26.51%		122	13	6.98%
11	101	11.63%		60	52	25.12%		122	82	6.98%
11	131	11.63%		60	142	24.19%		122	153	6.98%
11	293	11.63%		60	49	22.79%		122	34	6.98%
11	104	11.63%		60	97	18.60%		122	98	6.51%
11	66	11.16%		60	95	17.67%		122	18	6.51%
11	80	11.16%		60	57	17.21%		122	124	6.51%
11	117	11.16%		60	108	16.74%		122	65	6.51%
11	121	11.16%		60	63	16.28%		122	297	6.51%
11	297	11.16%		60	96	16.28%		122	76	6.05%
11	89	10.70%		60	303	11.63%		122	33	6.05%
11	92	10.70%		60	306	11.63%		122	259	6.05%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
11	127	10.70%		60	300	11.16%		122	101	6.05%
11	103	10.70%		60	301	11.16%		122	67	5.58%
11	98	10.23%		60	302	11.16%		122	66	5.58%
11	102	10.23%		60	307	11.16%		122	83	5.58%
11	129	10.23%		60	51	11.16%		122	56	5.58%
11	132	10.23%		60	305	10.70%		122	71	5.58%
11	83	9.77%		60	308	10.23%		122	143	5.58%
11	295	9.77%		60	304	10.23%		122	109	5.58%
11	128	9.77%		60	59	8.84%		122	68	5.12%
11	130	9.77%		60	299	8.37%		122	131	5.12%
11	64	9.30%		60	159	4.19%		122	81	5.12%
11	75	9.30%		60	257	3.72%		122	70	5.12%
11	120	9.30%		60	193	3.72%		122	77	5.12%
11	143	9.30%		60	224	3.72%		122	107	5.12%
11	81	8.84%		61	61	100.00%		122	117	5.12%
11	125	8.84%		61	60	37.67%		122	111	5.12%
11	111	8.84%		61	50	37.21%		122	84	4.65%
11	110	8.84%		61	53	37.21%		122	293	4.65%
11	122	8.37%		61	91	35.81%		122	42	4.65%
11	84	7.91%		61	142	25.58%		122	85	4.65%
11	126	7.91%		61	58	25.12%		122	126	4.65%
11	116	7.91%		61	52	23.72%		122	127	4.65%
11	67	7.44%		61	49	22.33%		122	110	4.65%
11	54	7.44%		61	95	20.00%		122	102	4.65%
11	74	7.44%		61	97	18.14%		122	74	4.19%
11	68	6.98%		61	63	17.67%		122	130	3.72%
11	105	6.51%		61	108	17.21%		122	105	3.72%
11	106	5.12%		61	57	17.21%		122	118	3.72%
11	119	4.65%		61	96	15.81%		122	119	3.72%
11	118	4.65%		61	307	12.56%		122	116	3.72%
11	90	4.19%		61	306	11.16%		122	90	3.26%
11	86	3.72%		61	305	10.23%		123	123	100.00%
12	12	100.00%		61	308	9.30%		124	124	100.00%
12	7	57.21%		61	303	8.84%		124	71	32.56%
12	8	56.28%		61	301	6.98%		124	109	32.09%
12	1	53.95%		61	300	6.98%		124	70	31.16%
12	6	53.95%		61	304	6.98%		124	64	30.23%
12	309	49.77%		61	302	6.98%		124	66	28.84%
12	15	45.12%		61	51	6.51%		124	76	26.98%
12	18	44.19%		61	299	5.58%		124	107	26.98%
12	24	42.33%		61	59	5.58%		124	101	26.51%
12	22	42.33%		61	193	5.12%		124	77	26.05%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
12	28	39.53%		61	255	4.65%		124	67	25.58%
12	2	38.60%		61	229	4.19%		124	65	25.58%
12	26	38.60%		61	99	3.72%		124	68	23.26%
12	25	38.14%		61	248	3.72%		124	131	22.79%
12	17	36.74%		61	257	3.72%		124	81	21.86%
12	16	36.74%		61	224	3.72%		124	293	21.40%
12	30	36.28%		62	62	100.00%		124	295	20.47%
12	9	36.28%		62	103	43.72%		124	130	20.47%
12	29	36.28%		62	55	43.26%		124	102	20.47%
12	11	36.28%		62	79	42.79%		124	117	20.00%
12	13	35.35%		62	78	41.86%		124	111	20.00%
12	21	35.35%		62	104	30.70%		124	80	19.53%
12	20	34.88%		62	121	30.70%		124	129	19.53%
12	23	34.42%		62	120	29.77%		124	89	18.60%
12	27	33.95%		62	122	22.79%		124	110	18.60%
12	10	33.95%		62	9	14.88%		124	74	18.14%
12	14	33.49%		62	309	14.88%		124	75	18.14%
12	19	33.02%		62	69	14.42%		124	132	17.67%
12	37	32.09%		62	30	13.95%		124	126	17.67%
12	31	29.30%		62	28	13.95%		124	128	17.21%
12	311	27.44%		62	20	13.95%		124	127	16.74%
12	41	26.98%		62	98	13.49%		124	25	14.88%
12	310	26.98%		62	11	13.02%		124	44	14.42%
12	312	26.51%		62	16	13.02%		124	28	13.95%
12	40	26.05%		62	15	12.56%		124	309	13.95%
12	34	25.58%		62	25	12.09%		124	259	13.95%
12	313	25.58%		62	24	12.09%		124	45	13.49%
12	39	25.12%		62	37	12.09%		124	15	13.49%
12	35	25.12%		62	92	11.63%		124	31	13.02%
12	298	25.12%		62	297	11.63%		124	69	13.02%
12	32	24.65%		62	17	11.63%		124	48	13.02%
12	36	24.65%		62	31	11.63%		124	16	13.02%
12	38	23.72%		62	27	11.63%		124	11	13.02%
12	43	23.72%		62	2	11.16%		124	9	12.56%
12	314	23.72%		62	77	11.16%		124	7	12.56%
12	69	23.26%		62	47	11.16%		124	20	12.56%
12	3	22.79%		62	26	11.16%		124	27	12.56%
12	153	22.33%		62	7	10.70%		124	47	12.09%
12	33	21.40%		62	293	10.70%		124	30	12.09%
12	42	20.47%		62	124	10.70%		124	294	12.09%
12	296	17.67%		62	29	10.70%		124	19	12.09%
12	294	16.28%		62	45	10.70%		124	6	11.63%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
12	45	13.02%		62	296	10.70%		124	24	11.63%
12	48	12.09%		62	1	10.23%		124	1	11.63%
12	46	11.63%		62	76	10.23%		124	14	11.63%
12	295	11.16%		62	6	10.23%		124	13	11.63%
12	47	10.70%		62	22	10.23%		124	23	11.63%
12	259	10.70%		62	65	9.77%		124	10	11.63%
12	297	10.70%		62	8	9.77%		124	296	11.63%
12	71	10.23%		62	43	9.77%		124	116	11.63%
12	124	10.23%		62	56	9.77%		124	22	11.16%
12	62	9.77%		62	19	9.77%		124	17	11.16%
12	79	9.77%		62	128	9.77%		124	121	11.16%
12	78	9.77%		62	310	9.77%		124	3	10.70%
12	131	9.77%		62	12	9.77%		124	37	10.70%
12	66	9.30%		62	44	9.77%		124	62	10.70%
12	55	9.30%		62	71	9.30%		124	21	10.70%
12	129	9.30%		62	10	9.30%		124	310	10.23%
12	128	9.30%		62	3	9.30%		124	92	10.23%
12	101	9.30%		62	21	9.30%		124	26	10.23%
12	70	8.84%		62	298	9.30%		124	12	10.23%
12	65	8.84%		62	153	9.30%		124	43	10.23%
12	56	8.84%		62	129	9.30%		124	2	10.23%
12	89	8.84%		62	23	9.30%		124	104	10.23%
12	76	8.84%		62	313	9.30%		124	313	9.77%
12	44	8.84%		62	38	9.30%		124	298	9.77%
12	109	8.84%		62	13	9.30%		124	312	9.77%
12	132	8.84%		62	64	8.84%		124	311	9.77%
12	81	8.37%		62	67	8.84%		124	18	9.77%
12	77	8.37%		62	14	8.84%		124	153	9.77%
12	105	8.37%		62	36	8.84%		124	35	9.30%
12	293	8.37%		62	18	8.84%		124	46	9.30%
12	127	8.37%		62	35	8.84%		124	8	9.30%
12	104	8.37%		62	109	8.84%		124	314	9.30%
12	67	7.91%		62	40	8.84%		124	29	8.84%
12	125	7.91%		62	311	8.84%		124	34	8.84%
12	110	7.91%		62	314	8.84%		124	40	8.84%
12	111	7.91%		62	68	8.37%		124	41	8.84%
12	130	7.91%		62	80	8.37%		124	32	8.84%
12	116	7.91%		62	107	8.37%		124	120	8.84%
12	92	7.44%		62	312	8.37%		124	36	8.37%
12	117	7.44%		62	117	8.37%		124	38	8.37%
12	103	7.44%		62	48	8.37%		124	106	8.37%
12	143	7.44%		62	294	8.37%		124	42	7.91%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
12	74	6.98%		62	70	7.91%		124	39	7.91%
12	98	6.98%		62	116	7.91%		124	103	7.91%
12	122	6.98%		62	259	7.91%		124	55	7.44%
12	107	6.98%		62	34	7.91%		124	56	7.44%
12	64	6.51%		62	39	7.44%		124	33	6.98%
12	102	6.51%		62	143	7.44%		124	54	6.98%
12	68	6.05%		62	81	6.98%		124	82	6.98%
12	80	6.05%		62	89	6.98%		124	143	6.51%
12	126	6.05%		62	101	6.98%		124	85	6.51%
12	118	6.05%		62	111	6.98%		124	79	6.51%
12	119	6.05%		62	126	6.98%		124	78	6.51%
12	75	5.58%		62	46	6.98%		124	122	6.51%
12	88	5.58%		62	41	6.98%		124	83	6.05%
12	106	5.58%		62	102	6.98%		124	84	6.05%
12	120	5.58%		62	130	6.51%		124	264	5.58%
12	121	5.58%		62	85	6.05%		124	125	5.58%
12	83	5.12%		62	131	6.05%		124	297	5.58%
12	85	4.65%		62	110	6.05%		124	251	5.58%
12	87	4.65%		62	32	6.05%		124	105	4.19%
12	84	3.72%		62	66	5.58%		124	119	3.72%
12	86	3.72%		62	82	5.58%		124	118	3.72%
12	174	3.26%		62	83	5.58%		124	138	3.26%
13	13	100.00%		62	127	5.58%		124	88	3.26%
13	14	85.12%		62	42	5.58%		125	125	100.00%
13	23	85.12%		62	295	5.58%		125	106	37.21%
13	19	84.65%		62	132	5.58%		125	105	12.09%
13	21	84.65%		62	125	5.58%		125	119	11.63%
13	10	84.19%		62	74	4.65%		125	118	11.16%
13	309	47.44%		62	86	4.65%		125	28	10.70%
13	15	44.65%		62	33	4.65%		125	9	9.30%
13	24	42.33%		62	54	4.65%		125	293	9.30%
13	8	41.86%		62	88	4.19%		125	15	9.30%
13	1	41.40%		62	84	4.19%		125	37	9.30%
13	6	41.40%		62	106	3.72%		125	20	9.30%
13	16	40.47%		62	90	3.26%		125	11	8.84%
13	25	40.47%		62	119	3.26%		125	309	8.37%
13	7	40.00%		63	63	100.00%		125	69	8.37%
13	11	37.67%		63	58	22.33%		125	30	8.37%
13	20	36.28%		63	142	19.07%		125	12	7.91%
13	12	35.35%		63	61	17.67%		125	27	7.91%
13	18	34.88%		63	97	17.21%		125	294	7.91%
13	9	34.42%		63	91	16.28%		125	25	7.91%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
13	26	33.49%		63	95	16.28%		125	17	7.91%
13	2	33.02%		63	60	16.28%		125	26	7.91%
13	29	33.02%		63	96	15.81%		125	2	7.91%
13	30	33.02%		63	53	15.35%		125	24	7.44%
13	22	32.56%		63	50	14.88%		125	8	7.44%
13	28	32.09%		63	52	14.42%		125	7	7.44%
13	17	31.63%		63	57	14.42%		125	6	7.44%
13	27	31.16%		63	108	13.02%		125	21	7.44%
13	31	27.44%		63	49	12.56%		125	45	7.44%
13	69	26.51%		63	51	4.65%		125	1	7.44%
13	37	26.05%		63	307	4.19%		125	39	7.44%
13	310	25.12%		63	306	3.72%		125	76	7.44%
13	311	24.65%		63	257	3.72%		125	77	7.44%
13	35	24.19%		63	303	3.26%		125	65	6.98%
13	312	24.19%		64	64	100.00%		125	40	6.98%
13	39	23.72%		64	75	39.53%		125	311	6.98%
13	40	23.72%		64	74	35.81%		125	80	6.98%
13	41	23.72%		64	67	32.09%		125	31	6.98%
13	3	23.26%		64	68	30.70%		125	130	6.98%
13	313	23.26%		64	124	30.23%		125	16	6.51%
13	314	23.26%		64	117	23.26%		125	13	6.51%
13	38	22.79%		64	66	22.79%		125	313	6.51%
13	298	22.79%		64	65	22.33%		125	3	6.51%
13	34	22.33%		64	70	22.33%		125	153	6.51%
13	32	22.33%		64	109	22.33%		125	41	6.51%
13	43	21.86%		64	101	21.86%		125	132	6.51%
13	36	21.40%		64	71	21.40%		125	102	6.51%
13	42	20.47%		64	76	20.93%		125	22	6.05%
13	33	17.67%		64	77	20.47%		125	42	6.05%
13	153	17.21%		64	131	20.47%		125	312	6.05%
13	48	14.88%		64	130	20.47%		125	310	6.05%
13	296	14.88%		64	107	20.00%		125	46	6.05%
13	294	13.95%		64	293	20.00%		125	295	6.05%
13	47	12.56%		64	102	19.53%		125	298	6.05%
13	117	12.56%		64	89	18.14%		125	18	6.05%
13	45	11.63%		64	295	18.14%		125	35	6.05%
13	71	11.63%		64	81	17.67%		125	81	6.05%
13	101	11.63%		64	80	17.67%		125	127	6.05%
13	124	11.63%		64	127	17.67%		125	29	6.05%
13	70	11.16%		64	132	16.74%		125	48	6.05%
13	129	11.16%		64	129	16.28%		125	44	6.05%
13	259	10.70%		64	128	15.81%		125	111	6.05%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
13	55	10.23%		64	126	14.88%		125	116	6.05%
13	92	10.23%		64	111	14.42%		125	107	6.05%
13	109	10.23%		64	9	12.09%		125	19	5.58%
13	46	9.77%		64	110	12.09%		125	23	5.58%
13	64	9.77%		64	69	11.63%		125	10	5.58%
13	66	9.77%		64	27	11.63%		125	43	5.58%
13	77	9.77%		64	309	11.63%		125	131	5.58%
13	89	9.77%		64	294	11.16%		125	34	5.58%
13	297	9.77%		64	44	10.70%		125	297	5.58%
13	44	9.30%		64	30	10.70%		125	62	5.58%
13	62	9.30%		64	25	10.70%		125	124	5.58%
13	65	9.30%		64	310	10.70%		125	110	5.58%
13	67	9.30%		64	28	10.23%		125	109	5.58%
13	76	9.30%		64	15	10.23%		125	14	5.12%
13	80	9.30%		64	48	10.23%		125	47	5.12%
13	107	9.30%		64	24	10.23%		125	314	5.12%
13	104	9.30%		64	6	9.77%		125	55	5.12%
13	131	8.84%		64	47	9.77%		125	296	5.12%
13	132	8.84%		64	55	9.77%		125	68	5.12%
13	130	8.84%		64	20	9.77%		125	67	5.12%
13	56	8.37%		64	45	9.77%		125	117	5.12%
13	128	8.37%		64	13	9.77%		125	71	4.65%
13	111	8.37%		64	7	9.30%		125	38	4.65%
13	295	8.37%		64	11	9.30%		125	259	4.65%
13	127	8.37%		64	16	9.30%		125	36	4.65%
13	293	7.91%		64	116	9.30%		125	78	4.65%
13	102	7.91%		64	1	8.84%		125	79	4.65%
13	68	7.44%		64	121	8.84%		125	32	4.65%
13	81	7.44%		64	62	8.84%		125	103	4.65%
13	79	6.98%		64	22	8.84%		125	129	4.19%
13	122	6.98%		64	298	8.84%		125	83	4.19%
13	121	6.98%		64	21	8.84%		125	64	4.19%
13	116	6.98%		64	259	8.84%		125	92	4.19%
13	74	6.51%		64	314	8.84%		125	70	4.19%
13	75	6.51%		64	40	8.84%		125	56	4.19%
13	78	6.51%		64	31	8.84%		125	89	4.19%
13	82	6.51%		64	311	8.84%		125	101	4.19%
13	85	6.51%		64	92	8.37%		125	98	3.72%
13	98	6.51%		64	10	8.37%		125	128	3.72%
13	126	6.51%		64	120	8.37%		125	143	3.72%
13	125	6.51%		64	43	8.37%		125	147	3.26%
13	143	6.51%		64	18	8.37%		125	104	3.26%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
13	83	6.05%		64	23	8.37%		126	126	100.00%
13	103	6.05%		64	17	8.37%		126	128	46.98%
13	120	6.05%		64	14	8.37%		126	129	45.12%
13	110	6.05%		64	296	8.37%		126	77	17.67%
13	86	5.12%		64	19	8.37%		126	124	17.67%
13	90	5.12%		64	3	7.91%		126	101	16.74%
13	84	4.65%		64	104	7.91%		126	76	16.28%
13	105	4.65%		64	312	7.91%		126	131	16.28%
13	106	4.65%		64	37	7.91%		126	71	16.28%
13	87	4.19%		64	41	7.91%		126	102	16.28%
13	238	3.72%		64	38	7.91%		126	107	16.28%
13	119	3.72%		64	39	7.91%		126	293	15.35%
13	251	3.26%		64	2	7.44%		126	117	15.35%
13	118	3.26%		64	8	7.44%		126	64	14.88%
14	23	100.00%		64	83	7.44%		126	109	14.42%
14	14	100.00%		64	122	7.44%		126	70	13.95%
14	10	99.53%		64	36	7.44%		126	80	13.49%
14	19	98.14%		64	313	7.44%		126	295	13.49%
14	21	91.63%		64	56	7.44%		126	89	13.02%
14	13	85.12%		64	42	7.44%		126	81	13.02%
14	309	46.51%		64	103	6.98%		126	127	13.02%
14	15	45.12%		64	153	6.98%		126	132	13.02%
14	8	41.40%		64	26	6.98%		126	44	12.56%
14	24	40.93%		64	35	6.98%		126	130	12.56%
14	6	40.00%		64	98	6.51%		126	66	12.09%
14	1	40.00%		64	12	6.51%		126	68	11.63%
14	25	39.53%		64	32	6.51%		126	65	11.16%
14	16	39.53%		64	297	6.51%		126	75	10.70%
14	7	38.60%		64	78	6.05%		126	45	10.23%
14	11	36.28%		64	79	6.05%		126	67	10.23%
14	20	35.81%		64	82	6.05%		126	69	9.77%
14	9	34.88%		64	54	6.05%		126	26	9.77%
14	30	33.95%		64	143	6.05%		126	74	9.30%
14	18	33.49%		64	34	6.05%		126	28	9.30%
14	12	33.49%		64	46	6.05%		126	294	9.30%
14	29	33.02%		64	84	5.58%		126	56	9.30%
14	26	33.02%		64	251	5.58%		126	17	9.30%
14	17	32.56%		64	86	5.12%		126	1	8.84%
14	2	32.09%		64	85	4.65%		126	110	8.84%
14	22	32.09%		64	105	4.65%		126	37	8.37%
14	27	31.63%		64	29	4.65%		126	55	8.37%
14	28	31.63%		64	106	4.65%		126	9	8.37%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
14	31	28.37%		64	33	4.65%		126	11	7.91%
14	37	25.58%		64	87	4.19%		126	20	7.91%
14	310	25.12%		64	88	4.19%		126	310	7.91%
14	69	24.19%		64	264	4.19%		126	43	7.91%
14	311	24.19%		64	119	4.19%		126	309	7.91%
14	3	23.72%		64	125	4.19%		126	111	7.91%
14	43	23.26%		64	118	3.72%		126	47	7.44%
14	39	23.26%		64	238	3.26%		126	30	7.44%
14	38	22.79%		65	65	100.00%		126	298	7.44%
14	313	22.79%		65	101	27.44%		126	27	7.44%
14	312	22.79%		65	124	25.58%		126	7	7.44%
14	314	22.79%		65	70	22.79%		126	22	7.44%
14	35	22.33%		65	64	22.33%		126	6	7.44%
14	40	22.33%		65	109	21.86%		126	18	7.44%
14	41	22.33%		65	71	20.93%		126	143	7.44%
14	34	21.86%		65	76	20.93%		126	25	7.44%
14	32	21.40%		65	107	20.93%		126	103	7.44%
14	298	21.40%		65	68	20.47%		126	15	6.98%
14	36	20.00%		65	67	20.00%		126	29	6.98%
14	42	19.53%		65	89	19.53%		126	3	6.98%
14	153	18.14%		65	77	19.53%		126	41	6.98%
14	33	16.74%		65	66	19.53%		126	36	6.98%
14	296	15.35%		65	102	19.07%		126	312	6.98%
14	48	14.42%		65	293	18.60%		126	62	6.98%
14	294	14.42%		65	132	18.14%		126	8	6.98%
14	45	13.02%		65	295	18.14%		126	79	6.98%
14	71	12.56%		65	131	17.67%		126	104	6.98%
14	117	12.09%		65	130	17.21%		126	13	6.51%
14	47	11.63%		65	111	17.21%		126	48	6.51%
14	101	11.63%		65	74	16.74%		126	297	6.51%
14	124	11.63%		65	81	16.28%		126	34	6.51%
14	297	10.70%		65	117	16.28%		126	21	6.51%
14	70	10.23%		65	80	15.81%		126	39	6.51%
14	92	10.23%		65	127	15.35%		126	42	6.51%
14	132	10.23%		65	110	14.88%		126	24	6.51%
14	129	10.23%		65	128	14.42%		126	259	6.51%
14	131	10.23%		65	75	13.95%		126	2	6.51%
14	259	10.23%		65	69	13.95%		126	92	6.51%
14	44	9.77%		65	20	13.49%		126	19	6.05%
14	89	9.77%		65	9	13.02%		126	14	6.05%
14	65	9.77%		65	129	13.02%		126	12	6.05%
14	66	9.77%		65	45	12.56%		126	31	6.05%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
14	109	9.77%		65	11	12.09%		126	78	6.05%
14	128	9.77%		65	30	11.63%		126	313	6.05%
14	104	9.77%		65	44	11.63%		126	120	6.05%
14	80	9.30%		65	294	11.63%		126	35	5.58%
14	46	9.30%		65	48	11.16%		126	213	5.58%
14	55	9.30%		65	126	11.16%		126	23	5.58%
14	67	8.84%		65	153	11.16%		126	16	5.58%
14	62	8.84%		65	296	10.70%		126	46	5.58%
14	107	8.84%		65	6	10.23%		126	314	5.58%
14	295	8.84%		65	15	10.23%		126	311	5.58%
14	127	8.84%		65	309	10.23%		126	121	5.58%
14	293	8.84%		65	25	10.23%		126	116	5.58%
14	76	8.37%		65	55	10.23%		126	10	5.12%
14	64	8.37%		65	116	10.23%		126	83	5.12%
14	77	8.37%		65	24	10.23%		126	40	5.12%
14	130	8.37%		65	3	9.77%		126	153	5.12%
14	56	7.91%		65	1	9.77%		126	38	5.12%
14	111	7.91%		65	7	9.77%		126	251	5.12%
14	121	7.91%		65	10	9.77%		126	296	5.12%
14	102	7.91%		65	22	9.77%		126	33	5.12%
14	81	7.44%		65	62	9.77%		126	32	5.12%
14	68	7.44%		65	21	9.77%		126	98	4.65%
14	79	7.44%		65	19	9.77%		126	122	4.65%
14	78	7.44%		65	16	9.77%		126	84	4.19%
14	110	7.44%		65	14	9.77%		126	54	4.19%
14	122	7.44%		65	23	9.77%		127	127	100.00%
14	116	7.44%		65	37	9.77%		127	293	44.19%
14	143	6.98%		65	27	9.77%		127	80	41.40%
14	75	6.51%		65	28	9.77%		127	101	19.53%
14	82	6.51%		65	8	9.30%		127	109	18.60%
14	103	6.51%		65	47	9.30%		127	64	17.67%
14	98	6.05%		65	13	9.30%		127	71	17.21%
14	126	6.05%		65	92	8.84%		127	70	17.21%
14	74	5.58%		65	311	8.84%		127	131	17.21%
14	83	5.58%		65	313	8.84%		127	130	17.21%
14	120	5.58%		65	31	8.84%		127	124	16.74%
14	85	5.12%		65	18	8.84%		127	67	15.35%
14	125	5.12%		65	310	8.84%		127	65	15.35%
14	105	5.12%		65	12	8.84%		127	129	14.88%
14	86	4.65%		65	2	8.37%		127	76	14.88%
14	106	4.65%		65	298	8.37%		127	68	14.42%
14	84	4.19%		65	43	8.37%		127	66	14.42%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
14	90	4.19%		65	312	8.37%		127	128	13.95%
14	88	3.72%		65	35	8.37%		127	77	13.95%
14	119	3.72%		65	26	8.37%		127	102	13.49%
14	118	3.26%		65	17	8.37%		127	107	13.49%
15	15	100.00%		65	39	8.37%		127	117	13.49%
15	309	60.00%		65	314	8.37%		127	74	13.02%
15	24	53.95%		65	42	8.37%		127	132	13.02%
15	7	50.23%		65	36	7.91%		127	126	13.02%
15	8	49.30%		65	41	7.91%		127	89	12.56%
15	1	47.91%		65	29	7.91%		127	69	12.09%
15	6	47.44%		65	103	7.44%		127	295	12.09%
15	25	46.51%		65	46	7.44%		127	7	12.09%
15	28	46.51%		65	34	7.44%		127	47	11.63%
15	21	45.58%		65	38	7.44%		127	75	11.63%
15	10	45.12%		65	125	6.98%		127	309	11.63%
15	23	45.12%		65	106	6.98%		127	9	11.63%
15	12	45.12%		65	56	6.98%		127	15	11.63%
15	14	45.12%		65	121	6.98%		127	16	11.63%
15	18	44.65%		65	259	6.98%		127	30	11.63%
15	20	44.65%		65	40	6.98%		127	111	11.63%
15	19	44.65%		65	104	6.98%		127	81	11.16%
15	16	44.65%		65	32	6.98%		127	1	11.16%
15	13	44.65%		65	78	6.51%		127	294	11.16%
15	9	43.26%		65	79	6.51%		127	45	10.70%
15	22	42.79%		65	83	6.51%		127	18	10.70%
15	2	41.40%		65	122	6.51%		127	6	10.70%
15	11	41.40%		65	297	6.51%		127	25	10.70%
15	30	40.93%		65	85	6.05%		127	11	10.70%
15	29	40.47%		65	54	6.05%		127	110	10.70%
15	17	40.00%		65	98	5.58%		127	116	10.70%
15	26	38.14%		65	82	5.58%		127	22	10.23%
15	27	38.14%		65	120	5.12%		127	29	10.23%
15	37	37.67%		65	143	5.12%		127	43	10.23%
15	31	36.74%		65	105	4.65%		127	311	10.23%
15	310	32.09%		65	264	3.72%		127	46	10.23%
15	40	31.16%		65	119	3.72%		127	20	10.23%
15	311	30.70%		65	118	3.72%		127	28	9.77%
15	41	30.23%		65	33	3.72%		127	31	9.77%
15	34	29.30%		66	66	100.00%		127	27	9.77%
15	39	29.30%		66	109	35.35%		127	298	9.30%
15	312	29.30%		66	71	34.88%		127	296	9.30%
15	32	28.84%		66	70	33.49%		127	17	9.30%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
15	3	28.84%		66	124	28.84%		127	10	9.30%
15	43	28.84%		66	64	22.79%		127	314	9.30%
15	298	28.84%		66	76	21.40%		127	39	9.30%
15	313	28.84%		66	101	20.93%		127	21	9.30%
15	35	28.37%		66	77	19.53%		127	44	8.84%
15	69	27.44%		66	65	19.53%		127	37	8.84%
15	314	27.44%		66	131	18.60%		127	312	8.84%
15	36	26.98%		66	67	18.14%		127	313	8.84%
15	38	26.98%		66	102	18.14%		127	42	8.84%
15	42	25.12%		66	107	18.14%		127	8	8.84%
15	33	24.19%		66	117	17.67%		127	2	8.84%
15	153	23.26%		66	68	16.74%		127	14	8.84%
15	296	19.07%		66	89	16.28%		127	19	8.84%
15	294	17.21%		66	75	16.28%		127	24	8.84%
15	48	16.74%		66	80	15.35%		127	23	8.84%
15	45	15.35%		66	128	14.88%		127	41	8.84%
15	47	13.95%		66	74	14.42%		127	26	8.84%
15	124	13.49%		66	295	14.42%		127	36	8.84%
15	109	13.02%		66	127	14.42%		127	40	8.37%
15	71	12.56%		66	130	13.95%		127	13	8.37%
15	70	12.56%		66	45	13.95%		127	12	8.37%
15	62	12.56%		66	111	13.95%		127	310	8.37%
15	44	12.56%		66	129	13.49%		127	34	8.37%
15	46	12.09%		66	293	13.49%		127	48	7.91%
15	295	12.09%		66	132	12.09%		127	3	7.44%
15	297	12.09%		66	126	12.09%		127	56	7.44%
15	92	11.63%		66	81	11.63%		127	35	7.44%
15	56	11.63%		66	110	11.63%		127	38	7.44%
15	101	11.63%		66	44	11.63%		127	92	6.98%
15	259	11.63%		66	309	11.63%		127	98	6.98%
15	127	11.63%		66	294	11.63%		127	259	6.98%
15	293	11.63%		66	6	11.16%		127	32	6.98%
15	85	10.70%		66	11	11.16%		127	106	6.98%
15	76	10.70%		66	37	11.16%		127	104	6.98%
15	67	10.70%		66	35	11.16%		127	121	6.98%
15	65	10.23%		66	9	10.70%		127	153	6.51%
15	55	10.23%		66	28	10.70%		127	297	6.51%
15	64	10.23%		66	19	10.70%		127	55	6.05%
15	117	10.23%		66	1	10.23%		127	125	6.05%
15	104	10.23%		66	3	10.23%		127	62	5.58%
15	89	9.77%		66	10	10.23%		127	79	5.58%
15	66	9.77%		66	310	10.23%		127	78	5.58%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
15	80	9.77%		66	25	10.23%		127	85	5.58%
15	81	9.77%		66	31	10.23%		127	83	5.58%
15	78	9.77%		66	23	10.23%		127	84	5.58%
15	79	9.77%		66	24	10.23%		127	54	5.58%
15	68	9.77%		66	298	9.77%		127	33	5.12%
15	129	9.77%		66	15	9.77%		127	143	4.65%
15	128	9.77%		66	311	9.77%		127	120	4.65%
15	82	9.30%		66	17	9.77%		127	122	4.65%
15	77	9.30%		66	27	9.77%		127	103	4.65%
15	122	9.30%		66	16	9.77%		127	86	3.72%
15	111	9.30%		66	20	9.77%		127	238	3.72%
15	131	9.30%		66	14	9.77%		128	128	100.00%
15	110	9.30%		66	47	9.77%		128	129	50.23%
15	130	9.30%		66	116	9.77%		128	126	46.98%
15	125	9.30%		66	13	9.77%		128	131	21.40%
15	83	8.84%		66	92	9.30%		128	76	18.14%
15	107	8.84%		66	69	9.30%		128	101	17.67%
15	103	8.84%		66	7	9.30%		128	77	17.21%
15	132	8.84%		66	36	9.30%		128	102	17.21%
15	102	8.84%		66	41	9.30%		128	124	17.21%
15	98	7.91%		66	26	9.30%		128	107	16.74%
15	116	7.91%		66	22	9.30%		128	130	16.28%
15	75	7.44%		66	43	9.30%		128	64	15.81%
15	84	7.44%		66	30	9.30%		128	293	15.81%
15	121	7.44%		66	12	9.30%		128	68	15.35%
15	126	6.98%		66	153	9.30%		128	70	15.35%
15	105	6.98%		66	21	9.30%		128	109	15.35%
15	74	6.51%		66	314	8.84%		128	89	14.88%
15	120	6.51%		66	313	8.84%		128	66	14.88%
15	118	6.51%		66	312	8.84%		128	67	14.88%
15	143	6.51%		66	296	8.84%		128	117	14.88%
15	106	6.05%		66	29	8.84%		128	71	14.42%
15	119	6.05%		66	40	8.37%		128	65	14.42%
15	54	5.58%		66	48	8.37%		128	44	13.95%
15	86	5.12%		66	38	7.91%		128	132	13.95%
15	88	5.12%		66	259	7.91%		128	127	13.95%
16	16	100.00%		66	18	7.91%		128	80	13.49%
16	309	53.02%		66	39	7.91%		128	74	13.02%
16	25	48.37%		66	34	7.91%		128	81	12.56%
16	24	44.65%		66	32	7.91%		128	22	12.56%
16	15	44.65%		66	8	7.44%		128	1	12.09%
16	7	41.40%		66	2	7.44%		128	75	12.09%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
16	8	41.40%		66	46	7.44%		128	7	12.09%
16	28	41.40%		66	42	7.44%		128	8	11.63%
16	20	41.40%		66	33	6.98%		128	6	11.63%
16	9	40.93%		66	56	6.98%		128	45	11.63%
16	1	40.93%		66	121	6.51%		128	17	11.63%
16	13	40.47%		66	55	6.51%		128	295	11.16%
16	10	39.53%		66	84	6.05%		128	309	11.16%
16	23	39.53%		66	54	6.05%		128	27	11.16%
16	6	39.53%		66	83	5.58%		128	48	10.70%
16	14	39.53%		66	122	5.58%		128	259	10.70%
16	11	39.53%		66	143	5.58%		128	294	10.70%
16	18	39.07%		66	62	5.58%		128	28	10.70%
16	19	39.07%		66	104	5.58%		128	29	10.70%
16	21	38.60%		66	82	5.12%		128	310	10.70%
16	22	36.74%		66	79	5.12%		128	47	10.23%
16	30	36.74%		66	103	5.12%		128	20	10.23%
16	12	36.74%		66	98	4.65%		128	313	10.23%
16	2	36.28%		66	78	4.65%		128	26	10.23%
16	26	34.88%		66	85	4.65%		128	37	10.23%
16	17	33.49%		66	264	4.65%		128	14	9.77%
16	27	33.49%		66	297	4.65%		128	10	9.77%
16	29	33.49%		66	106	4.65%		128	23	9.77%
16	31	32.56%		66	120	4.19%		128	19	9.77%
16	37	32.56%		67	67	100.00%		128	25	9.77%
16	310	29.30%		67	68	79.07%		128	15	9.77%
16	311	28.84%		67	64	32.09%		128	2	9.77%
16	40	28.37%		67	124	25.58%		128	24	9.77%
16	312	27.44%		67	74	20.93%		128	18	9.77%
16	69	26.98%		67	107	20.93%		128	62	9.77%
16	32	26.51%		67	75	20.00%		128	30	9.77%
16	3	26.51%		67	76	20.00%		128	11	9.77%
16	39	26.51%		67	65	20.00%		128	3	9.77%
16	34	26.05%		67	130	19.07%		128	9	9.77%
16	313	25.58%		67	109	18.60%		128	36	9.77%
16	35	25.12%		67	77	18.14%		128	43	9.77%
16	41	24.65%		67	66	18.14%		128	111	9.77%
16	298	24.65%		67	70	17.67%		128	110	9.77%
16	43	24.19%		67	101	17.67%		128	92	9.30%
16	314	24.19%		67	117	17.21%		128	40	9.30%
16	38	23.26%		67	131	16.74%		128	12	9.30%
16	42	22.79%		67	71	16.28%		128	298	9.30%
16	36	22.79%		67	102	15.81%		128	31	9.30%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
16	153	22.33%		67	127	15.35%		128	103	9.30%
16	296	20.00%		67	132	15.35%		128	21	8.84%
16	33	19.53%		67	81	14.88%		128	16	8.84%
16	45	18.60%		67	128	14.88%		128	312	8.84%
16	294	17.21%		67	295	13.95%		128	69	8.84%
16	48	15.35%		67	129	13.95%		128	311	8.84%
16	47	13.02%		67	111	13.95%		128	39	8.84%
16	89	13.02%		67	80	13.49%		128	296	8.84%
16	62	13.02%		67	110	12.56%		128	34	8.84%
16	101	13.02%		67	89	11.63%		128	13	8.37%
16	124	13.02%		67	293	11.63%		128	41	8.37%
16	46	12.56%		67	45	11.63%		128	35	8.37%
16	109	12.56%		67	294	11.63%		128	32	8.37%
16	71	12.09%		67	15	10.70%		128	104	8.37%
16	297	12.09%		67	309	10.23%		128	314	7.91%
16	70	11.63%		67	126	10.23%		128	55	7.91%
16	44	11.63%		67	16	10.23%		128	42	7.91%
16	56	11.63%		67	21	9.77%		128	116	7.91%
16	117	11.63%		67	6	9.30%		128	38	7.44%
16	127	11.63%		67	23	9.30%		128	122	7.44%
16	259	11.63%		67	27	9.30%		128	121	7.44%
16	67	10.23%		67	30	9.30%		128	56	6.98%
16	116	10.23%		67	48	9.30%		128	143	6.98%
16	77	9.77%		67	25	9.30%		128	153	6.98%
16	80	9.77%		67	20	9.30%		128	79	6.51%
16	65	9.77%		67	13	9.30%		128	297	6.05%
16	66	9.77%		67	10	8.84%		128	33	6.05%
16	79	9.77%		67	14	8.84%		128	78	5.58%
16	107	9.77%		67	310	8.84%		128	46	5.58%
16	295	9.77%		67	28	8.84%		128	213	5.58%
16	293	9.77%		67	35	8.84%		128	83	5.12%
16	64	9.30%		67	62	8.84%		128	98	5.12%
16	78	9.30%		67	311	8.84%		128	120	5.12%
16	92	9.30%		67	43	8.84%		128	88	4.65%
16	76	9.30%		67	7	8.37%		128	54	4.65%
16	68	9.30%		67	2	8.37%		128	86	4.19%
16	129	9.30%		67	1	8.37%		128	251	3.72%
16	75	8.84%		67	69	8.37%		128	105	3.72%
16	128	8.84%		67	24	8.37%		128	125	3.72%
16	111	8.84%		67	312	8.37%		128	106	3.72%
16	103	8.84%		67	26	8.37%		129	129	100.00%
16	121	8.84%		67	19	8.37%		129	128	50.23%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
16	81	8.37%		67	22	8.37%		129	126	45.12%
16	104	8.37%		67	32	8.37%		129	124	19.53%
16	106	8.37%		67	314	8.37%		129	293	18.14%
16	131	8.37%		67	3	7.91%		129	131	17.67%
16	55	7.91%		67	92	7.91%		129	89	17.67%
16	110	7.91%		67	41	7.91%		129	71	17.21%
16	130	7.91%		67	12	7.91%		129	70	17.21%
16	85	7.44%		67	31	7.91%		129	102	17.21%
16	132	7.44%		67	313	7.91%		129	101	17.21%
16	102	7.44%		67	42	7.91%		129	109	16.74%
16	120	6.98%		67	38	7.91%		129	64	16.28%
16	122	6.98%		67	36	7.91%		129	76	15.81%
16	98	6.51%		67	298	7.91%		129	80	15.81%
16	82	6.51%		67	8	7.44%		129	132	15.35%
16	125	6.51%		67	9	7.44%		129	44	14.88%
16	83	6.05%		67	153	7.44%		129	77	14.88%
16	143	6.05%		67	11	7.44%		129	45	14.88%
16	126	5.58%		67	18	7.44%		129	127	14.88%
16	119	5.12%		67	56	7.44%		129	107	14.88%
16	118	5.12%		67	55	6.98%		129	117	14.88%
16	84	4.65%		67	47	6.98%		129	75	14.42%
16	105	4.65%		67	29	6.98%		129	130	14.42%
16	238	4.19%		67	17	6.98%		129	67	13.95%
16	138	3.72%		67	79	6.51%		129	66	13.49%
16	86	3.26%		67	121	6.51%		129	65	13.02%
17	17	100.00%		67	104	6.51%		129	68	13.02%
17	26	71.63%		67	103	6.51%		129	1	13.02%
17	309	47.44%		67	39	6.51%		129	7	12.09%
17	9	46.51%		67	40	6.51%		129	295	12.09%
17	27	45.58%		67	37	6.51%		129	81	12.09%
17	11	43.26%		67	296	6.51%		129	6	12.09%
17	7	42.79%		67	78	6.05%		129	22	11.63%
17	1	41.86%		67	44	6.05%		129	74	11.63%
17	8	41.40%		67	34	6.05%		129	294	11.63%
17	6	41.40%		67	259	6.05%		129	309	11.63%
17	30	40.93%		67	98	5.58%		129	17	11.63%
17	25	40.47%		67	122	5.58%		129	26	11.63%
17	15	40.00%		67	120	5.58%		129	13	11.16%
17	24	38.60%		67	84	5.12%		129	110	11.16%
17	28	37.21%		67	116	5.12%		129	8	10.70%
17	37	36.74%		67	106	5.12%		129	27	10.70%
17	12	36.74%		67	125	5.12%		129	19	10.70%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
17	31	36.28%		67	82	4.65%		129	28	10.70%
17	18	35.81%		67	83	4.65%		129	25	10.70%
17	22	34.88%		67	251	4.65%		129	31	10.70%
17	20	34.88%		67	297	4.19%		129	9	10.70%
17	2	33.49%		67	105	3.72%		129	3	10.70%
17	16	33.49%		67	118	3.72%		129	111	10.70%
17	23	33.02%		67	119	3.72%		129	47	10.23%
17	10	32.56%		67	143	3.72%		129	18	10.23%
17	14	32.56%		67	174	3.26%		129	14	10.23%
17	310	32.56%		67	238	3.26%		129	23	10.23%
17	21	31.63%		68	68	100.00%		129	21	10.23%
17	13	31.63%		68	67	79.07%		129	11	10.23%
17	29	31.16%		68	64	30.70%		129	30	10.23%
17	19	30.23%		68	124	23.26%		129	55	10.23%
17	311	30.23%		68	74	20.93%		129	310	10.23%
17	41	29.77%		68	65	20.47%		129	15	9.77%
17	35	29.30%		68	75	20.00%		129	10	9.77%
17	39	29.30%		68	107	20.00%		129	2	9.77%
17	312	28.84%		68	76	19.53%		129	20	9.77%
17	34	28.37%		68	130	18.60%		129	41	9.77%
17	40	28.37%		68	77	17.67%		129	311	9.77%
17	32	27.44%		68	66	16.74%		129	39	9.77%
17	38	27.44%		68	109	16.74%		129	16	9.30%
17	314	27.44%		68	101	16.28%		129	29	9.30%
17	3	26.98%		68	131	16.28%		129	12	9.30%
17	42	26.51%		68	117	16.28%		129	313	9.30%
17	313	26.05%		68	70	15.81%		129	37	9.30%
17	43	25.12%		68	71	15.35%		129	62	9.30%
17	36	24.65%		68	102	15.35%		129	298	9.30%
17	33	24.19%		68	128	15.35%		129	116	9.30%
17	298	24.19%		68	132	14.88%		129	48	8.84%
17	69	23.72%		68	127	14.42%		129	92	8.84%
17	153	22.33%		68	81	13.02%		129	69	8.84%
17	296	18.60%		68	129	13.02%		129	34	8.84%
17	294	15.81%		68	111	12.56%		129	79	8.84%
17	259	15.81%		68	295	12.09%		129	259	8.37%
17	45	13.95%		68	45	11.63%		129	24	8.37%
17	48	13.02%		68	126	11.63%		129	43	8.37%
17	46	12.09%		68	89	11.16%		129	36	8.37%
17	62	11.63%		68	80	11.16%		129	35	8.37%
17	92	11.63%		68	294	11.16%		129	122	8.37%
17	76	11.63%		68	293	10.70%		129	121	8.37%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
17	128	11.63%		68	110	10.23%		129	312	7.91%
17	129	11.63%		68	15	9.77%		129	40	7.91%
17	107	11.63%		68	6	9.30%		129	78	7.91%
17	295	11.63%		68	311	9.30%		129	104	7.91%
17	130	11.63%		68	25	9.30%		129	46	7.44%
17	70	11.16%		68	309	9.30%		129	297	7.44%
17	56	11.16%		68	43	9.30%		129	56	7.44%
17	55	11.16%		68	16	9.30%		129	314	7.44%
17	117	11.16%		68	1	8.84%		129	42	7.44%
17	293	11.16%		68	310	8.84%		129	153	7.44%
17	124	11.16%		68	20	8.84%		129	143	7.44%
17	71	10.70%		68	314	8.84%		129	32	7.44%
17	103	10.70%		68	27	8.37%		129	103	7.44%
17	77	10.23%		68	30	8.37%		129	38	6.98%
17	78	10.23%		68	48	8.37%		129	83	6.98%
17	83	10.23%		68	312	8.37%		129	33	6.51%
17	79	10.23%		68	62	8.37%		129	296	6.51%
17	66	9.77%		68	42	8.37%		129	82	6.05%
17	81	9.77%		68	22	8.37%		129	85	6.05%
17	109	9.77%		68	38	8.37%		129	84	6.05%
17	111	9.77%		68	7	7.91%		129	213	5.58%
17	132	9.77%		68	3	7.91%		129	120	5.58%
17	47	9.30%		68	2	7.91%		129	98	4.65%
17	127	9.30%		68	92	7.91%		129	88	4.65%
17	297	9.30%		68	103	7.91%		129	54	4.65%
17	131	9.30%		68	21	7.91%		129	251	4.19%
17	126	9.30%		68	153	7.91%		129	125	4.19%
17	75	8.84%		68	28	7.91%		129	174	3.72%
17	101	8.84%		68	26	7.91%		129	106	3.72%
17	104	8.84%		68	35	7.91%		129	105	3.72%
17	106	8.84%		68	313	7.91%		129	119	3.26%
17	82	8.37%		68	69	7.44%		130	130	100.00%
17	65	8.37%		68	14	7.44%		130	132	50.23%
17	64	8.37%		68	24	7.44%		130	131	33.95%
17	44	8.37%		68	19	7.44%		130	64	20.47%
17	122	8.37%		68	41	7.44%		130	124	20.47%
17	121	8.37%		68	18	7.44%		130	67	19.07%
17	102	8.37%		68	298	7.44%		130	109	19.07%
17	110	8.37%		68	56	7.44%		130	76	18.60%
17	89	7.91%		68	36	7.44%		130	293	18.60%
17	125	7.91%		68	13	7.44%		130	71	18.60%
17	116	7.91%		68	8	6.98%		130	68	18.60%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
17	143	7.91%		68	9	6.98%		130	70	17.67%
17	80	7.44%		68	10	6.98%		130	107	17.67%
17	67	6.98%		68	11	6.98%		130	65	17.21%
17	68	6.98%		68	23	6.98%		130	80	17.21%
17	84	6.98%		68	39	6.98%		130	127	17.21%
17	85	6.51%		68	55	6.98%		130	77	16.28%
17	74	6.05%		68	47	6.98%		130	128	16.28%
17	120	6.05%		68	31	6.98%		130	89	14.42%
17	98	5.58%		68	17	6.98%		130	129	14.42%
17	105	5.58%		68	37	6.98%		130	66	13.95%
17	119	5.58%		68	32	6.98%		130	81	13.95%
17	118	5.58%		68	79	6.51%		130	117	13.95%
17	54	4.65%		68	296	6.51%		130	74	13.49%
17	251	4.19%		68	78	6.05%		130	75	13.02%
17	174	3.26%		68	34	6.05%		130	102	13.02%
18	18	100.00%		68	12	6.05%		130	101	12.56%
18	22	63.26%		68	259	6.05%		130	126	12.56%
18	2	60.47%		68	40	6.05%		130	111	12.09%
18	309	53.95%		68	104	5.58%		130	17	11.63%
18	6	53.49%		68	121	5.58%		130	295	11.63%
18	1	53.02%		68	120	5.58%		130	45	11.16%
18	7	52.09%		68	29	5.58%		130	44	11.16%
18	8	52.09%		68	84	5.12%		130	110	11.16%
18	24	45.12%		68	122	5.12%		130	26	10.70%
18	15	44.65%		68	44	5.12%		130	309	10.70%
18	12	44.19%		68	125	5.12%		130	28	10.23%
18	29	41.40%		68	82	4.65%		130	7	9.77%
18	16	39.07%		68	98	4.65%		130	9	9.77%
18	9	38.60%		68	106	4.65%		130	30	9.77%
18	25	38.60%		68	83	4.19%		130	310	9.77%
18	11	38.14%		68	116	4.19%		130	27	9.77%
18	28	37.67%		68	33	4.19%		130	69	9.77%
18	30	36.74%		68	105	3.72%		130	11	9.77%
18	26	36.74%		68	143	3.72%		130	116	9.77%
18	20	36.28%		68	251	3.26%		130	47	9.30%
18	27	35.81%		68	297	3.26%		130	43	9.30%
18	17	35.81%		68	119	3.26%		130	15	9.30%
18	13	34.88%		69	69	100.00%		130	8	9.30%
18	10	34.42%		69	309	33.49%		130	48	9.30%
18	23	34.42%		69	9	33.02%		130	21	9.30%
18	21	33.95%		69	11	32.09%		130	311	9.30%
18	19	33.49%		69	28	30.23%		130	37	9.30%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
18	14	33.49%		69	27	30.23%		130	22	8.84%
18	37	32.09%		69	7	29.30%		130	24	8.84%
18	31	30.70%		69	20	29.30%		130	13	8.84%
18	311	27.91%		69	30	29.30%		130	2	8.84%
18	35	27.44%		69	2	28.84%		130	29	8.37%
18	69	27.44%		69	25	28.37%		130	14	8.37%
18	310	27.44%		69	8	27.44%		130	23	8.37%
18	40	26.98%		69	22	27.44%		130	10	8.37%
18	39	26.51%		69	18	27.44%		130	19	8.37%
18	312	26.05%		69	15	27.44%		130	313	8.37%
18	34	25.58%		69	1	26.98%		130	312	8.37%
18	313	25.12%		69	16	26.98%		130	259	8.37%
18	43	24.65%		69	31	26.98%		130	42	8.37%
18	41	24.65%		69	6	26.51%		130	39	8.37%
18	3	24.65%		69	37	26.51%		130	16	7.91%
18	314	24.65%		69	310	26.51%		130	298	7.91%
18	42	24.19%		69	13	26.51%		130	12	7.91%
18	38	24.19%		69	24	26.05%		130	25	7.91%
18	298	23.72%		69	311	26.05%		130	18	7.91%
18	36	22.79%		69	26	25.58%		130	31	7.91%
18	32	22.33%		69	40	25.58%		130	40	7.91%
18	33	20.47%		69	21	25.58%		130	92	7.91%
18	45	19.07%		69	296	24.65%		130	6	7.91%
18	153	19.07%		69	19	24.65%		130	32	7.91%
18	294	18.60%		69	10	24.19%		130	153	7.44%
18	296	18.14%		69	29	24.19%		130	36	7.44%
18	71	14.42%		69	14	24.19%		130	35	7.44%
18	48	14.42%		69	23	24.19%		130	3	7.44%
18	44	13.49%		69	17	23.72%		130	297	7.44%
18	259	12.56%		69	32	23.26%		130	294	6.98%
18	70	12.09%		69	12	23.26%		130	20	6.98%
18	109	12.09%		69	35	23.26%		130	41	6.98%
18	297	11.63%		69	39	23.26%		130	314	6.98%
18	83	11.16%		69	41	22.79%		130	1	6.98%
18	46	11.16%		69	312	22.79%		130	125	6.98%
18	47	10.70%		69	3	22.33%		130	62	6.51%
18	127	10.70%		69	298	21.86%		130	38	6.51%
18	85	10.23%		69	294	21.86%		130	296	6.51%
18	89	10.23%		69	36	20.93%		130	55	6.51%
18	56	10.23%		69	56	20.93%		130	34	6.05%
18	129	10.23%		69	42	20.93%		130	98	6.05%
18	128	9.77%		69	313	20.93%		130	106	6.05%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
18	124	9.77%		69	34	20.47%		130	56	5.58%
18	84	9.30%		69	314	20.00%		130	251	5.58%
18	79	9.30%		69	33	19.53%		130	46	5.58%
18	117	9.30%		69	43	19.07%		130	79	5.12%
18	111	9.30%		69	153	19.07%		130	143	5.12%
18	65	8.84%		69	38	18.60%		130	54	4.65%
18	62	8.84%		69	77	16.74%		130	83	4.65%
18	295	8.84%		69	107	16.74%		130	78	4.65%
18	293	8.84%		69	45	16.74%		130	104	4.65%
18	102	8.84%		69	47	16.28%		130	120	4.65%
18	132	8.84%		69	48	15.81%		130	105	4.65%
18	82	8.37%		69	92	15.35%		130	103	4.65%
18	76	8.37%		69	76	14.88%		130	33	4.19%
18	64	8.37%		69	259	14.88%		130	238	4.19%
18	77	8.37%		69	102	14.42%		130	121	4.19%
18	92	8.37%		69	62	14.42%		130	119	4.19%
18	55	8.37%		69	65	13.95%		130	138	3.72%
18	107	8.37%		69	44	13.02%		130	122	3.72%
18	81	7.91%		69	124	13.02%		130	118	3.72%
18	66	7.91%		69	79	12.56%		131	131	100.00%
18	78	7.91%		69	295	12.56%		131	130	33.95%
18	101	7.91%		69	74	12.09%		131	132	28.84%
18	131	7.91%		69	89	12.09%		131	124	22.79%
18	110	7.91%		69	293	12.09%		131	109	22.79%
18	130	7.91%		69	127	12.09%		131	70	22.33%
18	143	7.91%		69	55	12.09%		131	71	21.86%
18	68	7.44%		69	101	12.09%		131	128	21.40%
18	67	7.44%		69	46	12.09%		131	76	20.93%
18	80	7.44%		69	78	11.63%		131	64	20.47%
18	104	7.44%		69	64	11.63%		131	77	20.00%
18	121	7.44%		69	297	11.63%		131	80	19.07%
18	126	7.44%		69	83	11.16%		131	293	19.07%
18	75	6.98%		69	75	11.16%		131	66	18.60%
18	103	6.98%		69	80	11.16%		131	65	17.67%
18	98	6.51%		69	117	11.16%		131	107	17.67%
18	122	6.51%		69	109	11.16%		131	129	17.67%
18	116	6.51%		69	82	10.70%		131	127	17.21%
18	74	6.05%		69	81	10.70%		131	67	16.74%
18	105	6.05%		69	111	10.70%		131	68	16.28%
18	120	6.05%		69	71	10.23%		131	126	16.28%
18	125	6.05%		69	131	10.23%		131	295	15.81%
18	119	5.58%		69	103	10.23%		131	89	15.35%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
18	118	5.58%		69	98	9.77%		131	81	15.35%
18	54	5.12%		69	70	9.77%		131	102	15.35%
18	106	4.65%		69	126	9.77%		131	117	15.35%
18	174	4.19%		69	121	9.77%		131	111	14.88%
18	90	3.72%		69	130	9.77%		131	101	14.88%
18	88	3.72%		69	85	9.30%		131	75	14.42%
18	251	3.72%		69	66	9.30%		131	74	13.95%
18	86	3.26%		69	116	9.30%		131	45	13.49%
19	19	100.00%		69	104	8.84%		131	44	13.02%
19	14	98.14%		69	129	8.84%		131	11	11.63%
19	23	97.67%		69	128	8.84%		131	110	11.63%
19	10	96.74%		69	110	8.84%		131	7	11.16%
19	21	91.16%		69	125	8.37%		131	9	11.16%
19	13	84.65%		69	67	8.37%		131	8	10.70%
19	309	46.51%		69	122	7.91%		131	6	10.70%
19	15	44.65%		69	84	7.44%		131	1	10.70%
19	8	40.93%		69	68	7.44%		131	14	10.23%
19	25	40.00%		69	106	7.44%		131	92	10.23%
19	24	40.00%		69	54	7.44%		131	69	10.23%
19	1	39.53%		69	132	7.44%		131	22	10.23%
19	16	39.07%		69	120	6.98%		131	36	10.23%
19	6	38.60%		69	143	6.51%		131	116	10.23%
19	7	38.14%		69	119	5.58%		131	47	9.77%
19	11	36.28%		69	118	5.12%		131	309	9.77%
19	20	35.35%		69	105	5.12%		131	12	9.77%
19	9	34.42%		70	70	100.00%		131	28	9.77%
19	18	33.49%		70	109	87.91%		131	298	9.77%
19	30	33.02%		70	71	74.42%		131	21	9.30%
19	12	33.02%		70	66	33.49%		131	25	9.30%
19	22	32.56%		70	124	31.16%		131	26	9.30%
19	26	32.56%		70	76	24.19%		131	15	9.30%
19	2	32.09%		70	101	24.19%		131	23	9.30%
19	29	31.63%		70	65	22.79%		131	10	9.30%
19	28	31.63%		70	77	22.33%		131	17	9.30%
19	27	30.70%		70	64	22.33%		131	20	9.30%
19	17	30.23%		70	131	22.33%		131	48	8.84%
19	31	27.91%		70	107	21.40%		131	19	8.84%
19	310	25.58%		70	295	20.00%		131	13	8.84%
19	37	24.65%		70	117	19.53%		131	296	8.84%
19	69	24.65%		70	102	18.60%		131	37	8.84%
19	311	24.19%		70	80	18.14%		131	54	8.37%
19	3	23.72%		70	111	18.14%		131	27	8.37%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
19	39	23.26%		70	293	18.14%		131	259	8.37%
19	35	22.79%		70	81	17.67%		131	294	8.37%
19	314	22.79%		70	89	17.67%		131	16	8.37%
19	41	22.33%		70	67	17.67%		131	2	7.91%
19	38	22.33%		70	130	17.67%		131	18	7.91%
19	312	22.33%		70	129	17.21%		131	310	7.91%
19	32	21.86%		70	127	17.21%		131	313	7.91%
19	43	21.86%		70	68	15.81%		131	30	7.91%
19	40	21.86%		70	128	15.35%		131	31	7.91%
19	313	21.86%		70	75	13.95%		131	312	7.91%
19	34	21.40%		70	126	13.95%		131	43	7.91%
19	298	21.40%		70	132	13.95%		131	314	7.44%
19	36	20.00%		70	309	13.95%		131	24	7.44%
19	42	19.53%		70	27	13.95%		131	29	7.44%
19	153	17.67%		70	1	13.49%		131	35	7.44%
19	33	16.74%		70	74	13.49%		131	153	7.44%
19	296	15.35%		70	25	13.49%		131	56	7.44%
19	294	14.42%		70	45	13.49%		131	311	6.98%
19	48	13.95%		70	294	13.49%		131	3	6.98%
19	117	13.02%		70	9	13.02%		131	106	6.98%
19	45	12.09%		70	110	13.02%		131	143	6.51%
19	124	12.09%		70	7	12.56%		131	83	6.51%
19	71	11.63%		70	8	12.56%		131	38	6.51%
19	101	11.63%		70	15	12.56%		131	42	6.51%
19	47	11.16%		70	30	12.56%		131	297	6.51%
19	70	10.70%		70	20	12.56%		131	32	6.51%
19	89	10.70%		70	6	12.09%		131	40	6.05%
19	66	10.70%		70	28	12.09%		131	39	6.05%
19	129	10.70%		70	18	12.09%		131	41	6.05%
19	62	9.77%		70	11	12.09%		131	62	6.05%
19	65	9.77%		70	2	11.63%		131	103	6.05%
19	55	9.77%		70	296	11.63%		131	264	5.58%
19	109	9.77%		70	16	11.63%		131	121	5.58%
19	128	9.77%		70	22	11.63%		131	125	5.58%
19	259	9.77%		70	17	11.16%		131	55	5.12%
19	297	9.77%		70	153	11.16%		131	33	5.12%
19	46	9.30%		70	116	11.16%		131	98	5.12%
19	295	9.30%		70	310	11.16%		131	34	5.12%
19	132	9.30%		70	35	11.16%		131	120	5.12%
19	293	9.30%		70	13	11.16%		131	122	5.12%
19	80	8.84%		70	3	10.70%		131	104	5.12%
19	92	8.84%		70	19	10.70%		131	251	4.65%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
19	77	8.84%		70	24	10.70%		131	79	4.19%
19	111	8.84%		70	311	10.70%		131	84	4.19%
19	131	8.84%		70	34	10.70%		131	78	4.19%
19	104	8.84%		70	10	10.23%		131	46	4.19%
19	127	8.84%		70	14	10.23%		131	82	3.72%
19	76	8.37%		70	23	10.23%		131	105	3.72%
19	44	8.37%		70	26	10.23%		132	132	100.00%
19	67	8.37%		70	314	10.23%		132	130	50.23%
19	64	8.37%		70	40	10.23%		132	131	28.84%
19	56	8.37%		70	29	10.23%		132	65	18.14%
19	107	8.37%		70	38	10.23%		132	124	17.67%
19	130	8.37%		70	39	10.23%		132	64	16.74%
19	81	7.91%		70	41	10.23%		132	76	16.74%
19	78	7.91%		70	31	10.23%		132	107	15.81%
19	110	7.91%		70	37	10.23%		132	67	15.35%
19	79	7.44%		70	21	9.77%		132	129	15.35%
19	68	7.44%		70	313	9.77%		132	68	14.88%
19	121	7.44%		70	69	9.77%		132	77	14.42%
19	122	7.44%		70	56	9.77%		132	71	13.95%
19	116	7.44%		70	48	9.30%		132	70	13.95%
19	102	7.44%		70	12	8.84%		132	128	13.95%
19	103	6.98%		70	43	8.84%		132	293	13.49%
19	143	6.51%		70	312	8.84%		132	109	13.49%
19	75	6.05%		70	47	8.84%		132	75	13.02%
19	74	6.05%		70	44	8.37%		132	127	13.02%
19	126	6.05%		70	298	8.37%		132	126	13.02%
19	82	5.58%		70	46	8.37%		132	295	12.56%
19	85	5.58%		70	42	8.37%		132	74	12.56%
19	98	5.58%		70	32	8.37%		132	117	12.56%
19	125	5.58%		70	92	7.91%		132	66	12.09%
19	120	5.58%		70	62	7.91%		132	81	12.09%
19	54	5.12%		70	36	7.91%		132	80	11.63%
19	83	4.65%		70	121	7.91%		132	101	11.16%
19	86	4.65%		70	104	7.44%		132	89	10.70%
19	105	4.65%		70	143	6.98%		132	309	10.70%
19	106	4.65%		70	259	6.98%		132	102	10.70%
19	90	3.26%		70	106	6.98%		132	14	10.23%
19	119	3.26%		70	84	6.05%		132	21	10.23%
20	20	100.00%		70	103	6.05%		132	25	10.23%
20	309	51.63%		70	78	5.58%		132	11	10.23%
20	28	48.84%		70	79	5.58%		132	28	10.23%
20	15	44.65%		70	33	5.58%		132	111	10.23%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
20	24	41.40%		70	55	5.58%		132	10	9.77%
20	25	41.40%		70	83	5.12%		132	310	9.77%
20	11	41.40%		70	122	5.12%		132	8	9.77%
20	16	41.40%		70	54	5.12%		132	26	9.77%
20	6	40.93%		70	251	5.12%		132	17	9.77%
20	1	40.47%		70	297	4.65%		132	19	9.30%
20	30	40.47%		70	98	4.19%		132	23	9.30%
20	9	40.00%		70	119	4.19%		132	30	9.30%
20	7	39.53%		70	118	4.19%		132	31	9.30%
20	8	38.60%		70	125	4.19%		132	6	9.30%
20	29	36.74%		70	88	3.72%		132	110	9.30%
20	10	36.28%		70	105	3.72%		132	44	8.84%
20	23	36.28%		70	238	3.72%		132	13	8.84%
20	2	36.28%		71	71	100.00%		132	3	8.84%
20	13	36.28%		71	109	74.88%		132	311	8.84%
20	18	36.28%		71	70	74.42%		132	15	8.84%
20	14	35.81%		71	66	34.88%		132	22	8.84%
20	37	35.35%		71	124	32.56%		132	18	8.84%
20	21	35.35%		71	76	24.19%		132	9	8.84%
20	19	35.35%		71	101	23.26%		132	27	8.84%
20	17	34.88%		71	77	21.86%		132	45	8.84%
20	12	34.88%		71	131	21.86%		132	12	8.84%
20	26	33.95%		71	64	21.40%		132	24	8.84%
20	27	33.95%		71	107	20.93%		132	7	8.37%
20	22	33.49%		71	65	20.93%		132	39	8.37%
20	31	33.02%		71	293	20.00%		132	1	8.37%
20	312	33.02%		71	295	19.53%		132	37	8.37%
20	310	31.63%		71	117	19.07%		132	2	8.37%
20	311	31.63%		71	80	18.60%		132	35	7.91%
20	313	31.63%		71	102	18.60%		132	48	7.91%
20	35	30.70%		71	130	18.60%		132	42	7.44%
20	38	30.23%		71	81	18.14%		132	20	7.44%
20	314	30.23%		71	89	17.21%		132	47	7.44%
20	298	30.23%		71	129	17.21%		132	41	7.44%
20	3	29.77%		71	127	17.21%		132	16	7.44%
20	39	29.30%		71	67	16.28%		132	259	7.44%
20	69	29.30%		71	126	16.28%		132	69	7.44%
20	32	28.84%		71	74	15.81%		132	32	7.44%
20	40	28.84%		71	68	15.35%		132	298	6.98%
20	43	28.84%		71	9	14.88%		132	40	6.98%
20	36	28.84%		71	27	14.88%		132	29	6.98%
20	41	28.37%		71	11	14.88%		132	36	6.98%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
20	34	27.44%		71	128	14.42%		132	54	6.98%
20	42	26.51%		71	18	14.42%		132	314	6.51%
20	153	23.26%		71	110	14.42%		132	34	6.51%
20	33	21.86%		71	111	14.42%		132	83	6.51%
20	296	20.47%		71	309	14.42%		132	38	6.51%
20	294	18.60%		71	22	14.42%		132	296	6.51%
20	45	18.14%		71	20	14.42%		132	297	6.51%
20	46	15.81%		71	314	14.42%		132	46	6.51%
20	47	15.35%		71	1	13.95%		132	125	6.51%
20	48	15.35%		71	132	13.95%		132	43	6.05%
20	71	14.42%		71	294	13.95%		132	56	6.05%
20	62	13.95%		71	35	13.95%		132	116	6.05%
20	65	13.49%		71	75	13.49%		132	312	5.58%
20	297	13.49%		71	7	13.49%		132	313	5.58%
20	56	13.02%		71	45	13.49%		132	294	5.58%
20	109	13.02%		71	25	13.49%		132	62	5.58%
20	70	12.56%		71	310	13.49%		132	153	5.12%
20	44	12.56%		71	311	13.49%		132	92	5.12%
20	124	12.56%		71	30	13.49%		132	143	5.12%
20	293	12.56%		71	38	13.49%		132	251	5.12%
20	259	12.56%		71	6	13.02%		132	98	5.12%
20	98	11.63%		71	3	13.02%		132	121	5.12%
20	76	11.63%		71	31	13.02%		132	55	4.65%
20	92	11.63%		71	28	13.02%		132	104	4.65%
20	104	11.63%		71	8	12.56%		132	106	4.65%
20	101	11.63%		71	15	12.56%		132	78	4.19%
20	79	11.16%		71	14	12.56%		132	79	4.19%
20	55	10.23%		71	10	12.09%		132	105	4.19%
20	128	10.23%		71	16	12.09%		132	174	3.72%
20	107	10.23%		71	153	12.09%		132	238	3.72%
20	117	10.23%		71	312	12.09%		132	120	3.26%
20	127	10.23%		71	2	11.63%		132	119	3.26%
20	75	9.77%		71	296	11.63%		133	133	100.00%
20	64	9.77%		71	37	11.63%		133	287	12.56%
20	78	9.77%		71	298	11.63%		133	237	5.12%
20	66	9.77%		71	313	11.63%		133	200	4.19%
20	85	9.77%		71	19	11.63%		133	222	3.72%
20	121	9.77%		71	23	11.63%		133	236	3.72%
20	129	9.77%		71	24	11.63%		134	134	100.00%
20	77	9.30%		71	41	11.63%		134	169	55.35%
20	82	9.30%		71	13	11.63%		134	249	7.44%
20	80	9.30%		71	26	11.16%		134	219	5.12%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
20	67	9.30%		71	36	11.16%		134	161	3.26%
20	131	9.30%		71	21	11.16%		134	217	3.26%
20	125	9.30%		71	34	11.16%		135	135	100.00%
20	83	8.84%		71	40	11.16%		135	168	48.37%
20	68	8.84%		71	17	10.70%		136	136	100.00%
20	89	8.84%		71	39	10.70%		136	192	33.95%
20	84	8.84%		71	12	10.23%		136	236	8.37%
20	102	8.84%		71	29	10.23%		136	237	7.44%
20	120	8.84%		71	69	10.23%		137	137	100.00%
20	143	8.84%		71	43	10.23%		137	145	15.35%
20	295	8.37%		71	48	10.23%		137	243	5.58%
20	103	8.37%		71	56	10.23%		137	179	4.19%
20	74	7.91%		71	92	9.77%		138	138	100.00%
20	126	7.91%		71	47	9.77%		138	22	3.72%
20	122	7.91%		71	116	9.77%		138	310	3.72%
20	110	7.91%		71	44	9.77%		138	311	3.72%
20	132	7.44%		71	32	9.77%		138	6	3.72%
20	106	7.44%		71	42	9.77%		138	26	3.72%
20	81	6.98%		71	62	9.30%		138	16	3.72%
20	54	6.98%		71	121	9.30%		138	130	3.72%
20	130	6.98%		71	259	8.84%		138	124	3.26%
20	116	6.51%		71	104	8.84%		138	294	2.79%
20	111	6.05%		71	46	6.98%		139	139	100.00%
20	118	5.58%		71	103	6.98%		139	164	28.84%
20	119	5.58%		71	98	6.51%		140	140	100.00%
20	105	5.12%		71	84	6.05%		141	141	100.00%
20	86	3.72%		71	83	6.05%		141	208	5.58%
21	21	100.00%		71	33	6.05%		141	284	4.65%
21	14	91.63%		71	143	6.05%		142	142	100.00%
21	19	91.16%		71	78	5.58%		142	58	39.07%
21	23	90.70%		71	55	5.58%		142	108	29.30%
21	10	90.70%		71	122	5.58%		142	91	26.51%
21	13	84.65%		71	54	5.58%		142	61	25.58%
21	309	46.51%		71	106	5.58%		142	52	25.58%
21	15	45.58%		71	79	5.12%		142	53	25.12%
21	8	42.79%		71	297	5.12%		142	50	25.12%
21	24	40.93%		71	125	4.65%		142	49	24.65%
21	1	40.47%		71	251	4.65%		142	60	24.19%
21	25	40.00%		71	119	4.19%		142	57	23.72%
21	6	39.53%		71	264	3.72%		142	97	20.93%
21	7	39.07%		71	105	3.72%		142	96	20.47%
21	16	38.60%		71	118	3.26%		142	63	19.07%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
21	20	35.35%		72	72	100.00%		142	95	18.60%
21	11	35.35%		72	197	57.67%		142	59	11.16%
21	12	35.35%		72	221	6.05%		142	303	10.70%
21	2	34.42%		72	248	3.26%		142	306	9.77%
21	29	33.95%		73	73	100.00%		142	308	9.77%
21	9	33.95%		74	74	100.00%		142	305	9.30%
21	30	33.95%		74	75	37.21%		142	307	9.30%
21	18	33.95%		74	64	35.81%		142	301	9.30%
21	22	33.02%		74	67	20.93%		142	300	8.84%
21	26	32.56%		74	68	20.93%		142	304	8.84%
21	28	32.56%		74	124	18.14%		142	302	7.91%
21	27	31.63%		74	101	17.21%		142	299	6.98%
21	17	31.63%		74	65	16.74%		142	51	6.51%
21	37	27.44%		74	71	15.81%		142	159	3.72%
21	31	27.44%		74	117	15.81%		142	246	3.72%
21	310	26.05%		74	77	15.35%		142	193	3.72%
21	69	25.58%		74	89	14.42%		142	224	3.26%
21	311	25.12%		74	66	14.42%		143	143	100.00%
21	3	24.65%		74	131	13.95%		143	30	10.23%
21	312	24.65%		74	107	13.95%		143	11	9.30%
21	313	24.19%		74	109	13.49%		143	31	8.84%
21	40	23.72%		74	130	13.49%		143	20	8.84%
21	32	23.26%		74	70	13.49%		143	1	8.84%
21	39	23.26%		74	293	13.49%		143	25	8.84%
21	41	23.26%		74	76	13.02%		143	45	8.37%
21	38	23.26%		74	128	13.02%		143	26	8.37%
21	314	23.26%		74	127	13.02%		143	44	8.37%
21	35	22.79%		74	102	12.56%		143	309	8.37%
21	43	22.79%		74	132	12.56%		143	28	8.37%
21	34	22.79%		74	295	12.56%		143	8	8.37%
21	298	22.79%		74	69	12.09%		143	9	8.37%
21	36	21.40%		74	80	11.63%		143	78	7.91%
21	42	20.47%		74	129	11.63%		143	297	7.91%
21	153	17.67%		74	81	11.16%		143	17	7.91%
21	33	17.21%		74	111	10.70%		143	6	7.91%
21	294	14.88%		74	309	9.77%		143	24	7.91%
21	48	14.42%		74	47	9.30%		143	22	7.91%
21	296	14.42%		74	126	9.30%		143	310	7.91%
21	117	12.56%		74	110	9.30%		143	18	7.91%
21	101	12.09%		74	92	8.84%		143	29	7.91%
21	47	11.63%		74	25	8.84%		143	7	7.91%
21	71	11.16%		74	153	8.84%		143	79	7.44%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
21	45	11.16%		74	27	8.84%		143	62	7.44%
21	124	10.70%		74	6	8.37%		143	12	7.44%
21	89	10.23%		74	43	8.37%		143	41	7.44%
21	92	10.23%		74	298	8.37%		143	296	7.44%
21	297	10.23%		74	36	7.91%		143	37	7.44%
21	132	10.23%		74	44	7.91%		143	126	7.44%
21	129	10.23%		74	310	7.91%		143	129	7.44%
21	70	9.77%		74	20	7.91%		143	109	7.44%
21	67	9.77%		74	294	7.91%		143	77	6.98%
21	80	9.77%		74	9	7.44%		143	70	6.98%
21	44	9.77%		74	8	7.44%		143	259	6.98%
21	65	9.77%		74	313	7.44%		143	153	6.98%
21	259	9.77%		74	30	7.44%		143	56	6.98%
21	62	9.30%		74	11	7.44%		143	2	6.98%
21	66	9.30%		74	38	7.44%		143	47	6.98%
21	77	9.30%		74	314	7.44%		143	314	6.98%
21	55	9.30%		74	3	6.98%		143	312	6.98%
21	56	9.30%		74	7	6.98%		143	14	6.98%
21	109	9.30%		74	28	6.98%		143	10	6.98%
21	131	9.30%		74	312	6.98%		143	48	6.98%
21	293	9.30%		74	22	6.98%		143	27	6.98%
21	127	9.30%		74	12	6.98%		143	39	6.98%
21	130	9.30%		74	37	6.98%		143	128	6.98%
21	76	8.84%		74	1	6.51%		143	102	6.98%
21	64	8.84%		74	15	6.51%		143	36	6.51%
21	46	8.84%		74	35	6.51%		143	46	6.51%
21	128	8.84%		74	311	6.51%		143	294	6.51%
21	111	8.84%		74	21	6.51%		143	13	6.51%
21	295	8.84%		74	40	6.51%		143	21	6.51%
21	116	8.84%		74	29	6.51%		143	40	6.51%
21	68	7.91%		74	13	6.51%		143	313	6.51%
21	81	7.44%		74	98	6.05%		143	19	6.51%
21	125	7.44%		74	103	6.05%		143	15	6.51%
21	104	7.44%		74	296	6.05%		143	38	6.51%
21	122	7.44%		74	18	6.05%		143	42	6.51%
21	102	7.44%		74	19	6.05%		143	23	6.51%
21	78	6.98%		74	17	6.05%		143	69	6.51%
21	79	6.98%		74	41	6.05%		143	32	6.51%
21	110	6.98%		74	24	6.05%		143	124	6.51%
21	74	6.51%		74	46	6.05%		143	131	6.51%
21	103	6.51%		74	39	6.05%		143	103	6.51%
21	126	6.51%		74	10	5.58%		143	298	6.05%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
21	121	6.51%		74	2	5.58%		143	3	6.05%
21	143	6.51%		74	45	5.58%		143	71	6.05%
21	75	6.05%		74	23	5.58%		143	64	6.05%
21	82	6.05%		74	48	5.58%		143	92	6.05%
21	86	6.05%		74	14	5.58%		143	55	6.05%
21	98	6.05%		74	55	5.58%		143	34	6.05%
21	107	5.58%		74	31	5.58%		143	43	6.05%
21	88	5.12%		74	79	5.12%		143	311	6.05%
21	105	5.12%		74	26	5.12%		143	16	6.05%
21	90	4.65%		74	116	5.12%		143	104	6.05%
21	106	4.65%		74	54	5.12%		143	101	6.05%
21	120	4.19%		74	32	5.12%		143	111	6.05%
21	119	3.72%		74	78	4.65%		143	110	6.05%
21	174	3.26%		74	56	4.65%		143	66	5.58%
21	118	3.26%		74	34	4.65%		143	84	5.58%
22	22	100.00%		74	62	4.65%		143	75	5.58%
22	2	64.65%		74	82	4.19%		143	76	5.58%
22	18	63.26%		74	122	4.19%		143	122	5.58%
22	8	54.42%		74	297	4.19%		143	107	5.58%
22	7	52.56%		74	104	3.72%		143	293	5.12%
22	309	50.70%		74	264	3.72%		143	65	5.12%
22	6	47.91%		74	143	3.72%		143	35	5.12%
22	1	47.91%		75	75	100.00%		143	83	5.12%
22	24	44.65%		75	64	39.53%		143	132	5.12%
22	15	42.79%		75	74	37.21%		143	130	5.12%
22	12	42.33%		75	67	20.00%		143	81	4.65%
22	29	41.40%		75	68	20.00%		143	80	4.65%
22	9	39.53%		75	124	18.14%		143	85	4.65%
22	25	39.07%		75	76	17.21%		143	295	4.65%
22	28	38.14%		75	89	16.28%		143	127	4.65%
22	11	37.21%		75	77	16.28%		143	117	4.65%
22	16	36.74%		75	66	16.28%		143	89	4.19%
22	30	36.28%		75	101	15.81%		143	82	4.19%
22	27	35.35%		75	107	15.35%		143	33	4.19%
22	17	34.88%		75	102	14.88%		143	88	3.72%
22	26	33.49%		75	131	14.42%		143	74	3.72%
22	20	33.49%		75	129	14.42%		143	68	3.72%
22	10	33.02%		75	117	14.42%		143	67	3.72%
22	21	33.02%		75	65	13.95%		143	121	3.72%
22	37	32.56%		75	70	13.95%		143	105	3.72%
22	23	32.56%		75	71	13.49%		143	106	3.72%
22	13	32.56%		75	132	13.02%		143	125	3.72%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
22	19	32.56%		75	130	13.02%		144	144	100.00%
22	14	32.09%		75	293	13.02%		144	255	4.65%
22	31	30.70%		75	109	13.02%		144	154	4.65%
22	69	27.44%		75	128	12.09%		144	146	3.26%
22	310	26.98%		75	127	11.63%		144	197	3.26%
22	40	25.58%		75	81	11.16%		145	145	100.00%
22	311	25.12%		75	80	11.16%		145	137	15.35%
22	35	24.65%		75	309	11.16%		145	243	4.19%
22	39	24.65%		75	69	11.16%		145	199	3.72%
22	34	24.65%		75	126	10.70%		145	237	3.26%
22	41	24.19%		75	44	10.70%		146	146	100.00%
22	312	24.19%		75	20	9.77%		146	113	7.44%
22	32	23.72%		75	295	9.77%		146	162	6.98%
22	313	23.72%		75	9	9.30%		146	267	6.51%
22	3	23.26%		75	47	9.30%		146	154	6.05%
22	42	23.26%		75	25	9.30%		146	248	5.12%
22	38	22.79%		75	27	9.30%		146	218	5.12%
22	298	22.79%		75	11	9.30%		146	282	4.19%
22	314	22.79%		75	92	8.84%		146	99	4.19%
22	43	22.33%		75	16	8.84%		146	204	3.72%
22	36	21.86%		75	24	8.84%		146	144	3.26%
22	33	20.00%		75	111	8.84%		147	147	100.00%
22	153	20.00%		75	30	8.84%		147	220	8.37%
22	45	19.07%		75	43	8.84%		147	188	8.37%
22	296	19.07%		75	17	8.84%		147	25	4.65%
22	294	18.14%		75	8	8.37%		147	309	4.19%
22	48	15.81%		75	28	8.37%		147	105	3.26%
22	71	14.42%		75	310	8.37%		147	125	3.26%
22	259	13.95%		75	37	8.37%		148	148	100.00%
22	44	12.56%		75	298	8.37%		148	152	5.12%
22	109	12.56%		75	26	8.37%		149	149	100.00%
22	128	12.56%		75	6	7.91%		150	150	100.00%
22	70	11.63%		75	296	7.91%		150	261	14.88%
22	92	11.63%		75	46	7.91%		151	151	100.00%
22	129	11.63%		75	3	7.44%		151	247	9.77%
22	76	11.16%		75	15	7.44%		152	152	100.00%
22	46	11.16%		75	294	7.44%		152	148	5.12%
22	124	11.16%		75	36	7.44%		153	153	100.00%
22	83	10.70%		75	7	6.98%		153	37	29.77%
22	77	10.70%		75	1	6.98%		153	310	29.77%
22	55	10.70%		75	45	6.98%		153	312	29.30%
22	107	10.70%		75	29	6.98%		153	311	28.37%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
22	47	10.23%		75	18	6.98%		153	35	27.91%
22	62	10.23%		75	153	6.98%		153	313	27.91%
22	127	10.23%		75	31	6.98%		153	314	27.44%
22	131	10.23%		75	40	6.51%		153	309	26.51%
22	297	10.23%		75	22	6.51%		153	38	26.51%
22	65	9.77%		75	14	6.51%		153	41	26.51%
22	79	9.77%		75	110	6.51%		153	3	26.05%
22	295	9.77%		75	13	6.51%		153	298	25.58%
22	102	9.77%		75	2	6.05%		153	34	25.58%
22	66	9.30%		75	10	6.05%		153	43	25.12%
22	89	9.30%		75	313	6.05%		153	40	24.65%
22	117	9.30%		75	19	6.05%		153	9	24.65%
22	293	9.30%		75	23	6.05%		153	11	24.19%
22	64	8.84%		75	55	6.05%		153	25	23.72%
22	56	8.84%		75	314	6.05%		153	24	23.72%
22	101	8.84%		75	104	6.05%		153	36	23.72%
22	130	8.84%		75	21	6.05%		153	39	23.72%
22	132	8.84%		75	38	6.05%		153	32	23.26%
22	81	8.37%		75	98	5.58%		153	15	23.26%
22	84	8.37%		75	12	5.58%		153	28	23.26%
22	67	8.37%		75	35	5.58%		153	31	23.26%
22	68	8.37%		75	312	5.58%		153	20	23.26%
22	80	7.91%		75	42	5.58%		153	27	22.79%
22	82	7.91%		75	56	5.58%		153	26	22.33%
22	78	7.91%		75	32	5.58%		153	16	22.33%
22	111	7.91%		75	143	5.58%		153	17	22.33%
22	143	7.91%		75	41	5.12%		153	30	22.33%
22	85	7.44%		75	311	5.12%		153	12	22.33%
22	110	7.44%		75	48	5.12%		153	7	22.33%
22	103	7.44%		75	39	5.12%		153	42	21.86%
22	126	7.44%		75	116	5.12%		153	6	20.93%
22	74	6.98%		75	259	4.65%		153	8	20.93%
22	122	6.98%		75	54	4.65%		153	1	20.47%
22	116	6.98%		75	297	4.65%		153	22	20.00%
22	75	6.51%		75	34	4.19%		153	33	20.00%
22	98	6.51%		75	83	3.26%		153	18	19.07%
22	121	6.51%		75	85	3.26%		153	69	19.07%
22	104	6.51%		76	76	100.00%		153	14	18.14%
22	125	6.05%		76	77	70.23%		153	10	17.67%
22	105	6.05%		76	107	65.58%		153	19	17.67%
22	118	5.58%		76	102	47.44%		153	21	17.67%
22	120	5.12%		76	124	26.98%		153	2	17.67%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
22	119	5.12%		76	81	25.12%		153	23	17.67%
22	106	4.65%		76	71	24.19%		153	29	17.67%
22	88	4.19%		76	70	24.19%		153	13	17.21%
22	90	4.19%		76	109	22.33%		153	294	17.21%
22	174	4.19%		76	295	22.33%		153	296	14.42%
22	86	3.72%		76	101	21.40%		153	45	13.95%
22	138	3.72%		76	66	21.40%		153	47	13.02%
22	251	3.26%		76	131	20.93%		153	92	13.02%
23	14	100.00%		76	64	20.93%		153	259	12.56%
23	23	100.00%		76	111	20.93%		153	71	12.09%
23	10	99.53%		76	65	20.93%		153	46	12.09%
23	19	97.67%		76	67	20.00%		153	101	12.09%
23	21	90.70%		76	68	19.53%		153	295	11.63%
23	13	85.12%		76	293	19.53%		153	48	11.63%
23	309	46.98%		76	130	18.60%		153	70	11.16%
23	15	45.12%		76	80	18.14%		153	65	11.16%
23	8	42.33%		76	128	18.14%		153	109	11.16%
23	24	41.40%		76	117	17.21%		153	56	10.70%
23	25	40.00%		76	75	17.21%		153	111	10.70%
23	1	40.00%		76	110	17.21%		153	76	9.77%
23	7	39.53%		76	132	16.74%		153	81	9.77%
23	6	39.53%		76	126	16.28%		153	102	9.77%
23	16	39.53%		76	129	15.81%		153	124	9.77%
23	11	36.74%		76	9	15.35%		153	77	9.30%
23	20	36.28%		76	89	15.35%		153	62	9.30%
23	9	34.42%		76	69	14.88%		153	79	9.30%
23	18	34.42%		76	127	14.88%		153	66	9.30%
23	12	34.42%		76	45	13.95%		153	107	9.30%
23	30	33.95%		76	310	13.95%		153	44	8.84%
23	29	33.02%		76	27	13.49%		153	74	8.84%
23	2	33.02%		76	3	13.02%		153	117	8.84%
23	26	33.02%		76	74	13.02%		153	293	8.37%
23	17	33.02%		76	11	13.02%		153	68	7.91%
23	22	32.56%		76	25	12.56%		153	89	7.91%
23	28	31.63%		76	35	12.09%		153	78	7.91%
23	27	31.16%		76	78	11.63%		153	80	7.91%
23	31	28.37%		76	20	11.63%		153	67	7.44%
23	37	25.58%		76	44	11.63%		153	55	7.44%
23	310	25.12%		76	28	11.63%		153	116	7.44%
23	311	24.65%		76	311	11.63%		153	130	7.44%
23	69	24.19%		76	103	11.63%		153	110	7.44%
23	3	23.72%		76	17	11.63%		153	129	7.44%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
23	39	23.26%		76	7	11.16%		153	103	7.44%
23	312	23.26%		76	6	11.16%		153	131	7.44%
23	35	22.79%		76	22	11.16%		153	64	6.98%
23	40	22.79%		76	296	11.16%		153	75	6.98%
23	43	22.79%		76	298	11.16%		153	143	6.98%
23	41	22.79%		76	30	11.16%		153	122	6.98%
23	313	22.79%		76	41	11.16%		153	128	6.98%
23	314	22.79%		76	34	11.16%		153	54	6.51%
23	38	22.33%		76	1	10.70%		153	127	6.51%
23	34	21.86%		76	79	10.70%		153	125	6.51%
23	32	21.40%		76	26	10.70%		153	82	6.05%
23	298	21.40%		76	15	10.70%		153	83	6.05%
23	36	20.00%		76	47	10.70%		153	297	6.05%
23	42	19.53%		76	259	10.70%		153	84	5.58%
23	153	17.67%		76	36	10.70%		153	121	5.58%
23	33	17.21%		76	309	10.70%		153	132	5.12%
23	296	15.35%		76	37	10.70%		153	126	5.12%
23	294	14.88%		76	312	10.70%		153	105	5.12%
23	48	14.42%		76	2	10.23%		153	85	4.65%
23	45	13.49%		76	39	10.23%		153	86	4.19%
23	117	12.09%		76	62	10.23%		153	120	4.19%
23	71	11.63%		76	294	10.23%		153	104	4.19%
23	47	11.63%		76	313	10.23%		153	88	3.72%
23	101	11.63%		76	153	9.77%		153	98	3.72%
23	124	11.63%		76	42	9.77%		153	174	3.72%
23	259	10.70%		76	32	9.77%		154	154	100.00%
23	70	10.23%		76	43	9.77%		154	146	6.05%
23	89	10.23%		76	40	9.77%		154	94	5.12%
23	92	10.23%		76	92	9.30%		154	99	5.12%
23	66	10.23%		76	31	9.30%		154	113	5.12%
23	129	10.23%		76	24	9.30%		154	282	4.65%
23	297	10.23%		76	46	9.30%		154	248	4.65%
23	46	9.77%		76	16	9.30%		154	93	4.65%
23	65	9.77%		76	314	9.30%		154	144	4.65%
23	109	9.77%		76	13	9.30%		154	162	4.19%
23	128	9.77%		76	8	8.84%		154	267	3.26%
23	293	9.77%		76	56	8.84%		154	204	3.26%
23	104	9.77%		76	116	8.84%		154	218	3.26%
23	67	9.30%		76	21	8.84%		155	155	100.00%
23	44	9.30%		76	48	8.84%		155	173	4.19%
23	62	9.30%		76	12	8.84%		156	156	100.00%
23	132	9.30%		76	98	8.37%		156	242	12.56%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
23	131	9.30%		76	10	8.37%		156	58	3.72%
23	77	8.84%		76	19	8.37%		156	160	3.72%
23	55	8.84%		76	23	8.37%		156	108	3.26%
23	295	8.84%		76	18	8.37%		157	157	100.00%
23	127	8.84%		76	14	8.37%		157	244	13.02%
23	76	8.37%		76	55	8.37%		157	202	10.23%
23	64	8.37%		76	29	8.37%		158	158	100.00%
23	56	8.37%		76	38	7.91%		158	273	13.95%
23	107	8.37%		76	83	7.44%		158	225	6.98%
23	130	8.37%		76	125	7.44%		158	277	6.98%
23	80	7.91%		76	106	7.44%		159	159	100.00%
23	79	7.91%		76	121	6.98%		159	255	15.81%
23	78	7.91%		76	297	6.98%		159	246	4.65%
23	111	7.91%		76	104	6.51%		159	209	4.65%
23	122	7.91%		76	120	6.05%		159	223	4.65%
23	102	7.91%		76	122	6.05%		159	60	4.19%
23	110	7.44%		76	33	6.05%		159	210	3.72%
23	121	7.44%		76	143	5.58%		159	91	3.72%
23	116	7.44%		76	85	4.65%		159	191	3.72%
23	81	6.98%		76	82	4.65%		159	142	3.72%
23	68	6.98%		76	54	4.65%		159	100	3.26%
23	143	6.51%		76	105	4.65%		160	160	100.00%
23	75	6.05%		76	118	4.65%		160	185	12.09%
23	83	6.05%		76	84	4.19%		160	94	5.58%
23	82	6.05%		76	86	4.19%		160	248	4.65%
23	103	6.05%		76	119	4.19%		160	282	4.19%
23	74	5.58%		76	174	3.26%		160	93	4.19%
23	98	5.58%		77	77	100.00%		160	267	3.72%
23	126	5.58%		77	76	70.23%		160	219	3.72%
23	125	5.58%		77	107	66.05%		160	162	3.72%
23	85	5.12%		77	102	46.05%		160	156	3.72%
23	105	5.12%		77	124	26.05%		160	228	3.26%
23	86	4.65%		77	81	24.19%		161	161	100.00%
23	106	4.65%		77	295	23.72%		161	240	31.63%
23	120	4.65%		77	70	22.33%		161	208	3.72%
23	84	4.19%		77	71	21.86%		161	93	3.26%
23	90	4.19%		77	111	21.40%		161	284	3.26%
23	88	3.72%		77	64	20.47%		161	134	3.26%
23	119	3.72%		77	101	20.47%		162	162	100.00%
23	118	3.26%		77	131	20.00%		162	267	50.70%
24	24	100.00%		77	109	19.53%		162	146	6.98%
24	309	61.40%		77	65	19.53%		162	248	6.05%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
24	15	53.95%		77	66	19.53%		162	99	5.12%
24	7	49.77%		77	293	18.60%		162	282	4.19%
24	6	49.30%		77	110	18.60%		162	154	4.19%
24	1	48.84%		77	80	18.14%		162	113	3.72%
24	8	47.91%		77	67	18.14%		162	160	3.72%
24	28	46.05%		77	126	17.67%		163	163	100.00%
24	25	45.12%		77	68	17.67%		163	183	20.93%
24	18	45.12%		77	128	17.21%		164	164	100.00%
24	22	44.65%		77	69	16.74%		164	139	28.84%
24	16	44.65%		77	130	16.28%		165	165	100.00%
24	9	44.19%		77	117	16.28%		165	172	28.84%
24	11	43.72%		77	75	16.28%		166	166	100.00%
24	30	43.26%		77	89	15.35%		167	167	100.00%
24	13	42.33%		77	74	15.35%		167	234	30.23%
24	12	42.33%		77	9	14.88%		168	168	100.00%
24	10	41.40%		77	129	14.88%		168	135	48.37%
24	20	41.40%		77	132	14.42%		169	169	100.00%
24	23	41.40%		77	11	14.42%		169	134	55.35%
24	14	40.93%		77	45	13.95%		169	249	6.51%
24	21	40.93%		77	127	13.95%		169	219	6.05%
24	2	40.47%		77	27	12.56%		169	248	4.65%
24	27	40.00%		77	294	12.56%		169	185	4.19%
24	26	40.00%		77	1	11.63%		169	230	3.26%
24	19	40.00%		77	28	11.63%		170	170	100.00%
24	31	39.07%		77	309	11.63%		170	203	34.42%
24	17	38.60%		77	310	11.63%		170	260	6.51%
24	29	36.28%		77	25	11.63%		170	256	4.65%
24	37	36.28%		77	3	11.16%		171	171	100.00%
24	310	32.09%		77	6	11.16%		171	177	13.95%
24	311	31.63%		77	44	11.16%		171	115	4.19%
24	3	29.30%		77	62	11.16%		171	114	3.72%
24	35	29.30%		77	56	11.16%		172	172	100.00%
24	39	29.30%		77	30	11.16%		172	165	28.84%
24	312	28.84%		77	259	11.16%		173	173	100.00%
24	40	28.37%		77	37	11.16%		173	155	4.19%
24	41	28.37%		77	35	11.16%		174	174	100.00%
24	38	27.44%		77	78	10.70%		174	25	4.65%
24	314	27.44%		77	22	10.70%		174	309	4.65%
24	298	26.98%		77	41	10.70%		174	18	4.19%
24	313	26.51%		77	311	10.70%		174	294	4.19%
24	32	26.05%		77	92	10.23%		174	1	4.19%
24	34	26.05%		77	7	10.23%		174	6	4.19%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
24	69	26.05%		77	79	10.23%		174	22	4.19%
24	36	25.58%		77	296	10.23%		174	8	4.19%
24	43	25.12%		77	103	10.23%		174	102	4.19%
24	42	24.65%		77	17	10.23%		174	2	3.72%
24	153	23.72%		77	26	10.23%		174	310	3.72%
24	33	22.33%		77	16	9.77%		174	129	3.72%
24	296	18.60%		77	298	9.77%		174	132	3.72%
24	294	17.67%		77	36	9.77%		174	153	3.72%
24	45	15.81%		77	39	9.77%		174	31	3.26%
24	48	14.88%		77	13	9.77%		174	67	3.26%
24	47	12.56%		77	2	9.30%		174	26	3.26%
24	62	12.09%		77	15	9.30%		174	46	3.26%
24	44	11.63%		77	55	9.30%		174	30	3.26%
24	71	11.63%		77	153	9.30%		174	79	3.26%
24	46	11.63%		77	20	9.30%		174	21	3.26%
24	124	11.63%		77	21	9.30%		174	76	3.26%
24	293	11.63%		77	314	9.30%		174	7	3.26%
24	295	11.63%		77	34	9.30%		174	12	3.26%
24	259	11.63%		77	10	8.84%		174	17	3.26%
24	70	10.70%		77	47	8.84%		174	35	3.26%
24	92	10.70%		77	19	8.84%		174	55	3.26%
24	55	10.70%		77	23	8.84%		174	107	3.26%
24	66	10.23%		77	312	8.84%		175	175	100.00%
24	64	10.23%		77	40	8.84%		175	224	4.19%
24	65	10.23%		77	48	8.84%		175	255	3.72%
24	109	10.23%		77	313	8.84%		176	176	100.00%
24	128	9.77%		77	106	8.37%		176	280	5.12%
24	117	9.77%		77	104	8.37%		176	232	3.72%
24	81	9.30%		77	18	8.37%		177	177	100.00%
24	98	9.30%		77	14	8.37%		177	171	13.95%
24	56	9.30%		77	12	8.37%		178	178	100.00%
24	76	9.30%		77	32	8.37%		178	182	13.02%
24	75	8.84%		77	8	7.91%		178	290	9.30%
24	120	8.84%		77	46	7.91%		179	179	100.00%
24	130	8.84%		77	43	7.91%		179	291	13.02%
24	101	8.84%		77	24	7.91%		179	199	6.51%
24	127	8.84%		77	31	7.91%		179	137	4.19%
24	102	8.84%		77	98	7.44%		179	250	3.72%
24	103	8.84%		77	38	7.44%		180	180	100.00%
24	132	8.84%		77	42	7.44%		180	255	3.26%
24	67	8.37%		77	116	7.44%		181	181	100.00%
24	82	8.37%		77	125	7.44%		181	239	26.98%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
24	79	8.37%		77	143	6.98%		182	182	100.00%
24	129	8.37%		77	29	6.98%		182	178	13.02%
24	111	8.37%		77	83	6.51%		182	290	4.65%
24	122	8.37%		77	121	6.51%		183	183	100.00%
24	104	8.37%		77	120	6.51%		183	163	20.93%
24	80	7.91%		77	33	6.51%		184	184	100.00%
24	77	7.91%		77	82	6.05%		184	256	16.28%
24	89	7.91%		77	297	5.58%		184	260	4.19%
24	78	7.91%		77	86	5.12%		185	185	100.00%
24	107	7.91%		77	85	5.12%		185	160	12.09%
24	143	7.91%		77	122	5.12%		185	193	4.65%
24	83	7.44%		77	105	4.65%		185	224	4.65%
24	68	7.44%		77	84	4.19%		185	169	4.19%
24	85	7.44%		77	54	3.72%		185	248	3.72%
24	131	7.44%		77	88	3.26%		185	235	3.26%
24	125	7.44%		77	119	3.26%		186	186	100.00%
24	121	7.44%		77	251	3.26%		186	201	26.51%
24	297	7.44%		77	118	3.26%		187	187	100.00%
24	54	6.98%		78	78	100.00%		188	188	100.00%
24	116	6.98%		78	79	88.84%		188	220	22.79%
24	110	6.98%		78	103	60.47%		188	147	8.37%
24	126	6.51%		78	62	41.86%		188	104	3.72%
24	105	6.51%		78	55	40.47%		189	189	100.00%
24	74	6.05%		78	121	29.30%		189	196	26.51%
24	118	6.05%		78	104	28.84%		190	190	100.00%
24	119	5.58%		78	120	26.05%		190	289	18.14%
24	106	5.12%		78	122	23.72%		190	288	17.67%
24	251	5.12%		78	98	14.42%		191	191	100.00%
24	84	4.65%		78	9	13.02%		191	210	23.72%
24	90	4.65%		78	11	12.56%		191	223	7.91%
24	88	3.72%		78	30	11.63%		191	209	6.05%
25	25	100.00%		78	69	11.63%		191	230	3.72%
25	309	60.47%		78	76	11.63%		191	159	3.72%
25	16	48.37%		78	27	11.16%		192	192	100.00%
25	9	46.98%		78	309	11.16%		192	136	33.95%
25	11	46.98%		78	296	11.16%		192	237	9.30%
25	28	46.51%		78	37	10.70%		192	236	6.51%
25	15	46.51%		78	77	10.70%		193	193	100.00%
25	24	45.12%		78	25	10.70%		193	224	39.53%
25	7	44.65%		78	1	10.23%		193	61	5.12%
25	8	43.72%		78	45	10.23%		193	108	4.65%
25	1	42.79%		78	17	10.23%		193	185	4.65%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
25	6	42.33%		78	6	9.77%		193	248	3.72%
25	20	41.40%		78	15	9.77%		193	60	3.72%
25	10	40.47%		78	20	9.77%		193	142	3.72%
25	13	40.47%		78	297	9.77%		193	58	3.26%
25	17	40.47%		78	48	9.77%		193	91	3.26%
25	30	40.00%		78	12	9.77%		193	51	3.26%
25	23	40.00%		78	28	9.77%		194	194	100.00%
25	19	40.00%		78	7	9.30%		194	229	62.79%
25	21	40.00%		78	56	9.30%		194	91	3.72%
25	26	39.53%		78	16	9.30%		194	50	3.26%
25	14	39.53%		78	313	9.30%		195	195	100.00%
25	22	39.07%		78	26	9.30%		195	270	26.51%
25	27	38.60%		78	312	9.30%		196	196	100.00%
25	18	38.60%		78	314	9.30%		196	189	26.51%
25	12	38.14%		78	31	8.84%		197	197	100.00%
25	2	37.67%		78	294	8.84%		197	72	57.67%
25	31	36.74%		78	311	8.84%		197	144	3.26%
25	37	35.35%		78	44	8.84%		198	198	100.00%
25	29	33.02%		78	298	8.84%		198	206	11.16%
25	310	32.09%		78	29	8.37%		199	199	100.00%
25	312	30.23%		78	35	8.37%		199	250	31.16%
25	311	30.23%		78	107	8.37%		199	179	6.51%
25	3	29.77%		78	92	7.91%		199	291	3.72%
25	39	28.84%		78	10	7.91%		199	145	3.72%
25	40	28.37%		78	8	7.91%		200	200	100.00%
25	69	28.37%		78	43	7.91%		200	222	17.67%
25	43	28.37%		78	47	7.91%		200	287	5.58%
25	35	27.91%		78	143	7.91%		200	133	4.19%
25	313	27.91%		78	19	7.91%		200	237	3.26%
25	298	27.44%		78	23	7.91%		201	201	100.00%
25	314	26.98%		78	153	7.91%		201	186	26.51%
25	41	26.51%		78	18	7.91%		201	239	3.26%
25	34	26.51%		78	22	7.91%		202	202	100.00%
25	36	26.05%		78	24	7.91%		202	157	10.23%
25	38	25.58%		78	38	7.91%		202	244	8.37%
25	32	25.12%		78	129	7.91%		203	203	100.00%
25	42	24.19%		78	14	7.44%		203	170	34.42%
25	153	23.72%		78	310	7.44%		203	260	6.51%
25	33	21.86%		78	34	7.44%		203	256	3.72%
25	296	20.00%		78	2	6.98%		204	204	100.00%
25	45	18.14%		78	21	6.98%		204	205	13.49%
25	294	16.74%		78	40	6.98%		204	146	3.72%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
25	47	16.28%		78	293	6.98%		204	154	3.26%
25	48	15.35%		78	36	6.98%		205	205	100.00%
25	124	14.88%		78	46	6.98%		205	204	13.49%
25	92	14.42%		78	259	6.98%		205	5	5.58%
25	109	13.95%		78	41	6.98%		205	59	3.26%
25	117	13.95%		78	102	6.98%		206	206	100.00%
25	70	13.49%		78	111	6.98%		206	198	11.16%
25	71	13.49%		78	3	6.51%		206	255	4.19%
25	46	13.49%		78	65	6.51%		207	207	100.00%
25	297	13.49%		78	124	6.51%		207	212	18.14%
25	259	13.49%		78	118	6.51%		208	208	100.00%
25	44	13.02%		78	119	6.51%		208	284	40.00%
25	76	12.56%		78	13	6.51%		208	141	5.58%
25	55	12.56%		78	83	6.05%		208	161	3.72%
25	62	12.09%		78	82	6.05%		209	209	100.00%
25	293	12.09%		78	68	6.05%		209	223	44.19%
25	89	11.63%		78	64	6.05%		209	210	6.05%
25	56	11.63%		78	67	6.05%		209	191	6.05%
25	77	11.63%		78	39	6.05%		209	159	4.65%
25	295	11.16%		78	42	6.05%		209	262	3.72%
25	103	11.16%		78	126	6.05%		209	255	3.26%
25	64	10.70%		78	32	6.05%		210	210	100.00%
25	78	10.70%		78	110	6.05%		210	191	23.72%
25	127	10.70%		78	85	5.58%		210	223	6.98%
25	129	10.70%		78	81	5.58%		210	209	6.05%
25	66	10.23%		78	128	5.58%		210	159	3.72%
25	85	10.23%		78	70	5.58%		210	217	3.26%
25	65	10.23%		78	127	5.58%		210	275	3.26%
25	101	10.23%		78	71	5.58%		211	211	100.00%
25	132	10.23%		78	117	5.58%		212	212	100.00%
25	80	9.77%		78	106	5.58%		212	207	18.14%
25	79	9.77%		78	101	5.12%		213	213	100.00%
25	128	9.77%		78	109	5.12%		213	245	40.00%
25	121	9.77%		78	33	5.12%		213	264	7.91%
25	107	9.77%		78	295	5.12%		213	126	5.58%
25	102	9.77%		78	80	4.65%		213	129	5.58%
25	104	9.77%		78	84	4.65%		213	128	5.58%
25	81	9.30%		78	74	4.65%		213	116	4.19%
25	83	9.30%		78	66	4.65%		213	293	3.72%
25	75	9.30%		78	130	4.65%		214	214	100.00%
25	68	9.30%		78	125	4.65%		214	271	35.81%
25	84	9.30%		78	116	4.65%		215	215	100.00%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
25	67	9.30%		78	89	4.19%		216	216	100.00%
25	131	9.30%		78	131	4.19%		216	269	42.79%
25	111	9.30%		78	132	4.19%		217	217	100.00%
25	110	9.30%		79	79	100.00%		217	242	3.26%
25	74	8.84%		79	78	88.84%		217	134	3.26%
25	122	8.84%		79	103	60.47%		217	210	3.26%
25	143	8.84%		79	62	42.79%		218	218	100.00%
25	98	8.37%		79	55	41.40%		218	235	46.05%
25	82	8.37%		79	121	30.23%		218	146	5.12%
25	120	7.91%		79	104	29.30%		218	248	3.72%
25	125	7.91%		79	120	26.51%		218	223	3.26%
25	130	7.91%		79	122	23.26%		218	154	3.26%
25	126	7.44%		79	98	14.42%		218	99	2.79%
25	116	6.98%		79	9	13.02%		219	219	100.00%
25	106	6.98%		79	69	12.56%		219	169	6.05%
25	54	5.12%		79	309	12.56%		219	134	5.12%
25	119	5.12%		79	27	12.09%		219	160	3.72%
25	118	5.12%		79	296	12.09%		220	220	100.00%
25	174	4.65%		79	11	12.09%		220	188	22.79%
25	105	4.65%		79	1	11.63%		220	147	8.37%
25	147	4.65%		79	6	11.63%		221	221	100.00%
25	251	3.26%		79	30	11.63%		221	72	6.05%
26	26	100.00%		79	20	11.16%		221	292	5.12%
26	17	71.63%		79	7	10.70%		221	242	5.12%
26	309	48.37%		79	45	10.70%		222	222	100.00%
26	9	46.98%		79	294	10.70%		222	200	17.67%
26	27	46.51%		79	26	10.70%		222	287	3.72%
26	11	45.12%		79	37	10.70%		222	133	3.72%
26	6	42.79%		79	76	10.70%		223	223	100.00%
26	1	42.79%		79	56	10.23%		223	209	44.19%
26	7	42.33%		79	17	10.23%		223	191	7.91%
26	30	42.33%		79	48	10.23%		223	210	6.98%
26	8	40.93%		79	77	10.23%		223	159	4.65%
26	24	40.00%		79	28	9.77%		223	255	4.19%
26	25	39.53%		79	15	9.77%		223	218	3.26%
26	12	38.60%		79	16	9.77%		224	224	100.00%
26	15	38.14%		79	311	9.77%		224	193	39.53%
26	28	37.21%		79	22	9.77%		224	185	4.65%
26	31	36.74%		79	31	9.77%		224	175	4.19%
26	18	36.74%		79	25	9.77%		224	108	4.19%
26	37	36.28%		79	12	9.77%		224	95	3.72%
26	16	34.88%		79	35	9.30%		224	61	3.72%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
26	29	33.95%		79	153	9.30%		224	58	3.72%
26	20	33.95%		79	297	9.30%		224	60	3.72%
26	13	33.49%		79	312	9.30%		224	253	3.72%
26	22	33.49%		79	18	9.30%		224	97	3.26%
26	2	33.02%		79	8	8.84%		224	59	3.26%
26	10	33.02%		79	313	8.84%		224	142	3.26%
26	14	33.02%		79	298	8.84%		225	225	100.00%
26	23	33.02%		79	107	8.84%		225	277	36.28%
26	19	32.56%		79	314	8.84%		225	276	7.91%
26	21	32.56%		79	129	8.84%		225	273	7.44%
26	310	30.70%		79	3	8.37%		225	268	6.98%
26	40	29.30%		79	92	8.37%		225	158	6.98%
26	41	28.37%		79	310	8.37%		226	226	100.00%
26	311	28.37%		79	24	8.37%		226	275	9.30%
26	34	27.44%		79	44	8.37%		226	255	3.72%
26	39	27.44%		79	10	7.91%		226	257	3.72%
26	35	26.98%		79	23	7.91%		227	227	100.00%
26	312	26.98%		79	34	7.91%		228	228	100.00%
26	313	26.05%		79	41	7.91%		228	91	3.26%
26	69	25.58%		79	38	7.91%		228	160	3.26%
26	43	25.12%		79	2	7.44%		229	229	100.00%
26	38	25.12%		79	47	7.44%		229	194	62.79%
26	3	24.65%		79	19	7.44%		229	57	4.65%
26	314	24.65%		79	40	7.44%		229	91	4.65%
26	32	24.19%		79	14	7.44%		229	53	4.19%
26	42	23.72%		79	143	7.44%		229	61	4.19%
26	36	23.26%		79	111	7.44%		229	50	4.19%
26	298	22.79%		79	39	7.44%		229	96	3.72%
26	33	22.33%		79	102	7.44%		230	230	100.00%
26	153	22.33%		79	29	6.98%		230	255	5.12%
26	296	18.60%		79	43	6.98%		230	191	3.72%
26	294	16.74%		79	21	6.98%		230	169	3.26%
26	46	14.88%		79	36	6.98%		231	231	100.00%
26	45	14.88%		79	259	6.98%		231	254	61.86%
26	259	14.88%		79	119	6.98%		232	232	100.00%
26	48	13.49%		79	126	6.98%		232	280	15.81%
26	44	12.56%		79	13	6.98%		232	289	3.72%
26	55	12.56%		79	82	6.51%		232	288	3.72%
26	56	11.63%		79	65	6.51%		232	176	3.72%
26	92	11.63%		79	68	6.51%		233	233	100.00%
26	117	11.63%		79	67	6.51%		233	255	3.72%
26	129	11.63%		79	42	6.51%		234	234	100.00%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
26	297	11.63%		79	124	6.51%		234	167	30.23%
26	47	11.16%		79	117	6.51%		235	235	100.00%
26	71	11.16%		79	128	6.51%		235	218	46.05%
26	62	11.16%		79	83	6.05%		235	185	3.26%
26	76	10.70%		79	293	6.05%		236	236	100.00%
26	83	10.70%		79	64	6.05%		236	237	16.74%
26	79	10.70%		79	118	6.05%		236	136	8.37%
26	293	10.70%		79	32	6.05%		236	192	6.51%
26	295	10.70%		79	110	6.05%		236	133	3.72%
26	130	10.70%		79	85	5.58%		237	237	100.00%
26	103	10.70%		79	81	5.58%		237	236	16.74%
26	70	10.23%		79	127	5.58%		237	192	9.30%
26	77	10.23%		79	46	5.58%		237	136	7.44%
26	124	10.23%		79	109	5.58%		237	133	5.12%
26	128	10.23%		79	33	5.58%		237	200	3.26%
26	107	10.23%		79	70	5.58%		237	145	3.26%
26	109	9.77%		79	80	5.12%		238	238	100.00%
26	101	9.77%		79	84	5.12%		238	251	16.74%
26	111	9.77%		79	101	5.12%		238	16	4.19%
26	126	9.77%		79	74	5.12%		238	295	4.19%
26	110	9.77%		79	66	5.12%		238	81	4.19%
26	132	9.77%		79	71	5.12%		238	117	4.19%
26	66	9.30%		79	106	5.12%		238	130	4.19%
26	78	9.30%		79	130	5.12%		238	13	3.72%
26	102	9.30%		79	295	5.12%		238	48	3.72%
26	131	9.30%		79	116	5.12%		238	70	3.72%
26	121	9.30%		79	125	4.65%		238	127	3.72%
26	104	9.30%		79	131	4.19%		238	132	3.72%
26	89	8.84%		79	132	4.19%		238	109	3.72%
26	105	8.84%		79	90	3.72%		238	64	3.26%
26	127	8.84%		79	174	3.26%		238	67	3.26%
26	116	8.84%		80	80	100.00%		239	239	100.00%
26	82	8.37%		80	293	59.07%		239	181	26.98%
26	81	8.37%		80	127	41.40%		239	201	3.26%
26	65	8.37%		80	101	21.86%		240	240	100.00%
26	67	8.37%		80	109	20.00%		240	161	31.63%
26	75	8.37%		80	124	19.53%		241	241	100.00%
26	143	8.37%		80	131	19.07%		241	243	5.12%
26	85	7.91%		80	71	18.60%		242	242	100.00%
26	68	7.91%		80	76	18.14%		242	156	12.56%
26	122	7.91%		80	77	18.14%		242	221	5.12%
26	125	7.91%		80	70	18.14%		242	108	3.72%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
26	106	7.91%		80	64	17.67%		242	217	3.26%
26	80	7.44%		80	130	17.21%		243	243	100.00%
26	84	6.98%		80	107	16.28%		243	137	5.58%
26	64	6.98%		80	295	16.28%		243	241	5.12%
26	119	6.98%		80	117	16.28%		243	145	4.19%
26	54	6.51%		80	89	15.81%		244	244	100.00%
26	120	6.51%		80	102	15.81%		244	157	13.02%
26	118	6.51%		80	129	15.81%		244	202	8.37%
26	98	6.05%		80	65	15.81%		245	245	100.00%
26	74	5.12%		80	66	15.35%		245	213	40.00%
26	251	4.19%		80	81	14.88%		245	264	3.72%
26	264	3.72%		80	111	13.95%		245	109	3.72%
26	138	3.72%		80	128	13.49%		246	246	100.00%
26	86	3.26%		80	67	13.49%		246	262	48.84%
26	88	3.26%		80	126	13.49%		246	285	6.05%
26	174	3.26%		80	110	12.56%		246	274	5.58%
27	27	100.00%		80	9	12.09%		246	159	4.65%
27	9	49.30%		80	132	11.63%		246	255	4.19%
27	30	46.51%		80	45	11.63%		246	100	4.19%
27	309	46.51%		80	74	11.63%		246	50	3.72%
27	26	46.51%		80	47	11.63%		246	303	3.72%
27	11	46.51%		80	116	11.63%		246	142	3.72%
27	17	45.58%		80	75	11.16%		247	247	100.00%
27	1	40.93%		80	44	11.16%		247	151	9.77%
27	7	40.47%		80	68	11.16%		247	277	3.72%
27	31	40.00%		80	69	11.16%		248	248	100.00%
27	24	40.00%		80	11	11.16%		248	282	41.86%
27	6	39.53%		80	30	11.16%		248	99	18.60%
27	37	38.60%		80	294	11.16%		248	267	7.44%
27	8	38.60%		80	46	10.23%		248	162	6.05%
27	25	38.60%		80	21	9.77%		248	93	5.58%
27	15	38.14%		80	15	9.77%		248	146	5.12%
27	28	37.21%		80	25	9.77%		248	154	4.65%
27	29	36.28%		80	16	9.77%		248	169	4.65%
27	18	35.81%		80	309	9.77%		248	160	4.65%
27	22	35.35%		80	98	9.30%		248	61	3.72%
27	310	34.88%		80	296	9.30%		248	95	3.72%
27	12	33.95%		80	14	9.30%		248	193	3.72%
27	20	33.95%		80	20	9.30%		248	185	3.72%
27	16	33.49%		80	27	9.30%		248	218	3.72%
27	2	32.56%		80	13	9.30%		248	72	3.26%
27	40	32.09%		80	19	8.84%		248	306	3.26%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
27	39	32.09%		80	297	8.84%		248	50	3.26%
27	311	32.09%		80	10	8.37%		249	249	100.00%
27	10	31.63%		80	3	8.37%		249	134	7.44%
27	34	31.63%		80	29	8.37%		249	169	6.51%
27	14	31.63%		80	28	8.37%		250	250	100.00%
27	21	31.63%		80	48	8.37%		250	199	31.16%
27	13	31.16%		80	62	8.37%		250	179	3.72%
27	23	31.16%		80	37	8.37%		251	251	100.00%
27	41	30.70%		80	7	7.91%		251	238	16.74%
27	35	30.70%		80	1	7.91%		251	64	5.58%
27	19	30.70%		80	6	7.91%		251	130	5.58%
27	69	30.23%		80	2	7.91%		251	124	5.58%
27	312	30.23%		80	22	7.91%		251	24	5.12%
27	3	29.77%		80	24	7.91%		251	70	5.12%
27	313	29.30%		80	23	7.91%		251	126	5.12%
27	43	28.84%		80	56	7.91%		251	132	5.12%
27	32	27.91%		80	153	7.91%		251	67	4.65%
27	36	27.44%		80	8	7.44%		251	71	4.65%
27	314	26.51%		80	26	7.44%		251	131	4.65%
27	298	26.51%		80	17	7.44%		251	295	4.19%
27	42	25.58%		80	35	7.44%		251	26	4.19%
27	38	25.58%		80	31	7.44%		251	17	4.19%
27	33	23.72%		80	310	7.44%		251	28	4.19%
27	153	22.79%		80	311	7.44%		251	101	4.19%
27	296	21.86%		80	54	7.44%		251	129	4.19%
27	294	19.07%		80	18	7.44%		251	109	4.19%
27	45	15.81%		80	92	6.98%		251	312	3.72%
27	259	15.81%		80	40	6.98%		251	81	3.72%
27	71	14.88%		80	313	6.98%		251	309	3.72%
27	48	14.88%		80	106	6.98%		251	45	3.72%
27	109	14.42%		80	125	6.98%		251	31	3.72%
27	70	13.95%		80	104	6.98%		251	18	3.72%
27	297	13.95%		80	103	6.51%		251	117	3.72%
27	76	13.49%		80	43	6.51%		251	128	3.72%
27	44	13.49%		80	312	6.51%		251	111	3.72%
27	55	13.02%		80	83	6.05%		251	13	3.26%
27	46	13.02%		80	42	6.05%		251	77	3.26%
27	107	13.02%		80	38	6.05%		251	68	3.26%
27	92	12.56%		80	314	6.05%		251	89	3.26%
27	77	12.56%		80	12	6.05%		251	43	3.26%
27	124	12.56%		80	85	5.58%		251	25	3.26%
27	79	12.09%		80	298	5.58%		251	22	3.26%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
27	64	11.63%		80	39	5.58%		252	252	100.00%
27	89	11.63%		80	121	5.58%		252	278	33.95%
27	56	11.63%		80	79	5.12%		252	286	24.19%
27	62	11.63%		80	32	5.12%		253	253	100.00%
27	101	11.63%		80	120	5.12%		253	263	19.53%
27	295	11.63%		80	41	5.12%		253	224	3.72%
27	293	11.63%		80	34	5.12%		254	254	100.00%
27	81	11.16%		80	82	4.65%		254	231	61.86%
27	47	11.16%		80	143	4.65%		254	266	4.19%
27	78	11.16%		80	78	4.65%		254	265	4.19%
27	102	11.16%		80	55	4.65%		255	255	100.00%
27	128	11.16%		81	81	100.00%		255	159	15.81%
27	103	10.70%		81	295	62.33%		255	230	5.12%
27	129	10.70%		81	111	36.28%		255	61	4.65%
27	117	10.70%		81	110	35.81%		255	144	4.65%
27	111	10.70%		81	76	25.12%		255	262	4.19%
27	122	10.23%		81	102	24.19%		255	100	4.19%
27	116	10.23%		81	77	24.19%		255	246	4.19%
27	66	9.77%		81	107	22.33%		255	223	4.19%
27	65	9.77%		81	124	21.86%		255	206	4.19%
27	104	9.77%		81	101	21.86%		255	275	3.72%
27	130	9.77%		81	71	18.14%		255	226	3.72%
27	127	9.77%		81	109	18.14%		255	175	3.72%
27	67	9.30%		81	89	17.67%		255	233	3.72%
27	75	9.30%		81	64	17.67%		255	91	3.26%
27	80	9.30%		81	70	17.67%		255	58	3.26%
27	121	9.30%		81	117	16.28%		255	180	3.26%
27	110	9.30%		81	65	16.28%		255	113	3.26%
27	74	8.84%		81	293	15.35%		255	209	3.26%
27	105	8.84%		81	131	15.35%		256	256	100.00%
27	132	8.84%		81	67	14.88%		256	184	16.28%
27	83	8.37%		81	80	14.88%		256	260	4.65%
27	85	8.37%		81	130	13.95%		256	170	4.65%
27	68	8.37%		81	68	13.02%		256	203	3.72%
27	82	8.37%		81	126	13.02%		257	257	100.00%
27	131	8.37%		81	128	12.56%		257	283	20.47%
27	125	7.91%		81	132	12.09%		257	63	3.72%
27	98	7.44%		81	294	12.09%		257	60	3.72%
27	126	7.44%		81	129	12.09%		257	61	3.72%
27	84	6.98%		81	66	11.63%		257	226	3.72%
27	54	6.98%		81	75	11.16%		258	258	100.00%
27	120	6.98%		81	27	11.16%		258	281	36.74%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
27	143	6.98%		81	127	11.16%		259	259	100.00%
27	106	6.51%		81	74	11.16%		259	48	32.09%
27	118	6.05%		81	43	11.16%		259	294	18.60%
27	119	6.05%		81	44	10.70%		259	310	17.21%
27	86	3.72%		81	309	10.70%		259	28	16.74%
27	90	3.72%		81	69	10.70%		259	35	16.28%
28	28	100.00%		81	32	10.70%		259	311	16.28%
28	309	53.49%		81	30	10.70%		259	37	16.28%
28	20	48.84%		81	116	10.23%		259	34	15.81%
28	15	46.51%		81	312	10.23%		259	31	15.81%
28	25	46.51%		81	298	10.23%		259	27	15.81%
28	24	46.05%		81	38	10.23%		259	309	15.81%
28	7	44.19%		81	310	10.23%		259	17	15.81%
28	6	43.72%		81	311	10.23%		259	41	15.35%
28	1	43.26%		81	9	9.77%		259	45	15.35%
28	8	42.79%		81	56	9.77%		259	312	14.88%
28	30	41.86%		81	313	9.77%		259	26	14.88%
28	9	41.86%		81	314	9.77%		259	39	14.88%
28	11	41.40%		81	15	9.77%		259	69	14.88%
28	16	41.40%		81	17	9.77%		259	3	14.42%
28	12	39.53%		81	153	9.77%		259	313	14.42%
28	31	38.14%		81	1	9.30%		259	11	14.42%
28	22	38.14%		81	8	9.30%		259	296	14.42%
28	18	37.67%		81	24	9.30%		259	298	13.95%
28	37	37.21%		81	25	9.30%		259	9	13.95%
28	17	37.21%		81	47	9.30%		259	22	13.95%
28	26	37.21%		81	37	9.30%		259	32	13.95%
28	27	37.21%		81	6	8.84%		259	124	13.95%
28	2	36.74%		81	7	8.84%		259	40	13.49%
28	29	36.28%		81	3	8.84%		259	42	13.49%
28	310	33.49%		81	36	8.84%		259	25	13.49%
28	21	32.56%		81	31	8.84%		259	92	13.49%
28	13	32.09%		81	11	8.84%		259	7	13.02%
28	311	32.09%		81	41	8.84%		259	36	13.02%
28	10	31.63%		81	22	8.37%		259	2	13.02%
28	312	31.63%		81	48	8.37%		259	314	13.02%
28	14	31.63%		81	26	8.37%		259	30	13.02%
28	19	31.63%		81	16	8.37%		259	1	13.02%
28	23	31.63%		81	28	8.37%		259	38	13.02%
28	40	30.70%		81	42	8.37%		259	18	12.56%
28	313	30.70%		81	34	8.37%		259	43	12.56%
28	35	30.23%		81	39	8.37%		259	6	12.56%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
28	69	30.23%		81	12	8.37%		259	20	12.56%
28	3	30.23%		81	92	7.91%		259	153	12.56%
28	298	30.23%		81	19	7.91%		259	8	12.09%
28	43	29.77%		81	18	7.91%		259	15	11.63%
28	32	29.30%		81	35	7.91%		259	16	11.63%
28	39	29.30%		81	2	7.44%		259	24	11.63%
28	314	29.30%		81	121	7.44%		259	46	11.63%
28	38	28.84%		81	21	7.44%		259	47	11.63%
28	41	28.84%		81	14	7.44%		259	29	11.16%
28	34	28.84%		81	259	7.44%		259	77	11.16%
28	36	28.37%		81	55	7.44%		259	76	10.70%
28	42	27.44%		81	45	7.44%		259	23	10.70%
28	153	23.26%		81	297	7.44%		259	13	10.70%
28	296	22.79%		81	13	7.44%		259	12	10.70%
28	33	21.86%		81	10	6.98%		259	128	10.70%
28	45	20.47%		81	40	6.98%		259	33	10.23%
28	48	18.14%		81	23	6.98%		259	14	10.23%
28	294	17.67%		81	62	6.98%		259	10	10.23%
28	259	16.74%		81	29	6.98%		259	19	9.77%
28	46	16.28%		81	20	6.98%		259	21	9.77%
28	47	14.42%		81	104	6.98%		259	56	9.77%
28	62	13.95%		81	46	6.51%		259	44	9.77%
28	124	13.95%		81	103	6.51%		259	297	9.77%
28	56	13.49%		81	98	6.05%		259	107	9.77%
28	71	13.02%		81	84	6.05%		259	111	9.77%
28	89	12.56%		81	33	6.05%		259	117	9.30%
28	297	12.56%		81	120	6.05%		259	110	9.30%
28	70	12.09%		81	296	6.05%		259	64	8.84%
28	109	12.09%		81	125	6.05%		259	71	8.84%
28	117	12.09%		81	82	5.58%		259	83	8.37%
28	101	12.09%		81	83	5.58%		259	101	8.37%
28	77	11.63%		81	106	5.58%		259	129	8.37%
28	55	11.63%		81	79	5.58%		259	131	8.37%
28	76	11.63%		81	78	5.58%		259	130	8.37%
28	104	11.63%		81	85	5.12%		259	66	7.91%
28	44	11.16%		81	122	5.12%		259	62	7.91%
28	92	11.16%		81	143	4.65%		259	109	7.91%
28	103	11.16%		81	86	4.19%		259	81	7.44%
28	295	11.16%		81	105	4.19%		259	132	7.44%
28	66	10.70%		81	238	4.19%		259	65	6.98%
28	125	10.70%		81	251	3.72%		259	79	6.98%
28	129	10.70%		82	82	100.00%		259	70	6.98%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
28	128	10.70%		82	85	78.14%		259	78	6.98%
28	293	10.70%		82	83	51.63%		259	84	6.98%
28	64	10.23%		82	84	49.77%		259	143	6.98%
28	98	10.23%		82	294	13.02%		259	127	6.98%
28	83	10.23%		82	11	11.63%		259	102	6.98%
28	107	10.23%		82	69	10.70%		259	293	6.51%
28	130	10.23%		82	6	9.77%		259	82	6.51%
28	132	10.23%		82	310	9.77%		259	55	6.51%
28	79	9.77%		82	309	9.77%		259	295	6.51%
28	65	9.77%		82	1	9.30%		259	98	6.51%
28	78	9.77%		82	15	9.30%		259	126	6.51%
28	121	9.77%		82	56	9.30%		259	89	6.05%
28	127	9.77%		82	28	9.30%		259	68	6.05%
28	122	9.77%		82	20	9.30%		259	67	6.05%
28	131	9.77%		82	45	9.30%		259	103	6.05%
28	85	9.30%		82	9	8.84%		259	122	6.05%
28	82	9.30%		82	31	8.84%		259	116	6.05%
28	126	9.30%		82	39	8.84%		259	106	5.58%
28	120	9.30%		82	17	8.37%		259	85	5.12%
28	116	9.30%		82	18	8.37%		259	75	4.65%
28	67	8.84%		82	26	8.37%		259	90	4.65%
28	106	8.84%		82	25	8.37%		259	88	4.65%
28	75	8.37%		82	24	8.37%		259	125	4.65%
28	81	8.37%		82	27	8.37%		259	104	4.19%
28	80	8.37%		82	47	8.37%		259	86	3.72%
28	143	8.37%		82	311	7.91%		259	105	3.72%
28	68	7.91%		82	42	7.91%		259	87	3.26%
28	84	7.44%		82	22	7.91%		259	119	3.26%
28	111	7.44%		82	296	7.91%		260	260	100.00%
28	110	7.44%		82	3	7.44%		260	170	6.51%
28	105	7.44%		82	293	7.44%		260	203	6.51%
28	74	6.98%		82	41	7.44%		260	256	4.65%
28	54	6.98%		82	48	7.44%		260	184	4.19%
28	102	6.98%		82	30	7.44%		261	261	100.00%
28	119	5.58%		82	37	7.44%		261	150	14.88%
28	86	4.65%		82	7	6.98%		262	262	100.00%
28	118	4.65%		82	36	6.98%		262	246	48.84%
28	88	4.19%		82	117	6.98%		262	285	5.12%
28	251	4.19%		82	35	6.98%		262	100	5.12%
28	90	3.72%		82	122	6.98%		262	274	4.19%
28	87	3.26%		82	104	6.98%		262	255	4.19%
28	264	3.26%		82	124	6.98%		262	209	3.72%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
29	29	100.00%		82	8	6.51%		263	263	100.00%
29	309	45.12%		82	2	6.51%		263	253	19.53%
29	1	43.26%		82	312	6.51%		264	264	100.00%
29	8	42.79%		82	34	6.51%		264	213	7.91%
29	6	42.79%		82	298	6.51%		264	124	5.58%
29	7	41.86%		82	314	6.51%		264	131	5.58%
29	18	41.40%		82	297	6.51%		264	66	4.65%
29	22	41.40%		82	16	6.51%		264	64	4.19%
29	15	40.47%		82	259	6.51%		264	101	4.19%
29	2	39.53%		82	40	6.51%		264	74	3.72%
29	20	36.74%		82	14	6.51%		264	26	3.72%
29	27	36.28%		82	46	6.51%		264	71	3.72%
29	12	36.28%		82	79	6.51%		264	65	3.72%
29	28	36.28%		82	102	6.51%		264	245	3.72%
29	24	36.28%		82	13	6.51%		264	28	3.26%
29	30	35.81%		82	89	6.05%		264	9	3.26%
29	9	34.42%		82	10	6.05%		265	265	100.00%
29	21	33.95%		82	313	6.05%		265	266	51.63%
29	26	33.95%		82	38	6.05%		265	254	4.19%
29	16	33.49%		82	153	6.05%		266	266	100.00%
29	10	33.02%		82	129	6.05%		266	265	51.63%
29	13	33.02%		82	121	6.05%		266	254	4.19%
29	14	33.02%		82	44	6.05%		267	267	100.00%
29	23	33.02%		82	64	6.05%		267	162	50.70%
29	25	33.02%		82	23	6.05%		267	248	7.44%
29	11	32.56%		82	21	6.05%		267	99	6.98%
29	19	31.63%		82	77	6.05%		267	146	6.51%
29	17	31.16%		82	78	6.05%		267	282	6.05%
29	31	26.98%		82	101	5.58%		267	94	4.19%
29	37	26.51%		82	81	5.58%		267	160	3.72%
29	310	25.58%		82	65	5.58%		267	154	3.26%
29	314	24.65%		82	19	5.58%		267	113	3.26%
29	38	24.19%		82	62	5.58%		268	268	100.00%
29	69	24.19%		82	103	5.58%		268	276	40.00%
29	298	24.19%		82	88	5.12%		268	225	6.98%
29	311	24.19%		82	43	5.12%		268	277	6.51%
29	36	23.72%		82	111	5.12%		269	269	100.00%
29	312	23.72%		82	66	5.12%		269	216	42.79%
29	32	23.26%		82	109	5.12%		270	270	100.00%
29	313	23.26%		82	68	4.65%		270	195	26.51%
29	35	22.79%		82	67	4.65%		270	89	3.72%
29	43	22.79%		82	29	4.65%		270	87	3.26%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
29	39	21.86%		82	80	4.65%		270	47	3.26%
29	41	21.86%		82	76	4.65%		270	48	3.26%
29	40	21.86%		82	55	4.65%		271	271	100.00%
29	42	21.40%		82	87	4.19%		271	214	35.81%
29	3	21.40%		82	74	4.19%		272	272	100.00%
29	34	19.53%		82	295	4.19%		272	279	15.35%
29	33	18.60%		82	120	4.19%		273	273	100.00%
29	153	17.67%		82	143	4.19%		273	158	13.95%
29	45	15.81%		82	86	3.72%		273	277	7.44%
29	296	14.88%		82	131	3.72%		273	225	7.44%
29	294	13.49%		82	54	3.26%		274	274	100.00%
29	293	12.56%		83	83	100.00%		274	285	26.98%
29	56	11.16%		83	85	54.42%		274	100	15.81%
29	259	11.16%		83	84	53.02%		274	246	5.58%
29	48	10.70%		83	82	51.63%		274	262	4.19%
29	62	10.70%		83	294	14.42%		275	275	100.00%
29	46	10.70%		83	69	11.16%		275	226	9.30%
29	109	10.70%		83	18	11.16%		275	283	4.19%
29	128	10.70%		83	47	11.16%		275	255	3.72%
29	71	10.23%		83	22	10.70%		275	210	3.26%
29	70	10.23%		83	56	10.70%		276	276	100.00%
29	127	10.23%		83	26	10.70%		276	268	40.00%
29	297	10.23%		83	45	10.23%		276	225	7.91%
29	44	9.77%		83	17	10.23%		276	277	6.51%
29	55	9.77%		83	28	10.23%		277	277	100.00%
29	47	9.77%		83	2	9.77%		277	225	36.28%
29	101	9.77%		83	9	9.77%		277	273	7.44%
29	98	9.30%		83	309	9.77%		277	158	6.98%
29	295	9.30%		83	11	9.77%		277	276	6.51%
29	129	9.30%		83	297	9.30%		277	268	6.51%
29	66	8.84%		83	25	9.30%		277	247	3.72%
29	124	8.84%		83	310	9.30%		278	278	100.00%
29	117	8.84%		83	117	9.30%		278	252	33.95%
29	80	8.37%		83	15	8.84%		278	286	17.21%
29	78	8.37%		83	20	8.84%		279	279	100.00%
29	76	8.37%		83	31	8.84%		279	272	15.35%
29	130	8.37%		83	39	8.84%		280	280	100.00%
29	92	7.91%		83	3	8.37%		280	232	15.81%
29	65	7.91%		83	7	8.37%		280	176	5.12%
29	122	7.91%		83	1	8.37%		280	288	4.65%
29	143	7.91%		83	27	8.37%		280	289	4.65%
29	131	7.44%		83	259	8.37%		281	281	100.00%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
29	102	7.44%		83	293	8.37%		281	258	36.74%
29	75	6.98%		83	296	8.37%		282	282	100.00%
29	79	6.98%		83	37	8.37%		282	248	41.86%
29	81	6.98%		83	6	7.91%		282	99	18.60%
29	67	6.98%		83	30	7.91%		282	267	6.05%
29	77	6.98%		83	35	7.91%		282	93	5.58%
29	107	6.98%		83	41	7.91%		282	154	4.65%
29	126	6.98%		83	42	7.91%		282	146	4.19%
29	132	6.98%		83	8	7.44%		282	162	4.19%
29	104	6.98%		83	24	7.44%		282	160	4.19%
29	116	6.98%		83	76	7.44%		282	94	3.72%
29	74	6.51%		83	34	7.44%		283	283	100.00%
29	89	6.51%		83	64	7.44%		283	257	20.47%
29	111	6.51%		83	314	6.98%		283	275	4.19%
29	110	6.05%		83	129	6.98%		284	284	100.00%
29	103	6.05%		83	102	6.98%		284	208	40.00%
29	125	6.05%		83	77	6.51%		284	141	4.65%
29	83	5.58%		83	44	6.51%		284	161	3.26%
29	68	5.58%		83	312	6.51%		285	285	100.00%
29	105	5.58%		83	36	6.51%		285	274	26.98%
29	119	5.58%		83	131	6.51%		285	100	15.81%
29	54	5.12%		83	46	6.51%		285	246	6.05%
29	84	5.12%		83	313	6.51%		285	262	5.12%
29	121	5.12%		83	48	6.51%		285	95	4.65%
29	118	5.12%		83	311	6.51%		285	53	3.26%
29	82	4.65%		83	132	6.51%		285	50	3.26%
29	85	4.65%		83	65	6.51%		286	286	100.00%
29	64	4.65%		83	92	6.05%		286	252	24.19%
29	106	4.19%		83	55	6.05%		286	278	17.21%
29	90	3.26%		83	16	6.05%		287	287	100.00%
30	30	100.00%		83	104	6.05%		287	133	12.56%
30	9	49.30%		83	124	6.05%		287	200	5.58%
30	309	49.30%		83	153	6.05%		287	222	3.72%
30	11	48.37%		83	23	6.05%		288	288	100.00%
30	31	47.91%		83	107	6.05%		288	289	78.60%
30	27	46.51%		83	38	6.05%		288	190	17.67%
30	24	43.26%		83	79	6.05%		288	280	4.65%
30	26	42.33%		83	71	6.05%		288	232	3.72%
30	6	41.86%		83	80	6.05%		289	289	100.00%
30	1	41.86%		83	78	6.05%		289	288	78.60%
30	28	41.86%		83	40	6.05%		289	190	18.14%
30	15	40.93%		83	13	6.05%		289	280	4.65%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
30	17	40.93%		83	10	5.58%		289	232	3.72%
30	20	40.47%		83	89	5.58%		290	290	100.00%
30	25	40.00%		83	121	5.58%		290	178	9.30%
30	7	39.53%		83	122	5.58%		290	182	4.65%
30	37	39.07%		83	29	5.58%		291	291	100.00%
30	8	38.60%		83	298	5.58%		291	179	13.02%
30	18	36.74%		83	81	5.58%		291	199	3.72%
30	16	36.74%		83	101	5.58%		292	292	100.00%
30	22	36.28%		83	66	5.58%		292	221	5.12%
30	12	36.28%		83	127	5.58%		293	293	100.00%
30	29	35.81%		83	14	5.58%		293	80	59.07%
30	10	33.95%		83	43	5.58%		293	127	44.19%
30	14	33.95%		83	103	5.58%		293	101	22.33%
30	23	33.95%		83	109	5.58%		293	124	21.40%
30	21	33.95%		83	62	5.58%		293	71	20.00%
30	310	33.49%		83	33	5.12%		293	64	20.00%
30	13	33.02%		83	12	5.12%		293	109	20.00%
30	19	33.02%		83	295	5.12%		293	76	19.53%
30	2	32.09%		83	126	5.12%		293	131	19.07%
30	40	30.23%		83	70	5.12%		293	77	18.60%
30	69	29.30%		83	128	5.12%		293	65	18.60%
30	311	29.30%		83	143	5.12%		293	130	18.60%
30	41	28.37%		83	32	5.12%		293	70	18.14%
30	312	27.91%		83	88	4.65%		293	129	18.14%
30	3	27.44%		83	19	4.65%		293	107	16.74%
30	35	26.98%		83	67	4.65%		293	102	15.81%
30	39	26.98%		83	54	4.65%		293	128	15.81%
30	313	26.98%		83	130	4.65%		293	295	15.35%
30	32	26.51%		83	120	4.19%		293	81	15.35%
30	34	26.51%		83	68	4.19%		293	126	15.35%
30	43	26.05%		83	125	4.19%		293	9	14.88%
30	42	24.65%		83	87	3.72%		293	111	14.88%
30	38	24.65%		83	86	3.72%		293	117	14.42%
30	298	24.65%		83	75	3.26%		293	89	13.49%
30	314	24.65%		84	84	100.00%		293	44	13.49%
30	36	23.26%		84	83	53.02%		293	66	13.49%
30	33	22.33%		84	82	49.77%		293	74	13.49%
30	153	22.33%		84	85	49.30%		293	30	13.49%
30	296	21.40%		84	294	13.49%		293	132	13.49%
30	294	18.14%		84	45	10.23%		293	75	13.02%
30	46	16.28%		84	18	9.30%		293	45	13.02%
30	45	15.81%		84	25	9.30%		293	47	12.56%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
30	48	15.35%		84	31	8.84%		293	29	12.56%
30	109	14.42%		84	20	8.84%		293	309	12.56%
30	62	13.95%		84	22	8.37%		293	20	12.56%
30	71	13.49%		84	3	7.91%		293	294	12.56%
30	293	13.49%		84	47	7.91%		293	110	12.56%
30	101	13.02%		84	11	7.91%		293	25	12.09%
30	259	13.02%		84	310	7.91%		293	69	12.09%
30	70	12.56%		84	296	7.91%		293	67	11.63%
30	117	12.56%		84	56	7.91%		293	24	11.63%
30	107	12.56%		84	9	7.44%		293	15	11.63%
30	295	12.56%		84	15	7.44%		293	27	11.63%
30	44	12.09%		84	312	7.44%		293	11	11.63%
30	47	12.09%		84	28	7.44%		293	17	11.16%
30	124	12.09%		84	311	7.44%		293	31	11.16%
30	103	12.09%		84	69	7.44%		293	1	11.16%
30	297	12.09%		84	2	6.98%		293	7	11.16%
30	65	11.63%		84	1	6.98%		293	116	11.16%
30	78	11.63%		84	26	6.98%		293	68	10.70%
30	79	11.63%		84	27	6.98%		293	62	10.70%
30	89	11.63%		84	36	6.98%		293	26	10.70%
30	56	11.63%		84	17	6.98%		293	46	10.70%
30	127	11.63%		84	259	6.98%		293	296	10.70%
30	80	11.16%		84	102	6.98%		293	6	10.70%
30	76	11.16%		84	7	6.51%		293	28	10.70%
30	77	11.16%		84	6	6.51%		293	37	10.23%
30	64	10.70%		84	44	6.51%		293	8	10.23%
30	81	10.70%		84	298	6.51%		293	104	10.23%
30	92	10.70%		84	309	6.51%		293	23	9.77%
30	55	10.23%		84	42	6.51%		293	16	9.77%
30	129	10.23%		84	297	6.51%		293	56	9.77%
30	121	10.23%		84	109	6.51%		293	10	9.30%
30	143	10.23%		84	35	6.05%		293	48	9.30%
30	102	9.77%		84	46	6.05%		293	19	9.30%
30	111	9.77%		84	81	6.05%		293	21	9.30%
30	128	9.77%		84	66	6.05%		293	298	9.30%
30	130	9.77%		84	70	6.05%		293	22	9.30%
30	110	9.77%		84	71	6.05%		293	125	9.30%
30	66	9.30%		84	293	6.05%		293	92	8.84%
30	85	9.30%		84	39	6.05%		293	2	8.84%
30	67	9.30%		84	124	6.05%		293	18	8.84%
30	98	9.30%		84	313	6.05%		293	3	8.84%
30	132	9.30%		84	314	6.05%		293	14	8.84%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
30	75	8.84%		84	30	6.05%		293	43	8.84%
30	116	8.84%		84	129	6.05%		293	55	8.37%
30	68	8.37%		84	8	5.58%		293	83	8.37%
30	104	8.37%		84	86	5.58%		293	12	8.37%
30	125	8.37%		84	92	5.58%		293	36	8.37%
30	83	7.91%		84	88	5.58%		293	312	8.37%
30	120	7.91%		84	153	5.58%		293	311	8.37%
30	122	7.91%		84	41	5.58%		293	153	8.37%
30	131	7.91%		84	64	5.58%		293	13	7.91%
30	74	7.44%		84	34	5.58%		293	54	7.91%
30	82	7.44%		84	38	5.58%		293	40	7.91%
30	126	7.44%		84	48	5.58%		293	42	7.91%
30	105	7.44%		84	120	5.58%		293	314	7.91%
30	84	6.05%		84	127	5.58%		293	35	7.91%
30	106	6.05%		84	143	5.58%		293	38	7.91%
30	119	6.05%		84	117	5.12%		293	297	7.91%
30	118	6.05%		84	68	5.12%		293	121	7.91%
30	54	5.12%		84	67	5.12%		293	82	7.44%
30	86	5.12%		84	101	5.12%		293	98	7.44%
30	87	4.19%		84	121	5.12%		293	85	7.44%
30	174	3.26%		84	29	5.12%		293	39	7.44%
31	31	100.00%		84	37	5.12%		293	34	7.44%
31	30	47.91%		84	79	5.12%		293	313	7.44%
31	9	43.26%		84	40	5.12%		293	310	7.44%
31	309	41.86%		84	54	5.12%		293	78	6.98%
31	11	40.00%		84	87	4.65%		293	41	6.98%
31	27	40.00%		84	89	4.65%		293	120	6.98%
31	37	39.07%		84	90	4.65%		293	32	6.51%
31	24	39.07%		84	122	4.65%		293	106	6.51%
31	28	38.14%		84	24	4.65%		293	259	6.51%
31	25	36.74%		84	78	4.65%		293	79	6.05%
31	15	36.74%		84	16	4.65%		293	84	6.05%
31	26	36.74%		84	55	4.65%		293	103	5.58%
31	7	36.28%		84	103	4.65%		293	143	5.12%
31	17	36.28%		84	13	4.65%		293	122	4.65%
31	1	33.49%		84	10	4.19%		293	86	4.19%
31	8	33.02%		84	76	4.19%		293	105	4.19%
31	6	33.02%		84	131	4.19%		293	33	3.72%
31	20	33.02%		84	43	4.19%		293	213	3.72%
31	16	32.56%		84	126	4.19%		293	88	3.26%
31	310	31.63%		84	77	4.19%		293	119	3.26%
31	22	30.70%		84	23	4.19%		293	118	3.26%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
31	18	30.70%		84	14	4.19%		294	294	100.00%
31	2	29.77%		84	62	4.19%		294	69	21.86%
31	12	29.30%		84	32	4.19%		294	296	21.86%
31	311	28.84%		84	12	3.72%		294	11	20.47%
31	3	28.37%		84	104	3.72%		294	9	20.00%
31	14	28.37%		85	85	100.00%		294	27	19.07%
31	23	28.37%		85	82	78.14%		294	311	19.07%
31	10	27.91%		85	83	54.42%		294	37	19.07%
31	34	27.91%		85	84	49.30%		294	18	18.60%
31	19	27.91%		85	294	13.49%		294	309	18.60%
31	312	27.91%		85	11	12.56%		294	6	18.60%
31	41	27.44%		85	15	10.70%		294	41	18.60%
31	13	27.44%		85	309	10.70%		294	20	18.60%
31	21	27.44%		85	18	10.23%		294	35	18.60%
31	39	26.98%		85	25	10.23%		294	259	18.60%
31	69	26.98%		85	31	9.77%		294	22	18.14%
31	29	26.98%		85	20	9.77%		294	7	18.14%
31	40	26.51%		85	9	9.30%		294	30	18.14%
31	313	26.51%		85	28	9.30%		294	31	18.14%
31	35	25.58%		85	30	9.30%		294	2	17.67%
31	43	25.58%		85	69	9.30%		294	1	17.67%
31	32	25.12%		85	6	8.84%		294	28	17.67%
31	38	24.65%		85	45	8.84%		294	24	17.67%
31	314	24.65%		85	1	8.37%		294	34	17.67%
31	42	23.72%		85	27	8.37%		294	16	17.21%
31	36	23.26%		85	56	8.37%		294	3	17.21%
31	153	23.26%		85	296	8.37%		294	310	17.21%
31	298	23.26%		85	26	7.91%		294	8	17.21%
31	296	20.47%		85	47	7.91%		294	15	17.21%
31	33	19.07%		85	7	7.44%		294	153	17.21%
31	294	18.14%		85	310	7.44%		294	39	16.74%
31	46	16.74%		85	22	7.44%		294	26	16.74%
31	48	15.81%		85	293	7.44%		294	25	16.74%
31	259	15.81%		85	16	7.44%		294	45	16.74%
31	45	15.35%		85	24	7.44%		294	43	16.28%
31	47	14.42%		85	39	7.44%		294	313	16.28%
31	71	13.02%		85	42	6.98%		294	312	16.28%
31	124	13.02%		85	8	6.51%		294	12	16.28%
31	109	12.56%		85	2	6.51%		294	40	15.81%
31	92	11.63%		85	17	6.51%		294	314	15.81%
31	62	11.63%		85	41	6.51%		294	17	15.81%
31	293	11.16%		85	124	6.51%		294	36	15.35%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
31	56	10.70%		85	121	6.51%		294	48	15.35%
31	129	10.70%		85	35	6.51%		294	32	15.35%
31	66	10.23%		85	13	6.51%		294	23	14.88%
31	44	10.23%		85	3	6.05%		294	21	14.88%
31	70	10.23%		85	314	6.05%		294	298	14.88%
31	297	10.23%		85	104	6.05%		294	38	14.88%
31	85	9.77%		85	311	6.05%		294	10	14.42%
31	79	9.77%		85	313	6.05%		294	14	14.42%
31	101	9.77%		85	312	6.05%		294	19	14.42%
31	127	9.77%		85	65	6.05%		294	83	14.42%
31	103	9.77%		85	129	6.05%		294	109	14.42%
31	76	9.30%		85	62	6.05%		294	71	13.95%
31	122	9.30%		85	102	6.05%		294	13	13.95%
31	132	9.30%		85	36	5.58%		294	42	13.95%
31	128	9.30%		85	80	5.58%		294	84	13.49%
31	82	8.84%		85	38	5.58%		294	85	13.49%
31	65	8.84%		85	127	5.58%		294	33	13.49%
31	81	8.84%		85	297	5.58%		294	70	13.49%
31	84	8.84%		85	19	5.58%		294	29	13.49%
31	89	8.84%		85	79	5.58%		294	46	13.49%
31	83	8.84%		85	78	5.58%		294	82	13.02%
31	78	8.84%		85	10	5.12%		294	47	13.02%
31	64	8.84%		85	117	5.12%		294	56	13.02%
31	55	8.84%		85	298	5.12%		294	102	13.02%
31	143	8.84%		85	48	5.12%		294	77	12.56%
31	117	8.37%		85	34	5.12%		294	293	12.56%
31	107	8.37%		85	81	5.12%		294	81	12.09%
31	111	8.37%		85	44	5.12%		294	297	12.09%
31	110	8.37%		85	14	5.12%		294	124	12.09%
31	67	7.91%		85	103	5.12%		294	66	11.63%
31	77	7.91%		85	23	5.12%		294	67	11.63%
31	295	7.91%		85	77	5.12%		294	65	11.63%
31	131	7.91%		85	40	5.12%		294	92	11.63%
31	130	7.91%		85	259	5.12%		294	129	11.63%
31	80	7.44%		85	98	4.65%		294	111	11.63%
31	121	7.44%		85	89	4.65%		294	107	11.63%
31	120	7.44%		85	88	4.65%		294	64	11.16%
31	102	7.44%		85	76	4.65%		294	295	11.16%
31	68	6.98%		85	101	4.65%		294	68	11.16%
31	75	6.98%		85	29	4.65%		294	80	11.16%
31	106	6.98%		85	122	4.65%		294	101	11.16%
31	125	6.98%		85	12	4.65%		294	127	11.16%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
31	104	6.98%		85	64	4.65%		294	79	10.70%
31	105	6.51%		85	66	4.65%		294	44	10.70%
31	116	6.05%		85	153	4.65%		294	110	10.70%
31	126	6.05%		85	37	4.65%		294	128	10.70%
31	74	5.58%		85	120	4.65%		294	76	10.23%
31	54	5.58%		85	143	4.65%		294	117	10.23%
31	98	5.12%		85	86	4.19%		294	55	9.30%
31	86	4.65%		85	87	3.72%		294	126	9.30%
31	90	4.65%		85	55	3.72%		294	104	9.30%
31	88	3.72%		85	75	3.26%		294	121	9.30%
31	118	3.72%		85	295	3.26%		294	89	8.84%
31	251	3.72%		86	86	100.00%		294	78	8.84%
31	119	3.72%		86	88	51.63%		294	62	8.37%
31	174	3.26%		86	87	49.30%		294	131	8.37%
32	32	100.00%		86	90	45.12%		294	103	8.37%
32	40	62.33%		86	102	6.51%		294	74	7.91%
32	311	60.93%		86	21	6.05%		294	125	7.91%
32	310	59.07%		86	84	5.58%		294	122	7.91%
32	312	57.21%		86	44	5.58%		294	75	7.44%
32	41	56.74%		86	1	5.12%		294	130	6.98%
32	313	56.74%		86	64	5.12%		294	116	6.98%
32	39	53.95%		86	77	5.12%		294	98	6.51%
32	34	52.56%		86	15	5.12%		294	120	6.51%
32	33	51.63%		86	314	5.12%		294	143	6.51%
32	43	51.63%		86	309	5.12%		294	132	5.58%
32	3	51.16%		86	30	5.12%		294	106	4.65%
32	314	50.23%		86	297	5.12%		294	174	4.19%
32	35	49.77%		86	13	5.12%		294	88	3.72%
32	42	49.30%		86	7	4.65%		294	86	3.72%
32	298	49.30%		86	9	4.65%		294	138	2.79%
32	36	48.84%		86	6	4.65%		295	295	100.00%
32	38	46.98%		86	10	4.65%		295	81	62.33%
32	37	38.60%		86	28	4.65%		295	111	40.00%
32	11	29.30%		86	39	4.65%		295	110	38.60%
32	28	29.30%		86	41	4.65%		295	101	24.19%
32	309	29.30%		86	62	4.65%		295	77	23.72%
32	15	28.84%		86	31	4.65%		295	76	22.33%
32	20	28.84%		86	19	4.65%		295	102	21.86%
32	9	28.37%		86	45	4.65%		295	107	20.93%
32	27	27.91%		86	23	4.65%		295	124	20.47%
32	17	27.44%		86	14	4.65%		295	70	20.00%
32	16	26.51%		86	92	4.19%		295	109	20.00%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
32	30	26.51%		86	8	4.19%		295	71	19.53%
32	1	26.05%		86	2	4.19%		295	89	19.07%
32	7	26.05%		86	153	4.19%		295	64	18.14%
32	24	26.05%		86	107	4.19%		295	65	18.14%
32	6	25.58%		86	81	4.19%		295	117	17.21%
32	25	25.12%		86	128	4.19%		295	80	16.28%
32	31	25.12%		86	117	4.19%		295	131	15.81%
32	8	24.65%		86	103	4.19%		295	293	15.35%
32	12	24.65%		86	76	4.19%		295	66	14.42%
32	26	24.19%		86	111	4.19%		295	67	13.95%
32	22	23.72%		86	293	4.19%		295	309	13.49%
32	69	23.26%		86	38	4.19%		295	126	13.49%
32	21	23.26%		86	85	4.19%		295	69	12.56%
32	29	23.26%		86	55	4.19%		295	7	12.56%
32	153	23.26%		86	120	4.19%		295	30	12.56%
32	13	22.33%		86	116	4.19%		295	74	12.56%
32	18	22.33%		86	32	4.19%		295	132	12.56%
32	2	21.86%		86	312	3.72%		295	68	12.09%
32	19	21.86%		86	310	3.72%		295	15	12.09%
32	10	21.40%		86	42	3.72%		295	129	12.09%
32	14	21.40%		86	27	3.72%		295	127	12.09%
32	23	21.40%		86	127	3.72%		295	27	11.63%
32	296	17.67%		86	43	3.72%		295	24	11.63%
32	294	15.35%		86	313	3.72%		295	17	11.63%
32	47	13.95%		86	83	3.72%		295	153	11.63%
32	259	13.95%		86	294	3.72%		295	130	11.63%
32	48	13.49%		86	11	3.72%		295	25	11.16%
32	92	13.02%		86	259	3.72%		295	28	11.16%
32	45	12.56%		86	82	3.72%		295	12	11.16%
32	46	11.63%		86	22	3.72%		295	32	11.16%
32	295	11.16%		86	20	3.72%		295	128	11.16%
32	81	10.70%		86	12	3.72%		295	294	11.16%
32	71	9.77%		86	109	3.72%		295	1	10.70%
32	76	9.77%		86	18	3.26%		295	9	10.70%
32	107	9.77%		86	26	3.26%		295	8	10.70%
32	297	9.77%		86	47	3.26%		295	26	10.70%
32	44	9.30%		86	16	3.26%		295	6	10.23%
32	101	8.84%		87	87	100.00%		295	44	9.77%
32	109	8.84%		87	88	63.72%		295	75	9.77%
32	124	8.84%		87	90	49.77%		295	16	9.77%
32	67	8.37%		87	86	49.30%		295	22	9.77%
32	70	8.37%		87	84	4.65%		295	11	9.77%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
32	77	8.37%		87	12	4.65%		295	37	9.77%
32	128	8.37%		87	8	4.19%		295	116	9.77%
32	66	7.91%		87	45	4.19%		295	29	9.30%
32	102	7.91%		87	64	4.19%		295	47	9.30%
32	110	7.91%		87	30	4.19%		295	2	9.30%
32	116	7.91%		87	82	4.19%		295	19	9.30%
32	130	7.91%		87	309	4.19%		295	43	9.30%
32	56	7.44%		87	13	4.19%		295	56	8.84%
32	111	7.44%		87	7	3.72%		295	21	8.84%
32	117	7.44%		87	2	3.72%		295	10	8.84%
32	122	7.44%		87	298	3.72%		295	23	8.84%
32	129	7.44%		87	55	3.72%		295	14	8.84%
32	132	7.44%		87	83	3.72%		295	18	8.84%
32	65	6.98%		87	314	3.72%		295	312	8.37%
32	68	6.98%		87	46	3.72%		295	310	8.37%
32	89	6.98%		87	85	3.72%		295	298	8.37%
32	104	6.98%		87	6	3.26%		295	13	8.37%
32	127	6.98%		87	28	3.26%		295	314	8.37%
32	55	6.51%		87	38	3.26%		295	20	8.37%
32	64	6.51%		87	259	3.26%		295	48	8.37%
32	98	6.51%		87	270	3.26%		295	313	7.91%
32	103	6.51%		88	88	100.00%		295	311	7.91%
32	121	6.51%		88	87	63.72%		295	38	7.91%
32	131	6.51%		88	86	51.63%		295	39	7.91%
32	143	6.51%		88	90	50.23%		295	34	7.91%
32	293	6.51%		88	92	6.05%		295	45	7.91%
32	62	6.05%		88	121	6.05%		295	31	7.91%
32	78	6.05%		88	7	5.58%		295	36	7.44%
32	79	6.05%		88	120	5.58%		295	46	7.44%
32	106	6.05%		88	12	5.58%		295	42	7.44%
32	75	5.58%		88	309	5.58%		295	35	7.44%
32	74	5.12%		88	44	5.58%		295	296	6.98%
32	80	5.12%		88	84	5.58%		295	55	6.98%
32	83	5.12%		88	1	5.12%		295	40	6.98%
32	126	5.12%		88	15	5.12%		295	41	6.98%
32	125	4.65%		88	21	5.12%		295	297	6.98%
32	84	4.19%		88	82	5.12%		295	121	6.98%
32	86	4.19%		88	8	4.65%		295	92	6.51%
32	105	3.72%		88	2	4.65%		295	98	6.51%
32	120	3.72%		88	6	4.65%		295	33	6.51%
33	33	100.00%		88	129	4.65%		295	3	6.51%
33	40	58.14%		88	128	4.65%		295	259	6.51%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
33	311	52.56%		88	259	4.65%		295	125	6.05%
33	32	51.63%		88	297	4.65%		295	106	6.05%
33	39	50.23%		88	83	4.65%		295	62	5.58%
33	310	49.77%		88	85	4.65%		295	120	5.58%
33	41	49.30%		88	47	4.65%		295	103	5.58%
33	313	47.44%		88	39	4.19%		295	83	5.12%
33	312	46.98%		88	40	4.19%		295	79	5.12%
33	34	46.05%		88	64	4.19%		295	78	5.12%
33	42	45.12%		88	28	4.19%		295	104	4.65%
33	298	44.19%		88	62	4.19%		295	143	4.65%
33	43	42.79%		88	55	4.19%		295	82	4.19%
33	36	42.33%		88	46	4.19%		295	105	4.19%
33	314	42.33%		88	22	4.19%		295	251	4.19%
33	35	41.40%		88	109	4.19%		295	238	4.19%
33	3	40.00%		88	10	3.72%		295	85	3.26%
33	38	39.53%		88	143	3.72%		295	54	2.79%
33	37	33.49%		88	311	3.72%		296	296	100.00%
33	309	25.58%		88	45	3.72%		296	69	24.65%
33	11	24.65%		88	153	3.72%		296	11	24.65%
33	1	24.19%		88	70	3.72%		296	9	23.26%
33	15	24.19%		88	313	3.72%		296	28	22.79%
33	17	24.19%		88	312	3.72%		296	27	21.86%
33	27	23.72%		88	314	3.72%		296	294	21.86%
33	6	23.26%		88	294	3.72%		296	309	21.40%
33	9	23.26%		88	24	3.72%		296	30	21.40%
33	8	22.79%		88	18	3.72%		296	37	21.40%
33	7	22.33%		88	14	3.72%		296	7	20.47%
33	24	22.33%		88	23	3.72%		296	31	20.47%
33	30	22.33%		88	31	3.72%		296	20	20.47%
33	26	22.33%		88	77	3.26%		296	25	20.00%
33	28	21.86%		88	124	3.26%		296	16	20.00%
33	20	21.86%		88	26	3.26%		296	35	20.00%
33	25	21.86%		88	293	3.26%		296	45	20.00%
33	12	21.40%		88	110	3.26%		296	8	19.53%
33	18	20.47%		88	111	3.26%		296	6	19.53%
33	22	20.00%		88	117	3.26%		296	40	19.53%
33	153	20.00%		89	89	100.00%		296	15	19.07%
33	69	19.53%		89	101	23.72%		296	22	19.07%
33	16	19.53%		89	65	19.53%		296	310	19.07%
33	2	19.07%		89	295	19.07%		296	311	19.07%
33	31	19.07%		89	124	18.60%		296	47	18.60%
33	29	18.60%		89	117	18.14%		296	17	18.60%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
33	13	17.67%		89	64	18.14%		296	26	18.60%
33	23	17.21%		89	81	17.67%		296	24	18.60%
33	21	17.21%		89	129	17.67%		296	18	18.14%
33	10	16.74%		89	109	17.67%		296	1	18.14%
33	19	16.74%		89	70	17.67%		296	3	18.14%
33	14	16.74%		89	71	17.21%		296	32	17.67%
33	296	13.95%		89	107	16.28%		296	12	17.67%
33	294	13.49%		89	75	16.28%		296	41	17.21%
33	45	12.56%		89	66	16.28%		296	313	17.21%
33	47	10.70%		89	80	15.81%		296	39	17.21%
33	48	10.70%		89	111	15.81%		296	34	17.21%
33	259	10.23%		89	102	15.35%		296	298	16.74%
33	46	9.30%		89	131	15.35%		296	48	16.74%
33	92	9.30%		89	77	15.35%		296	2	16.28%
33	56	7.91%		89	76	15.35%		296	43	16.28%
33	66	6.98%		89	128	14.88%		296	10	15.81%
33	297	6.98%		89	74	14.42%		296	36	15.81%
33	124	6.98%		89	130	14.42%		296	312	15.81%
33	77	6.51%		89	293	13.49%		296	19	15.35%
33	295	6.51%		89	309	13.49%		296	14	15.35%
33	109	6.51%		89	126	13.02%		296	23	15.35%
33	129	6.51%		89	16	13.02%		296	13	14.88%
33	71	6.05%		89	127	12.56%		296	29	14.88%
33	44	6.05%		89	110	12.56%		296	92	14.88%
33	76	6.05%		89	28	12.56%		296	42	14.88%
33	81	6.05%		89	9	12.09%		296	314	14.88%
33	107	6.05%		89	45	12.09%		296	21	14.42%
33	122	6.05%		89	69	12.09%		296	56	14.42%
33	128	6.05%		89	67	11.63%		296	38	14.42%
33	102	6.05%		89	47	11.63%		296	153	14.42%
33	70	5.58%		89	27	11.63%		296	259	14.42%
33	79	5.58%		89	30	11.63%		296	33	13.95%
33	103	5.58%		89	25	11.63%		296	79	12.09%
33	83	5.12%		89	68	11.16%		296	44	12.09%
33	55	5.12%		89	132	10.70%		296	109	12.09%
33	78	5.12%		89	19	10.70%		296	71	11.63%
33	127	5.12%		89	11	10.70%		296	70	11.63%
33	131	5.12%		89	10	10.23%		296	297	11.63%
33	111	5.12%		89	7	10.23%		296	124	11.63%
33	110	5.12%		89	1	10.23%		296	76	11.16%
33	126	5.12%		89	6	10.23%		296	78	11.16%
33	116	5.12%		89	23	10.23%		296	46	11.16%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
33	64	4.65%		89	18	10.23%		296	103	11.16%
33	62	4.65%		89	21	10.23%		296	62	10.70%
33	104	4.65%		89	15	9.77%		296	65	10.70%
33	68	4.19%		89	14	9.77%		296	102	10.70%
33	101	4.19%		89	13	9.77%		296	293	10.70%
33	130	4.19%		89	8	9.30%		296	55	10.23%
33	121	4.19%		89	48	9.30%		296	77	10.23%
33	143	4.19%		89	22	9.30%		296	107	10.23%
33	65	3.72%		89	310	8.84%		296	104	9.77%
33	293	3.72%		89	312	8.84%		296	101	9.77%
33	98	3.26%		89	116	8.84%		296	80	9.30%
34	34	100.00%		89	294	8.84%		296	120	9.30%
34	41	78.60%		89	31	8.84%		296	127	9.30%
34	311	69.30%		89	26	8.84%		296	121	9.30%
34	310	63.72%		89	12	8.84%		296	111	9.30%
34	312	62.79%		89	20	8.84%		296	66	8.84%
34	39	61.40%		89	43	8.37%		296	122	8.84%
34	313	60.93%		89	40	8.37%		296	117	8.84%
34	35	56.74%		89	298	7.91%		296	131	8.84%
34	298	56.28%		89	37	7.91%		296	128	8.84%
34	36	55.81%		89	296	7.91%		296	98	8.37%
34	43	55.81%		89	153	7.91%		296	64	8.37%
34	314	54.88%		89	44	7.91%		296	83	8.37%
34	40	53.49%		89	314	7.91%		296	85	8.37%
34	3	53.49%		89	24	7.91%		296	110	8.37%
34	42	53.49%		89	17	7.91%		296	75	7.91%
34	32	52.56%		89	2	7.44%		296	89	7.91%
34	38	50.70%		89	3	7.44%		296	84	7.91%
34	33	46.05%		89	122	7.44%		296	82	7.91%
34	37	38.14%		89	41	7.44%		296	116	7.91%
34	11	32.56%		89	313	7.44%		296	143	7.44%
34	309	32.56%		89	311	7.44%		296	295	6.98%
34	27	31.63%		89	35	7.44%		296	106	6.98%
34	9	29.30%		89	38	6.98%		296	68	6.51%
34	1	29.30%		89	62	6.98%		296	67	6.51%
34	15	29.30%		89	32	6.98%		296	132	6.51%
34	28	28.84%		89	92	6.51%		296	130	6.51%
34	6	28.37%		89	56	6.51%		296	129	6.51%
34	17	28.37%		89	36	6.51%		296	74	6.05%
34	8	27.91%		89	46	6.51%		296	54	6.05%
34	31	27.91%		89	29	6.51%		296	81	6.05%
34	7	27.44%		89	259	6.05%		296	105	6.05%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
34	20	27.44%		89	82	6.05%		296	125	5.12%
34	26	27.44%		89	98	5.58%		296	126	5.12%
34	25	26.51%		89	55	5.58%		296	119	4.19%
34	30	26.51%		89	39	5.58%		296	118	3.72%
34	16	26.05%		89	34	5.58%		297	297	100.00%
34	24	26.05%		89	83	5.58%		297	45	14.88%
34	18	25.58%		89	103	5.12%		297	309	14.42%
34	153	25.58%		89	121	5.12%		297	310	14.42%
34	12	25.58%		89	42	5.12%		297	27	13.95%
34	22	24.65%		89	297	5.12%		297	25	13.49%
34	2	22.79%		89	105	5.12%		297	9	13.49%
34	21	22.79%		89	85	4.65%		297	20	13.49%
34	13	22.33%		89	84	4.65%		297	3	13.02%
34	14	21.86%		89	120	4.19%		297	311	12.56%
34	23	21.86%		89	104	4.19%		297	28	12.56%
34	10	21.40%		89	78	4.19%		297	40	12.09%
34	19	21.40%		89	143	4.19%		297	39	12.09%
34	69	20.47%		89	125	4.19%		297	16	12.09%
34	29	19.53%		89	106	3.72%		297	15	12.09%
34	294	17.67%		89	119	3.72%		297	30	12.09%
34	296	17.21%		89	270	3.72%		297	294	12.09%
34	259	15.81%		89	251	3.26%		297	62	11.63%
34	48	13.02%		89	118	3.26%		297	35	11.63%
34	45	12.56%		90	90	100.00%		297	47	11.63%
34	46	11.63%		90	88	50.23%		297	18	11.63%
34	109	11.63%		90	87	49.77%		297	26	11.63%
34	101	11.63%		90	86	45.12%		297	69	11.63%
34	71	11.16%		90	7	5.58%		297	296	11.63%
34	76	11.16%		90	8	5.12%		297	312	11.16%
34	92	10.70%		90	13	5.12%		297	1	11.16%
34	70	10.70%		90	6	4.65%		297	7	11.16%
34	47	9.77%		90	45	4.65%		297	11	11.16%
34	56	9.77%		90	259	4.65%		297	56	11.16%
34	297	9.77%		90	31	4.65%		297	6	11.16%
34	77	9.30%		90	24	4.65%		297	41	10.70%
34	107	9.30%		90	48	4.65%		297	14	10.70%
34	124	8.84%		90	21	4.65%		297	12	10.70%
34	129	8.84%		90	84	4.65%		297	21	10.23%
34	128	8.84%		90	10	4.19%		297	23	10.23%
34	81	8.37%		90	11	4.19%		297	22	10.23%
34	102	8.37%		90	309	4.19%		297	314	10.23%
34	127	8.37%		90	314	4.19%		297	31	10.23%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
34	66	7.91%		90	38	4.19%		297	29	10.23%
34	79	7.91%		90	14	4.19%		297	37	10.23%
34	62	7.91%		90	23	4.19%		297	36	9.77%
34	295	7.91%		90	22	4.19%		297	13	9.77%
34	65	7.44%		90	297	4.19%		297	34	9.77%
34	98	7.44%		90	1	3.72%		297	10	9.77%
34	83	7.44%		90	2	3.72%		297	78	9.77%
34	44	7.44%		90	18	3.72%		297	2	9.77%
34	78	7.44%		90	28	3.72%		297	19	9.77%
34	293	7.44%		90	79	3.72%		297	8	9.77%
34	55	6.98%		90	27	3.72%		297	32	9.77%
34	121	6.98%		90	92	3.26%		297	259	9.77%
34	104	6.98%		90	29	3.26%		297	83	9.30%
34	122	6.98%		90	122	3.26%		297	298	9.30%
34	82	6.51%		90	62	3.26%		297	79	9.30%
34	126	6.51%		90	19	3.26%		297	38	9.30%
34	132	6.51%		90	120	3.26%		297	17	9.30%
34	111	6.51%		91	91	100.00%		297	55	8.84%
34	116	6.51%		91	60	36.74%		297	92	8.84%
34	68	6.05%		91	61	35.81%		297	44	8.84%
34	67	6.05%		91	53	33.02%		297	42	8.84%
34	64	6.05%		91	50	32.56%		297	48	8.84%
34	117	6.05%		91	52	26.51%		297	80	8.84%
34	110	6.05%		91	142	26.51%		297	103	8.84%
34	103	6.05%		91	58	25.12%		297	313	8.37%
34	130	6.05%		91	49	24.19%		297	121	8.37%
34	143	6.05%		91	57	20.47%		297	43	7.91%
34	84	5.58%		91	95	19.53%		297	143	7.91%
34	89	5.58%		91	97	19.07%		297	111	7.91%
34	125	5.58%		91	96	18.14%		297	293	7.91%
34	85	5.12%		91	63	16.28%		297	118	7.91%
34	80	5.12%		91	108	15.81%		297	46	7.44%
34	131	5.12%		91	303	12.09%		297	24	7.44%
34	106	5.12%		91	307	11.63%		297	81	7.44%
34	74	4.65%		91	306	11.16%		297	129	7.44%
34	105	4.65%		91	300	10.23%		297	130	7.44%
34	75	4.19%		91	308	9.77%		297	110	7.44%
34	119	4.19%		91	302	9.77%		297	119	7.44%
34	120	4.19%		91	305	9.30%		297	33	6.98%
35	35	100.00%		91	304	9.30%		297	76	6.98%
35	311	61.86%		91	59	9.30%		297	104	6.98%
35	41	58.14%		91	301	8.84%		297	295	6.98%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
35	313	57.21%		91	51	8.84%		297	82	6.51%
35	310	57.21%		91	299	6.51%		297	84	6.51%
35	312	57.21%		91	229	4.65%		297	65	6.51%
35	34	56.74%		91	159	3.72%		297	64	6.51%
35	3	52.56%		91	194	3.72%		297	126	6.51%
35	43	52.09%		91	100	3.26%		297	122	6.51%
35	314	52.09%		91	255	3.26%		297	132	6.51%
35	39	51.63%		91	228	3.26%		297	127	6.51%
35	298	51.16%		91	193	3.26%		297	102	6.51%
35	38	50.70%		92	92	100.00%		297	131	6.51%
35	36	50.70%		92	310	17.21%		297	101	6.05%
35	32	49.77%		92	69	15.35%		297	128	6.05%
35	40	49.30%		92	35	14.88%		297	106	6.05%
35	42	45.12%		92	36	14.88%		297	153	6.05%
35	33	41.40%		92	296	14.88%		297	109	6.05%
35	37	40.00%		92	3	14.42%		297	85	5.58%
35	309	32.09%		92	298	14.42%		297	77	5.58%
35	11	31.16%		92	312	14.42%		297	124	5.58%
35	20	30.70%		92	311	14.42%		297	120	5.58%
35	27	30.70%		92	25	14.42%		297	125	5.58%
35	28	30.23%		92	313	13.95%		297	89	5.12%
35	9	29.77%		92	37	13.49%		297	71	5.12%
35	24	29.30%		92	314	13.49%		297	98	5.12%
35	17	29.30%		92	38	13.49%		297	86	5.12%
35	1	28.84%		92	259	13.49%		297	105	5.12%
35	8	28.37%		92	32	13.02%		297	107	5.12%
35	6	28.37%		92	43	13.02%		297	117	5.12%
35	15	28.37%		92	153	13.02%		297	116	5.12%
35	7	27.91%		92	27	12.56%		297	70	4.65%
35	25	27.91%		92	7	12.09%		297	66	4.65%
35	153	27.91%		92	41	12.09%		297	75	4.65%
35	18	27.44%		92	309	12.09%		297	88	4.65%
35	26	26.98%		92	40	12.09%		297	67	4.19%
35	30	26.98%		92	15	11.63%		297	90	4.19%
35	31	25.58%		92	47	11.63%		297	74	4.19%
35	16	25.12%		92	31	11.63%		297	54	3.72%
35	12	25.12%		92	17	11.63%		297	68	3.26%
35	22	24.65%		92	20	11.63%		298	298	100.00%
35	13	24.19%		92	45	11.63%		298	36	87.91%
35	2	23.72%		92	22	11.63%		298	312	74.42%
35	69	23.26%		92	26	11.63%		298	313	73.02%
35	10	22.79%		92	62	11.63%		298	43	72.09%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
35	23	22.79%		92	294	11.63%		298	311	64.65%
35	21	22.79%		92	9	11.16%		298	314	60.00%
35	19	22.79%		92	42	11.16%		298	310	60.00%
35	29	22.79%		92	28	11.16%		298	41	57.21%
35	14	22.33%		92	39	11.16%		298	34	56.28%
35	296	20.00%		92	48	11.16%		298	39	54.88%
35	294	18.60%		92	1	10.70%		298	38	54.42%
35	259	16.28%		92	34	10.70%		298	35	51.16%
35	48	15.35%		92	24	10.70%		298	3	50.70%
35	92	14.88%		92	30	10.70%		298	40	49.77%
35	71	13.95%		92	11	10.70%		298	32	49.30%
35	45	12.56%		92	10	10.23%		298	42	47.91%
35	109	12.56%		92	6	10.23%		298	33	44.19%
35	46	12.09%		92	8	10.23%		298	37	37.21%
35	76	12.09%		92	56	10.23%		298	20	30.23%
35	47	11.63%		92	77	10.23%		298	309	30.23%
35	56	11.63%		92	124	10.23%		298	28	30.23%
35	297	11.63%		92	21	10.23%		298	15	28.84%
35	70	11.16%		92	23	10.23%		298	25	27.44%
35	66	11.16%		92	131	10.23%		298	8	27.44%
35	77	11.16%		92	55	10.23%		298	24	26.98%
35	101	11.16%		92	14	10.23%		298	7	26.98%
35	107	10.23%		92	13	10.23%		298	11	26.51%
35	79	9.30%		92	107	9.77%		298	1	26.51%
35	124	9.30%		92	71	9.77%		298	6	26.51%
35	55	8.84%		92	128	9.30%		298	27	26.51%
35	67	8.84%		92	66	9.30%		298	9	25.58%
35	62	8.84%		92	104	9.30%		298	153	25.58%
35	111	8.84%		92	76	9.30%		298	12	25.12%
35	103	8.84%		92	16	9.30%		298	16	24.65%
35	65	8.37%		92	33	9.30%		298	30	24.65%
35	78	8.37%		92	116	9.30%		298	29	24.19%
35	117	8.37%		92	74	8.84%		298	17	24.19%
35	128	8.37%		92	293	8.84%		298	18	23.72%
35	129	8.37%		92	129	8.84%		298	31	23.26%
35	102	8.37%		92	19	8.84%		298	22	22.79%
35	81	7.91%		92	103	8.84%		298	21	22.79%
35	83	7.91%		92	65	8.84%		298	13	22.79%
35	68	7.91%		92	75	8.84%		298	26	22.79%
35	44	7.91%		92	297	8.84%		298	69	21.86%
35	132	7.91%		92	109	8.84%		298	10	21.86%
35	110	7.91%		92	98	8.37%		298	14	21.40%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
35	293	7.91%		92	2	8.37%		298	2	21.40%
35	98	7.44%		92	64	8.37%		298	19	21.40%
35	80	7.44%		92	79	8.37%		298	23	21.40%
35	89	7.44%		92	18	8.37%		298	296	16.74%
35	122	7.44%		92	70	7.91%		298	294	14.88%
35	127	7.44%		92	81	7.91%		298	92	14.42%
35	130	7.44%		92	101	7.91%		298	47	13.95%
35	295	7.44%		92	29	7.91%		298	259	13.95%
35	131	7.44%		92	67	7.91%		298	46	13.49%
35	82	6.98%		92	68	7.91%		298	48	13.02%
35	64	6.98%		92	78	7.91%		298	45	12.56%
35	121	6.98%		92	44	7.91%		298	71	11.63%
35	104	6.98%		92	111	7.91%		298	76	11.16%
35	74	6.51%		92	130	7.91%		298	81	10.23%
35	85	6.51%		92	46	7.91%		298	66	9.77%
35	84	6.05%		92	117	7.44%		298	77	9.77%
35	54	6.05%		92	12	7.44%		298	107	9.77%
35	106	6.05%		92	102	7.44%		298	124	9.77%
35	125	6.05%		92	122	6.98%		298	101	9.77%
35	75	5.58%		92	127	6.98%		298	122	9.77%
35	126	5.58%		92	121	6.98%		298	131	9.77%
35	116	5.58%		92	80	6.98%		298	62	9.30%
35	143	5.12%		92	110	6.98%		298	127	9.30%
35	105	5.12%		92	295	6.51%		298	297	9.30%
35	119	5.12%		92	89	6.51%		298	293	9.30%
35	118	4.65%		92	126	6.51%		298	128	9.30%
35	120	4.19%		92	120	6.05%		298	129	9.30%
35	174	3.26%		92	83	6.05%		298	109	9.30%
36	36	100.00%		92	88	6.05%		298	55	8.84%
36	298	87.91%		92	143	6.05%		298	64	8.84%
36	312	72.56%		92	54	5.58%		298	98	8.84%
36	313	71.63%		92	84	5.58%		298	44	8.84%
36	43	71.16%		92	132	5.12%		298	79	8.84%
36	311	63.72%		92	86	4.19%		298	78	8.84%
36	310	60.00%		92	125	4.19%		298	65	8.37%
36	314	58.14%		92	105	3.72%		298	70	8.37%
36	41	57.67%		92	90	3.26%		298	74	8.37%
36	34	55.81%		93	93	100.00%		298	75	8.37%
36	39	54.88%		93	94	40.93%		298	295	8.37%
36	38	52.56%		93	282	5.58%		298	104	8.37%
36	35	50.70%		93	248	5.58%		298	102	8.37%
36	40	49.30%		93	113	5.12%		298	89	7.91%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
36	32	48.84%		93	154	4.65%		298	56	7.91%
36	3	48.37%		93	160	4.19%		298	67	7.91%
36	42	47.91%		93	161	3.26%		298	111	7.91%
36	33	42.33%		94	94	100.00%		298	110	7.91%
36	37	37.21%		94	93	40.93%		298	130	7.91%
36	309	29.30%		94	160	5.58%		298	68	7.44%
36	20	28.84%		94	154	5.12%		298	103	7.44%
36	28	28.37%		94	267	4.19%		298	126	7.44%
36	27	27.44%		94	282	3.72%		298	117	7.44%
36	15	26.98%		95	95	100.00%		298	121	6.98%
36	1	26.51%		95	97	23.26%		298	132	6.98%
36	8	26.05%		95	61	20.00%		298	116	6.98%
36	6	26.05%		95	58	20.00%		298	82	6.51%
36	25	26.05%		95	91	19.53%		298	84	6.51%
36	7	25.58%		95	53	18.60%		298	143	6.05%
36	11	25.58%		95	142	18.60%		298	125	6.05%
36	24	25.58%		95	50	18.14%		298	80	5.58%
36	12	24.65%		95	60	17.67%		298	83	5.58%
36	17	24.65%		95	52	17.21%		298	119	5.58%
36	9	24.19%		95	63	16.28%		298	85	5.12%
36	29	23.72%		95	49	15.81%		298	105	4.19%
36	153	23.72%		95	57	14.88%		298	87	3.72%
36	31	23.26%		95	108	14.42%		298	106	3.72%
36	30	23.26%		95	96	12.56%		299	299	100.00%
36	26	23.26%		95	306	11.16%		299	304	72.09%
36	16	22.79%		95	308	10.70%		299	301	69.77%
36	18	22.79%		95	307	9.30%		299	302	69.30%
36	22	21.86%		95	301	8.37%		299	300	68.84%
36	13	21.40%		95	303	8.37%		299	308	35.35%
36	21	21.40%		95	305	8.37%		299	307	34.88%
36	69	20.93%		95	300	6.98%		299	305	34.88%
36	2	20.47%		95	304	6.98%		299	303	34.42%
36	10	20.00%		95	302	6.98%		299	306	33.49%
36	14	20.00%		95	51	6.98%		299	51	10.70%
36	19	20.00%		95	299	6.05%		299	96	9.77%
36	23	20.00%		95	100	4.65%		299	59	9.77%
36	296	15.81%		95	285	4.65%		299	57	8.84%
36	294	15.35%		95	59	4.19%		299	60	8.37%
36	92	14.88%		95	224	3.72%		299	97	7.44%
36	47	13.49%		95	248	3.72%		299	108	7.44%
36	259	13.02%		96	96	100.00%		299	142	6.98%
36	48	12.09%		96	57	67.91%		299	91	6.51%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
36	46	11.63%		96	58	23.72%		299	58	6.51%
36	71	11.16%		96	108	22.33%		299	95	6.05%
36	45	10.70%		96	142	20.47%		299	53	6.05%
36	76	10.70%		96	91	18.14%		299	61	5.58%
36	131	10.23%		96	60	16.28%		299	50	5.58%
36	77	9.77%		96	61	15.81%		300	300	100.00%
36	297	9.77%		96	53	15.81%		300	302	75.35%
36	128	9.77%		96	63	15.81%		300	304	73.95%
36	66	9.30%		96	52	15.35%		300	301	73.49%
36	107	9.30%		96	50	14.88%		300	299	68.84%
36	122	9.30%		96	97	14.42%		300	308	38.60%
36	81	8.84%		96	49	13.95%		300	305	37.21%
36	98	8.84%		96	95	12.56%		300	306	37.21%
36	62	8.84%		96	306	12.09%		300	307	36.74%
36	101	8.84%		96	307	11.63%		300	303	36.28%
36	127	8.84%		96	308	11.16%		300	51	13.02%
36	56	8.37%		96	305	11.16%		300	59	11.63%
36	55	8.37%		96	300	10.23%		300	60	11.16%
36	44	8.37%		96	303	9.77%		300	96	10.23%
36	124	8.37%		96	304	9.77%		300	91	10.23%
36	109	8.37%		96	299	9.77%		300	57	9.30%
36	129	8.37%		96	302	9.30%		300	142	8.84%
36	293	8.37%		96	301	8.84%		300	58	8.37%
36	74	7.91%		96	59	7.91%		300	108	8.37%
36	65	7.91%		96	51	7.91%		300	97	7.91%
36	70	7.91%		96	99	3.72%		300	53	7.44%
36	67	7.91%		96	229	3.72%		300	50	7.44%
36	110	7.91%		97	97	100.00%		300	95	6.98%
36	104	7.91%		97	58	23.72%		300	61	6.98%
36	102	7.91%		97	95	23.26%		300	52	4.65%
36	64	7.44%		97	142	20.93%		301	301	100.00%
36	75	7.44%		97	50	19.07%		301	304	73.95%
36	68	7.44%		97	53	19.07%		301	302	73.49%
36	295	7.44%		97	91	19.07%		301	300	73.49%
36	111	7.44%		97	60	18.60%		301	299	69.77%
36	130	7.44%		97	61	18.14%		301	308	38.60%
36	82	6.98%		97	63	17.21%		301	303	37.21%
36	79	6.98%		97	52	15.35%		301	306	34.88%
36	78	6.98%		97	108	15.35%		301	305	33.95%
36	84	6.98%		97	57	14.88%		301	307	33.95%
36	117	6.98%		97	96	14.42%		301	59	13.02%
36	132	6.98%		97	49	13.95%		301	51	11.63%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
36	126	6.98%		97	300	7.91%		301	60	11.16%
36	89	6.51%		97	302	7.91%		301	142	9.30%
36	83	6.51%		97	59	7.91%		301	96	8.84%
36	143	6.51%		97	304	7.44%		301	91	8.84%
36	121	6.51%		97	308	7.44%		301	95	8.37%
36	85	5.58%		97	306	7.44%		301	57	7.91%
36	116	5.58%		97	299	7.44%		301	58	7.44%
36	103	5.58%		97	307	7.44%		301	53	7.44%
36	119	5.12%		97	303	7.44%		301	50	7.44%
36	125	4.65%		97	305	6.98%		301	61	6.98%
36	106	4.19%		97	301	6.05%		301	108	6.51%
36	118	3.72%		97	51	4.19%		301	97	6.05%
37	37	100.00%		97	224	3.26%		301	52	4.65%
37	310	47.91%		98	98	100.00%		301	49	3.72%
37	311	43.26%		98	78	14.42%		302	302	100.00%
37	9	42.33%		98	79	14.42%		302	304	75.35%
37	40	42.33%		98	62	13.49%		302	300	75.35%
37	309	41.86%		98	103	12.09%		302	301	73.49%
37	3	40.93%		98	20	11.63%		302	299	69.30%
37	41	40.47%		98	9	11.16%		302	308	40.47%
37	39	40.47%		98	104	11.16%		302	305	39.53%
37	312	40.47%		98	55	11.16%		302	307	38.60%
37	11	40.47%		98	28	10.23%		302	306	38.14%
37	35	40.00%		98	120	10.23%		302	303	37.67%
37	31	39.07%		98	11	10.23%		302	59	11.63%
37	314	39.07%		98	56	9.77%		302	60	11.16%
37	30	39.07%		98	69	9.77%		302	51	10.70%
37	32	38.60%		98	121	9.77%		302	91	9.77%
37	27	38.60%		98	29	9.30%		302	96	9.30%
37	42	38.14%		98	24	9.30%		302	57	9.30%
37	34	38.14%		98	80	9.30%		302	108	8.37%
37	38	37.67%		98	30	9.30%		302	58	7.91%
37	15	37.67%		98	6	8.84%		302	97	7.91%
37	28	37.21%		98	312	8.84%		302	142	7.91%
37	36	37.21%		98	36	8.84%		302	53	7.44%
37	298	37.21%		98	298	8.84%		302	95	6.98%
37	17	36.74%		98	1	8.37%		302	61	6.98%
37	26	36.28%		98	3	8.37%		302	50	6.98%
37	24	36.28%		98	76	8.37%		302	52	4.65%
37	313	36.28%		98	296	8.37%		303	303	100.00%
37	43	35.35%		98	25	8.37%		303	308	50.70%
37	25	35.35%		98	92	8.37%		303	307	47.91%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
37	20	35.35%		98	43	7.91%		303	306	46.51%
37	1	33.49%		98	117	7.91%		303	305	46.51%
37	33	33.49%		98	309	7.91%		303	302	37.67%
37	7	33.02%		98	15	7.91%		303	301	37.21%
37	6	33.02%		98	8	7.44%		303	300	36.28%
37	8	32.56%		98	313	7.44%		303	304	35.81%
37	22	32.56%		98	311	7.44%		303	299	34.42%
37	16	32.56%		98	35	7.44%		303	51	14.88%
37	18	32.09%		98	77	7.44%		303	91	12.09%
37	12	32.09%		98	293	7.44%		303	60	11.63%
37	2	30.23%		98	314	7.44%		303	59	11.16%
37	153	29.77%		98	38	7.44%		303	57	10.70%
37	21	27.44%		98	310	7.44%		303	142	10.70%
37	69	26.51%		98	34	7.44%		303	58	10.23%
37	29	26.51%		98	27	7.44%		303	96	9.77%
37	13	26.05%		98	7	6.98%		303	61	8.84%
37	10	25.58%		98	45	6.98%		303	95	8.37%
37	14	25.58%		98	40	6.98%		303	97	7.44%
37	23	25.58%		98	107	6.98%		303	50	6.98%
37	19	24.65%		98	44	6.98%		303	108	6.98%
37	296	21.40%		98	127	6.98%		303	52	6.05%
37	294	19.07%		98	12	6.98%		303	53	5.58%
37	45	16.28%		98	122	6.51%		303	49	4.65%
37	259	16.28%		98	37	6.51%		303	246	3.72%
37	46	14.42%		98	64	6.51%		303	63	3.26%
37	48	14.42%		98	16	6.51%		304	304	100.00%
37	92	13.49%		98	48	6.51%		304	302	75.35%
37	62	12.09%		98	295	6.51%		304	300	73.95%
37	47	11.63%		98	41	6.51%		304	301	73.95%
37	71	11.63%		98	71	6.51%		304	299	72.09%
37	56	11.63%		98	294	6.51%		304	308	37.67%
37	109	11.63%		98	259	6.51%		304	305	37.21%
37	66	11.16%		98	32	6.51%		304	307	36.74%
37	77	11.16%		98	18	6.51%		304	306	35.81%
37	103	11.16%		98	22	6.51%		304	303	35.81%
37	55	10.70%		98	13	6.51%		304	59	11.63%
37	78	10.70%		98	10	6.05%		304	51	11.16%
37	76	10.70%		98	2	6.05%		304	60	10.23%
37	79	10.70%		98	81	6.05%		304	96	9.77%
37	44	10.70%		98	47	6.05%		304	57	9.77%
37	107	10.70%		98	74	6.05%		304	91	9.30%
37	101	10.70%		98	26	6.05%		304	142	8.84%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
37	124	10.70%		98	14	6.05%		304	53	8.37%
37	117	10.70%		98	21	6.05%		304	108	8.37%
37	70	10.23%		98	130	6.05%		304	50	7.91%
37	293	10.23%		98	102	6.05%		304	97	7.44%
37	128	10.23%		98	17	5.58%		304	58	7.44%
37	297	10.23%		98	65	5.58%		304	95	6.98%
37	65	9.77%		98	75	5.58%		304	61	6.98%
37	295	9.77%		98	101	5.58%		304	52	5.12%
37	81	9.30%		98	67	5.58%		305	305	100.00%
37	102	9.30%		98	89	5.58%		305	308	75.35%
37	129	9.30%		98	19	5.58%		305	307	70.70%
37	125	9.30%		98	23	5.58%		305	306	69.30%
37	130	9.30%		98	110	5.12%		305	303	46.51%
37	127	8.84%		98	31	5.12%		305	302	39.53%
37	106	8.84%		98	131	5.12%		305	300	37.21%
37	131	8.84%		98	46	5.12%		305	304	37.21%
37	75	8.37%		98	128	5.12%		305	299	34.88%
37	80	8.37%		98	297	5.12%		305	301	33.95%
37	83	8.37%		98	109	5.12%		305	59	12.09%
37	104	8.37%		98	132	5.12%		305	57	11.63%
37	126	8.37%		98	85	4.65%		305	51	11.63%
37	111	8.37%		98	129	4.65%		305	96	11.16%
37	132	8.37%		98	66	4.65%		305	60	10.70%
37	89	7.91%		98	39	4.65%		305	61	10.23%
37	64	7.91%		98	68	4.65%		305	108	9.77%
37	110	7.91%		98	126	4.65%		305	91	9.30%
37	82	7.44%		98	111	4.19%		305	142	9.30%
37	120	7.44%		98	70	4.19%		305	58	8.84%
37	121	7.44%		98	42	4.19%		305	50	8.37%
37	122	7.44%		98	116	4.19%		305	95	8.37%
37	143	7.44%		98	153	3.72%		305	53	7.44%
37	74	6.98%		98	125	3.72%		305	97	6.98%
37	68	6.98%		98	33	3.26%		305	52	6.51%
37	98	6.51%		99	99	100.00%		305	49	5.58%
37	54	6.51%		99	248	18.60%		306	306	100.00%
37	67	6.51%		99	282	18.60%		306	308	72.09%
37	105	6.51%		99	267	6.98%		306	307	69.77%
37	116	6.05%		99	154	5.12%		306	305	69.30%
37	84	5.12%		99	162	5.12%		306	303	46.51%
37	118	5.12%		99	146	4.19%		306	302	38.14%
37	85	4.65%		99	61	3.72%		306	300	37.21%
37	119	4.65%		99	108	3.72%		306	304	35.81%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
38	38	100.00%		99	53	3.72%		306	301	34.88%
38	314	80.47%		99	96	3.72%		306	299	33.49%
38	312	65.58%		99	50	3.26%		306	51	15.35%
38	313	64.19%		99	218	2.79%		306	59	13.49%
38	311	58.14%		100	100	100.00%		306	57	13.02%
38	310	56.74%		100	274	15.81%		306	96	12.09%
38	43	56.28%		100	285	15.81%		306	60	11.63%
38	298	54.42%		100	262	5.12%		306	61	11.16%
38	41	53.49%		100	50	4.65%		306	95	11.16%
38	36	52.56%		100	95	4.65%		306	91	11.16%
38	35	50.70%		100	53	4.19%		306	108	11.16%
38	34	50.70%		100	246	4.19%		306	50	10.23%
38	3	49.77%		100	255	4.19%		306	142	9.77%
38	39	48.84%		100	52	3.72%		306	58	9.30%
38	40	47.44%		100	91	3.26%		306	53	8.37%
38	32	46.98%		100	159	3.26%		306	52	7.44%
38	42	44.19%		101	101	100.00%		306	97	7.44%
38	33	39.53%		101	65	27.44%		306	49	6.05%
38	37	37.67%		101	124	26.51%		306	63	3.72%
38	309	31.16%		101	70	24.19%		306	248	3.26%
38	20	30.23%		101	109	24.19%		307	307	100.00%
38	28	28.84%		101	295	24.19%		307	308	74.88%
38	11	27.91%		101	111	23.72%		307	305	70.70%
38	7	27.44%		101	89	23.72%		307	306	69.77%
38	8	27.44%		101	71	23.26%		307	303	47.91%
38	9	27.44%		101	293	22.33%		307	302	38.60%
38	1	27.44%		101	80	21.86%		307	304	36.74%
38	24	27.44%		101	81	21.86%		307	300	36.74%
38	17	27.44%		101	64	21.86%		307	299	34.88%
38	15	26.98%		101	102	21.40%		307	301	33.95%
38	153	26.51%		101	76	21.40%		307	51	13.02%
38	6	26.05%		101	66	20.93%		307	61	12.56%
38	25	25.58%		101	107	20.47%		307	96	11.63%
38	27	25.58%		101	117	20.47%		307	91	11.63%
38	26	25.12%		101	110	20.47%		307	59	11.63%
38	31	24.65%		101	77	20.47%		307	57	11.16%
38	30	24.65%		101	127	19.53%		307	60	11.16%
38	29	24.19%		101	67	17.67%		307	58	9.77%
38	18	24.19%		101	128	17.67%		307	108	9.77%
38	12	23.72%		101	129	17.21%		307	50	9.30%
38	16	23.26%		101	74	17.21%		307	95	9.30%
38	21	23.26%		101	126	16.74%		307	142	9.30%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
38	13	22.79%		101	68	16.28%		307	53	8.37%
38	14	22.79%		101	75	15.81%		307	97	7.44%
38	22	22.79%		101	131	14.88%		307	52	6.05%
38	2	22.33%		101	45	13.95%		307	49	4.65%
38	23	22.33%		101	16	13.02%		307	63	4.19%
38	19	22.33%		101	30	13.02%		308	308	100.00%
38	10	21.86%		101	9	12.56%		308	305	75.35%
38	69	18.60%		101	130	12.56%		308	307	74.88%
38	294	14.88%		101	69	12.09%		308	306	72.09%
38	296	14.42%		101	21	12.09%		308	303	50.70%
38	47	13.95%		101	153	12.09%		308	302	40.47%
38	92	13.49%		101	28	12.09%		308	301	38.60%
38	71	13.49%		101	309	12.09%		308	300	38.60%
38	259	13.02%		101	15	11.63%		308	304	37.67%
38	48	11.63%		101	14	11.63%		308	299	35.35%
38	46	11.16%		101	10	11.63%		308	57	13.02%
38	45	10.70%		101	23	11.63%		308	51	13.02%
38	81	10.23%		101	27	11.63%		308	59	12.56%
38	70	10.23%		101	19	11.63%		308	96	11.16%
38	109	9.77%		101	13	11.63%		308	95	10.70%
38	62	9.30%		101	11	11.63%		308	60	10.23%
38	101	9.30%		101	34	11.63%		308	91	9.77%
38	297	9.30%		101	20	11.63%		308	108	9.77%
38	56	8.84%		101	35	11.16%		308	142	9.77%
38	55	8.84%		101	44	11.16%		308	61	9.30%
38	110	8.84%		101	132	11.16%		308	50	8.84%
38	103	8.84%		101	294	11.16%		308	58	8.84%
38	68	8.37%		101	41	10.70%		308	53	8.37%
38	104	8.37%		101	37	10.70%		308	97	7.44%
38	124	8.37%		101	116	10.70%		308	52	6.05%
38	102	8.37%		101	47	10.23%		308	49	5.12%
38	66	7.91%		101	6	10.23%		309	309	100.00%
38	64	7.91%		101	25	10.23%		309	24	61.40%
38	67	7.91%		101	313	9.77%		309	25	60.47%
38	79	7.91%		101	7	9.77%		309	15	60.00%
38	76	7.91%		101	1	9.77%		309	1	60.00%
38	78	7.91%		101	311	9.77%		309	7	59.53%
38	117	7.91%		101	31	9.77%		309	8	59.07%
38	295	7.91%		101	314	9.77%		309	6	59.07%
38	107	7.91%		101	56	9.77%		309	18	53.95%
38	122	7.91%		101	312	9.77%		309	28	53.49%
38	293	7.91%		101	48	9.77%		309	16	53.02%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
38	98	7.44%		101	26	9.77%		309	11	51.63%
38	74	7.44%		101	298	9.77%		309	20	51.63%
38	77	7.44%		101	296	9.77%		309	9	51.16%
38	65	7.44%		101	29	9.77%		309	22	50.70%
38	44	7.44%		101	40	9.30%		309	12	49.77%
38	128	7.44%		101	8	9.30%		309	30	49.30%
38	111	7.44%		101	3	9.30%		309	2	48.84%
38	127	7.44%		101	310	9.30%		309	26	48.37%
38	89	6.98%		101	38	9.30%		309	17	47.44%
38	129	6.98%		101	12	9.30%		309	10	47.44%
38	131	6.51%		101	36	8.84%		309	13	47.44%
38	132	6.51%		101	22	8.84%		309	23	46.98%
38	130	6.51%		101	42	8.84%		309	27	46.51%
38	143	6.51%		101	24	8.84%		309	14	46.51%
38	82	6.05%		101	17	8.84%		309	21	46.51%
38	75	6.05%		101	32	8.84%		309	19	46.51%
38	83	6.05%		101	259	8.37%		309	29	45.12%
38	80	6.05%		101	39	8.37%		309	31	41.86%
38	85	5.58%		101	2	8.37%		309	37	41.86%
38	84	5.58%		101	121	7.91%		309	310	37.21%
38	121	5.58%		101	92	7.91%		309	311	36.28%
38	116	5.58%		101	18	7.91%		309	312	35.81%
38	126	5.12%		101	43	7.91%		309	313	34.88%
38	125	4.65%		101	46	7.91%		309	40	33.49%
38	105	4.65%		101	54	7.44%		309	39	33.49%
38	86	4.19%		101	104	7.44%		309	69	33.49%
38	90	4.19%		101	55	7.44%		309	34	32.56%
38	87	3.26%		101	106	7.44%		309	35	32.09%
39	39	100.00%		101	62	6.98%		309	43	32.09%
39	311	69.77%		101	122	6.05%		309	3	32.09%
39	310	65.12%		101	297	6.05%		309	314	32.09%
39	41	64.65%		101	120	6.05%		309	41	31.63%
39	312	64.65%		101	143	6.05%		309	38	31.16%
39	313	63.72%		101	82	5.58%		309	298	30.23%
39	42	63.26%		101	98	5.58%		309	32	29.30%
39	34	61.40%		101	83	5.58%		309	36	29.30%
39	40	57.21%		101	79	5.12%		309	42	29.30%
39	43	56.28%		101	84	5.12%		309	153	26.51%
39	36	54.88%		101	103	5.12%		309	33	25.58%
39	298	54.88%		101	78	5.12%		309	296	21.40%
39	32	53.95%		101	105	5.12%		309	45	18.60%
39	314	53.02%		101	85	4.65%		309	48	18.60%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
39	35	51.63%		101	33	4.19%		309	294	18.60%
39	33	50.23%		101	264	4.19%		309	47	16.28%
39	3	49.77%		101	251	4.19%		309	259	15.81%
39	38	48.84%		101	119	4.19%		309	46	15.35%
39	37	40.47%		101	118	4.19%		309	62	14.88%
39	309	33.49%		101	125	4.19%		309	71	14.42%
39	27	32.09%		102	102	100.00%		309	297	14.42%
39	11	30.70%		102	76	47.44%		309	109	14.42%
39	9	29.30%		102	77	46.05%		309	70	13.95%
39	15	29.30%		102	107	43.26%		309	124	13.95%
39	28	29.30%		102	81	24.19%		309	117	13.95%
39	20	29.30%		102	111	21.86%		309	89	13.49%
39	24	29.30%		102	295	21.86%		309	295	13.49%
39	17	29.30%		102	101	21.40%		309	44	13.02%
39	25	28.84%		102	124	20.47%		309	56	13.02%
39	7	27.91%		102	64	19.53%		309	79	12.56%
39	8	27.44%		102	65	19.07%		309	293	12.56%
39	1	27.44%		102	110	19.07%		309	92	12.09%
39	6	27.44%		102	70	18.60%		309	55	12.09%
39	26	27.44%		102	71	18.60%		309	101	12.09%
39	31	26.98%		102	109	18.60%		309	66	11.63%
39	30	26.98%		102	66	18.14%		309	64	11.63%
39	16	26.51%		102	128	17.21%		309	77	11.63%
39	18	26.51%		102	129	17.21%		309	129	11.63%
39	12	25.12%		102	126	16.28%		309	127	11.63%
39	22	24.65%		102	67	15.81%		309	75	11.16%
39	2	24.19%		102	80	15.81%		309	78	11.16%
39	13	23.72%		102	117	15.81%		309	128	11.16%
39	153	23.72%		102	293	15.81%		309	107	11.16%
39	10	23.26%		102	68	15.35%		309	103	11.16%
39	69	23.26%		102	89	15.35%		309	81	10.70%
39	19	23.26%		102	131	15.35%		309	85	10.70%
39	14	23.26%		102	75	14.88%		309	76	10.70%
39	21	23.26%		102	69	14.42%		309	130	10.70%
39	23	23.26%		102	127	13.49%		309	111	10.70%
39	29	21.86%		102	45	13.02%		309	132	10.70%
39	296	17.21%		102	130	13.02%		309	65	10.23%
39	294	16.74%		102	294	13.02%		309	67	10.23%
39	47	16.28%		102	44	12.56%		309	102	10.23%
39	46	14.88%		102	74	12.56%		309	104	10.23%
39	259	14.88%		102	6	11.16%		309	110	10.23%
39	48	13.49%		102	27	11.16%		309	82	9.77%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
39	45	13.02%		102	310	11.16%		309	80	9.77%
39	297	12.09%		102	1	10.70%		309	83	9.77%
39	92	11.16%		102	56	10.70%		309	74	9.77%
39	56	11.16%		102	132	10.70%		309	116	9.77%
39	71	10.70%		102	296	10.70%		309	121	9.77%
39	70	10.23%		102	9	10.23%		309	131	9.77%
39	76	10.23%		102	11	10.23%		309	68	9.30%
39	109	10.23%		102	48	10.23%		309	122	9.30%
39	77	9.77%		102	309	10.23%		309	125	8.37%
39	107	9.77%		102	7	9.77%		309	143	8.37%
39	129	9.77%		102	22	9.77%		309	98	7.91%
39	102	9.30%		102	25	9.77%		309	126	7.91%
39	127	9.30%		102	30	9.77%		309	54	7.44%
39	82	8.84%		102	153	9.77%		309	120	7.44%
39	83	8.84%		102	3	9.30%		309	84	6.51%
39	44	8.84%		102	26	9.30%		309	106	6.51%
39	128	8.84%		102	37	9.30%		309	118	6.51%
39	55	8.37%		102	39	9.30%		309	105	6.05%
39	65	8.37%		102	41	9.30%		309	119	6.05%
39	81	8.37%		102	55	9.30%		309	88	5.58%
39	101	8.37%		102	120	9.30%		309	86	5.12%
39	111	8.37%		102	311	9.30%		309	174	4.65%
39	110	8.37%		102	15	8.84%		309	90	4.19%
39	132	8.37%		102	18	8.84%		309	87	4.19%
39	130	8.37%		102	20	8.84%		309	147	4.19%
39	66	7.91%		102	24	8.84%		309	251	3.72%
39	64	7.91%		102	103	8.84%		310	310	100.00%
39	295	7.91%		102	312	8.84%		310	311	77.21%
39	124	7.91%		102	314	8.84%		310	312	72.09%
39	79	7.44%		102	2	8.37%		310	313	70.23%
39	85	7.44%		102	17	8.37%		310	3	68.37%
39	62	7.44%		102	34	8.37%		310	41	66.51%
39	117	7.44%		102	35	8.37%		310	39	65.12%
39	293	7.44%		102	38	8.37%		310	43	64.19%
39	125	7.44%		102	121	8.37%		310	34	63.72%
39	68	6.98%		102	298	8.37%		310	40	61.40%
39	122	6.98%		102	8	7.91%		310	314	60.93%
39	143	6.98%		102	10	7.91%		310	36	60.00%
39	67	6.51%		102	13	7.91%		310	298	60.00%
39	126	6.51%		102	14	7.91%		310	32	59.07%
39	104	6.51%		102	23	7.91%		310	42	59.07%
39	84	6.05%		102	36	7.91%		310	35	57.21%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
39	74	6.05%		102	47	7.91%		310	38	56.74%
39	78	6.05%		102	104	7.91%		310	33	49.77%
39	131	6.05%		102	116	7.91%		310	37	47.91%
39	116	6.05%		102	32	7.91%		310	309	37.21%
39	103	6.05%		102	313	7.91%		310	11	35.35%
39	80	5.58%		102	16	7.44%		310	27	34.88%
39	89	5.58%		102	19	7.44%		310	9	33.95%
39	121	5.58%		102	21	7.44%		310	28	33.49%
39	106	5.58%		102	29	7.44%		310	30	33.49%
39	75	5.12%		102	31	7.44%		310	17	32.56%
39	86	4.65%		102	42	7.44%		310	25	32.09%
39	98	4.65%		102	43	7.44%		310	24	32.09%
39	105	4.65%		102	46	7.44%		310	15	32.09%
39	88	4.19%		102	79	7.44%		310	20	31.63%
39	119	3.72%		102	92	7.44%		310	31	31.63%
40	40	100.00%		102	28	6.98%		310	1	31.16%
40	311	63.72%		102	40	6.98%		310	8	30.70%
40	32	62.33%		102	62	6.98%		310	26	30.70%
40	310	61.40%		102	78	6.98%		310	6	30.23%
40	41	58.14%		102	83	6.98%		310	7	29.77%
40	312	58.14%		102	84	6.98%		310	153	29.77%
40	33	58.14%		102	143	6.98%		310	16	29.30%
40	39	57.21%		102	259	6.98%		310	18	27.44%
40	313	56.74%		102	12	6.51%		310	22	26.98%
40	34	53.49%		102	82	6.51%		310	12	26.98%
40	43	50.70%		102	86	6.51%		310	69	26.51%
40	314	50.70%		102	125	6.51%		310	21	26.05%
40	42	49.77%		102	297	6.51%		310	19	25.58%
40	3	49.77%		102	33	6.05%		310	2	25.58%
40	298	49.77%		102	85	6.05%		310	29	25.58%
40	35	49.30%		102	98	6.05%		310	13	25.12%
40	36	49.30%		102	105	4.65%		310	14	25.12%
40	38	47.44%		102	106	4.65%		310	10	25.12%
40	37	42.33%		102	122	4.65%		310	23	25.12%
40	309	33.49%		102	54	4.19%		310	296	19.07%
40	27	32.09%		102	119	4.19%		310	92	17.21%
40	11	31.63%		102	174	4.19%		310	294	17.21%
40	9	31.16%		102	118	3.72%		310	259	17.21%
40	15	31.16%		103	103	100.00%		310	45	16.28%
40	28	30.70%		103	78	60.47%		310	46	15.81%
40	30	30.23%		103	79	60.47%		310	47	14.88%
40	26	29.30%		103	62	43.72%		310	297	14.42%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
40	1	28.84%		103	55	41.86%		310	76	13.95%
40	7	28.84%		103	121	31.16%		310	71	13.49%
40	20	28.84%		103	104	27.44%		310	48	13.49%
40	6	28.37%		103	120	26.98%		310	107	12.56%
40	25	28.37%		103	122	22.33%		310	77	11.63%
40	24	28.37%		103	9	12.56%		310	109	11.63%
40	16	28.37%		103	98	12.09%		310	70	11.16%
40	17	28.37%		103	30	12.09%		310	102	11.16%
40	8	27.91%		103	76	11.63%		310	64	10.70%
40	18	26.98%		103	296	11.16%		310	128	10.70%
40	31	26.51%		103	28	11.16%		310	66	10.23%
40	12	26.05%		103	25	11.16%		310	81	10.23%
40	69	25.58%		103	37	11.16%		310	124	10.23%
40	22	25.58%		103	309	11.16%		310	117	10.23%
40	2	24.65%		103	27	10.70%		310	122	10.23%
40	153	24.65%		103	17	10.70%		310	129	10.23%
40	13	23.72%		103	11	10.70%		310	82	9.77%
40	21	23.72%		103	26	10.70%		310	62	9.77%
40	23	22.79%		103	1	10.23%		310	132	9.77%
40	10	22.33%		103	3	10.23%		310	130	9.77%
40	14	22.33%		103	77	10.23%		310	56	9.30%
40	19	21.86%		103	69	10.23%		310	83	9.30%
40	29	21.86%		103	6	10.23%		310	44	9.30%
40	296	19.53%		103	31	9.77%		310	104	9.30%
40	294	15.81%		103	45	9.30%		310	101	9.30%
40	45	14.88%		103	56	9.30%		310	111	9.30%
40	47	14.42%		103	7	9.30%		310	89	8.84%
40	48	13.95%		103	128	9.30%		310	68	8.84%
40	46	13.49%		103	313	8.84%		310	65	8.84%
40	259	13.49%		103	44	8.84%		310	67	8.84%
40	92	12.09%		103	92	8.84%		310	55	8.84%
40	297	12.09%		103	312	8.84%		310	75	8.37%
40	56	11.63%		103	16	8.84%		310	79	8.37%
40	71	11.16%		103	107	8.84%		310	295	8.37%
40	70	10.23%		103	15	8.84%		310	110	8.37%
40	109	10.23%		103	297	8.84%		310	127	8.37%
40	44	9.77%		103	48	8.84%		310	103	8.37%
40	76	9.77%		103	24	8.84%		310	74	7.91%
40	111	9.77%		103	35	8.84%		310	84	7.91%
40	101	9.30%		103	38	8.84%		310	131	7.91%
40	128	9.30%		103	102	8.84%		310	126	7.91%
40	107	9.30%		103	43	8.37%		310	143	7.91%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
40	64	8.84%		103	20	8.37%		310	85	7.44%
40	62	8.84%		103	311	8.37%		310	98	7.44%
40	77	8.84%		103	314	8.37%		310	78	7.44%
40	124	8.84%		103	294	8.37%		310	80	7.44%
40	110	8.84%		103	310	8.37%		310	116	7.44%
40	104	8.84%		103	68	7.91%		310	293	7.44%
40	66	8.37%		103	124	7.91%		310	121	6.98%
40	89	8.37%		103	8	7.91%		310	105	6.05%
40	122	8.37%		103	65	7.44%		310	125	6.05%
40	121	8.37%		103	40	7.44%		310	54	5.58%
40	127	8.37%		103	298	7.44%		310	106	5.58%
40	117	7.91%		103	47	7.44%		310	118	5.12%
40	129	7.91%		103	22	7.44%		310	119	5.12%
40	293	7.91%		103	129	7.44%		310	120	4.65%
40	130	7.91%		103	2	7.44%		310	86	3.72%
40	55	7.44%		103	153	7.44%		310	138	3.72%
40	79	7.44%		103	12	7.44%		310	174	3.72%
40	103	7.44%		103	126	7.44%		311	311	100.00%
40	116	7.44%		103	64	6.98%		311	312	80.00%
40	81	6.98%		103	19	6.98%		311	313	79.07%
40	98	6.98%		103	71	6.98%		311	310	77.21%
40	78	6.98%		103	18	6.98%		311	41	73.49%
40	80	6.98%		103	111	6.98%		311	39	69.77%
40	65	6.98%		103	21	6.51%		311	34	69.30%
40	295	6.98%		103	14	6.51%		311	43	66.51%
40	132	6.98%		103	67	6.51%		311	298	64.65%
40	125	6.98%		103	80	6.51%		311	40	63.72%
40	102	6.98%		103	81	6.51%		311	36	63.72%
40	75	6.51%		103	41	6.51%		311	42	63.72%
40	74	6.51%		103	46	6.51%		311	314	63.26%
40	82	6.51%		103	143	6.51%		311	35	61.86%
40	67	6.51%		103	32	6.51%		311	32	60.93%
40	143	6.51%		103	74	6.05%		311	3	60.93%
40	68	6.05%		103	10	6.05%		311	38	58.14%
40	83	6.05%		103	29	6.05%		311	33	52.56%
40	131	6.05%		103	131	6.05%		311	37	43.26%
40	106	5.58%		103	23	6.05%		311	309	36.28%
40	105	5.58%		103	13	6.05%		311	11	33.95%
40	84	5.12%		103	259	6.05%		311	28	32.09%
40	85	5.12%		103	109	6.05%		311	27	32.09%
40	126	5.12%		103	70	6.05%		311	20	31.63%
40	119	5.12%		103	34	6.05%		311	24	31.63%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
40	54	4.65%		103	39	6.05%		311	9	31.63%
40	88	4.19%		103	117	5.58%		311	15	30.70%
40	120	4.19%		103	293	5.58%		311	1	30.70%
41	41	100.00%		103	36	5.58%		311	25	30.23%
41	34	78.60%		103	295	5.58%		311	8	30.23%
41	311	73.49%		103	33	5.58%		311	17	30.23%
41	312	67.91%		103	83	5.58%		311	6	30.23%
41	313	66.98%		103	82	5.58%		311	7	29.30%
41	310	66.51%		103	89	5.12%		311	30	29.30%
41	39	64.65%		103	66	5.12%		311	31	28.84%
41	43	59.07%		103	85	5.12%		311	16	28.84%
41	40	58.14%		103	116	5.12%		311	26	28.37%
41	35	58.14%		103	110	5.12%		311	153	28.37%
41	36	57.67%		103	101	5.12%		311	18	27.91%
41	314	57.67%		103	84	4.65%		311	12	27.44%
41	298	57.21%		103	119	4.65%		311	69	26.05%
41	32	56.74%		103	127	4.65%		311	21	25.12%
41	42	54.88%		103	130	4.65%		311	22	25.12%
41	38	53.49%		103	42	4.65%		311	23	24.65%
41	3	53.02%		103	125	4.65%		311	10	24.65%
41	33	49.30%		103	86	4.19%		311	13	24.65%
41	37	40.47%		103	118	4.19%		311	14	24.19%
41	309	31.63%		103	106	4.19%		311	19	24.19%
41	11	30.70%		104	104	100.00%		311	2	24.19%
41	27	30.70%		104	120	40.47%		311	29	24.19%
41	15	30.23%		104	121	40.00%		311	294	19.07%
41	1	29.77%		104	62	30.70%		311	296	19.07%
41	17	29.77%		104	55	30.23%		311	259	16.28%
41	9	29.30%		104	122	30.23%		311	47	15.81%
41	6	29.30%		104	79	29.30%		311	46	15.35%
41	28	28.84%		104	78	28.84%		311	45	14.88%
41	20	28.37%		104	103	27.44%		311	92	14.42%
41	24	28.37%		104	20	11.63%		311	48	13.95%
41	26	28.37%		104	9	11.63%		311	71	13.49%
41	30	28.37%		104	28	11.63%		311	297	12.56%
41	8	27.91%		104	11	11.63%		311	76	11.63%
41	7	27.44%		104	48	11.63%		311	109	11.63%
41	31	27.44%		104	98	11.16%		311	110	11.16%
41	12	26.98%		104	1	11.16%		311	56	10.70%
41	25	26.51%		104	6	11.16%		311	70	10.70%
41	153	26.51%		104	293	10.23%		311	77	10.70%
41	16	24.65%		104	309	10.23%		311	111	10.70%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
41	18	24.65%		104	124	10.23%		311	122	10.70%
41	22	24.19%		104	15	10.23%		311	55	10.23%
41	13	23.72%		104	296	9.77%		311	81	10.23%
41	21	23.26%		104	27	9.77%		311	127	10.23%
41	69	22.79%		104	14	9.77%		311	107	10.23%
41	23	22.79%		104	10	9.77%		311	66	9.77%
41	10	22.33%		104	25	9.77%		311	79	9.77%
41	14	22.33%		104	23	9.77%		311	101	9.77%
41	19	22.33%		104	7	9.77%		311	124	9.77%
41	2	21.86%		104	310	9.30%		311	129	9.77%
41	29	21.86%		104	92	9.30%		311	68	9.30%
41	294	18.60%		104	294	9.30%		311	44	9.30%
41	296	17.21%		104	45	9.30%		311	102	9.30%
41	48	15.35%		104	13	9.30%		311	130	9.30%
41	259	15.35%		104	26	9.30%		311	65	8.84%
41	45	12.56%		104	56	8.84%		311	67	8.84%
41	92	12.09%		104	312	8.84%		311	78	8.84%
41	47	11.63%		104	69	8.84%		311	62	8.84%
41	71	11.63%		104	314	8.84%		311	64	8.84%
41	76	11.16%		104	19	8.84%		311	128	8.84%
41	46	11.16%		104	17	8.84%		311	132	8.84%
41	77	10.70%		104	71	8.84%		311	104	8.37%
41	101	10.70%		104	40	8.84%		311	103	8.37%
41	109	10.70%		104	128	8.37%		311	293	8.37%
41	297	10.70%		104	313	8.37%		311	82	7.91%
41	70	10.23%		104	311	8.37%		311	295	7.91%
41	56	9.77%		104	77	8.37%		311	117	7.91%
41	129	9.77%		104	43	8.37%		311	121	7.91%
41	66	9.30%		104	16	8.37%		311	98	7.44%
41	107	9.30%		104	38	8.37%		311	89	7.44%
41	102	9.30%		104	37	8.37%		311	84	7.44%
41	81	8.84%		104	298	8.37%		311	80	7.44%
41	127	8.84%		104	24	8.37%		311	116	7.44%
41	124	8.84%		104	30	8.37%		311	54	6.98%
41	111	8.37%		104	12	8.37%		311	131	6.98%
41	110	8.37%		104	3	8.37%		311	125	6.98%
41	128	8.37%		104	47	7.91%		311	74	6.51%
41	65	7.91%		104	64	7.91%		311	83	6.51%
41	83	7.91%		104	36	7.91%		311	105	6.51%
41	67	7.91%		104	109	7.91%		311	106	6.51%
41	64	7.91%		104	129	7.91%		311	85	6.05%
41	55	7.91%		104	8	7.91%		311	119	6.05%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
41	44	7.91%		104	102	7.91%		311	143	6.05%
41	79	7.91%		104	107	7.44%		311	120	5.58%
41	122	7.91%		104	21	7.44%		311	126	5.58%
41	82	7.44%		104	70	7.44%		311	75	5.12%
41	89	7.44%		104	18	7.44%		311	118	4.65%
41	68	7.44%		104	44	7.44%		311	88	3.72%
41	132	7.44%		104	46	7.44%		311	138	3.72%
41	143	7.44%		104	2	7.44%		312	312	100.00%
41	62	6.98%		104	101	7.44%		312	313	84.19%
41	78	6.98%		104	126	6.98%		312	311	80.00%
41	295	6.98%		104	41	6.98%		312	298	74.42%
41	104	6.98%		104	34	6.98%		312	43	73.95%
41	126	6.98%		104	82	6.98%		312	314	73.02%
41	130	6.98%		104	29	6.98%		312	36	72.56%
41	293	6.98%		104	81	6.98%		312	310	72.09%
41	85	6.51%		104	127	6.98%		312	41	67.91%
41	98	6.51%		104	65	6.98%		312	38	65.58%
41	121	6.51%		104	35	6.98%		312	39	64.65%
41	103	6.51%		104	31	6.98%		312	34	62.79%
41	125	6.51%		104	297	6.98%		312	3	59.07%
41	74	6.05%		104	80	6.98%		312	42	58.60%
41	131	6.05%		104	32	6.98%		312	40	58.14%
41	105	6.05%		104	76	6.51%		312	32	57.21%
41	116	6.05%		104	67	6.51%		312	35	57.21%
41	84	5.58%		104	39	6.51%		312	33	46.98%
41	106	5.58%		104	22	6.51%		312	37	40.47%
41	75	5.12%		104	85	6.05%		312	309	35.81%
41	80	5.12%		104	75	6.05%		312	20	33.02%
41	119	5.12%		104	143	6.05%		312	11	32.09%
41	86	4.65%		104	83	6.05%		312	28	31.63%
41	120	4.65%		104	68	5.58%		312	9	30.70%
41	118	4.65%		104	42	5.58%		312	25	30.23%
41	117	4.65%		104	66	5.58%		312	27	30.23%
42	42	100.00%		104	131	5.12%		312	7	29.77%
42	311	63.72%		104	116	5.12%		312	1	29.77%
42	39	63.26%		104	295	4.65%		312	15	29.30%
42	310	59.07%		104	132	4.65%		312	8	29.30%
42	312	58.60%		104	33	4.65%		312	153	29.30%
42	313	56.28%		104	130	4.65%		312	24	28.84%
42	41	54.88%		104	89	4.19%		312	6	28.84%
42	34	53.49%		104	259	4.19%		312	17	28.84%
42	43	50.70%		104	153	4.19%		312	31	27.91%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
42	40	49.77%		104	74	3.72%		312	30	27.91%
42	32	49.30%		104	84	3.72%		312	16	27.44%
42	298	47.91%		104	188	3.72%		312	26	26.98%
42	36	47.91%		104	54	3.72%		312	12	26.51%
42	314	47.91%		104	110	3.26%		312	18	26.05%
42	35	45.12%		104	125	3.26%		312	21	24.65%
42	33	45.12%		105	105	100.00%		312	13	24.19%
42	38	44.19%		105	118	48.84%		312	22	24.19%
42	3	43.72%		105	119	48.37%		312	29	23.72%
42	37	38.14%		105	106	16.28%		312	2	23.72%
42	309	29.30%		105	125	12.09%		312	10	23.26%
42	28	27.44%		105	26	8.84%		312	23	23.26%
42	11	26.98%		105	27	8.84%		312	14	22.79%
42	20	26.51%		105	12	8.37%		312	69	22.79%
42	17	26.51%		105	8	7.91%		312	19	22.33%
42	27	25.58%		105	28	7.44%		312	294	16.28%
42	1	25.12%		105	30	7.44%		312	47	15.81%
42	15	25.12%		105	9	6.98%		312	296	15.81%
42	9	24.65%		105	1	6.98%		312	46	14.88%
42	6	24.65%		105	15	6.98%		312	259	14.88%
42	24	24.65%		105	6	6.51%		312	92	14.42%
42	30	24.65%		105	11	6.51%		312	48	13.49%
42	8	24.19%		105	37	6.51%		312	45	13.02%
42	18	24.19%		105	311	6.51%		312	71	12.09%
42	25	24.19%		105	31	6.51%		312	297	11.16%
42	26	23.72%		105	24	6.51%		312	76	10.70%
42	31	23.72%		105	310	6.05%		312	122	10.70%
42	22	23.26%		105	41	6.05%		312	81	10.23%
42	16	22.79%		105	296	6.05%		312	55	9.77%
42	7	22.33%		105	18	6.05%		312	56	9.77%
42	2	22.33%		105	309	6.05%		312	101	9.77%
42	153	21.86%		105	22	6.05%		312	124	9.77%
42	29	21.40%		105	7	6.05%		312	110	9.77%
42	69	20.93%		105	313	5.58%		312	109	9.77%
42	13	20.47%		105	312	5.58%		312	79	9.30%
42	12	20.47%		105	48	5.58%		312	78	9.30%
42	21	20.47%		105	29	5.58%		312	111	9.30%
42	14	19.53%		105	40	5.58%		312	107	9.30%
42	23	19.53%		105	17	5.58%		312	66	8.84%
42	19	19.53%		105	23	5.12%		312	89	8.84%
42	10	19.07%		105	10	5.12%		312	98	8.84%
42	296	14.88%		105	14	5.12%		312	70	8.84%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
42	294	13.95%		105	45	5.12%		312	44	8.84%
42	45	13.49%		105	297	5.12%		312	77	8.84%
42	47	13.49%		105	153	5.12%		312	104	8.84%
42	259	13.49%		105	89	5.12%		312	127	8.84%
42	46	12.09%		105	35	5.12%		312	128	8.84%
42	48	11.63%		105	44	5.12%		312	103	8.84%
42	92	11.16%		105	20	5.12%		312	102	8.84%
42	76	9.77%		105	69	5.12%		312	65	8.37%
42	71	9.77%		105	21	5.12%		312	67	8.37%
42	107	9.77%		105	101	5.12%		312	68	8.37%
42	56	9.30%		105	13	4.65%		312	62	8.37%
42	101	8.84%		105	19	4.65%		312	295	8.37%
42	127	8.84%		105	64	4.65%		312	117	8.37%
42	109	8.84%		105	43	4.65%		312	130	8.37%
42	297	8.84%		105	34	4.65%		312	293	8.37%
42	70	8.37%		105	39	4.65%		312	64	7.91%
42	81	8.37%		105	107	4.65%		312	121	7.91%
42	68	8.37%		105	314	4.65%		312	129	7.91%
42	65	8.37%		105	111	4.65%		312	131	7.91%
42	111	8.37%		105	77	4.65%		312	84	7.44%
42	110	8.37%		105	38	4.65%		312	116	7.44%
42	130	8.37%		105	110	4.65%		312	74	6.98%
42	82	7.91%		105	76	4.65%		312	126	6.98%
42	83	7.91%		105	130	4.65%		312	143	6.98%
42	67	7.91%		105	16	4.65%		312	82	6.51%
42	44	7.91%		105	109	4.65%		312	83	6.51%
42	124	7.91%		105	65	4.65%		312	80	6.51%
42	117	7.91%		105	25	4.65%		312	85	6.05%
42	293	7.91%		105	102	4.65%		312	125	6.05%
42	128	7.91%		105	3	4.19%		312	75	5.58%
42	55	7.44%		105	298	4.19%		312	105	5.58%
42	66	7.44%		105	124	4.19%		312	132	5.58%
42	77	7.44%		105	47	4.19%		312	120	5.12%
42	64	7.44%		105	295	4.19%		312	119	5.12%
42	295	7.44%		105	293	4.19%		312	54	4.65%
42	132	7.44%		105	132	4.19%		312	118	4.65%
42	129	7.44%		105	81	4.19%		312	86	3.72%
42	102	7.44%		105	70	3.72%		312	88	3.72%
42	85	6.98%		105	71	3.72%		312	251	3.72%
42	79	6.51%		105	68	3.72%		313	313	100.00%
42	84	6.51%		105	259	3.72%		313	312	84.19%
42	126	6.51%		105	122	3.72%		313	311	79.07%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
42	131	6.51%		105	128	3.72%		313	298	73.02%
42	143	6.51%		105	129	3.72%		313	314	72.09%
42	80	6.05%		105	55	3.72%		313	36	71.63%
42	78	6.05%		105	42	3.72%		313	43	71.16%
42	125	6.05%		105	143	3.72%		313	310	70.23%
42	75	5.58%		105	67	3.72%		313	41	66.98%
42	62	5.58%		105	92	3.72%		313	38	64.19%
42	104	5.58%		105	131	3.72%		313	39	63.72%
42	116	5.58%		105	32	3.72%		313	34	60.93%
42	54	5.12%		105	147	3.26%		313	3	58.14%
42	89	5.12%		106	106	100.00%		313	35	57.21%
42	106	5.12%		106	125	37.21%		313	32	56.74%
42	122	4.65%		106	118	16.74%		313	40	56.74%
42	103	4.65%		106	105	16.28%		313	42	56.28%
42	98	4.19%		106	119	15.81%		313	33	47.44%
42	86	3.72%		106	37	8.84%		313	37	36.28%
42	105	3.72%		106	28	8.84%		313	309	34.88%
42	119	3.72%		106	17	8.84%		313	20	31.63%
43	43	100.00%		106	77	8.37%		313	28	30.70%
43	312	73.95%		106	124	8.37%		313	11	30.23%
43	298	72.09%		106	16	8.37%		313	9	29.77%
43	36	71.16%		106	26	7.91%		313	27	29.30%
43	313	71.16%		106	69	7.44%		313	7	28.84%
43	311	66.51%		106	20	7.44%		313	8	28.84%
43	310	64.19%		106	76	7.44%		313	15	28.84%
43	314	62.79%		106	101	7.44%		313	1	28.84%
43	41	59.07%		106	296	6.98%		313	25	27.91%
43	38	56.28%		106	65	6.98%		313	6	27.91%
43	39	56.28%		106	127	6.98%		313	153	27.91%
43	34	55.81%		106	70	6.98%		313	30	26.98%
43	3	54.88%		106	80	6.98%		313	31	26.51%
43	35	52.09%		106	131	6.98%		313	24	26.51%
43	32	51.63%		106	25	6.98%		313	26	26.05%
43	40	50.70%		106	9	6.98%		313	17	26.05%
43	42	50.70%		106	31	6.98%		313	16	25.58%
43	33	42.79%		106	107	6.98%		313	12	25.58%
43	37	35.35%		106	47	6.51%		313	18	25.12%
43	309	32.09%		106	293	6.51%		313	21	24.19%
43	28	29.77%		106	45	6.51%		313	22	23.72%
43	20	28.84%		106	309	6.51%		313	13	23.26%
43	15	28.84%		106	109	6.51%		313	29	23.26%
43	27	28.84%		106	27	6.51%		313	2	23.26%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
43	9	28.37%		106	44	6.51%		313	14	22.79%
43	25	28.37%		106	311	6.51%		313	23	22.79%
43	11	27.91%		106	15	6.05%		313	10	22.33%
43	7	27.44%		106	35	6.05%		313	19	21.86%
43	8	26.98%		106	48	6.05%		313	69	20.93%
43	1	26.98%		106	30	6.05%		313	296	17.21%
43	6	26.51%		106	130	6.05%		313	294	16.28%
43	30	26.05%		106	297	6.05%		313	259	14.42%
43	31	25.58%		106	295	6.05%		313	92	13.95%
43	24	25.12%		106	32	6.05%		313	47	13.49%
43	26	25.12%		106	12	5.58%		313	45	13.02%
43	153	25.12%		106	117	5.58%		313	48	12.09%
43	17	25.12%		106	40	5.58%		313	71	11.63%
43	18	24.65%		106	46	5.58%		313	46	11.16%
43	16	24.19%		106	41	5.58%		313	76	10.23%
43	12	23.72%		106	3	5.58%		313	122	10.23%
43	14	23.26%		106	2	5.58%		313	128	10.23%
43	10	22.79%		106	39	5.58%		313	109	10.23%
43	21	22.79%		106	81	5.58%		313	81	9.77%
43	23	22.79%		106	71	5.58%		313	56	9.77%
43	29	22.79%		106	310	5.58%		313	70	9.77%
43	22	22.33%		106	259	5.58%		313	101	9.77%
43	2	21.86%		106	78	5.58%		313	124	9.77%
43	19	21.86%		106	7	5.12%		313	107	9.77%
43	13	21.86%		106	313	5.12%		313	78	9.30%
43	69	19.07%		106	24	5.12%		313	62	9.30%
43	294	16.28%		106	42	5.12%		313	129	9.30%
43	296	16.28%		106	116	5.12%		313	111	9.30%
43	47	14.42%		106	111	5.12%		313	110	9.30%
43	92	13.02%		106	11	5.12%		313	66	8.84%
43	259	12.56%		106	34	5.12%		313	65	8.84%
43	45	11.63%		106	110	5.12%		313	55	8.84%
43	46	11.63%		106	79	5.12%		313	79	8.84%
43	81	11.16%		106	67	5.12%		313	77	8.84%
43	48	11.16%		106	23	4.65%		313	103	8.84%
43	71	10.23%		106	10	4.65%		313	127	8.84%
43	127	10.23%		106	19	4.65%		313	104	8.37%
43	124	10.23%		106	1	4.65%		313	297	8.37%
43	62	9.77%		106	14	4.65%		313	121	8.37%
43	76	9.77%		106	13	4.65%		313	130	8.37%
43	107	9.77%		106	8	4.65%		313	68	7.91%
43	122	9.77%		106	64	4.65%		313	44	7.91%

node 1	node 2	AS %		node 1	node 2	AS %		node 1	node 2	AS %
43	128	9.77%		106	22	4.65%		313	67	7.91%
43	56	9.30%		106	21	4.65%		313	295	7.91%
43	66	9.30%		106	294	4.65%		313	131	7.91%
43	68	9.30%		106	43	4.65%		313	102	7.91%
43	295	9.30%		106	66	4.65%		313	98	7.44%
43	130	9.30%		106	132	4.65%		313	74	7.44%
43	70	8.84%		106	18	4.65%		313	64	7.44%
43	75	8.84%		106	68	4.65%		313	89	7.44%
43	67	8.84%		106	102	4.65%		313	293	7.44%
43	109	8.84%		106	6	4.19%		313	80	6.98%
43	293	8.84%		106	29	4.19%		313	117	6.98%
43	65	8.37%		106	36	4.19%		313	83	6.51%
43	74	8.37%		106	103	4.19%		313	116	6.51%
43	64	8.37%		106	89	3.72%		313	125	6.51%
43	89	8.37%		106	129	3.72%		313	143	6.51%
43	104	8.37%		106	298	3.72%		313	82	6.05%
43	103	8.37%		106	62	3.72%		313	75	6.05%
43	129	8.37%		106	143	3.72%		313	85	6.05%
43	98	7.91%		106	128	3.72%		313	84	6.05%
43	78	7.91%		106	314	3.26%		313	120	6.05%
43	77	7.91%		107	107	100.00%		313	126	6.05%
43	101	7.91%		107	77	66.05%		313	54	5.58%
43	297	7.91%		107	76	65.58%		313	105	5.58%
43	131	7.91%		107	102	43.26%		313	132	5.58%
43	111	7.91%		107	124	26.98%		313	106	5.12%
43	126	7.91%		107	111	23.72%		313	119	5.12%
43	55	7.44%		107	81	22.33%		313	88	3.72%
43	121	7.44%		107	70	21.40%		313	86	3.72%
43	102	7.44%		107	110	21.40%		314	314	100.00%
43	79	6.98%		107	67	20.93%		314	38	80.47%
43	44	6.98%		107	71	20.93%		314	312	73.02%
43	117	6.98%		107	295	20.93%		314	313	72.09%
43	110	6.98%		107	65	20.93%		314	311	63.26%
43	116	6.98%		107	109	20.47%		314	43	62.79%
43	80	6.51%		107	101	20.47%		314	310	60.93%
43	132	6.05%		107	68	20.00%		314	298	60.00%
43	143	6.05%		107	64	20.00%		314	36	58.14%
43	83	5.58%		107	66	18.14%		314	41	57.67%
43	125	5.58%		107	131	17.67%		314	34	54.88%
43	82	5.12%		107	130	17.67%		314	3	53.02%
43	119	5.12%		107	128	16.74%		314	39	53.02%
43	105	4.65%		107	117	16.74%		314	35	52.09%

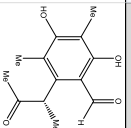
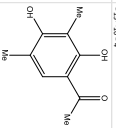
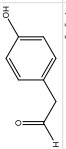
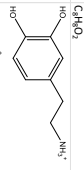
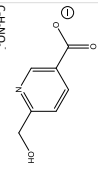
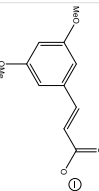
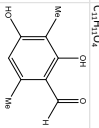
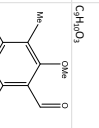
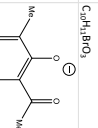
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43	106	4.65%		107	293	16.74%		314	32	50.23%
43	84	4.19%		107	126	16.28%		314	42	47.91%
43	86	3.72%		107	89	16.28%		314	33	42.33%
43	54	3.72%		107	80	16.28%		314	37	39.07%
43	251	3.26%		107	132	15.81%		314	309	32.09%
44	44	100.00%		107	75	15.35%		314	20	30.23%
44	129	14.88%		107	129	14.88%		314	28	29.30%
44	45	14.42%		107	9	14.88%		314	11	29.30%
44	124	14.42%		107	74	13.95%		314	9	28.84%
44	128	13.95%		107	127	13.49%		314	8	27.91%
44	18	13.49%		107	11	13.49%		314	15	27.44%
44	293	13.49%		107	45	13.02%		314	1	27.44%
44	27	13.49%		107	27	13.02%		314	17	27.44%
44	69	13.02%		107	30	12.56%		314	24	27.44%
44	9	13.02%		107	310	12.56%		314	153	27.44%
44	48	13.02%		107	294	11.63%		314	7	26.98%
44	309	13.02%		107	17	11.63%		314	25	26.98%
44	131	13.02%		107	44	11.16%		314	27	26.51%
44	25	13.02%		107	309	11.16%		314	6	26.51%
44	6	12.56%		107	37	10.70%		314	18	24.65%
44	102	12.56%		107	22	10.70%		314	29	24.65%
44	126	12.56%		107	2	10.70%		314	26	24.65%
44	11	12.56%		107	28	10.23%		314	31	24.65%
44	26	12.56%		107	296	10.23%		314	30	24.65%
44	20	12.56%		107	20	10.23%		314	16	24.19%
44	22	12.56%		107	311	10.23%		314	12	23.72%
44	15	12.56%		107	26	10.23%		314	21	23.26%
44	1	12.09%		107	35	10.23%		314	13	23.26%
44	55	12.09%		107	56	9.77%		314	23	22.79%
44	7	12.09%		107	16	9.77%		314	19	22.79%
44	30	12.09%		107	7	9.77%		314	14	22.79%
44	296	12.09%		107	92	9.77%		314	2	22.79%
44	66	11.63%		107	43	9.77%		314	22	22.79%
44	65	11.63%		107	298	9.77%		314	10	22.33%
44	76	11.63%		107	259	9.77%		314	69	20.00%
44	24	11.63%		107	313	9.77%		314	294	15.81%
44	16	11.63%		107	25	9.77%		314	296	14.88%
44	80	11.16%		107	6	9.77%		314	71	14.42%
44	77	11.16%		107	47	9.77%		314	47	13.95%
44	107	11.16%		107	39	9.77%		314	92	13.49%
44	101	11.16%		107	42	9.77%		314	48	13.02%

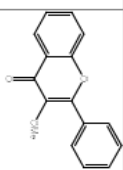
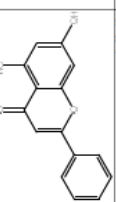
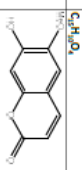
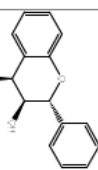
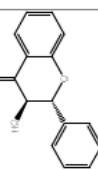
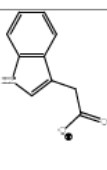
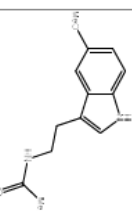
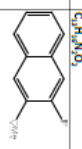
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44	130	11.16%		107	13	9.30%		314	46	11.63%
44	81	10.70%		107	153	9.30%		314	45	11.16%
44	64	10.70%		107	1	9.30%		314	70	10.23%
44	75	10.70%		107	36	9.30%		314	297	10.23%
44	2	10.70%		107	48	9.30%		314	109	10.23%
44	47	10.70%		107	314	9.30%		314	81	9.77%
44	110	10.70%		107	3	9.30%		314	55	9.77%
44	294	10.70%		107	41	9.30%		314	56	9.77%
44	37	10.70%		107	34	9.30%		314	101	9.77%
44	111	10.23%		107	312	9.30%		314	110	9.77%
44	31	10.23%		107	40	9.30%		314	77	9.30%
44	71	9.77%		107	14	8.84%		314	76	9.30%
44	10	9.77%		107	15	8.84%		314	78	9.30%
44	8	9.77%		107	79	8.84%		314	107	9.30%
44	56	9.77%		107	103	8.84%		314	127	9.30%
44	62	9.77%		107	23	8.37%		314	124	9.30%
44	14	9.77%		107	10	8.37%		314	66	8.84%
44	295	9.77%		107	19	8.37%		314	64	8.84%
44	29	9.77%		107	55	8.37%		314	68	8.84%
44	21	9.77%		107	116	8.37%		314	79	8.84%
44	40	9.77%		107	62	8.37%		314	62	8.84%
44	259	9.77%		107	31	8.37%		314	104	8.84%
44	3	9.30%		107	78	8.37%		314	102	8.84%
44	23	9.30%		107	18	8.37%		314	65	8.37%
44	311	9.30%		107	24	7.91%		314	67	8.37%
44	310	9.30%		107	8	7.91%		314	111	8.37%
44	32	9.30%		107	38	7.91%		314	295	8.37%
44	13	9.30%		107	104	7.44%		314	122	8.37%
44	78	8.84%		107	98	6.98%		314	103	8.37%
44	127	8.84%		107	46	6.98%		314	89	7.91%
44	153	8.84%		107	29	6.98%		314	44	7.91%
44	103	8.84%		107	12	6.98%		314	128	7.91%
44	132	8.84%		107	106	6.98%		314	293	7.91%
44	122	8.84%		107	33	6.05%		314	98	7.44%
44	298	8.84%		107	83	6.05%		314	74	7.44%
44	312	8.84%		107	125	6.05%		314	131	7.44%
44	12	8.84%		107	121	5.58%		314	129	7.44%
44	39	8.84%		107	54	5.58%		314	83	6.98%
44	297	8.84%		107	143	5.58%		314	117	6.98%
44	120	8.84%		107	21	5.58%		314	130	6.98%
44	70	8.37%		107	122	5.12%		314	143	6.98%

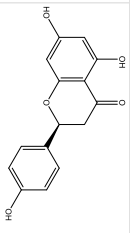
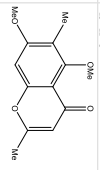
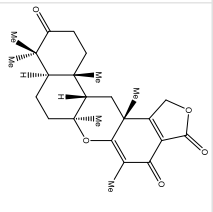
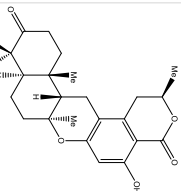
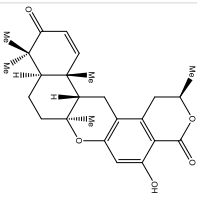
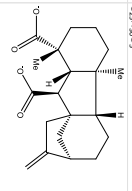
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44	79	8.37%		107	297	5.12%		314	82	6.51%
44	117	8.37%		107	120	4.65%		314	132	6.51%
44	19	8.37%		107	105	4.65%		314	85	6.05%
44	109	8.37%		107	86	4.19%		314	75	6.05%
44	36	8.37%		107	119	4.19%		314	84	6.05%
44	143	8.37%		107	118	3.72%		314	80	6.05%
44	17	8.37%		107	174	3.26%		314	116	6.05%
44	74	7.91%		108	108	100.00%		314	121	5.58%
44	89	7.91%		108	142	29.30%		314	126	5.58%
44	92	7.91%		108	57	23.72%		314	86	5.12%
44	46	7.91%		108	58	22.79%		314	125	5.12%
44	313	7.91%		108	96	22.33%		314	119	5.12%
44	41	7.91%		108	61	17.21%		314	105	4.65%
44	42	7.91%		108	60	16.74%		314	120	4.65%
44	314	7.91%		108	91	15.81%		314	54	4.19%
44	35	7.91%		108	97	15.35%		314	90	4.19%
44	104	7.44%		108	53	15.35%		314	88	3.72%
44	34	7.44%		108	50	15.35%		314	87	3.72%
				108	95	14.42%		314	106	3.26%

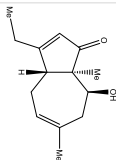
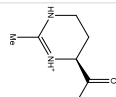
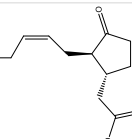
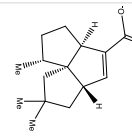
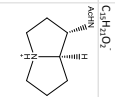
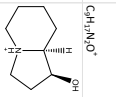
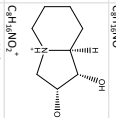
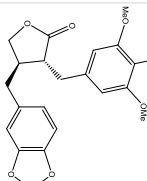
16. Summary of substrates in reaction database

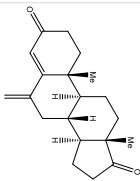
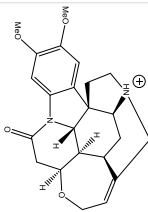
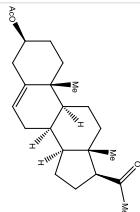
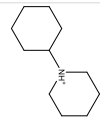
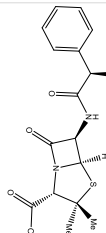
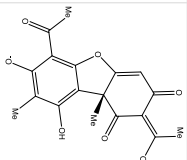
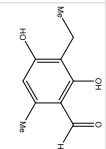
Supplemental Table S6. Substrate table for all substrate in chemical space. Literature reaction annotates if the substrate has been identified as compatible with an enzyme in aKGLib1 in the literature (T = true, F = false). Screened substrate represents if the substrate was screened against aKGLib1 (T = true, F = false). Visible by Mz describes if the substrate offered good ionization under the LC-MS method (T = true, F = false, NS = substrate not screened). Observed reaction describes if the substrate was observed to undergo biocatalytic chemistry with aKGLib1 (T = true, F = false, NS = substrate not screened, NV = substrate wasn't visible by LC-MS method). Train and test denote the assignment of the substrate to the train or test split for model training (T = true, F = false). PC0, PC1, PC2, PC3, and PC4 reflect the coordinates in the principal component analysis later referred to as PC1, PC2, PC3, PC4, PC5.

Substrate ¹	STRUCTURE	SMILES	IUPAC NAME	Literature Reactivity	Screened Substrate	Visible by Mz	Observed Reaction	Train	Test	PC 0	PC 1	PC 2	PC 3	PC 4
1		<chem>OCC=C(Cl(H)-O)C(Cl(=O)(C)C)C(=O)C(C)C=O</chem>	(S)-2,4-dihydroxy-3,5-dimethyl-6-(3-oxobutan-2-yl)benzaldehyde	T	F	NS	NS	F	T	-2.08221	1.664418	-0.69667	0.587217	-0.24311
2		<chem>OCC=C(C)O-C=C(C)C(C)C=O</chem>	1,12,4-dihydroxy-3,5-dimethylphenylethan-1-one	T	T	T	T	T	F	-2.24488	-1.21207	-0.70596	0.025221	0.411006
3		<chem>OCC=C=C=C(Cl(C)O)=O</chem>	2-hydroxybenzoate	T	T	T	F	F	T	-5.1865	1.451085	-0.20295	-0.19406	-0.43965
4		<chem>OCC=CC=C(Cl(H)-O)C=Cl</chem>	2-(4-hydroxyphenyl)acetaldehyde	T	F	NS	NS	F	T	-3.03171	-1.68063	0.116002	0.317247	0.103175
5		<chem>OCC=C(O)C=C(Cl(NH3+))C=Cl</chem>	2-(3,5-dihydroxyphenyl)ethan-1-aminium	T	T	T	F	T	F	-3.27801	-0.19726	0.44077	0.141527	-0.18806
6		<chem>[O]C(Cl=C(Cl)C(CO)C=O)=O</chem>	[6-(hydroxymethyl)pyridin-3-yl]1-oxidanemethanone	F	F	NS	NS	F	T	-4.38406	1.072099	-0.83612	0.443976	-0.05491
7		<chem>[O]C(Cl=C(Cl)C(CO)C=O)=O</chem>	(E)-3,6,5-dimethoxyphenylacetate	F	T	T	T	F	T	-2.96239	1.482386	1.051021	0.23745	0.174453
8		<chem>OCC=C(C)C(C)C(Cl(H)-O)C=O</chem>	2,4-dihydroxy-3,6-dimethylbenzaldehyde	F	T	T	T	F	T	-2.65941	-1.25736	-0.90849	0.864667	-0.06822
9		<chem>O=C(Cl=C(Cl)C=C(Cl)C(C)C=O</chem>	6-bromo-2,4-dimethoxy-3-methylbenzaldehyde	F	T	T	F	T	F	-1.94737	-0.37383	-0.7267	-0.38416	0.241332
10		<chem>OCC=C(Cl(C)O)=C(Cl)C=O</chem>	6-acetyl-3-hydroxy-2-methylphenolate	F	T	T	T	F	T	-3.49529	0.665029	-0.06004	0.49462	0.385757

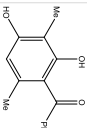
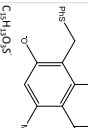
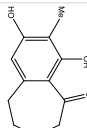
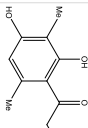
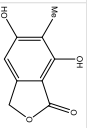
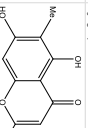
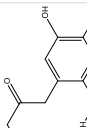
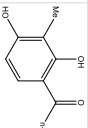
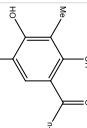
11		<chem>O=C1C=CC(=C(C=C1)OC)C2=CC=CC=C2</chem>	3-methoxy-2-phenyl-4H-chromen-4-one	F	F	NS	NS	F	T	-0.76005	-0.1084	-0.75464	0.392286	0.142398
12		<chem>O=C1C=CC(=C(C=C1)C2=CC=CC=C2C(=C3C=CC(=C3)O)O)C4=CC=CC=C4</chem>	5,7-dihydroxy-2-phenyl-4H-chromen-4-one	F	F	NS	NS	F	T	-2.01528	1.916189	-0.27957	0.550342	0.56473
13		<chem>O=C1OC=C(C(=O)C=C1)OC2=CC=CC=C2</chem>	7-hydroxy-6-methoxy-2H-chromen-2-one	T	T	F	NV	T	F	-2.47893	-0.70664	-0.15393	-0.32787	-0.5732
14		<chem>O[C@@H]1C=CC(=C(C=C1)C2=CC=CC=C2)C3=CC(=C(C=C3)C[C@H]1O</chem>	(2R,3S,4S)-2-phenylchromane-3,4-diol	F	F	NS	NS	T	F	-0.82216	-0.82593	-0.13435	0.086069	-0.37191
15		<chem>O=C1C=CC(=C(C=C1)C2=CC=CC=C2)C[C@H]3C=C[C@@H](O)C3</chem>	(2R,3R)-3-hydroxy-2-phenylchroman-4-one	F	F	NS	NS	T	F	-1.36448	-0.00645	-0.18916	-0.05631	-0.75941
16		<chem>O=C1C(=C(C=C1)OC2=CC=CC=C2)C3=CC=CC=C3</chem>	Unable to generate value	T	T	T	T	F	T	-3.14513	0.438311	-1.17273	0.507207	-0.33978
17		<chem>CC(=O)NCCc1c[nH]c2cc(OC)ccc12</chem>	N-(2-(5-methoxy-1H-indol-3-yl)ethyl)acetamide	T	T	T	F	F	T	-0.73909	-1.29801	0.641331	-0.17176	-0.09601
18		<chem>COc1cc(F)ccc1-c2ccccc2</chem>	2-fluoro-3-methoxyphenylbenzene	F	T	F	NV	F	T	-2.32504	-1.24816	-0.17112	0.289621	0.251901

19		<chem>O=C1C(=C2C(=C(C=C2)O)C(=C(C=C1)O)C3=CC=CC=C3)C4=CC=CC=C4</chem>	(5)-5,7-dihydroxy-2,4-hydroxyphenylchroman-4-one	T	F	NS	NS	F	T	-0.80374	-0.02308	0.155984	0.249058	-0.10517
20		<chem>O=C1C(=C2C(=C(C=C2)OC)C(=C(C=C1)OC)C3=CC(OC)=CC(OC)=C3)C4=CC=CC=C4</chem>	5,7-dimethoxy-2,5-dimethyl-4H-chromen-4-one	F	T	T	T	F	T	-1.18497	-0.94774	-0.55178	0.501061	0.568339
21		<chem>O=C1C(=C2C(=C(C=C2)C1C(=C3C(=C(C=C3)C)C(=C(C=C1)C)C)C)C4=CC=CC=C4</chem>	(6aS,8aR,12aS,12bS,13aR)-5,6a,9,9,12a,13a-hexamethyl-7,8,8a,9,11,12,12a,12b,13,13a-decalhydro-3H-benzo[a]furo[3,4-j]xanthene-3,4,10(1H,6aH)-trione	T	F	NS	NS	T	F	1.465456	1.618434	-1.36104	-0.69182	-1.42633
22		<chem>O=C1C(=C2C(=C(C=C2)C1C(=C3C(=C(C=C3)C)C(=C(C=C1)C)C)C)C4=CC=CC=C4</chem>	(2R,7aS,9aR,13aS,13bS)-5-methoxy-2,7a,10,10,13a-pentamethyl-1,8,9,9a,10,12,13a,13b,14-decalhydro-2H,4H-benzo[h]pyrro[3,4-j]xanthene-4,11(7H)-dione	T	F	NS	NS	T	F	1.746242	1.025944	-1.06762	-0.15317	-0.98107
23		<chem>O=C1C(=C2C(=C(C=C2)C1C(=C3C(=C(C=C3)C)C(=C(C=C1)C)C)C)C4=CC=CC=C4</chem>	(2R,7aS,9aR,13aS,13bS)-5-methoxy-2,7a,10,10,13a-pentamethyl-1,8,9,9a,10,13a,13b,14-decalhydro-2H,4H-benzo[h]pyrro[3,4-j]xanthene-4,11(7aH)-dione	T	F	NS	NS	F	T	0.577406	2.913609	-0.38621	-0.85799	-0.92462
24		<chem>O=C1C(=C2C(=C(C=C2)C1C(=C3C(=C(C=C3)C)C(=C(C=C1)C)C)C)C4=CC=CC=C4</chem>	(1R,4aS,4bS,7a,9aR,10S,10aS)-1,4a-dimethyl-3-methylene-6,6-dimethyl-7,9a-methanobenzo[h]julene-1,10-dicarboxylate	T	F	NS	NS	T	F	-1.13976	3.340129	0.472548	-1.03557	-0.15944

58		<chem>O=C(C=C(C(C(C@H)2C(C(C1C(=O)C(C1)C(C2)C)C)C)C)C)C)C1=CC=C(C=C1)O</chem>	(3aR,5aR)-3-ethyl-3-hydroxy-6,8a-dimethyl-4,7,8a,9-tetrahydroazulen-1(3aH)-one	T	F	NS	NS	F	T	-1.25986	-0.88763	-0.24714	-0.27525	0.37317
59		<chem>CC1=NC(=O)C(=O)N1C(=O)O</chem>	(S)-2-methyl-3,4,5,6-tetrahydropyrimidin-1(1H)-one-5-carboxylate	T	F	NS	NS	T	F	-2.71065	-2.55673	-0.21048	0.73713	1.260978
60		<chem>CCCC(=O)OCC1CC(=O)N1C(=O)C(=O)C</chem>	2-((1R,2R)-3-oxo-2-((2S)-pent-2-en-1-yl)pyrrolidin-1-yl)propanoate	T	F	NS	NS	F	T	-2.47148	1.53864	-0.45094	-0.36401	0.120512
61		<chem>CC1=CC2C(C1)C(C(C2)C(C(C3C(C(C3)C)C)C)C)C(=O)O</chem>	(1R,3aR,5aR)-1,2,7-trimethyl-1,2,3a,5a,6,7,8-octahydrocyclopenta(c)pentaline-4-carboxylate	T	F	NS	NS	F	T	-1.85403	1.647	-1.87832	1.28216	0.302399
62		<chem>CC(=O)N[C@@H]1C[C@H](N)C(C1)=O</chem>	(1S,7aR)-1-acetamidooctahydro-1H-indolizin-4-ium	T	F	NS	NS	T	F	-1.38965	-2.53026	0.36277	0.328344	-0.33937
63		<chem>O[C@@H]1C[C@H](N)C(C1)=O</chem>	(1S,5aR)-1-hydroxyoctahydro-1H-indolizin-4-ium	T	F	NS	NS	T	F	-1.43128	-5.28789	2.891841	1.147886	-1.590683
64		<chem>O[C@@H]1C[C@H](N)C(C1)=O</chem>	(1S,2R,8aR)-1,2-dihydrooctahydro-1H-indolizin-4-ium	T	F	NS	NS	F	T	-1.31936	-4.61603	2.206738	1.492175	-2.73053
65		<chem>COc1cc(OC)c(OC)cc1CCOC(=O)C1COC2=CC=CC=C2O1</chem>	(3R,4R)-4-benzod(1,3)dioxol-5-ylmethyl-3-(3,4,5-trimethoxyphenyl)dihydrofuran-2(3H)-one	T	F	NS	NS	T	F	1.894639	0.490256	0.076792	-0.73996	0.169475

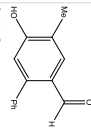
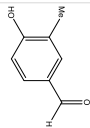
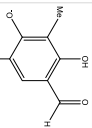
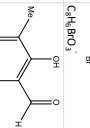
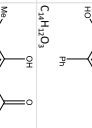
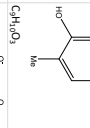
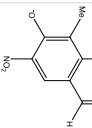
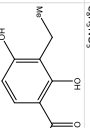
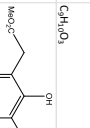
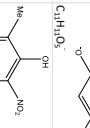
78		<chem>O=C(C=C1C(C(C@21[H])(C@2[H])(C@31C(C(C@3[H])(C@3C(=O)C2=O)C1=O)C1=O)C1=O)C1=O)C1=O</chem>	(8R,9S,10R,13S,14S)-10,13-dimethyl-6-methylene-1,5,7,8,9,10,11,12,13,14,15,16-dodecalyn-3-yl-dodecalyn-3-yl-dione	F	T	T	T	F	T	0.13063	0.27853	-1.33072	0.859061	-0.4674
79		<chem>O=C(C(C@11[H])(C@1[H])(C@21C(C@2[H])(C@2C(=O)C1=O)C1=O)C1=O)C1=O</chem>	(4aR,4a1R,5aS,6S,8a,9a1S,15a)-10,11-dimethyl-14-oxo-4a,4a1,5,5a,7,8,8a1,15,15a-octahydro-2H,14H-4b-methanobenzofuro[3,2-b]pyridine-2,3+de[pyridine]2,3-biquinoline-6-ylm-7-ylm	F	T	T	T	F	T	1.7626	-0.09321	-0.796	-0.08657	0.133984
80		<chem>O=C(C(C@11[H])(C@1[H])(C@21C(C@2[H])(C@2C(=O)C1=O)C1=O)C1=O)C1=O</chem>	(3S,8R,9S,10R,13S,14S,17S)-17-acetyl-10,13-dimethyl-2,3,4,7,8,9,10,11,12,13,14,15,16,17-tetraethyl-1H-cyclopentadecylphenanthrene-3-yl acetate	F	T	F	NV	F	T	1.278707	0.436388	0.267212	-0.1948	-0.08877
81		<chem>Cl([NH2]C(CCC(C)C)CCCC1</chem>	1-cyclohexylpiperidin-1-ium	F	T	T	T	F	T	-0.40911	-4.68156	2.726325	1.209013	-2.35827
82		<chem>[O-]C(C(C@11[H])(C@1[H])(C@21C(C@2[H])(C@2C(=O)C1=O)C1=O)C1=O)C1=O</chem>	(2S,5R,6R)-6-(R)-2-amino-2-phenylacetamido-3,3-dimethyl-7-oxo-4-thia-1-azabicyclo[3.2.0]heptane-2-carboxylate	F	T	T	F	F	T	-0.17549	2.788427	-1.29584	1.232515	-0.1741
83		<chem>O=C(C(C@11[H])(C@1[H])(C@21C(C@2[H])(C@2C(=O)C1=O)C1=O)C1=O)C1=O</chem>	(R2)-4-acetyl-1-hydroxy-2,9a-dimethyl-8-(1-oxododecylidene)-7,2-dioxo-7,8,9,9a-tetrahydrobenzofuro[3,2-b]furan-3-olite	F	T	T	T	T	F	-0.69447	2.455526	0.362931	-0.72696	-0.07614
84		<chem>OC1=C(C(C(C(=O)C1(C(=O)C(=O)C1=O)C1=O)C1=O)C1=O)C1=O</chem>	3-ethyl-2,4-dihydroxy-6-methylbenzaldehyde	F	F	NS	NS	F	T	-3.37942	0.755386	0.529699	-0.19738	-0.35958

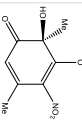
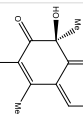
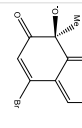
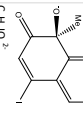
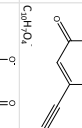
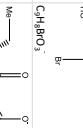
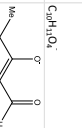
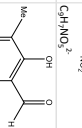
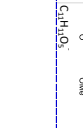
85		<chem>CC1=C(C(=O)O)C(C)=C(C(=O)O)C=C1</chem>	2,4-dihydroxy-3,5,6-trimethylbenzaldehyde	F	F	NS	NS	F	T	-3.13325	0.725696	-0.851345	0.530987	0.136616
86		<chem>CC1=C(C(=O)O)C(C)=C(C(=O)O)C=C1</chem>	5-bromo-4-formyl-3-hydroxy-2-methylphenol	F	F	NS	NS	F	T	-2.40706	-0.7757	-0.95277	-0.44936	-0.51261
87		<chem>CC1=C(C(=O)O)C(C)=C(C(=O)O)C=C1</chem>	4-formyl-3-hydroxy-5-iodo-2-methylphenol	F	F	NS	NS	F	T	-3.56741	2.199972	-0.48022	0.163316	0.016154
88		<chem>CC1=C(C(=O)O)C(C)=C(C(=O)O)C=C1</chem>	5-ethyl-4-formyl-3-hydroxy-2-methylphenol	F	F	NS	NS	T	F	-3.46	0.687006	0.062219	-0.49551	1.792211
89		<chem>CC1=C(C(=O)O)C(C)=C(C(=O)O)C=C1</chem>	3,5-dihydroxy-4-methyl-1,1'-biphenyl-2-carbaldehyde	T	F	NS	NS	T	F	-2.17638	1.461492	-0.66695	0.099715	0.169688
90		<chem>CC1=C(C(=O)O)C(C)=C(C(=O)O)C=C1</chem>	1-(2,4-dihydroxy-3,6-dimethylphenyl)ethan-1-one	F	F	NS	NS	T	F	-3.19038	0.690666	-0.79266	0.154023	0.713129
91		<chem>CC1=C(C(=O)O)C(C)=C(C(=O)O)C=C1</chem>	methyl 2,4-dihydroxy-3,6-dimethylbenzoate	T	F	NS	NS	T	F	-3.65987	1.526576	0.391154	-0.05293	0.534422
92		<chem>CC1=C(C(=O)O)C(C)=C(C(=O)O)C=C1</chem>	1-(2,4-dihydroxy-3,6-dimethylphenyl)pentan-1-one	F	F	NS	NS	F	T	-2.3707	1.210513	0.173187	-0.15687	0.027664
93		<chem>CC1=C(C(=O)O)C(C)=C(C(=O)O)C=C1</chem>	3-hydroxy-2,5-dimethyl-4-nitrophenol	F	F	NS	NS	F	T	-4.23479	2.121559	0.160366	0.415033	-0.6704
94		<chem>CC1=C(C(=O)O)C(C)=C(C(=O)O)C=C1</chem>	(E)-2,5-dimethyl-4-(methylimino)methylbenzene-1,3-diol	F	F	NS	NS	T	F	-3.27094	1.146971	0.388878	0.253857	0.597867
95		<chem>CC1=C(C(=O)O)C(C)=C(C(=O)O)C=C1</chem>	(E)-2,4-dihydroxy-3,6-dimethylbenzaldehyde oxime	F	F	NS	NS	F	T	-3.86563	1.00413	0.657739	-0.47125	0.969359

96		OC1=C(C(CO)=C(C(C)C=C-C-2)O)C(C)C1	(2,4-dihydroxy-3,6-dimethylphenyl)phenylmethanone	F	F	NS	NS	F	T	-1.03064	-0.22513	-0.78817	0.55817	-0.44384
97		[O-] C1=C(C(C)C=C-C-C2(C)O=C(C)(H)O)C(C)=C1	4-formyl-3-hydroxy-5-methyl-2-(phenylthiomethyl)phenolate	F	F	NS	NS	F	T	-1.25451	1.792085	-0.10617	-1.13685	0.14107
98		OC1=C(C(CO)=C2C(C(CCC2=O)=C1	2,4-dihydroxy-3-methyl-6,7,8,9-tetrahydro-5H-benzo[7]annulen-5-one	F	F	NS	NS	T	F	-1.54732	-1.14998	-0.29513	0.673526	-1.14553
99		OC1=C(C(C(C)C)=O)C(C)C(CO)=C1C	1-(2,4-dihydroxy-3,6-dimethylphenyl)-3-methylbutan-1-one	F	F	NS	NS	F	T	-0.95327	-0.82825	0.09279	-0.11174	-0.12532
100		O=C1OC(C=C(CO)=C(CO)C=C1	5,7-dihydroxy-6-methylisobenzofuran-1(3H)-one	F	F	NS	NS	T	F	-2.57677	-0.91461	-0.55335	0.290329	-1.40179
101		OC1=C2C(OC(C=C2=O)=CCO)=C(C	5,7-dihydroxy-2,6-dimethyl-4H-chromen-4-one	F	F	NS	NS	T	F	-2.6912	0.679813	-0.63616	0.18134	1.277353
102		O=C1C(C)=C(OC)C=C(CO)C(C(C	5,7-dimethoxy-2,3,6-trimethyl-4H-chromen-4-one	F	F	NS	NS	T	F	-0.86827	-0.81113	-0.22358	-0.53624	0.897789
103		OC1=C(C(CO)=C(C(CO)C(CO)C(C	2,4-dihydroxy-3-methyl-6-(2-oxopropyl)benzaldehyde	F	F	NS	NS	T	F	-2.17945	1.69782	0.558524	-0.65007	0.590481
104		OC1=C(C(CO)=C(C(CO)C(CO)C(C	1-(2,4-dihydroxy-3-methylphenyl)pentan-1-one	F	F	NS	NS	F	T	-3.13317	1.887016	0.65898	-0.10152	0.535501
105		OC1=C(C(CCC1=O)C(C(CO)C(CO	1-(5-ethyl-2,4-dihydroxy-3-methylphenyl)pentan-1-one	F	F	NS	NS	T	F	-0.98564	-0.82689	0.042384	-0.60689	0.694043

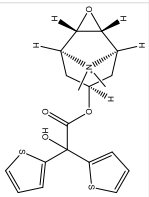
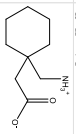
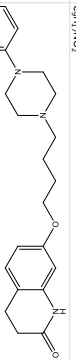
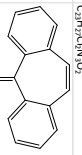
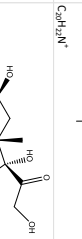
106		<chem>CC1=C(C(=O)C=CC(C)=O)C=C(C)C1</chem>	1-(2,4-dihydroxy-3,5-dimethylphenyl)pentan-1-one	F	F	NS	NS	F	T	-2.63693	1.839522	0.843719	-0.10437	-0.18956
106		<chem>CC1=C(C(=O)C=CC(C)=O)C=C(C)C1</chem>	1-(2,4-dihydroxy-3,5-dimethylphenyl)butan-1-one	F	F	NS	NS	F	T	-2.63693	1.839522	0.843719	-0.10437	-0.18956
106		<chem>OC1=C(C(=O)C=CC(C)=O)C=C(C)C1=O</chem>	4-formyl-3,5-dihydroxy-2-methylphenol	F	F	NS	NS	F	T	-2.63693	1.839522	0.843719	-0.10437	-0.18956
106		<chem>OC1=C(C(=O)C=CC(C)=O)C=C(C)C1=O</chem>	4-hydroxy-2,6-dimethoxy-3-methylbenzaldehyde	F	F	NS	NS	F	T	-2.63693	1.839522	0.843719	-0.10437	-0.18956
106		<chem>OC1=C(C(=O)C=CC(C)=O)C=C(C)C1</chem>	5-methylbenzene-1,3-diol	F	F	NS	NS	F	T	-2.63693	1.839522	0.843719	-0.10437	-0.18956
106		<chem>OC1=C(C(=O)C=CC(C)=O)C=C(C)C1</chem>	2,5-dimethylbenzene-1,3-diol	F	F	NS	NS	F	T	-2.63693	1.839522	0.843719	-0.10437	-0.18956
106		<chem>CC1=C(C(=O)C=CC(C)=O)C=C(C)C1</chem>	1-(2-hydroxy-4-methoxy-3-methylphenyl)ethan-1-one	F	F	NS	NS	F	T	-2.63693	1.839522	0.843719	-0.10437	-0.18956
106		<chem>CC1=C(C(=O)C=CC(C)=O)C=C(C)C1</chem>	3-methylbenzene-1,2-diol	F	F	NS	NS	F	T	-2.63693	1.839522	0.843719	-0.10437	-0.18956
106		<chem>CC1=C(C(=O)C=CC(C)=O)C=C(C)C1</chem>	o-cresol	F	F	NS	NS	F	T	-2.63693	1.839522	0.843719	-0.10437	-0.18956
106		<chem>CC1=C(C(=O)C=CC(C)=O)C=C(C)C1</chem>	m-cresol	F	F	NS	NS	F	T	-2.63693	1.839522	0.843719	-0.10437	-0.18956
106		<chem>CC1=C(C(=O)C=CC(C)=O)C=C(C)C1</chem>	2,4-dihydroxy-3-methylbenzoate	F	F	NS	NS	F	T	-2.63693	1.839522	0.843719	-0.10437	-0.18956

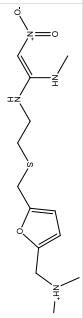
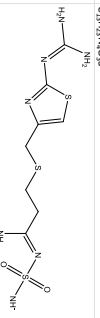
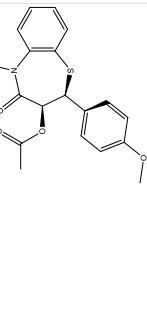
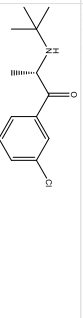
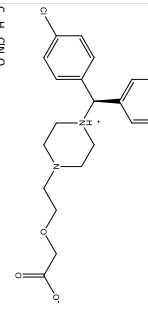
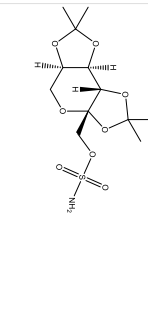
117		<chem>CC1=C(C(=O)O)C=C(C)C=C1</chem>	2-hydroxy-3,6-dimethylbenzaldehyde	F	F	NS	NS	F	T	-3.54359	0.566601	-0.10147	0.29538	-0.46505
118		<chem>CC1=C(C(=O)O)C(=O)C=C(C)C1</chem>	2,5-dihydroxy-3-methylbenzaldehyde	F	F	NS	NS	T	F	-4.01734	0.657439	0.087195	0.421691	0.00772
119		<chem>CC1=C(C(=O)O)C(=O)C=C(C)C1</chem>	2,4-dihydroxy-3-methylbenzaldehyde	F	F	NS	NS	F	T	-4.10567	0.789583	-0.34547	0.346098	-0.0129
120		<chem>CC1=C(C(=O)O)C(=O)C=C(C)C1</chem>	4,6-dihydroxy-2,3-dimethylbenzaldehyde	F	F	NS	NS	F	T	-3.45823	0.565021	-1.07588	-0.13974	-0.37897
121		<chem>CC1=C(C(=O)O)C(=O)C=C(C)C1</chem>	4-formyl-3-hydroxy-5-methylphenolate	F	F	NS	NS	F	T	-4.14196	0.868528	-0.83159	0.44129	0.231019
122		<chem>CC1=C(C(=O)O)C(=O)C=C(C)C1</chem>	6-(hydroxymethyl)-2-methylpyridin-1-ium-3-olate	F	F	NS	NS	F	T	-3.9619	0.165004	-0.21619	0.045554	0.393405
123		<chem>CC1=C(C(=O)O)C(=O)C=C(C)C1</chem>	6-formyl-2-methylpyridin-1-ium-3-olate	F	F	NS	NS	T	F	-4.44389	0.502245	-0.20921	0.04404	0.380513
124		<chem>CC1=C(C(=O)O)C(=O)C=C(C)C1</chem>	4-hydroxy-5-methyl-2-(naphthalen-2-yl)benzaldehyde	F	F	NS	NS	T	F	-1.24997	1.785448	-0.8832	-0.19543	0.062423
125		<chem>CC1=C(C(=O)O)C(=O)C=C(C)C1</chem>	4-hydroxy-2,5-dimethylbenzaldehyde	F	F	NS	NS	T	F	-2.65907	-1.22066	-0.40649	0.76657	-0.42311
126		<chem>CC1=C(C(=O)O)C(=O)C=C(C)C1</chem>	5-bromo-4-formyl-2-methylphenolate	F	F	NS	NS	F	T	-2.54618	-0.71476	-1.07333	-0.08792	-0.48864

127		<chem>CC1=CC(=C(C(=O)O)C(=O)C=C(C)C=C1)C=C(C)C=C1</chem>	5-hydroxy-4-methyl-1,1'-biphenyl-2-carbaldehyde	F	F	NS	NS	F	T	-2.31889	1.417525	-0.61735	-0.101	0.128954
128		<chem>CC1=CC(=C(C(=O)O)C=C(C)C=C1)C=C(C)C=C1</chem>	4-hydroxy-3-methylbenzaldehyde	F	F	NS	NS	T	F	-4.34459	0.471944	-0.40414	0.140753	0.554019
129		<chem>CC1=CC(=C(C(=O)O)C=C(C(=O)O)C=C(C)C=C1)C=C(C)C=C1</chem>	6-bromo-4-formyl-3-hydroxy-2-methylphenolate	F	F	NS	NS	F	T	-2.24862	-0.76955	-1.80533	0.969486	-0.89967
130		<chem>CC1=CC(=C(C(=O)O)C=C(C(=O)O)C=C(C)C=C1)C=C(C)C=C1</chem>	4,6-dihydroxy-5-methyl-1,1'-biphenyl-3-carbaldehyde	F	F	NS	NS	T	F	-2.46888	1.876026	-0.17737	0.322577	0.870441
131		<chem>CC1=CC(=C(C(=O)O)C=C(C(=O)O)C=C(C)C=C1)C=C(C)C=C1</chem>	2,4-dihydroxy-3,5-dimethylbenzaldehyde	T	F	NS	NS	T	F	-4.10026	1.375813	0.174295	0.451414	0.123833
132		<chem>CC1=CC(=C(C(=O)O)C=C(C(=O)O)C=C(C)C=C1)C=C(C)C=C1</chem>	4-formyl-2-methyl-6-nitrobenzene-1,3-bis(diolate)	F	F	NS	NS	T	F	-4.52118	2.398253	-0.23938	0.822888	0.420775
133		<chem>CC1=CC(=C(C(=O)O)C=C(C(=O)O)C=C(C)C=C1)C=C(C)C=C1</chem>	3-ethyl-2,4-dihydroxybenzaldehyde	F	F	NS	NS	T	F	-3.7452	0.846529	0.078228	-0.40051	-0.18164
134		<chem>CC1=CC(=C(C(=O)O)C=C(C(=O)O)C=C(C)C=C1)C=C(C)C=C1</chem>	4-formyl-3-hydroxy-2-(2-methoxy-2-oxoethyl)-5-methylphenolate	F	F	NS	NS	F	T	-2.85591	1.36538	1.017924	-1.13219	0.339563
135		<chem>CC1=CC(=C(C(=O)O)C=C(C(=O)O)C=C(C)C=C1)C=C(C)C=C1</chem>	3-hydroxy-2,6-dimethyl-4-nitrophenolate	F	F	NS	NS	F	T	-4.3276	1.7462	-0.62294	0.387301	0.678855
136		<chem>CC1=CC(=C(C(=O)O)C=C(C(=O)O)C=C(C)C=C1)C=C(C)C=C1</chem>	6-bromo-3-hydroxy-2-methyl-4-nitrophenolate	F	F	NS	NS	T	F	-2.57942	0.062945	-0.77587	0.831728	-0.70318

137		<chem>O=C1C@O(C(C(=O)1)C(=O)C=C1)O=C1C=C1</chem>	(S)-6-hydroxy-3,6-dimethyl-2-nitro-5-oxocyclohex-1-en-1-olite	T	F	NS	NS	T	F	-3.09913	0.003374	-0.74873	-0.10009	-0.4832
138		<chem>O=C(C(C(=O)O)=C(C(C(=O)O)C=C1O)1)C@O(C)C=C1O</chem>	(S)-5-hydroxy-3-(methoxycarbonyl)-2,5-dimethyl-4,6-dioxocyclohex-2-en-1-ylidene)methanolate	F	F	NS	NS	T	F	-3.02019	1.858653	0.231393	0.003098	0.948354
139		<chem>O=C(C=C(Br)/C=C/O)1C@O(C)1O=C(C(=O)O)C=C1O</chem>	(R,E)-4-bromo-1-methyl-5-(oxodimethyl)enyl-2,6-dioxocyclohex-3-en-1-olite	T	F	NS	NS	T	F	-2.56867	0.074839	-1.6243	0.284461	-0.43546
140		<chem>O=C(C=C(I)/C=C/O)1C@O(C)1O=C(C(=O)O)C=C1O</chem>	(R,E)-4-iodo-1-methyl-5-(oxodimethyl)enyl-2,6-dioxocyclohex-3-en-1-olite	T	F	NS	NS	F	T	-2.68815	0.217425	-1.34136	0.308373	-0.50686
141		<chem>O=C(C=C(C#O)/C=C/O)1C@O(C)1O=C(C(=O)O)C=C1O</chem>	(R,2)-2-ethyl-5-hydroxy-5-methyl-4,6-dioxocyclohex-2-en-1-ylidene)methanolate	F	F	NS	NS	T	F	-3.90425	1.574581	0.880183	-0.94957	0.908915
142		<chem>CC1=C(C(C(=O)O)1)C(C(=O)O)=C(Br)C=C1O</chem>	6-acetyl-4-bromo-3-hydroxy-2-methylphenolate	F	F	NS	NS	F	T	-2.13884	-0.77822	-0.7564	0.436578	0.622983
143		<chem>O=C(C=C(C(=O)O)1C@O(C)1O=C(C(=O)O)C=C1O)1C@O(C)O=C1O</chem>	(R,2)-1,5-ethyl-5-hydroxy-2-methyl-4,6-dioxocyclohex-2-en-1-ylidene)methanolate	T	F	NS	NS	F	T	-2.7793	-0.60935	1.080297	-1.14484	0.453416
144		<chem>[O-]C1=C(C(=O)O)O=C(C=C1N+)[O-]</chem>	4-formyl-2,5-dimethyl-5-nitrobenzene-1,3-bis(ol)ate	F	F	NS	NS	F	T	-3.88979	2.435423	-0.58123	0.523621	0.63081
145		<chem>[O-]C1=C(C(=O)O)C(C(=O)O)C=C1C(=O)O</chem>	4-formyl-3-hydroxy-5-(methoxycarbonyl)-2,5-dimethylphenolate	F	F	NS	NS	T	F	-3.35759	2.062281	0.443369	0.289559	0.667302

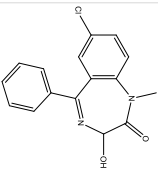
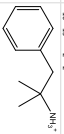
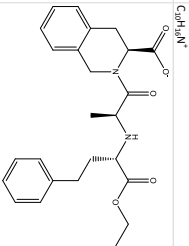
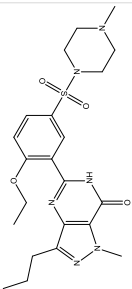
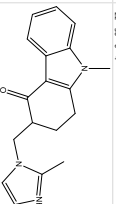
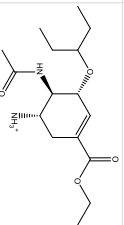
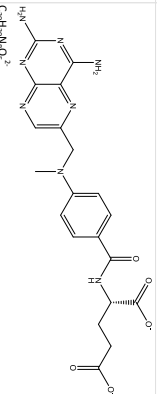
171		<chem>O=C(COC1=C(C=C(C=C1)C(C(=O)O)C2=CC=CC=C2)C3=CC=CC=C3)C4=CC=CC=C4</chem>	(R)-2-oxo-3-(3-oxo-1-phenylbutyl)-2H-chromen-4-ol	F	F	NS	NS	F	T	0.130817	0.343269	-1.27099	0.937812	-0.07831
172		<chem>O=C(COC1=C(C=C(C=C1)C(C(=O)O)C2=CC=CC=C2)C3=CC=CC=C3)C4=CC=CC=C4</chem>	2-(4-(2-chlorophenyl)-3-(ethoxycarbonyl)-5-(methoxycarbonyl)-6-methyl-1,4-dihydropyridin-2-yl)methoxyketan-1-aminium	F	F	NS	NS	T	F	3.058811	-0.4663	-1.14579	-0.39833	0.788176
173		<chem>O=C(COC1=C(C=C(C=C1)C(C(=O)O)C2=CC=CC=C2)C3=CC=CC=C3)C4=CC=CC=C4</chem>	(R)-4,4,5,7,8,12,15,14-hydroxy-9-methoxy-3-methyl-7-oxo-2,3,4,4a,5,6,7,7a-octahydro-1H-4,12-methanobenzo(fur)(3,2-e)isoquinolin-3-ium	F	F	NS	NS	T	F	0.101908	-0.51365	-0.39807	-0.88263	1.130071
174		<chem>O=C(COC1=C(C=C(C=C1)C(C(=O)O)C2=CC=CC=C2)C3=CC=CC=C3)C4=CC=CC=C4</chem>	2-(2-(4-(benzo[b][1,1']thiazepin-11-yl)pyrrolidin-3-yl)methoxyketan-1-ol	F	F	NS	NS	T	F	4.66465	-2.79015	2.61414	0.650099	2.178662
175		<chem>O=C(COC1=C(C=C(C=C1)C(C(=O)O)C2=CC=CC=C2)C3=CC=CC=C3)C4=CC=CC=C4</chem>	(S)-N,N-dimethyl-1-(10H-phenothiazin-10-yl)propan-2-aminium	F	F	NS	NS	F	T	0.766408	-0.92943	-1.09387	-0.18468	-0.43421
176		<chem>O=C(COC1=C(C=C(C=C1)C(C(=O)O)C2=CC=CC=C2)C3=CC=CC=C3)C4=CC=CC=C4</chem>	(6S,8S,9R,10S,11S,13S,14S,16R,17R)-6,9-difluoro-17-((fluoromethyl)phosphonyl)-11-hydroxy-10,13,16-trimethyl-3-oxo-6,7,8,9,10,11,12,13,14,15,16,17-dodecahydro-3H-cyclopenta[3]phenanthren-17-yl propionate	F	F	NS	NS	F	T	2.20818	2.206427	-0.72522	-1.08262	-1.56864

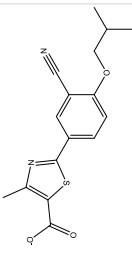
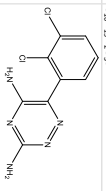
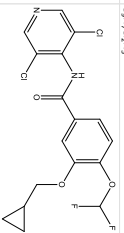
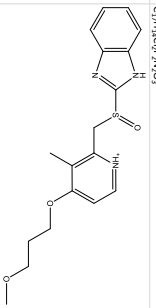
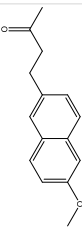
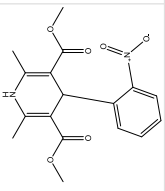
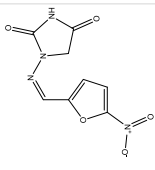
183		<chem>[H]C1C2C1C11C@H3C[C@@H]C(C1C@21N+3)C(C1H)OC(C1C=C(C5H4)C=C(C5D)=O1H1H1H1)</chem>	(1R,2R,4S,5S,3a,7,12-hydroxy-2,2-dithienophen-2-ylideneoxy)-3-oxa-9-azabicyclo[3.3.1]nonan-9-ylidene	F	F	NS	NS	F	T	3.509975	-1.72767	-0.42325	0.60238	1.420642
184		<chem>O=C(C1CCCC1C(N)N)[O-]</chem>	2-(1-(dimethylamino)cyclohexyl)acetate	F	F	NS	NS	F	T	-2.5013	-2.43378	1.003875	-0.29509	-0.03657
185		<chem>ClC1=CC=C(C=C1)N2CCN(CCC2)C(=O)C3=CC=C(C(C3)=O)C4=CC=CC=C4</chem>	7-(4-(4-(2,3-dichlorophenyl)piperazin-1-ylideneoxy)-3,4-dihydroquinolin-2(1H)-one	F	F	NS	NS	T	F	2.972631	0.584701	-0.21885	-0.02346	-2.31725
186		<chem>C1=CC=C2C(=C1)C(=C3C=CC=C3C=C2)N(C)C</chem>	3-(5H-fluoreno[9,8,7,6,5,4,3,2,1,0]undec-5-ylidene)-N,N-dimethylpropan-1-aminium	F	F	NS	NS	T	F	2.421884	-2.16512	-0.97813	1.23121	0.210917
187		<chem>O=C(C1C2C(C1)C(C2)C(C3C4C(C3)C(C4)C(C5C6C(C5)C(C6)C(C7C8C(C7)C(C8)C(C9C10C(C9)C(C10)C(C11C12C(C11)C(C12)C(C13C14C(C13)C(C14)C(C15C16C(C15)C(C16)C(C17C18C(C17)C(C18)C(C19C20C(C19)C(C20)C(C21C22C(C21)C(C22)C(C23C24C(C23)C(C24)C(C25C26C(C25)C(C26)C(C27C28C(C27)C(C28)C(C29C30C(C29)C(C30)C(C31C32C(C31)C(C32)C(C33C34C(C33)C(C34)C(C35C36C(C35)C(C36)C(C37C38C(C37)C(C38)C(C39C40C(C39)C(C40)C(C41C42C(C41)C(C42)C(C43C44C(C43)C(C44)C(C45C46C(C45)C(C46)C(C47C48C(C47)C(C48)C(C49C50C(C49)C(C50)C(C51C52C(C51)C(C52)C(C53C54C(C53)C(C54)C(C55C56C(C55)C(C56)C(C57C58C(C57)C(C58)C(C59C60C(C59)C(C60)C(C61C62C(C61)C(C62)C(C63C64C(C63)C(C64)C(C65C66C(C65)C(C66)C(C67C68C(C67)C(C68)C(C69C70C(C69)C(C70)C(C71C72C(C71)C(C72)C(C73C74C(C73)C(C74)C(C75C76C(C75)C(C76)C(C77C78C(C77)C(C78)C(C79C80C(C79)C(C80)C(C81C82C(C81)C(C82)C(C83C84C(C83)C(C84)C(C85C86C(C85)C(C86)C(C87C88C(C87)C(C88)C(C89C90C(C89)C(C90)C(C91C92C(C91)C(C92)C(C93C94C(C93)C(C94)C(C95C96C(C95)C(C96)C(C97C98C(C97)C(C98)C(C99C100C(C99)C(C100)C(C101C102C(C101)C(C102)C(C103C104C(C103)C(C104)C(C105C106C(C105)C(C106)C(C107C108C(C107)C(C108)C(C109C110C(C109)C(C110)C(C111C112C(C111)C(C112)C(C113C114C(C113)C(C114)C(C115C116C(C115)C(C116)C(C117C118C(C117)C(C118)C(C119C120C(C119)C(C120)C(C121C122C(C121)C(C122)C(C123C124C(C123)C(C124)C(C125C126C(C125)C(C126)C(C127C128C(C127)C(C128)C(C129C130C(C129)C(C130)C(C131C132C(C131)C(C132)C(C133C134C(C133)C(C134)C(C135C136C(C135)C(C136)C(C137C138C(C137)C(C138)C(C139C140C(C139)C(C140)C(C141C142C(C141)C(C142)C(C143C144C(C143)C(C144)C(C145C146C(C145)C(C146)C(C147C148C(C147)C(C148)C(C149C150C(C149)C(C150)C(C151C152C(C151)C(C152)C(C153C154C(C153)C(C154)C(C155C156C(C155)C(C156)C(C157C158C(C157)C(C158)C(C159C160C(C159)C(C160)C(C161C162C(C161)C(C162)C(C163C164C(C163)C(C164)C(C165C166C(C165)C(C166)C(C167C168C(C167)C(C168)C(C169C170C(C169)C(C170)C(C171C172C(C171)C(C172)C(C173C174C(C173)C(C174)C(C175C176C(C175)C(C176)C(C177C178C(C177)C(C178)C(C179C180C(C179)C(C180)C(C181C182C(C181)C(C182)C(C183C184C(C183)C(C184)C(C185C186C(C185)C(C186)C(C187C188C(C187)C(C188)C(C189C190C(C189)C(C190)C(C191C192C(C191)C(C192)C(C193C194C(C193)C(C194)C(C195C196C(C195)C(C196)C(C197C198C(C197)C(C198)C(C199C200C(C199)C(C200)C(C201C202C(C201)C(C202)C(C203C204C(C203)C(C204)C(C205C206C(C205)C(C206)C(C207C208C(C207)C(C208)C(C209C210C(C209)C(C210)C(C211C212C(C211)C(C212)C(C213C214C(C213)C(C214)C(C215C216C(C215)C(C216)C(C217C218C(C217)C(C218)C(C219C220C(C219)C(C220)C(C221C222C(C221)C(C222)C(C223C224C(C223)C(C224)C(C225C226C(C225)C(C226)C(C227C228C(C227)C(C228)C(C229C230C(C229)C(C230)C(C231C232C(C231)C(C232)C(C233C234C(C233)C(C234)C(C235C236C(C235)C(C236)C(C237C238C(C237)C(C238)C(C239C240C(C239)C(C240)C(C241C242C(C241)C(C242)C(C243C244C(C243)C(C244)C(C245C246C(C245)C(C246)C(C247C248C(C247)C(C248)C(C249C250C(C249)C(C250)C(C251C252C(C251)C(C252)C(C253C254C(C253)C(C254)C(C255C256C(C255)C(C256)C(C257C258C(C257)C(C258)C(C259C260C(C259)C(C260)C(C261C262C(C261)C(C262)C(C263C264C(C263)C(C264)C(C265C266C(C265)C(C266)C(C267C268C(C267)C(C268)C(C269C270C(C269)C(C270)C(C271C272C(C271)C(C272)C(C273C274C(C273)C(C274)C(C275C276C(C275)C(C276)C(C277C278C(C277)C(C278)C(C279C280C(C279)C(C280)C(C281C282C(C281)C(C282)C(C283C284C(C283)C(C284)C(C285C286C(C285)C(C286)C(C287C288C(C287)C(C288)C(C289C290C(C289)C(C290)C(C291C292C(C291)C(C292)C(C293C294C(C293)C(C294)C(C295C296C(C295)C(C296)C(C297C298C(C297)C(C298)C(C299C300C(C299)C(C300)C(C301C302C(C301)C(C302)C(C303C304C(C303)C(C304)C(C305C306C(C305)C(C306)C(C307C308C(C307)C(C308)C(C309C310C(C309)C(C310)C(C311C312C(C311)C(C312)C(C313C314C(C313)C(C314)C(C315C316C(C315)C(C316)C(C317C318C(C317)C(C318)C(C319C320C(C319)C(C320)C(C321C322C(C321)C(C322)C(C323C324C(C323)C(C324)C(C325C326C(C325)C(C326)C(C327C328C(C327)C(C328)C(C329C330C(C329)C(C330)C(C331C332C(C331)C(C332)C(C333C334C(C333)C(C334)C(C335C336C(C335)C(C336)C(C337C338C(C337)C(C338)C(C339C340C(C339)C(C340)C(C341C342C(C341)C(C342)C(C343C344C(C343)C(C344)C(C345C346C(C345)C(C346)C(C347C348C(C347)C(C348)C(C349C350C(C349)C(C350)C(C351C352C(C351)C(C352)C(C353C354C(C353)C(C354)C(C355C356C(C355)C(C356)C(C357C358C(C357)C(C358)C(C359C360C(C359)C(C360)C(C361C362C(C361)C(C362)C(C363C364C(C363)C(C364)C(C365C366C(C365)C(C366)C(C367C368C(C367)C(C368)C(C369C370C(C369)C(C370)C(C371C372C(C371)C(C372)C(C373C374C(C373)C(C374)C(C375C376C(C375)C(C376)C(C377C378C(C377)C(C378)C(C379C380C(C379)C(C380)C(C381C382C(C381)C(C382)C(C383C384C(C383)C(C384)C(C385C386C(C385)C(C386)C(C387C388C(C387)C(C388)C(C389C390C(C389)C(C390)C(C391C392C(C391)C(C392)C(C393C394C(C393)C(C394)C(C395C396C(C395)C(C396)C(C397C398C(C397)C(C398)C(C399C400C(C399)C(C400)C(C401C402C(C401)C(C402)C(C403C404C(C403)C(C404)C(C405C406C(C405)C(C406)C(C407C408C(C407)C(C408)C(C409C410C(C409)C(C410)C(C411C412C(C411)C(C412)C(C413C414C(C413)C(C414)C(C415C416C(C415)C(C416)C(C417C418C(C417)C(C418)C(C419C420C(C419)C(C420)C(C421C422C(C421)C(C422)C(C423C424C(C423)C(C424)C(C425C426C(C425)C(C426)C(C427C428C(C427)C(C428)C(C429C430C(C429)C(C430)C(C431C432C(C431)C(C432)C(C433C434C(C433)C(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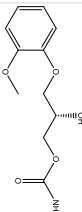
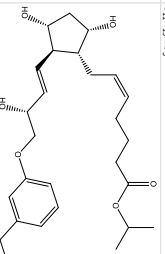
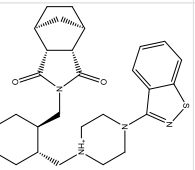
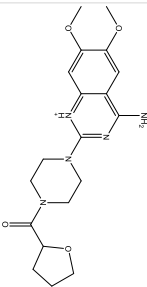
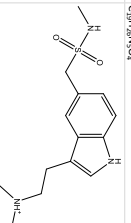
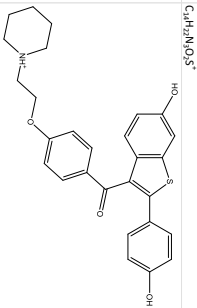
237		<chem>CC(C)N(C)CC(C)CC(C)C(=O)C1N=[NH+]C(C)C(=C1N+)(C(=O)O)O</chem>	(E)-N,N-dimethyl-1-(5-((2-((1-methylamino)-2-methylprop-1-en-1-yl)thio)propylidene)sulfamoyl)amino)-2-ylmethaniminium	F	F	NS	NS	F	T	0.398788	0.074497	-0.05385	-1.51911	-0.24191
238		<chem>NC(C)N(C)CC(C)CC(C)C(=O)C1N=[NH+]C(C)C(=C1N+)(C(=O)O)O</chem>	(Z)-N-(4-amino-3-((Z)-((E)-N,N-dimethyl-1-(5-((2-((1-methylamino)-2-methylprop-1-en-1-yl)thio)propylidene)sulfamoyl)amino)-2-ylmethaniminium 2-ylmethaniminium	F	F	NS	NS	T	F	1.505422	-1.39613	-1.02385	-1.95978	0.719039
239		<chem>CC(C)N(C)CC(C)CC(C)C(=O)C1N=[NH+]C(C)C(=C1N+)(C(=O)O)O</chem>	2-((Z)-N,N-dimethyl-1-(5-((2-((1-methylamino)-2-methylprop-1-en-1-yl)thio)propylidene)sulfamoyl)amino)-2-ylmethaniminium	F	F	NS	NS	T	F	3.806379	-1.00937	-1.26588	-1.27258	0.265937
240		<chem>CC(C)N(C)CC(C)CC(C)C(=O)C1N=[NH+]C(C)C(=C1N+)(C(=O)O)O</chem>	(S)-2-(tert-butylamino)-1-(3-chlorophenyl)propan-1-one	F	F	NS	NS	F	T	0.522239	-2.36789	-0.40985	-1.40177	-0.85972
241		<chem>CC(C)N(C)CC(C)CC(C)C(=O)C1N=[NH+]C(C)C(=C1N+)(C(=O)O)O</chem>	(R)-2-(2-((4-chlorophenyl)phenyl)methyl)pyrrolidine-1-ol	F	F	NS	NS	F	T	1.512514	0.215401	-1.02836	-1.61803	0.622197
242		<chem>CC(C)N(C)CC(C)CC(C)C(=O)C1N=[NH+]C(C)C(=C1N+)(C(=O)O)O</chem>	(3a,5aR,8bR,8bS)-2,2,7,7-tetramethyltetrahydro-3aH-benz[1,3]dioxolo[4,5-b,c]-5,6-dipyrano-3a-ylmethyl sulfate	F	F	NS	NS	F	T	0.546546	-1.28108	-0.4316	0.996752	-1.8933
243		<chem>CC(C)N(C)CC(C)CC(C)C(=O)C1N=[NH+]C(C)C(=C1N+)(C(=O)O)O</chem>	(E)-N,N-dimethyl-1-(5-((2-((1-methylamino)-2-methylprop-1-en-1-yl)thio)propylidene)sulfamoyl)amino)-2-ylmethaniminium	F	F	NS	NS	T	F	1.879637	-2.5754	-0.32215	-1.58697	-0.3965

255		<chem>CC1=CC(C1N+1)CCN1([C@@H](C3=C(C=C(C=C3)C)C)C=C(C=C4C1C2)=CC=C4C2)=CC=C1</chem>	5-(4-(4-chlorophenyl)phenyl)methyl-1-(3-methylbenzyl)piperazine-1-ium	F	F	NS	NS	T	F	2.379507	0.643034	-0.21426	-0.07186	-0.21663
256		<chem>CC1=NC=C(N1CCO)[N+](=O)[O-]=O</chem>	2-(2-methyl-5-nitro-1H-imidazol-1-yl)ethan-1-ol	F	F	NS	NS	F	T	-3.63454	-0.77671	1.108967	-0.26264	-0.28757
257		<chem>O=C1CC(C@12)C(C@3)H(C(C@4)H(C@5H)O)CC(C@6)4H)H(C@3)H)CC2=C1</chem>	(8R,9S,10R,13S,14S,17S,17'-hydroxy-10,13-dimethyl-1,2,6,7,9,10,11,12,13,14,15,16,17-tetrahydro-3H-cyclopenta[a]phenanthren-3-one	F	F	NS	NS	T	F	-0.17769	-0.22506	0.068804	0.617384	-0.21907
258		<chem>O=C1NC=C(C(C(C1N+1)CCC)CC)C=C(C)C1</chem>	N-(2-(2-oxoindol-4-yl)ethyl)-N-propylpropan-1-aminium	F	F	NS	NS	F	T	0.187549	-0.79465	0.521757	-0.11977	-0.65135
259		<chem>O=C1C(C(C1N+1)CC(C)CC)C3=NC(C=C(C=C3)C)C=C(C)C=C1N</chem>	4-(6-fluorobenzo[d]isoxazol-3-yl)-1-(2-(2-methyl-4-oxo-5,7,8,9-tetrahydro-4H-pyrido[1,2-a]pyrimidin-3-yl)ethyl)piperidin-1-ium	F	F	NS	NS	T	F	1.946467	1.1464	-0.21652	-0.52031	-0.39261
260		<chem>C1N+H(C=C(C=C1C2=C(C=C(C=C2)C)C)C)OC(=O)C</chem>	(Z)-2-(11-(3-(dimethylammonio)propylidene)-6,11-dihydrobenzo[b]oxepin-2-yl)acetate	F	F	NS	NS	T	F	1.709755	-0.55709	0.153449	-4.14458	-1.88412
261		<chem>[O-]C(=O)C1=CC=C(C=C1C2=CC(C=C(C=C2)C)C)C(=O)N(C3CC3)C4=CC=C(C=C4)C5=O</chem>	1-(5-cyclopropyl-5-fluoro-8-methoxy-7-(4aS,7aS)-octahydro-6H-pyrido[3,4-b]pyridin-1-ium-6-yl)-4-oxo-1,4-dihydroquinoline-3-carboxylate	F	F	NS	NS	T	F	3.420211	-0.6563	-2.11007	6.197392	2.785018

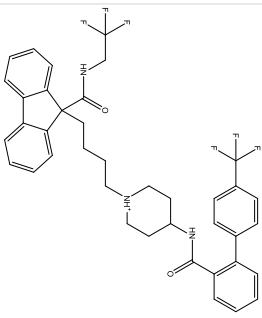
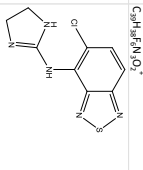
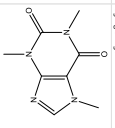
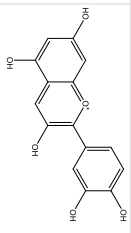
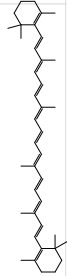
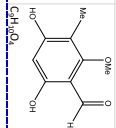
262		<chem>COCC(C@H)(C1=CC=C(C=C1)C@H1CCCC1N2)J2=O</chem>	(R)-2-((R)-2-methoxy-2-oxo-1-phenylethyl)pyrrolidine-1-ium	F	F	NS	NS	T	F	0.881809	-3.48211	0.489995	-1.2905	0.08571
263		<chem>CC(C)N(C1=CC=C(C=C1)C2CC(C)N+)(C2)CC(C3=CC=C(C3)=O)</chem>	1-phenethyl-4-(N-phenylpropionamido)pyrrolidine-1-ium	F	F	NS	NS	T	F	4.025531	-2.97544	0.237505	-1.7467	2.143669
264		<chem>CC(NH+)(C(=O)O(C1=CC=CC=C1)C2=CC=CC=C2)C2=CC=CC=C2</chem>	2-((1,1-bicyclohexene)-1-carbonyloxy)-N,N-diethylethan-1-aminium	F	F	NS	NS	F	T	3.517171	-3.81174	1.549992	0.623949	0.910603
265		<chem>C[NH2+](C(C@H)(C1=CC=C(C=C1)1)CC2=CC=C(C=C2)C=C</chem>	(R)-N-methyl-3-phenyl-3-(o-tolyl)oxy)propan-1-aminium	F	F	NS	NS	T	F	0.234512	-0.669591	-0.56466	0.08146	-0.38212
266		<chem>OC[C@H](COC(C1=CC=C(C=C1)C=C1)COC(C(=O)C(C)C)N+)(C(C)C</chem>	(S)-2-hydroxy-3-(4-((Z)-isopropoxyethoxy)methyl)phenoxyl-N-isopropylpropan-1-aminium	F	F	NS	NS	T	F	4.175091	-3.12619	2.845239	0.352488	1.815706
267		<chem>CC(=O)O[C@@H]1C[C@H]2[C@@H](C(C)C)C[C@H]3[C@@H](C(=O)O)C[C@H]4[C@@H](C(=O)O)C[C@H]14</chem>	(ZS,3aS,6aS)-1-((S)-1-ethoxy-1-oxo-4-phenylbutan-2-yl)-1-(4-aminyl)octahydrocyclopent[1b]pyrrole-2-carboxylate	F	F	NS	NS	T	F	1.631734	-0.880099	0.642773	-1.47084	0.325065

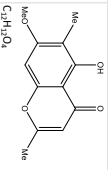
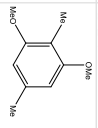
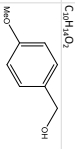
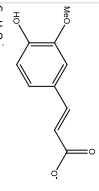
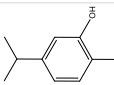
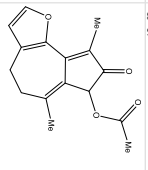
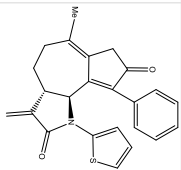
268		<chem>O=C1NC2=C(C(=CC=C2)C(=O)N1)C(=O)C(C(=O)C2)C</chem>	7-chloro-3-hydroxy-1-methyl-5-phenyl-1,3-dihydro-2H-benzotriazin-2-one	F	F	NS	NS	F	T	-0.12209	0.42426	-0.90491	-0.21029	-0.83911
269		<chem>[NH3+]C(C)CC1=C=CC=CC1</chem>	2-methyl-1-phenylpropan-2-aminium	F	F	NS	NS	T	F	0.324842	-5.05155	0.32157	-0.52999	-0.99648
270		<chem>O=C([O-])[C@@H]1CC2=C(C=C(C=C2)N1C[C@@H](CN)[C@@H](CC)C=C=C[C@@H](OCC)C(=O)O)</chem>	(S)-2-((S)-1-ethoxy-1-oxo-4-phenylbutan-2-yl)-L-alanyl-L-2,3,4-tetrahydroquinoline-3-carboxylate	F	F	NS	NS	T	F	1.341341	3.534989	0.786645	-1.48193	-0.03593
271		<chem>CN1CCN(CC18C(=O)C2=C(C(C(=N2)C=C(C(N3)CO)N1N=C4CC(C)C(=O)CC=C4C2=O)C3)C(=O)O</chem>	5-(2-ethoxy-5-(4-methylpiperazin-1-yl)sulfonyl)phenyl-1-methyl-3-propyl-1,6-dihydro-7H-pyrazolo[4,3-d]pyrimidin-7-one	F	F	NS	NS	F	T	3.205393	0.874886	0.632002	-0.01872	-0.15326
272		<chem>CN1C2=C(C(C(C2)CN3C=C(NH+)=C3)O)C4=C(C=C(C4)C1)C</chem>	2-methyl-1-(9-methyl-4-oxo-2,3,4,9-tetrahydro-1H-carbazol-3-yl)pyridin-3-ium	F	F	NS	NS	T	F	0.476851	0.145445	-0.42746	-0.41168	-1.08792
273		<chem>CCOC(C1=C(C(=O)O[C@@H]1C[C@H](C1)N)N3)N(C(=O)O)C(C(=O)O</chem>	(1S,5R,6R)-6-acetamido-3-(ethoxycarbonyl)-5-(tert-butyl)oxycyclohex-3-en-1-aminium	F	F	NS	NS	T	F	0.375426	0.23312	-0.35325	-0.470798	0.418268
274		<chem>CN(C)=CC=C(C(NC(=O)[C](O-)=O)CC([O-])=O)O=C(C1CC2=C(N=C(C(=O)N=C3N=CN=C3N)N)C=C1)C</chem>	(4-((1,2,4-diaminopyridin-6-yl)methyl)(methylamino)benzoyl)-L-glutamate	F	F	NS	NS	F	T	0.5446	4.411672	0.810731	-1.81664	-0.04756

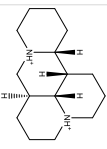
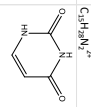
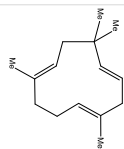
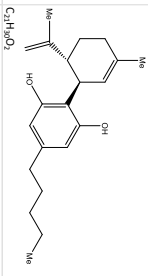
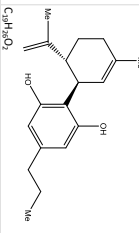
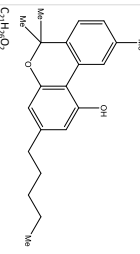
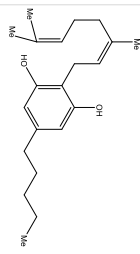
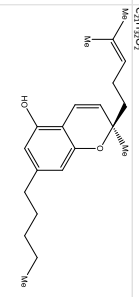
294		<chem>O=C([O-])C1=CN=C(S1C2=CC=C(C(C#N)=C2)CC(=O)C</chem>	2-(3-cyano-4-isobutoxyphenyl)-4-methylimidazole-5-carboxylate	F	F	NS	NS	F	T	-0.85344	2.642912	-0.31822	1.34115	1.122603
295		<chem>Nc1nc(N)c2cc(Cl)c(Cl)nc2n1</chem>	6-(2,3-dichlorophenyl)-1,2,4-triazine-3,5-diamine	F	F	NS	NS	T	F	-0.9547	-0.75783	0.202842	-0.97981	0.269758
296		<chem>FC1=CC=C(C=C1OC2=CC=C(Cl)C(=O)N2)C(=O)N3C=CC(=C3)OC4=CC=CC=C4F</chem>	3-(cyclopropylmethoxy)-N-(3,5-dichloropyridin-4-yl)-4-(difluoromethoxy)benzamide	F	F	NS	NS	T	F	-0.31178	3.20023	0.539799	-0.09749	0.241526
297		<chem>CC(C)OC(=O)C1=CC=C(C=C1)N2C=CC(=C2)C3=CC=CC=C3C4=CC=CC=C4N5C=CC(=C5)C6=CC=CC=C6S(=O)(=O)N7C=CC8=CC=CC=C8N7C6</chem>	2-((1H-benz[d]imidazol-2-ylsulfonyl)methyl)-4-(3-methoxypropoxy)-3-methylpyridin-1-ium	F	F	NS	NS	T	F	1.46447	0.79773	-0.20846	-1.60125	0.795532
298		<chem>CC(=O)CC1=CC2=CC=CC(OC)=CC2=CC=C1</chem>	4-(6-methoxynaphthalen-2-yl)butan-2-one	F	F	NS	NS	F	T	-0.70032	-0.69159	0.070597	-0.11776	0.086931
299		<chem>COC(=O)C1=CC=C(C=C1C2=CC(=C(C=C2)C)C(=O)OC)C(=O)OC</chem>	dimethyl 2,6-dimethyl-4-(2-nitrophenyl)-1,4-dihydropyridine-3,5-dicarboxylate	F	F	NS	NS	T	F	0.316811	0.66286	0.579597	-1.83939	0.789518
300		<chem>O=C1NC(C(=O)N1=CC2=CC=C(C(=O)N2C)C3=CC=CC=C3[N+](=O)[O-])C4=CC=CC=C4</chem>	(2)-1-((5-nitrofur-2-yl)methyl)pyrimidin-2,4-dione	F	F	NS	NS	F	T	-3.49344	2.27599	-0.44961	1.24601	-0.27289

308		<chem>O=C@H([C@@N](O)CO)C(=O)C=C</chem> C-C1OC	(S)-2-hydroxy-3-(2-methoxyphenyl)propyl carbamate	F	F	NS	NS	F	T	-2.47207	1.420883	0.093449	-0.76085	0.389401
309		<chem>CC(C)OC(=O)C=C(C)C@H1[C@@H]([C@@H]([C@@H]1)C=C(C)C@H([C@@H]2C=C(C(C(F)(F)F)O)O)O)O</chem> D>O>C	isopropyl (2S,3S,4S)-3,5-dihydroxy-2-((R)-3-hydroxy-4-(3-(trifluoromethyl)phenoxymethyl)-1-phenyl)-5-oxopent-1-en-1-yl)-2-methylpropanoate	F	F	NS	NS	F	T	3.462045	2.132535	0.034832	0.600506	0.390428
310		<chem>O=C1C@H)2C@H)3C(C(C@H)1([C@@H]2C(N1C(C@H)4C(CCC1)C@H4C(N1+1)SCN(C6=NSC7=C(C=C4C67)CC5)=OC3</chem> 4-benzal(iso)thiazol-3-yl-1-((1R,2R)-2-((3aR,4S,7R,7aS)-1,3-dioxocyclohex-2-yl)methyl)-5-(cyclohexylmethyl)pyrrolidin-1-ium	F	F	NS	NS	F	F						
311		<chem>O=C(C1CCCC1)N2C(N)(C2)C3=NC(N)C4C=C(C(=O)C=C4[NH+])3OC</chem> 4-amino-6,7-dimethoxy-2-(4-(tetrahydrofuran-2-carbonyl)pyrazol-1-yl)quinazolin-1-ium	F	F	NS	NS	T	F		2.891855	-1.12676	0.039438	0.077379	1.300166
312		<chem>O=S(=O)(C)CC2=C(NC=C2C([NH+])C)C(C)C1(NC)NC=O</chem> N,N-dimethyl-2-(6-(N-methylsulfonylphenyl)-1H-indol-3-yl)ethan-1-aminium	F	F	NS	NS	F	T	0.561848	-0.57196	-1.31838	-1.06075	-0.05489	
313		<chem>O=C(C1=CC=C(C(=O)C(N1)2CCCC2)C(C1)C3=C(C4C=C4C(C(=O)O)=C4)C5=CC(C(=O)C=C5</chem> 1-(2-(4-(6-hydroxy-2-(4-(hydroxyphenyl)benzoyl)thiophene-3-carbonyl)phenoxymethyl)pyrrolidin-1-ium	F	F	NS	NS	T	F	2.392484	3.339439	-0.52058	0.628712	0.623999	

322		<chem>O=C1C(C=C(C=C1)C2=CC=C(C=C2)N)C3=CC=C(C=C3)N=C(C#N)C=C4</chem>	1-(2-chlorophenyl)phenylmethoxy-1H-imidazole	F	F	NS	NS	F	T	1.01396	0.52062	-0.9773	-0.74072	-0.45898
323		<chem>O=C1NC(C2=CC=CC=C2)N(C3=CC=C(C=C3)O)C4=CC=CC=C4</chem>	5,5-diphenylimidazolidine-2,4-dione	F	F	NS	NS	F	T	-2.00944	2.090645	0.271714	-0.78755	-0.73458
324		<chem>[NH3+][C@H](C1=CC=CC=C1)C2=CC=CC=C2</chem>	(S)-1-phenylpropan-2-aminium	F	F	NS	NS	T	F	-0.08405	-5.3034	0.127278	-1.16335	0.13825
325		<chem>CC(C)N2+1[C@H]1CCC2=C(C1)S(C)N2</chem>	(S)-2-amino-N-propyl-4,5,6,7-tetrahydrobenzo[d]thiazole-6-aminium	F	F	NS	NS	F	T	1.140575	-4.78846	0.905958	-1.96023	0.848011
326		<chem>CC(C)C1=NC2=C(C(N1C@H3C(C@H3C=C(C)N(C=C4)N1)N=NN(C@H)5C(C@H)4C@H(C@H)1(C@H)5O)O)CCO</chem>	(1S,2S,3R,5S)-3-(7-((1R,2S)-2-(3,4-difluorophenyl)pydopropyl)amino)-5-(propylthio)-3H-1,2,3-triazole-4,5-dipyrroldin-3-yl)-5-(2-hydroxyethoxy)pyclopentane-1,2-diol	F	F	NS	NS	T	F	3.061932	2.356799	0.177698	-0.08724	-0.40145
327		<chem>[O-]C(=O)C=C(C1=CC=C(C=C1)N2=CC=C(C=C2)Cl)C3=CC=C(C=C3)Cl</chem>	2-(R)-2-(5-chlorophenyl)amino phenylacetate	F	F	NS	NS	F	T	-1.01011	2.015648	-0.53404	0.205346	-0.82544
328		<chem>[NH3+][C@H]1(C2CC3CC(C2)C(C3)C1)OCC(N4(C@H)5C(C@H)5SC(C@H)4C(N)=O</chem>	(1S)-2-((1S,3S,5S)-3-c-amino-2-azabicyclo[3.1.0]hexan-2-yl)-1-(4-hydroxyadamantan-1-yl)-2-oxoethan-1-aminium	F	F	NS	NS	F	T	3.083506	-4.13867	0.117758	-1.06826	-0.159916

329		<chem>Fc1ccc(cc1)NC(=O)c2ccccc2</chem>	1-(4-(2,2,2-trifluoroethyl)phenyl)-9H-fluoren-9-ylidene-4-(4-(trifluoromethyl)-1,1'-biphenyl)-2-carboxamido)piperidin-1-ium	NS	NS	F	T	5.937159	3.727752	0.037666	0.239767	-0.650213
330		<chem>Cc1cc2nc3ccccc3n2c1C(F)(F)F</chem>	5-chloro-N-(4,5-dihydro-1H-imidazo-2-yl)benzo[1,1,2,5]thiadiazol-4-amine	NS	NS	F	F	0.163508	-1.68916	-0.61875	-0.13287	0.994183
331		<chem>Cc1nc2c(ncn2C(F)(F)F)c1=O</chem>	1,3,7-trimethyl-3,7-dihydro-1H-purine-2,6-dione	NS	NS	F	F	-2.40251	-1.1226	0.167073	0.401355	-0.402215
332		<chem>CCCCCCCCCCCC(=O)O</chem>	decanoate	NS	NS	T	F	-3.31045	1.072656	-0.09932	0.166077	0.987044
333		<chem>Oc1cc(O)c2c(c1)oc3cc(O)c(C(F)(F)F)c3c2</chem>	2-(3,4-dihydroxyphenyl)-3,5,7-trimethoxyphenonium	NS	NS	T	F	-2.50779	3.267705	0.289731	0.546204	-0.23674
334		<chem>Oc1cc(O)c2c(c1)oc3cc(O)c(C(F)(F)F)c3c2</chem>	22-(10E,3E,5E,7E,9E,11E,13E,15E,17E)-3,7,12,16-tetraethyloctadeca-1,3,5,7,9,11,13,15,17-nonaene-1,18-diyldibutyl,3,3-trimethylcyclohex-1-ene)	NS	NS	T	F	6.455196	3.307844	0.561197	-0.83338	0.075263
335		<chem>Oc1cc(O)c2c(c1)oc3cc(O)c(C(F)(F)F)c3c2</chem>	4,6-dihydroxy-2-methoxy-3-methylbenzaldehyde	NS	NS	T	F	-3.70195	1.04625	-0.2381	0.329974	0.428763

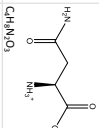
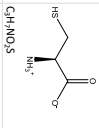
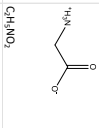
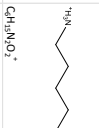
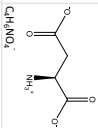
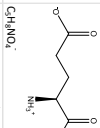
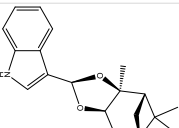
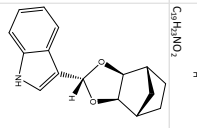
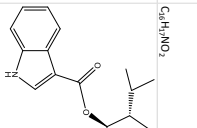
336		<chem>O=C1C=C(C(OC)=C(COC)C(C)C1)OC1</chem>	5-hydroxy-7-methoxy-2,6-dimethyl-4H-chromen-4-one	F	F	NS	NS	F	T	-2.32239	1.059077	0.579544	-0.31624	-0.55689
337		<chem>COCC1=CC(OC)=C(C)C=C1C</chem>	1,3-dimethoxy-2,5-dimethylbenzene	F	T	F	NV	F	T	-1.74427	-2.12324	0.879394	0.034615	-0.39366
338		<chem>OCC1=CC=C(OC)C=C1</chem>	(4-methoxyphenyl)methanol	F	T	F	NV	T	F	-2.80677	-2.12263	0.686764	-0.00962	-0.20238
339		<chem>OC1=CC(OC)=C(/C=C/C(=O)O)C=C1</chem>	(E)-3-(4-hydroxy-3-methoxyphenyl)acrylate	F	T	T	F	F	T	-3.3809	0.888032	-0.24025	-0.65099	1.072729
340		<chem>CC(C)C1=CC=C(C)C(C)=C1</chem>	5-isopropyl-2-methylphenol	F	T	F	NV	F	T	-2.06128	-2.05429	0.245947	0.408636	-0.93378
341		<chem>CC(=O)OC1=C(C)OC(=O)C2=C(C)C3=CC=CC=C3C2=C1</chem>	6,9-dimethyl-3-oxo-4,5,7,8-tetrahydrozulen(6,5-b)furan-7-yl acetate	F	T	T	T	F	T	-0.63106	0.326483	-0.2714	-1.15704	-0.45275
342		<chem>O=C1C2C=C(C)C(C)=CC1(C)C3=CC=CC=C3C2=C1C4=CC(=C(C=C4)N)C5=CC=CC=C5C6=CC=CC=C6C7=CC=CC=C7C8=CC=CC=C8C9=CC=CC=C9C10=CC=CC=C10C11=CC=CC=C11C12=CC=CC=C12C13=CC=CC=C13C14=CC=CC=C14C15=CC=CC=C15C16=CC=CC=C16C17=CC=CC=C17C18=CC=CC=C18C19=CC=CC=C19C20=CC=CC=C20C21=CC=CC=C21C22=CC=CC=C22C23=CC=CC=C23C24=CC=CC=C24C25=CC=CC=C25C26=CC=CC=C26C27=CC=CC=C27C28=CC=CC=C28C29=CC=CC=C29C30=CC=CC=C30C31=CC=CC=C31C32=CC=CC=C32C33=CC=CC=C33C34=CC=CC=C34C35=CC=CC=C35C36=CC=CC=C36C37=CC=CC=C37C38=CC=CC=C38C39=CC=CC=C39C40=CC=CC=C40C41=CC=CC=C41C42=CC=CC=C42C43=CC=CC=C43C44=CC=CC=C44C45=CC=CC=C45C46=CC=CC=C46C47=CC=CC=C47C48=CC=CC=C48C49=CC=CC=C49C50=CC=CC=C50C51=CC=CC=C51C52=CC=CC=C52C53=CC=CC=C53C54=CC=CC=C54C55=CC=CC=C55C56=CC=CC=C56C57=CC=CC=C57C58=CC=CC=C58C59=CC=CC=C59C60=CC=CC=C60C61=CC=CC=C61C62=CC=CC=C62C63=CC=CC=C63C64=CC=CC=C64C65=CC=CC=C65C66=CC=CC=C66C67=CC=CC=C67C68=CC=CC=C68C69=CC=CC=C69C70=CC=CC=C70C71=CC=CC=C71C72=CC=CC=C72C73=CC=CC=C73C74=CC=CC=C74C75=CC=CC=C75C76=CC=CC=C76C77=CC=CC=C77C78=CC=CC=C78C79=CC=CC=C79C80=CC=CC=C80C81=CC=CC=C81C82=CC=CC=C82C83=CC=CC=C83C84=CC=CC=C84C85=CC=CC=C85C86=CC=CC=C86C87=CC=CC=C87C88=CC=CC=C88C89=CC=CC=C89C90=CC=CC=C90C91=CC=CC=C91C92=CC=CC=C92C93=CC=CC=C93C94=CC=CC=C94C95=CC=CC=C95C96=CC=CC=C96C97=CC=CC=C97C98=CC=CC=C98C99=CC=CC=C99C100=CC=CC=C100C101=CC=CC=C101C102=CC=CC=C102C103=CC=CC=C103C104=CC=CC=C104C105=CC=CC=C105C106=CC=CC=C106C107=CC=CC=C107C108=CC=CC=C108C109=CC=CC=C109C110=CC=CC=C110C111=CC=CC=C111C112=CC=CC=C112C113=CC=CC=C113C114=CC=CC=C114C115=CC=CC=C115C116=CC=CC=C116C117=CC=CC=C117C118=CC=CC=C118C119=CC=CC=C119C120=CC=CC=C120C121=CC=CC=C121C122=CC=CC=C122C123=CC=CC=C123C124=CC=CC=C124C125=CC=CC=C125C126=CC=CC=C126C127=CC=CC=C127C128=CC=CC=C128C129=CC=CC=C129C130=CC=CC=C130C131=CC=CC=C131C132=CC=CC=C132C133=CC=CC=C133C134=CC=CC=C134C135=CC=CC=C135C136=CC=CC=C136C137=CC=CC=C137C138=CC=CC=C138C139=CC=CC=C139C140=CC=CC=C140C141=CC=CC=C141C142=CC=CC=C142C143=CC=CC=C143C144=CC=CC=C144C145=CC=CC=C145C146=CC=CC=C146C147=CC=CC=C147C148=CC=CC=C148C149=CC=CC=C149C150=CC=CC=C150C151=CC=CC=C151C152=CC=CC=C152C153=CC=CC=C153C154=CC=CC=C154C155=CC=CC=C155C156=CC=CC=C156C157=CC=CC=C157C158=CC=CC=C158C159=CC=CC=C159C160=CC=CC=C160C161=CC=CC=C161C162=CC=CC=C162C163=CC=CC=C163C164=CC=CC=C164C165=CC=CC=C165C166=CC=CC=C166C167=CC=CC=C167C168=CC=CC=C168C169=CC=CC=C169C170=CC=CC=C170C171=CC=CC=C171C172=CC=CC=C172C173=CC=CC=C173C174=CC=CC=C174C175=CC=CC=C175C176=CC=CC=C176C177=CC=CC=C177C178=CC=CC=C178C179=CC=CC=C179C180=CC=CC=C180C181=CC=CC=C181C182=CC=CC=C182C183=CC=CC=C183C184=CC=CC=C184C185=CC=CC=C185C186=CC=CC=C186C187=CC=CC=C187C188=CC=CC=C188C189=CC=CC=C189C190=CC=CC=C190C191=CC=CC=C191C192=CC=CC=C192C193=CC=CC=C193C194=CC=CC=C194C195=CC=CC=C195C196=CC=CC=C196C197=CC=CC=C197C198=CC=CC=C198C199=CC=CC=C199C200=CC=CC=C200C201=CC=CC=C201C202=CC=CC=C202C203=CC=CC=C203C204=CC=CC=C204C205=CC=CC=C205C206=CC=CC=C206C207=CC=CC=C207C208=CC=CC=C208C209=CC=CC=C209C210=CC=CC=C210C211=CC=CC=C211C212=CC=CC=C212C213=CC=CC=C213C214=CC=CC=C214C215=CC=CC=C215C216=CC=CC=C216C217=CC=CC=C217C218=CC=CC=C218C219=CC=CC=C219C220=CC=CC=C220C221=CC=CC=C221C222=CC=CC=C222C223=CC=CC=C223C224=CC=CC=C224C225=CC=CC=C225C226=CC=CC=C226C227=CC=CC=C227C228=CC=CC=C228C229=CC=CC=C229C230=CC=CC=C230C231=CC=CC=C231C232=CC=CC=C232C233=CC=CC=C233C234=CC=CC=C234C235=CC=CC=C235C236=CC=CC=C236C237=CC=CC=C237C238=CC=CC=C238C239=CC=CC=C239C240=CC=CC=C240C241=CC=CC=C241C242=CC=CC=C242C243=CC=CC=C243C244=CC=CC=C244C245=CC=CC=C245C246=CC=CC=C246C247=CC=CC=C247C248=CC=CC=C248C249=CC=CC=C249C250=CC=CC=C250C251=CC=CC=C251C252=CC=CC=C252C253=CC=CC=C253C254=CC=CC=C254C255=CC=CC=C255C256=CC=CC=C256C257=CC=CC=C257C258=CC=CC=C258C259=CC=CC=C259C260=CC=CC=C260C261=CC=CC=C261C262=CC=CC=C262C263=CC=CC=C263C264=CC=CC=C264C265=CC=CC=C265C266=CC=CC=C266C267=CC=CC=C267C268=CC=CC=C268C269=CC=CC=C269C270=CC=CC=C270C271=CC=CC=C271C272=CC=CC=C272C273=CC=CC=C273C274=CC=CC=C274C275=CC=CC=C275C276=CC=CC=C276C277=CC=CC=C277C278=CC=CC=C278C279=CC=CC=C279C280=CC=CC=C280C281=CC=CC=C281C282=CC=CC=C282C283=CC=CC=C283C284=CC=CC=C284C285=CC=CC=C285C286=CC=CC=C286C287=CC=CC=C287C288=CC=CC=C288C289=CC=CC=C289C290=CC=CC=C290C291=CC=CC=C291C292=CC=CC=C292C293=CC=CC=C293C294=CC=CC=C294C295=CC=CC=C295C296=CC=CC=C296C297=CC=CC=C297C298=CC=CC=C298C299=CC=CC=C299C300=CC=CC=C300C301=CC=CC=C301C302=CC=CC=C302C303=CC=CC=C303C304=CC=CC=C304C305=CC=CC=C305C306=CC=CC=C306C307=CC=CC=C307C308=CC=CC=C308C309=CC=CC=C309C310=CC=CC=C310C311=CC=CC=C311C312=CC=CC=C312C313=CC=CC=C313C314=CC=CC=C314C315=CC=CC=C315C316=CC=CC=C316C317=CC=CC=C317C318=CC=CC=C318C319=CC=CC=C319C320=CC=CC=C320C321=CC=CC=C321C322=CC=CC=C322C323=CC=CC=C323C324=CC=CC=C324C325=CC=CC=C325C326=CC=CC=C326C327=CC=CC=C327C328=CC=CC=C328C329=CC=CC=C329C330=CC=CC=C330C331=CC=CC=C331C332=CC=CC=C332C333=CC=CC=C333C334=CC=CC=C334C335=CC=CC=C335C336=CC=CC=C336C337=CC=CC=C337C338=CC=CC=C338C339=CC=CC=C339C340=CC=CC=C340C341=CC=CC=C341C342=CC=CC=C342C343=CC=CC=C343C344=CC=CC=C344C345=CC=CC=C345C346=CC=CC=C346C347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355		<chem>[H]C@@12[NH+]C(C@3[C@@H](4R,7AS,13AS)hexadecahydro-1H-4H-pyridine-2,1-f3,2,1-[1]1,6naphthyridine-4,9-dium</chem>	F	T	T	T	F	2.907822	-5.88549	1.835237	0.446805	-0.58807	
356		<chem>O=C(N1)NC=CC1=O</chem>	F	T	F	NV	F	T	-4.60382	-1.54139	0.426904	0.24711	-1.28873
357		<chem>C/C1=C/C(C(C)=C/C(C)C)/C=C/C1</chem>	F	T	T	T	F	T	-0.21894	-1.39044	-0.96128	0.559742	-1.26791
358		<chem>OC1=C(C(C@H)2C=C(C)C(C@2-4)1,2,3,4-tetrahydro-1,1,2,6-tetraol</chem>	F	T	T	F	F	T	1.295627	-0.29321	0.738669	-0.06325	0.027349
359		<chem>OC1=C(C(C@H)2C=C(C)C(C@2-4)1,2,3,4-tetrahydro-1,1,2,6-tetraol</chem>	F	T	T	T	F	T	-0.5515	2.037875	-0.10279	0.094154	0.57051
360		<chem>OC1=C(C(C(C(C)C)C)C)C(C)C(C)C1</chem>	F	T	T	F	F	T	0.027952	1.803149	0.543894	-0.5563	0.213283
361		<chem>OC1=C(C(C(C(C)C)C)C)C(C)C(C)C1</chem>	F	F	NS	NS	T	F	0.807844	1.818479	-0.30502	0.527636	0.758795
362		<chem>OC1=C(C(C(C(C)C)C)C)C(C)C(C)C1</chem>	F	F	NS	NS	T	F	1.254771	-0.04618	0.753506	-0.44065	0.33204

382		<chem>N[C@@H](CC(C(=O)OC)=O)C(=O)O</chem>	methyl L-tyrosinate	F	T	F	NV	F	T	-1.05694	-1.3079	-2.07536	-0.70559	0.907087
383		<chem>N[C@@H](CCCC(N)=O)C(=O)O</chem>	(S)-5-amino-6-methoxy-6-oxohexan-1-amine	F	T	F	NV	F	T	-2.28674	-2.33748	1.729561	-0.09891	0.053869
384		<chem>N[C@@H](CC(C(=O)O)=O)C(=O)O</chem>	(S)-4-amino-5-methoxy-5-oxopentylammoniummethanaminium	F	T	F	NV	T	F	1.704637	-6.43844	1.176691	-1.2681	1.237955
385		<chem>N[C@@H](C(=O)O)C(=O)O</chem>	methyl L-alaninate	F	T	F	NV	T	F	-4.31455	-2.93804	2.148512	0.27106	-0.36588
386		<chem>N[C@@H](CC(C(=O)O)=O)C(=O)O</chem>	methyl L-methioninate	F	T	T	F	F	T	-2.36371	-2.06875	0.827562	-0.44887	-0.18296
387		<chem>N[C@@H](CC(C(=O)O)=O)C(=O)O</chem>	(S)-4-amino-5-methoxy-5-oxopentanoate	F	T	F	NV	F	T	-4.80343	0.627227	0.418138	-0.39159	1.081987
388		<chem>N[C@@H](C(C(=O)O)=O)C(=O)O</chem>	methyl L-isoleucinate	F	T	T	F	F	T	-2.87982	-2.50516	1.120328	0.438065	-0.09147
389		<chem>N[C@@H](C(C(=O)O)=O)C(=O)O</chem>	methyl L-tryptophanate	F	T	T	T	F	T	-0.76794	-1.30826	-0.63732	0.391611	-0.31521
390		<chem>N[C@@H](C(C(=O)O)=O)C(=O)O</chem>	methyl L-valinate	F	T	T	F	T	F	-3.16947	-2.56857	1.33664	0.738644	-0.52653
391		<chem>[NH3+][C@@H](C(=O)O)C(=O)O</chem>	(S)-3-ammonio-4-methoxy-4-oxobutanoate	F	T	F	NV	T	F	-5.56185	0.86023	0.726168	-0.11399	1.331855
392		<chem>O=C(C(=O)C(C(=O)O)=O)C(=O)O</chem>	(6aR,8E,12E,15aS)-4-methoxy-1,6a,10,10,13-pentamethyl-6a,7,10,11,14,15,16-octahydro-3H-cyclohepta[b]cycloundec[e]pyran-3-one	F	T	T	T	T	F	1.688696	0.795379	0.46734	-1.03228	0.512956

393		<chem>[H][C@1]2[C@]3(C)[C@H]1C=C(N+)[C]C3=C(N4=C3C2=C(C)C4</chem>	(6aR,9R,7,9-dimethyl-4,6,6a,9,10,10a-hexahydroindolo[4,3-f]quinolin-7-ylum	T	F	NS	NS	T	F	0.746515	-2.542	-0.83191	-0.00124	0.181053
394		<chem>O=C1C2=C(O)C=C(O)C=C2O[C@H]1C3=CC(O)=C(O)C(O)=C3C1</chem>	(R)-5,7-dihydroxy-2-[3,4,5-trihydroxyphenyl]chroman-4-one	T	F	NS	NS	F	T	-1.78727	2.605727	-0.42035	-0.13419	-0.00545
395		<chem>O=C1C2=C(O)C=C(O)C=C2O[C@H]1C3=CC=C(O)C=C3C1</chem>	(R)-5,7-dihydroxy-2-(4-hydroxyphenyl)chroman-4-one	T	F	NS	NS	T	F	-1.80089	2.01248	0.137664	0.068039	0.876666
396		<chem>O=C1C2=C(O)C=C(O)C=C2O[C@H]1C3=CC=C(O)C=C3C1O</chem>	(2R,3R)-3,5,7-trihydroxy-2-(4-hydroxyphenyl)chroman-4-one	T	F	NS	NS	F	T	-1.53349	2.028989	0.23075	0.04512	-0.0903
397		<chem>O=C1C2=C(O)C=C(O)C=C2O[C@H]1C3=CC(O)=C(O)C=C3C1</chem>	(R)-2-[3,4-dihydroxyphenyl]-5,7-dihydroxychroman-4-one	T	F	NS	NS	T	F	-2.44139	3.11884	0.871291	0.15446	1.327321
398		<chem>O=C1C2=C(O)C=C(O)C=C2O[C@H]1C3=CC(O)=C(O)C=C3C1</chem>	(S)-2-[3,4-dihydroxyphenyl]-5,7-dihydroxychroman-4-one	T	F	NS	NS	F	T	-2.27364	3.339153	0.453361	0.355119	-0.1672
399		<chem>O=C1C2=C(O)C=C(O)C=C2O[C@H]1C3=CC(O)=C(O)C=C3C1</chem>	(S)-5,7-dihydroxy-2-[3,4,5-trihydroxyphenyl]chroman-4-one	T	F	NS	NS	T	F	-2.80055	4.815316	0.913175	0.84028	-0.3028
400		<chem>O[C@H]1C2=C(O)C=C(O)C=C2O[C@H]1C3=CC=C(O)C(O)=C3C1O</chem>	(2R,3S,4S)-2-[3,4-dihydroxyphenyl]chromene-3,4,5,7-tetraol	T	F	NS	NS	F	T	-1.2824	1.729874	0.084191	-0.64419	0.55835

[illegible]

433		[NH3+][C@@H](C(=O)O)[C@H](O)=O	(S)-4-amino-2-oxobutanoate	F	T	F	NV	F	T	-5.29401	0.66316	0.827045	0.538826	0.07917
434		[NH3+][C@@H](C(=O)O)=O	(R)-2-amino-3-mercaptopropionate	F	T	F	NV	T	F	-5.11776	0.312429	-0.518643	0.133788	0.580739
435		[NH3+][C](O)=O	2-aminoacetate	F	T	T	F	F	T	-7.18637	-0.28072	0.943766	-0.12385	0.513935
436		[NH3+][C@@H](C(=O)O)=O	(S)-2,6-diaminohexanoate	F	T	T	F	F	T	-0.20705	-6.01287	2.337649	0.95963	-0.3705
437		[NH3+][C@@H](C(=O)O)=O	(S)-2-aminoisobutyrate	F	T	F	NV	F	T	-6.1385	2.059257	0.188583	0.814656	-0.51649
438		[NH3+][C@@H](C(=O)O)=O	(S)-2-ammoniopentamethionate	F	T	F	NV	T	F	-4.96517	1.024545	0.290774	-0.02676	-0.56719
439		C1C@@H1C(=O)C@H2C3C4C=C(C=C4)C(=O)C(=O)C2C3C@H1C3C1C	3-((2R,3aS,4S,6S,7aR)-3a,5,5-trimethylhexahydro-4,6-methanobenzo[d][1,3]dioxol-2-yl)-1H-indole	F	F	NS	NS	F	T	0.363353	-0.63139	0.238828	-0.09514	-0.86652
440		[H]1C@H1C(=O)C@H2C3C4C=C(C=C4)C(=O)C2C3C@H1C3C1C	3-((2R,3aR,4S,7R)-2,5,1-hexahydro-4,7-methanobenzo[d][1,3]dioxol-2-yl)-1H-indole	F	F	NS	NS	T	F	-0.32827	-1.05712	-0.14619	0.497207	-0.81694
441		O=C(O)C@H1C(=O)C(=O)C(=O)C1C@H1C(=O)C(=O)C(=O)C1C	(1R,2S,5R)-2-isopropyl-5-methylpyridin-1H-indole-3-carboxylate	F	F	NS	NS	T	F	0.353525	-0.06115	0.077535	0.468215	-1.26654

450		<chem>[O-][C@H]1[NH2+](CCCC1)=O</chem>	(S)-piperidin-1-ium-2-carboxylate	F	T	T	F	F	T	-3.40557	-2.59761	0.795008	0.306311	-1.47897
451		<chem>OC1=C(Br)C=C(CCN1H)[O]CC2C3=C(C=CC=C3)K2=C1</chem>	7-bromo-8-hydroxy-3-methyl-1-phenyl-2,3,4,5-tetrahydro-1H-benzo[d]azepin-3-ium	F	T	T	T	F	T	1041279	-1.7362	-2.96039	0.571864	2.895677
452		<chem>NC1=CC=C(N2CCOCC2)C=C1</chem>	4-morpholineaniline	F	T	T	F	T	F	-1.11217	-2.38968	0.486595	0.196528	-0.23402
453		<chem>OC[C@H]1C[C@@H]2C[C@H]3[C@@H](O)[C@H]1C=C4C=CC(=C3C=C4)OC</chem>	(R)-6-methoxyquinolin-4-yl[(1S,4S)-5-vinylquinidin-2-yl]methanol	F	T	T	T	F	T	9.944309	10.85149	16.67226	-2.02237	0.553127

17. MORFEUS descriptors for all substrates

Supplemental Table S7. MORFEUS descriptors for all substrates. Substrate ID reflects those identified in Supplemental Table S6. Descriptors are consistent with the entirety of the MORFEUS set.⁸⁹ Substrates not compatible with the MORFEUS workflow are left blank and ultimately not included in the chemical space representation.

Substrate ID	sasa_area	sasa_volume	disp_area	disp_volume	disp_p_int	disp_p_max	disp_p_min	ip	ea	homo	lumo	electrophilicity	nucleophilicity	electrofugality	nucleofugality	dipole_x	dipole_y	dipole_z	mass	radius	charge
1	414.487	660.434	288.148	288.687	18.547	48.796	9.467	12.964	8.354	-0.401	-0.396	3.664	-8.118	11.783	0.157	1.033	0.802	0.662	235.256	4.176	-1
2	360.088	539.797	235.716	224.945	17.511	44.967	8.919	12.860	4.758	-0.379	-0.276	0.969	-8.014	8.984	1.057	-0.860	-1.882	0.051	180.200	3.967	0
3	287.487	405.197	170.334	151.424	16.856	39.864	9.011	14.541	8.840	-0.431	-0.429	4.109	-9.695	13.803	0.115	-3.308	0.512	0.038	136.105	3.133	-2
4	312.308	445.419	194.010	174.093	16.697	43.650	8.534	13.123	4.170	-0.387	-0.267	0.807	-8.277	9.084	1.483	0.817	-0.446	0.129	136.148	3.625	0
5	338.798	490.734	217.410	197.414	16.677	41.854	8.788	12.449	7.033	-0.387	-0.363	2.212	-7.603	9.815	0.025	-2.488	0.471	1.241	152.171	4.063	-1
6	314.106	447.699	188.626	170.106	16.823	42.368	9.223	14.110	8.460	-0.433	-0.424	3.669	-9.264	12.933	0.055	-1.654	-0.610	0.903	152.127	3.608	-1
7	418.358	622.543	268.727	250.466	17.452	42.204	8.174	13.261	8.155	-0.410	-0.406	3.365	-8.415	11.780	0.056	2.809	2.395	0.266	207.203	5.186	-1
8	334.848	495.154	211.617	200.679	17.258	43.948	9.022	13.031	4.936	-0.386	-0.285	1.057	-8.185	9.242	0.967	-0.283	-1.186	1.479	166.174	3.444	0
9	392.371	600.380	262.987	254.836	18.460	46.165	8.503	13.139	5.403	-0.397	-0.296	1.266	-8.293	9.559	0.709	-2.065	-1.176	0.161	259.097	4.178	0
10	334.548	493.964	212.621	199.439	17.112	44.042	8.753	13.201	7.888	-0.396	-0.391	3.056	-8.355	11.411	0.014	1.762	0.513	0.442	165.166	4.003	-1
11	449.282	697.948	302.159	294.826	19.263	45.121	9.146	12.372	5.533	-0.372	-0.285	1.233	-7.526	8.758	0.546	0.574	-0.640	0.805	252.265	5.573	0
12	433.849	669.891	280.895	274.254	19.460	43.854	9.282	13.175	8.336	-0.412	-0.401	3.609	-8.329	11.937	0.119	2.987	-0.144	0.070	253.230	5.605	-1
13	360.928	533.720	228.220	213.225	17.827	43.844	8.262	13.041	5.260	-0.390	-0.289	1.191	-8.195	9.386	0.777	-3.023	0.957	0.872	192.168	4.650	0
14	434.921	679.791	299.984	295.141	18.833	42.048	9.396	12.592	4.109	-0.380	-0.229	0.724	-7.746	8.470	1.461	0.084	-0.398	-0.205	242.270	5.571	0
15	427.491	663.028	289.081	282.852	19.096	40.874	9.343	12.951	5.362	-0.398	-0.295	1.224	-8.105	9.329	0.708	-0.335	1.103	-0.014	240.254	5.539	0
16	350.109	516.569	224.898	207.705	17.798	42.367	9.284	12.802	7.599	-0.410	-0.378	2.755	-7.956	10.711	0.002	-2.851	-0.343	1.748	174.176	3.860	-1
17	466.110	710.439	320.586	300.530	17.785	41.916	8.282	11.903	3.859	-0.354	-0.230	0.573	-7.057	7.630	1.559	-1.201	0.246	0.632	232.278	6.016	0
18	351.951	519.629	223.254	209.515	17.691	45.263	8.168	12.901	4.617	-0.381	-0.265	0.924	-8.055	8.980	1.153	-0.276	-0.628	1.039	176.187	4.586	0
19	460.847	717.794	310.120	303.226	19.106	43.749	8.694	12.566	5.202	-0.387	-0.282	1.107	-7.720	8.827	0.751	1.725	0.863	0.464	272.253	5.992	0
20	431.100	663.893	294.007	283.476	18.124	46.336	8.469	12.379	4.646	-0.372	-0.262	0.869	-7.533	8.403	1.069	0.141	-1.690	1.265	234.248	4.646	0
21	590.757	1047.084	453.474	511.974	20.174	48.230	10.643	12.504	5.955	-0.391	-0.303	1.467	-7.658	9.125	0.358	-3.360	0.463	-0.620	412.519	6.403	0
22	603.397	1051.621	454.461	508.836	19.976	51.017	9.763	12.274	5.036	-0.384	-0.257	1.002	-7.428	8.430	0.813	-2.280	-0.048	0.597	412.519	6.563	0
23	600.827	1041.563	449.262	497.303	20.158	45.725	9.880	12.455	8.048	-0.396	-0.389	3.315	-7.609	10.924	0.113	-2.912	1.454	-0.562	409.495	6.563	-1
24	492.596	851.503	366.472	411.978	19.457	48.779	10.054	13.094	9.015	-0.411	-0.410	4.725	-8.248	12.973	0.556	1.571	1.416	-3.343	330.418	5.108	-2
25	547.226	978.391	417.466	480.430	20.290	50.834	10.920	12.626	5.927	-0.391	-0.291	1.465	-7.780	9.245	0.384	0.685	1.032	-1.547	394.503	5.432	0
26	565.317	1015.903	430.188	505.001	19.925	45.742	9.644	12.459	5.418	-0.388	-0.284	1.190	-7.613	8.803	0.617	0.573	1.046	-1.516	416.507	5.092	0
27	490.645	837.550	370.087	396.504	19.406	54.304	10.013	13.143	8.457	-0.417	-0.411	3.783	-8.297	12.080	0.172	0.519	-1.861	-0.517	331.383	4.979	-1
28	493.485	848.629	367.597	400.753	19.438	55.772	9.993	13.236	8.713	-0.422	-0.416	4.152	-8.390	12.542	0.285	1.408	0.896	-1.122	347.382	5.019	-1
29	428.018	714.758	308.242	346.287	18.070	39.405	10.429	13.035	2.117	-0.403	-0.223	0.341	-8.189	8.530	3.070	2.006	-0.489	0.880	250.376	4.605	0
30	553.586	999.561	420.492	497.058	20.050	46.223	10.957	12.856	5.178	-0.397	-0.273	1.133	-8.010	9.144	0.801	1.308	1.800	-3.078	412.519	5.406	0
31	599.867	1102.185	472.994	557.027	20.311	54.900	9.791	12.524	5.534	-0.397	-0.296	1.252	-7.678	8.930	0.563	-1.676	0.406	-1.635	460.560	5.660	0
32	561.147	1008.647	429.280	503.073	19.844	47.009	10.729	12.577	5.255	-0.394	-0.290	1.131	-7.731	8.862	0.722	1.431	-1.987	-0.938	402.524	5.327	0
33	338.068	510.688	226.810	222.089	16.677	37.713	9.125	12.513	2.473	-0.361	-0.213	0.349	-7.667	8.016	2.722	1.025	-0.312	-0.846	174.201	3.604	0
34	273.807	378.739	167.639	147.951	15.036	34.460	8.845	14.009	7.762	-0.429	-0.403	2.920	-9.163	12.083	0.003	-2.472	-1.154	-0.579	114.123	2.788	-1
35	315.887	456.065	205.838	190.193	15.520	39.102	9.072	13.669	2.014	-0.397	-0.227	0.365	-8.823	9.208	3.217	-1.100	1.230	-1.494	131.173	3.493	0
36	360.776	532.870	227.232	212.804	17.330	40.076	9.559	13.565	8.786	-0.413	-0.409	4.191	-8.719	12.911	0.251	0.821	0.618	0.858	179.173	4.478	-2
37	310.265	442.612	191.357	173.782	15.979	38.737	8.655	13.674	8.378	-0.426	-0.413	3.588	-9.028	12.616	0.056	0.751	-1.502	0.411	145.137	3.313	-1
38	308.337	448.849	201.439	188.404	15.608	39.529	8.606	13.642	2.049	-0.396	-0.227	0.388	-8.796	9.185	3.185	0.555	-1.836	1.083	131.173	3.029	0
39	313.668	455.740	200.908	183.687	16.704	44.187	8.673	13.056	3.057	-0.381	-0.219	0.515	-8.210	8.725	2.305	1.082	0.516	1.221	155.155	3.228	0
40	389.148	592.130	260.390	245.640	18.122	45.147	9.380	12.672	7.655	-0.392	-0.382	2.818	-7.826	10.643	0.009	2.679	-2.371	-0.455	203.217	4.542	-1
41	335.878	501.807	219.610	207.990	17.351	46.185	9.261	13.408	7.787	-0.415	-0.399	2.943	-8.562	11.505	0.002	0.829	0.844	-1.404	164.181	3.569	-1

Substrate ID	sasa_area	sasa_volume	disp_area	disp_volume	disp_p_int	disp_p_max	disp_p_min	ip	ea	homo	lumo	electrophilicity	nucleophilicity	electrofugality	nucleofugality	dipole_x	dipole_y	dipole_z	mass	radius	charge
42	588.683	1032.207	462.042	508.037	21.112	56.791	9.895	7.034	3.302	-0.320	-0.189	0.014	-2.188	2.202	1.558	0.576	-1.712	1.951	399.551	6.127	1
43	516.790	845.644	376.499	380.506	19.770	51.625	8.324	9.755	4.912	-0.372	-0.265	0.639	-4.909	5.547	0.573	1.254	0.256	1.292	311.355	6.214	1
44	657.621	1165.135	515.691	579.137	20.245	51.777	10.103	10.901	3.960	-0.327	-0.237	0.481	-6.055	6.536	1.367	-0.032	0.260	-0.663	449.628	7.807	0
45	774.481	1392.156	621.686	675.304	21.746	54.421	9.995	8.221	4.778	-0.341	-0.236	0.397	-3.375	3.772	0.465	-1.957	3.003	1.140	566.670	8.169	1
46	582.450	1021.177	451.218	500.348	20.144	63.858	8.535	6.846	2.905	-0.179	-0.178	0.000	-2.000	2.000	1.941	0.325	-1.941	0.171	400.511	5.974	2
47	724.509	1254.518	564.115	594.463	20.576	53.270	8.697	8.551	4.127	-0.335	-0.218	0.252	-3.705	3.957	0.971	0.535	-0.073	-1.551	480.576	7.603	1
48	429.060	701.637	318.711	339.732	18.039	45.845	9.973	3.454	-1.777	-0.321	-0.027	1.535	1.392	0.143	8.158	-0.095	-0.144	0.037	235.388	4.657	1
49	434.859	712.704	319.028	342.736	18.215	43.425	10.184	8.044	0.575	-0.338	-0.154	0.019	-3.196	3.216	4.290	-2.202	-1.916	1.210	249.372	4.597	1
50	754.811	1344.863	615.708	639.769	21.319	56.759	9.097	11.904	5.498	-0.368	-0.281	1.160	-7.058	8.218	0.508	-2.292	0.933	1.229	500.625	6.943	0
51	344.724	516.134	219.978	205.727	17.546	39.944	9.641	14.222	9.037	-0.434	-0.430	4.438	-9.376	13.814	0.246	0.622	-1.931	0.634	195.149	3.271	-1
52	553.131	993.979	453.451	492.224	20.856	56.350	10.115	12.153	4.340	-0.367	-0.239	0.740	-7.307	8.047	1.246	2.596	-0.549	-0.251	387.476	5.794	0
53	424.571	687.439	308.006	323.880	17.777	40.280	9.726	12.556	1.773	-0.374	-0.191	0.249	-7.710	7.959	3.323	-0.763	0.240	0.353	220.350	4.552	0
54	469.920	716.643	336.606	313.531	16.997	42.288	8.712	12.141	3.699	-0.367	-0.244	0.560	-7.295	7.855	1.707	-0.385	-0.132	1.088	194.313	5.932	0
55	343.226	515.370	223.060	211.597	17.351	40.053	9.833	13.687	8.523	-0.415	-0.410	3.793	-8.841	12.634	0.116	1.381	-0.501	-1.132	181.165	3.219	-1
56	506.900	827.070	374.611	382.404	18.877	44.956	9.514	6.292	1.961	-0.309	-0.142	0.060	-1.446	1.506	2.945	8.803	0.721	-2.070	290.377	6.063	1
57	459.870	691.340	322.560	299.235	17.232	46.815	8.596	5.948	1.646	-0.140	-0.139	0.128	-1.102	1.229	3.328	2.459	-0.667	-1.734	212.295	5.555	2
58	419.089	668.500	300.324	305.891	17.886	45.575	8.804	12.544	4.384	-0.376	-0.271	0.802	-7.698	8.501	1.264	-0.542	-1.378	-0.394	220.307	4.832	0
59	306.158	440.358	196.027	180.545	16.111	40.503	9.142	12.243	3.769	-0.338	-0.257	0.589	-7.397	7.986	1.666	2.740	-3.163	-0.330	142.156	2.886	0
60	424.186	658.007	298.558	284.491	17.499	49.148	8.676	13.200	8.178	-0.411	-0.406	3.400	-8.354	11.754	0.067	-2.382	0.045	0.209	209.262	5.176	-1
61	422.388	668.337	303.339	318.176	18.040	51.781	10.152	13.280	7.909	-0.422	-0.402	3.076	-8.434	11.510	0.013	1.745	-2.099	1.445	233.326	4.121	-1
62	367.959	548.071	251.812	237.326	16.600	50.891	8.621	12.528	1.573	-0.350	-0.200	0.222	-7.682	7.904	3.495	-0.750	-1.106	0.296	168.236	4.375	0
63	317.839	468.091	216.315	205.472	16.005	39.412	8.700	12.413	-3.258	-0.341	0.028	0.002	-7.567	7.570	8.106	-0.546	-0.441	0.251	141.211	3.387	0
64	328.108	490.047	225.031	216.119	16.230	39.684	9.511	12.764	-2.508	-0.350	-0.004	0.003	-7.918	7.920	7.357	-0.718	0.607	0.746	157.210	3.438	0
65	589.618	1022.578	462.639	474.917	20.560	52.513	8.849	11.698	4.412	-0.351	-0.240	0.707	-6.852	7.558	1.141	1.640	0.351	-1.336	400.422	6.054	0
66	478.839	790.613	348.419	367.431	19.168	46.287	8.587	6.745	2.101	-0.308	-0.161	0.019	-1.899	1.919	2.764	5.800	-2.321	-1.262	300.372	5.302	1
67	509.440	832.863	373.501	381.282	19.276	50.659	8.521	11.495	4.041	-0.343	-0.237	0.573	-6.649	7.221	1.378	-0.839	-0.156	-0.296	311.375	5.386	0
68	1233.765	2126.846	911.396	950.976	21.316	51.238	8.451	12.548	10.446	-0.424	-0.423	10.523	-7.702	18.225	4.923	12.843	6.458	-4.111	939.671	14.891	-4
69	1242.495	2099.318	903.587	926.249	20.762	54.466	9.167	12.655	10.674	-0.429	-0.429	11.735	-7.809	19.545	5.907	10.468	5.018	-1.598	907.629	17.680	-6
70	1558.884	2687.180	1217.565	1267.363	20.131	57.439	8.374	11.547	9.619	-0.381	-0.391	8.537	-6.701	15.238	3.764	-8.028	-3.559	-3.270	961.217	25.338	-3
71																					
72	590.532	978.588	434.333	434.200	18.973	46.917	9.765	13.015	9.537	-0.416	-0.415	5.944	-8.169	14.113	1.253	-0.150	0.762	-0.362	361.414	5.601	-2
73	577.582	934.120	406.828	409.944	18.629	42.328	10.086	12.875	8.703	-0.413	-0.409	4.234	-8.029	12.263	0.376	-1.116	3.353	2.654	358.380	6.978	-1
74	589.481	931.497	407.722	397.311	18.836	54.730	9.816	13.031	9.470	-0.414	-0.414	5.758	-8.185	13.944	1.135	-0.896	-2.955	2.184	355.366	7.347	-2
75	693.700	1213.308	542.978	578.406	19.164	48.392	9.005	6.524	1.059	-0.309	-0.129	0.102	-1.678	1.780	3.888	-3.134	1.403	-0.552	498.499	7.540	1
76																					
77	516.804	837.683	365.192	367.153	18.598	44.225	9.297	12.677	4.619	-0.393	-0.268	0.897	-7.831	8.729	1.124	-0.090	0.066	0.144	343.286	5.566	0
78	493.698	834.138	366.137	397.360	19.214	43.890	10.471	12.429	5.363	-0.382	-0.284	1.161	-7.583	8.744	0.644	0.898	-1.182	0.713	298.419	5.460	0
79	564.229	967.565	423.512	461.956	20.307	53.404	8.686	11.424	4.121	-0.348	-0.227	0.586	-6.578	7.165	1.311	-1.186	-1.140	0.951	394.464	5.999	0
80	586.139	1000.775	439.945	484.137	18.981	47.476	8.780	12.235	4.255	-0.380	-0.245	0.724	-7.389	8.112	1.315	-0.125	-0.279	0.270	358.514	7.918	0
81	374.990	574.316	266.105	264.895	16.659	39.438	9.478	12.158	-3.035	-0.335	0.017	0.003	-7.312	7.315	7.884	-0.029	0.243	0.021	167.291	4.565	0
82	506.936	855.459	366.650	392.358	20.035	56.815	9.746	12.831	8.435	-0.405	-0.401	3.809	-7.985	11.794	0.220	2.904	0.316	1.536	348.387	5.514	-1

Substrate ID	sasa_area	sasa_volume	disp_area	disp_volume	disp_p_int	disp_p_max	disp_p_min	ip	ea	homo	lumo	electrophilicity	nucleophilicity	electrofugality	nucleofugality	dipole_x	dipole_y	dipole_z	mass	radius	charge
83	516.426	847.156	366.259	373.127	19.674	47.077	9.159	12.596	8.327	-0.394	-0.389	3.693	-7.750	11.443	0.212	0.751	1.794	-1.307	343.308	6.075	-1
84	357.748	538.682	235.822	223.904	17.383	39.696	8.641	13.053	7.904	-0.391	-0.388	3.081	-8.207	11.288	0.023	-0.370	2.326	0.023	179.193	4.108	-1
85	350.398	528.945	228.721	221.623	17.651	42.722	9.705	13.047	7.946	-0.397	-0.388	3.129	-8.201	11.330	0.030	0.544	-0.524	0.227	179.193	3.466	-1
86	338.369	503.634	214.496	205.635	18.486	44.610	9.140	13.162	5.239	-0.388	-0.292	1.197	-8.316	9.512	0.803	-3.041	-0.276	-0.166	231.043	3.469	0
87	345.749	515.950	219.016	211.060	19.373	41.582	9.344	13.854	9.116	-0.424	-0.423	4.652	-9.008	13.660	0.382	-0.863	-0.195	-0.068	276.028	3.483	-2
88	350.079	518.867	220.402	205.079	17.656	44.405	8.121	13.105	8.037	-0.394	-0.391	3.234	-8.259	11.494	0.043	1.228	-1.730	-1.078	175.161	4.204	-1
89	418.268	645.064	277.002	268.843	18.859	44.614	9.398	12.970	8.138	-0.400	-0.394	3.371	-8.124	11.495	0.079	-0.282	-0.235	0.157	227.235	5.088	-1
90	351.768	529.935	229.520	220.402	17.502	45.468	9.045	13.104	7.902	-0.397	-0.389	3.076	-8.258	11.334	0.020	-0.181	-1.306	0.131	179.193	3.743	-1
91	373.228	560.902	244.635	229.964	17.345	42.880	8.330	13.491	8.496	-0.407	-0.407	3.783	-8.645	12.428	0.133	-0.212	0.240	0.074	194.184	4.139	-2
92	430.568	671.440	299.827	293.595	17.926	42.742	8.582	12.865	7.877	-0.396	-0.387	3.060	-8.019	11.079	0.029	-0.662	1.098	0.386	221.272	4.824	-1
93	338.376	502.001	212.258	199.061	17.155	43.843	9.397	14.223	9.123	-0.431	-0.431	4.569	-9.377	13.946	0.292	0.517	1.834	-0.085	181.145	3.459	-2
94	370.809	551.511	241.403	214.241	17.192	40.983	7.645	13.194	8.082	-0.395	-0.388	3.443	-8.348	11.791	0.077	-1.557	-0.145	0.163	179.173	4.424	-2
95	358.027	530.862	229.421	226.724	17.274	45.268	8.472	12.942	8.082	-0.389	-0.388	3.302	-8.096	11.399	0.067	1.570	0.599	0.130	177.200	4.408	-2
96	432.179	680.360	294.996	291.808	19.154	42.657	9.507	12.702	5.318	-0.381	-0.284	1.174	-7.856	9.031	0.702	0.072	-0.148	0.955	242.270	5.271	0
97	477.429	747.015	322.013	318.711	19.440	44.804	9.348	12.433	8.170	-0.387	-0.384	3.491	-7.587	11.078	0.167	-1.938	0.441	-1.480	273.327	6.328	-1
98	383.248	592.028	261.228	257.435	17.952	43.923	9.240	12.638	4.185	-0.374	-0.253	0.752	-7.792	8.544	1.413	-0.505	1.167	1.281	206.238	4.272	0
99	433.869	679.108	310.817	302.041	18.018	45.827	9.202	12.494	4.158	-0.374	-0.253	0.726	-7.648	8.374	1.414	1.217	-0.053	-0.872	222.280	4.916	0
100	333.957	493.311	210.434	197.368	17.619	45.546	9.465	13.449	4.645	-0.401	-0.271	1.009	-8.653	9.662	1.209	-1.141	1.351	0.352	180.157	3.459	-1
101	377.218	568.405	242.028	229.207	17.914	44.728	9.043	12.862	7.780	-0.384	-0.382	2.960	-8.016	10.975	0.016	0.401	-2.369	0.053	205.187	4.585	-1
102	449.711	703.068	312.405	305.124	18.287	47.328	8.514	12.208	4.608	-0.368	-0.259	0.835	-7.362	8.197	1.073	-0.140	-1.830	-0.740	248.274	4.986	0
103	438.217	681.160	300.045	292.142	17.931	46.967	8.500	12.899	8.368	-0.396	-0.394	3.697	-8.053	11.749	0.174	0.688	0.869	-1.009	235.256	5.779	-1
104	415.458	634.351	282.029	267.082	17.527	42.069	8.508	13.293	8.632	-0.410	-0.409	4.013	-8.447	12.459	0.227	0.304	0.395	-0.191	206.238	5.047	-2
105	470.459	732.598	333.318	323.897	17.745	42.694	8.586	12.474	4.379	-0.375	-0.258	0.792	-7.629	8.421	1.259	-1.493	-2.051	-0.558	236.307	5.656	0
106	440.308	678.822	303.030	290.842	17.687	41.721	8.744	12.974	8.355	-0.397	-0.397	3.664	-8.128	11.792	0.156	0.344	2.051	-0.153	220.264	4.951	-2
107	412.249	631.288	280.821	270.408	17.579	43.570	8.553	12.767	7.820	-0.395	-0.384	2.999	-7.921	10.920	0.025	-0.067	0.585	-1.055	207.246	4.739	-1
108	319.676	466.396	195.648	181.100	17.342	42.928	9.354	14.155	8.942	-0.426	-0.425	4.308	-9.309	13.617	0.213	-0.809	-0.800	-0.304	166.131	3.334	-2
109	376.118	568.887	248.533	235.648	17.396	41.446	8.415	13.273	8.135	-0.404	-0.396	3.339	-8.427	11.767	0.050	-0.693	0.278	0.206	195.192	4.142	-1
110	289.618	405.107	175.514	156.019	16.274	40.251	8.757	13.475	7.267	-0.396	-0.382	2.459	-8.629	11.088	0.038	1.686	1.689	0.626	123.129	2.933	-1
111	313.809	451.394	199.302	182.502	16.452	43.781	8.953	12.754	2.742	-0.370	-0.209	0.419	-7.888	8.307	2.522	1.011	-0.170	-0.030	138.164	3.418	0
112	363.179	542.452	236.416	223.154	17.193	41.587	8.297	13.056	7.834	-0.393	-0.388	3.002	-8.210	11.212	0.014	-2.033	0.373	-0.241	179.193	4.735	-1
113	284.349	401.010	174.304	158.483	16.376	43.813	9.207	13.062	2.806	-0.370	-0.216	0.465	-8.216	8.681	2.505	1.233	-0.231	-0.027	124.137	2.929	0
114	272.110	376.214	164.292	145.241	16.149	38.687	8.897	13.170	7.085	-0.391	-0.374	2.292	-8.324	10.616	0.053	-0.482	-1.534	-0.050	107.130	2.933	-1
115	277.440	384.038	168.888	149.718	16.078	42.993	8.567	13.294	2.813	-0.378	-0.218	0.491	-8.448	8.939	2.524	0.672	0.407	-0.068	108.138	2.929	0
116	320.036	466.119	194.547	180.113	17.320	42.602	9.374	14.426	9.174	-0.436	-0.434	4.603	-9.580	14.183	0.276	-1.673	0.572	-0.077	166.131	3.467	-2
117	322.249	471.092	205.005	190.734	17.128	44.579	9.104	13.117	7.829	-0.390	-0.388	2.994	-8.271	11.265	0.011	0.692	2.023	0.239	149.167	3.453	-1
118	310.308	447.955	190.023	175.304	17.122	40.169	9.086	13.442	8.056	-0.403	-0.397	3.235	-8.596	11.831	0.025	1.728	1.148	-0.019	151.139	3.467	-1
119	309.968	448.176	191.023	176.407	17.171	40.293	9.390	13.618	8.212	-0.416	-0.402	3.407	-8.772	12.179	0.041	0.550	0.287	-0.075	151.139	3.344	-1
120	330.157	488.569	207.727	198.192	17.453	42.652	9.820	13.197	7.928	-0.393	-0.391	3.101	-8.351	11.452	0.019	-2.860	-0.224	-0.079	165.166	3.399	-1
121	308.897	449.030	187.729	174.870	17.083	42.167	9.576	13.871	8.302	-0.416	-0.409	3.496	-9.025	12.521	0.040	0.155	-0.898	0.007	151.139	3.215	-1
122	311.398	441.775	193.710	173.179	16.344	43.075	8.997	13.263	7.563	-0.389	-0.388	2.719	-8.417	11.135	0.002	0.452	-0.032	-0.389	138.144	3.206	-1
123	302.668	426.651	183.207	162.616	16.637	39.042	8.998	13.661	8.148	-0.407	-0.404	3.329	-8.815	12.144	0.027	-0.520	-0.390	-0.153	136.128	3.350	-1

Substrate ID	sasa_area	sasa_volume	disp_area	disp_volume	disp_p_int	disp_p_max	disp_p_min	ip	ea	homo	lumo	electrophilicity	nucleophilicity	electrofugality	nucleofugality	dipole_x	dipole_y	dipole_z	mass	radius	charge
124	477.410	748.106	322.868	315.652	19.585	44.931	9.415	12.546	8.127	-0.393	-0.388	3.411	-7.700	11.111	0.130	-1.224	-0.005	0.136	261.295	6.181	-1
125	326.139	477.681	209.502	196.111	17.123	43.427	9.531	13.159	4.692	-0.386	-0.277	0.983	-8.313	9.296	1.137	1.901	0.027	0.148	150.175	3.480	0
126	332.260	487.946	211.382	198.717	18.268	46.378	9.058	13.297	5.338	-0.394	-0.297	1.256	-8.451	9.707	0.764	-2.399	-0.293	0.390	215.044	3.390	0
127	412.959	629.861	273.388	261.554	18.743	45.010	9.328	13.025	8.112	-0.403	-0.394	3.333	-8.179	11.511	0.067	-0.700	-0.097	-0.072	211.236	5.068	-1
128	305.879	435.006	186.212	168.633	16.703	39.266	9.062	13.579	8.091	-0.412	-0.400	3.268	-8.733	12.001	0.023	-0.507	-1.029	-0.025	135.140	3.456	-1
129	342.979	508.529	215.597	205.808	18.458	44.079	9.734	13.225	5.226	-0.395	-0.293	1.199	-8.379	9.578	0.819	-2.575	-1.022	2.125	231.043	3.460	0
130	417.049	640.936	273.298	263.722	18.879	44.376	9.262	13.010	8.520	-0.398	-0.397	3.902	-8.164	12.066	0.227	2.054	-0.918	-0.434	226.227	4.818	-2
131	338.077	496.378	213.432	196.590	17.120	40.282	9.146	13.616	8.589	-0.410	-0.410	3.894	-8.770	12.663	0.151	1.009	0.502	-0.013	164.158	3.488	-2
132	349.304	518.110	213.678	198.953	17.367	41.208	9.369	14.517	9.685	-0.447	-0.446	5.447	-9.671	15.118	0.608	0.061	-1.360	0.167	195.129	3.536	-2
133	337.518	498.233	214.427	200.227	17.281	42.727	8.621	13.462	8.070	-0.402	-0.398	3.249	-8.616	11.865	0.026	-1.572	1.375	-0.117	165.166	3.945	-1
134	406.246	622.159	268.652	256.043	17.879	42.980	8.258	13.153	8.098	-0.396	-0.394	3.304	-8.307	11.610	0.052	0.388	1.983	-1.792	223.202	4.911	-1
135	343.276	506.928	216.158	200.107	17.108	42.173	9.179	14.111	9.095	-0.428	-0.428	4.552	-9.265	13.817	0.302	-1.299	-2.108	0.353	181.145	3.422	-2
136	347.667	518.048	218.024	208.447	18.478	42.896	9.821	13.870	5.870	-0.417	-0.317	1.577	-9.024	10.601	0.553	2.484	0.602	0.088	248.031	3.404	0
137	345.715	522.835	223.570	214.662	17.456	41.025	9.877	13.908	6.355	-0.415	-0.335	1.849	-9.062	10.911	0.340	-0.184	-0.125	-1.021	199.161	3.257	0
138	412.675	641.777	278.286	267.957	17.734	44.272	8.597	13.583	8.777	-0.421	-0.413	4.174	-8.737	12.911	0.243	1.788	-0.526	-0.499	239.201	4.431	-1
139	349.497	526.955	224.327	216.145	18.453	43.646	9.834	13.726	6.255	-0.410	-0.326	1.772	-8.880	10.652	0.362	-0.203	-0.565	-0.104	247.043	3.393	0
140	358.878	544.406	231.334	226.206	19.282	41.268	9.984	13.657	6.241	-0.410	-0.325	1.756	-8.811	10.566	0.361	-0.284	-0.597	-0.065	294.043	3.488	0
141	360.277	540.502	228.559	214.671	17.745	42.572	8.129	13.776	8.809	-0.420	-0.417	4.184	-8.930	13.114	0.220	1.069	0.677	-1.940	191.670	3.996	-1
142	363.900	548.478	235.895	228.760	18.504	42.640	8.894	13.167	4.994	-0.395	-0.280	1.097	-8.321	9.418	0.949	0.753	-2.181	0.366	245.070	4.031	0
143	363.406	559.141	244.256	237.175	17.471	40.319	8.225	13.050	5.581	-0.384	-0.304	1.337	-8.204	9.542	0.602	1.803	1.265	-2.539	196.200	3.585	0
144	362.575	549.982	230.671	220.295	17.841	46.614	9.460	14.226	9.485	-0.438	-0.437	5.183	-9.380	14.562	0.543	0.811	-1.659	-0.247	209.156	3.462	-2
145	399.467	611.964	263.454	251.489	17.874	42.984	8.445	13.571	8.897	-0.417	-0.416	4.366	-8.725	13.091	0.315	1.055	0.005	0.273	222.194	4.512	-2
146	634.594	1043.011	457.161	475.475	23.533	50.188	10.368	12.799	5.923	-0.405	-0.289	1.482	-7.953	9.436	0.406	-0.370	-1.573	-0.908	776.870	6.931	0
147	462.109	773.503	344.024	364.388	19.589	51.594	8.807	11.599	5.029	-0.346	-0.283	0.915	-6.753	7.668	0.732	-1.329	-0.895	-0.747	299.364	5.120	0
148	569.504	929.649	405.884	407.545	19.649	50.615	10.149	12.850	9.207	-0.407	-0.406	5.247	-8.004	13.251	0.885	-1.636	0.166	1.841	363.388	6.068	-2
149	635.775	1093.619	482.760	505.507	19.935	54.118	9.608	12.685	9.203	-0.408	-0.403	5.341	-7.839	13.180	0.984	-1.592	0.891	-1.983	403.472	7.195	-2
150	580.090	928.333	411.573	404.893	19.360	44.910	8.226	11.978	5.127	-0.370	-0.259	1.003	-7.132	8.135	0.721	0.164	-0.377	-0.577	345.416	7.925	0
151	834.117	1449.837	651.176	673.937	21.563	54.368	9.774	12.196	8.666	-0.397	-0.395	4.418	-7.350	11.768	0.598	-5.468	-0.791	1.287	557.632	8.963	-1
152	660.778	1158.283	521.656	561.378	19.754	49.061	9.393	12.232	4.483	-0.370	-0.240	0.795	-7.386	8.182	1.159	-1.232	-0.148	-1.350	418.566	6.728	0
153	507.271	822.957	365.323	371.306	20.178	51.773	8.929	8.240	4.388	-0.373	-0.231	0.280	-3.394	3.674	0.738	-0.712	0.502	-0.584	322.830	5.628	1
154	883.503	1521.950	661.756	709.224	21.367	50.360	10.557	11.757	8.131	-0.380	-0.378	3.584	-6.911	10.486	0.299	1.832	1.336	0.335	585.175	8.695	-1
155	711.244	1210.869	529.755	545.034	20.568	48.217	9.698	12.623	8.643	-0.404	-0.401	4.206	-7.777	11.984	0.410	-3.233	0.154	0.455	480.530	7.581	-1
156	525.490	843.098	387.313	378.129	17.943	45.614	8.701	6.061	1.232	-0.292	-0.123	0.149	-1.215	1.364	3.763	-5.669	1.258	0.728	268.372	6.742	1
157	561.851	915.427	407.017	409.013	19.617	50.209	9.586	12.244	5.220	-0.350	-0.282	1.075	-7.398	8.473	0.701	1.343	0.146	0.158	324.392	5.666	0
158	973.569	1875.138	835.408	990.552	21.000	55.992	9.147	4.973	0.814	-0.289	-0.102	0.458	-0.127	0.585	4.491	6.394	1.288	3.840	749.992	7.929	1
159	465.378	732.561	328.516	325.342	17.548	43.553	9.094	12.058	3.408	-0.345	-0.235	0.482	-7.212	7.694	1.919	-0.170	-0.530	-0.092	239.311	5.642	0
160	412.484	642.148	269.468	267.410	20.604	47.266	9.742	13.776	8.802	-0.431	-0.425	4.173	-8.903	13.102	0.217	-1.950	3.467	-1.972	296.771	4.309	-1
161	316.310	448.715	205.676	185.516	15.800	35.307	8.581	6.931	-0.586	-0.145	-0.083	0.186	-2.085	2.271	5.618	0.203	0.113	-0.075	131.180	3.794	2
162	494.652	801.475	358.286	365.499	20.133	46.096	9.432	12.173	4.468	-0.356	-0.248	0.783	-7.327	8.110	1.162	-0.804	-0.391	1.074	306.230	5.126	0
163	429.899	664.019	301.919	290.093	17.699	46.484	9.194	12.824	7.757	-0.426	-0.384	2.925	-7.978	10.903	0.014	-2.429	0.550	1.516	205.273	5.075	-1
164	564.242	901.266	404.336	395.853	19.257	45.476	9.426	11.716	4.443	-0.353	-0.241	0.719	-6.870	7.589	1.122	-0.884	-1.841	-1.307	307.380	6.364	0

Substrate ID	sasa_area	sasa_volume	disp_area	disp_volume	disp_p_int	disp_p_max	disp_p_min	ip	ea	homo	lumo	electrophilicity	nucleophilicity	electrofugality	nucleofugality	dipole_x	dipole_y	dipole_z	mass	radius	charge
165	482.145	765.597	320.947	320.679	20.269	45.684	8.832	13.634	9.615	-0.431	-0.427	5.716	-8.788	14.505	0.947	-2.892	1.252	1.026	328.728	5.037	-2
166	577.551	923.317	406.872	402.360	19.368	48.704	8.230	11.913	5.068	-0.367	-0.258	0.970	-7.067	8.037	0.748	-0.072	-0.714	1.080	345.416	8.111	0
167	615.622	995.599	441.561	443.654	19.675	43.667	9.474	11.346	5.259	-0.343	-0.280	0.982	-6.500	7.482	0.568	-1.027	-0.030	0.643	371.864	7.867	0
168	689.399	1174.684	526.955	542.412	20.255	52.648	8.740	12.329	5.570	-0.392	-0.284	1.246	-7.483	8.729	0.522	2.823	0.667	-2.588	435.519	8.426	0
169	477.880	779.797	351.205	364.284	18.448	48.251	8.469	11.987	2.969	-0.356	-0.217	0.384	-7.141	7.526	2.261	0.119	1.141	0.261	263.375	5.024	0
170	532.683	851.159	382.964	378.210	19.732	46.100	8.461	11.770	4.771	-0.360	-0.249	0.838	-6.924	7.761	0.913	-0.764	-0.464	0.203	297.415	6.253	0
171	506.790	825.405	361.896	365.140	19.891	46.777	9.563	12.481	5.379	-0.386	-0.283	1.174	-7.635	8.809	0.641	1.008	-1.230	1.535	308.328	5.561	0
172	590.419	1036.985	481.532	495.417	20.848	55.717	9.349	8.719	4.471	-0.381	-0.241	0.360	-3.873	4.233	0.735	2.085	-1.083	-0.519	409.884	5.399	1
173	480.128	798.941	347.644	370.515	19.216	50.298	8.574	11.964	4.251	-0.365	-0.258	0.690	-7.118	7.807	1.285	-0.303	-2.473	-1.347	315.364	5.374	0
174	641.731	1053.316	472.194	478.706	19.874	47.874	7.680	6.826	2.565	-0.171	-0.157	0.003	-1.980	1.983	2.283	11.876	2.120	-0.131	385.523	8.524	2
175	484.093	791.663	347.866	363.353	20.090	48.850	9.758	11.162	4.067	-0.333	-0.232	0.540	-6.316	6.857	1.319	-1.641	-0.598	0.010	284.471	4.954	0
176	639.326	1150.678	496.348	561.669	20.620	54.511	9.632	12.626	6.031	-0.381	-0.291	1.523	-7.780	9.303	0.338	-2.951	2.280	-0.597	500.571	6.480	0
177	499.162	796.473	343.717	345.897	20.295	49.291	9.572	12.483	5.704	-0.370	-0.291	1.331	-7.637	8.967	0.473	0.515	-2.153	0.006	308.765	5.050	0
178	485.977	770.831	327.608	324.016	20.326	47.491	9.700	13.147	8.847	-0.417	-0.408	4.400	-8.301	12.701	0.399	0.851	0.707	0.239	314.703	4.685	-1
179	680.928	1150.373	519.625	521.285	20.178	48.504	9.181	12.450	8.246	-0.400	-0.394	3.601	-7.604	11.205	0.201	-1.848	2.205	-1.363	423.482	7.441	-1
180	530.818	851.063	369.137	369.212	20.502	46.200	9.324	9.824	5.708	-0.377	-0.283	1.036	-4.978	6.014	0.174	-0.025	2.346	-0.751	352.409	7.219	1
181	575.751	927.707	411.910	412.695	19.432	49.316	9.357	12.113	5.288	-0.346	-0.283	1.088	-7.267	8.356	0.647	1.034	0.115	0.148	324.392	6.526	0
182	554.806	894.792	392.849	387.470	19.804	47.423	9.433	7.459	9.260	-0.403	-0.401	4.906	-7.913	12.820	0.722	-1.456	-2.438	-2.507	345.373	6.851	-2
183	533.219	923.238	400.345	441.057	21.025	55.778	9.763	7.457	3.260	-0.324	-0.195	0.031	-2.611	2.643	1.617	8.510	-0.857	-1.109	392.512	5.586	1
184	343.647	527.763	233.044	237.143	16.643	36.276	9.134	13.254	1.706	-0.392	-0.211	0.300	-8.408	8.708	3.441	-0.123	-1.992	-1.940	171.237	3.618	0
185	606.751	1069.128	465.408	513.626	21.544	48.737	10.643	10.940	4.268	-0.314	-0.243	0.570	-6.094	6.664	1.148	1.196	4.383	-0.462	448.385	5.815	0
186	481.283	803.736	361.242	375.833	20.228	55.073	9.773	7.843	3.518	-0.321	-0.207	0.081	-2.997	3.077	1.408	5.423	0.543	1.222	276.395	4.824	1
187	552.926	961.733	413.966	466.898	19.589	52.403	10.250	12.386	5.657	-0.373	-0.287	1.296	-7.540	8.836	0.484	1.619	0.384	-1.376	374.471	6.168	0
188	441.721	696.940	316.397	315.034	18.405	46.658	8.965	7.473	2.343	-0.346	-0.179	0.000	-2.627	2.627	2.504	-3.483	0.489	0.502	224.314	4.823	1
189	691.561	1265.292	549.689	635.254	21.674	62.834	9.947	11.121	4.472	-0.318	-0.228	0.655	-6.275	6.930	1.028	0.572	-4.339	-0.122	501.656	6.633	0
190	622.973	1069.680	479.939	498.838	20.769	48.670	9.757	7.353	3.841	-0.330	-0.205	0.080	-2.507	2.587	1.085	-1.953	2.847	0.563	407.482	6.237	1
191	469.269	761.749	345.729	347.275	17.815	45.400	8.815	13.234	8.458	-0.413	-0.412	3.769	-8.388	12.157	0.157	0.140	0.858	-0.039	259.322	4.985	-1
192	1028.223	1887.080	824.965	953.500	20.177	54.800	9.854	11.984	4.508	-0.394	-0.277	0.773	-7.138	7.911	1.111	0.631	-1.289	0.175	780.938	13.734	0
193	357.900	565.329	257.503	269.457	16.948	33.264	10.265	12.598	-3.073	-0.358	0.026	0.000	-7.752	7.752	7.919	0.426	-0.155	0.232	179.302	3.409	0
194	518.328	813.312	369.613	356.270	17.816	47.988	8.627	12.233	7.790	-0.381	-0.378	3.003	-7.387	10.389	0.059	-3.537	0.291	-0.220	265.328	7.104	-1
195	476.761	752.506	328.768	327.453	19.978	45.127	9.548	12.541	5.469	-0.376	-0.283	1.223	-7.695	8.918	0.600	-0.171	-1.350	0.278	284.740	4.888	0
196	401.802	629.250	260.604	257.968	20.005	48.294	9.148	14.778	10.364	-0.463	-0.460	6.759	-9.932	16.691	1.242	5.602	-0.144	-0.799	279.081	4.513	-4
197	703.762	1124.731	481.414	469.064	19.372	44.158	8.889	12.777	9.827	-0.419	-0.415	7.063	-7.931	14.995	2.082	6.775	0.798	1.577	438.374	10.653	-3
198	687.988	1158.213	507.624	523.276	20.605	48.082	9.379	12.843	9.529	-0.413	-0.412	6.065	-7.997	14.062	1.381	0.260	-1.226	2.861	444.486	7.238	-2
199	530.685	914.035	394.270	436.774	19.662	52.377	10.151	12.504	5.871	-0.378	-0.293	1.421	-7.658	9.079	0.396	1.998	1.416	0.960	358.428	6.328	0
200	596.633	1029.505	438.590	471.098	20.718	50.877	9.060	12.574	9.022	-0.398	-0.397	4.986	-7.728	12.714	0.810	1.391	6.299	2.603	441.411	6.499	-3
201	365.001	566.738	236.220	237.367	19.094	45.199	9.513	14.886	10.350	-0.468	-0.464	6.659	-10.040	16.699	1.155	3.991	0.674	2.296	246.072	3.657	-3
202	522.647	877.970	383.378	392.067	20.688	66.521	8.881	12.943	8.854	-0.405	-0.404	4.479	-8.097	12.577	0.471	-2.508	1.914	0.177	382.362	5.435	-1
203	609.740	1052.207	467.906	493.126	20.885	51.685	9.047	10.767	4.376	-0.275	-0.253	0.581	-5.921	6.503	1.051	-4.576	0.871	6.934	408.512	5.994	0
204	443.331	680.014	295.788	286.467	19.254	45.251	8.869	11.471	5.056	-0.329	-0.270	0.910	-6.625	7.535	0.701	0.651	-0.586	-0.126	253.263	5.957	0
205	543.209	886.800	391.182	397.519	19.355	45.754	8.826	6.930	2.826	-0.324	-0.176	0.000	-2.084	2.084	2.020	-2.226	-7.582	1.843	330.373	5.862	1

Substrate ID	sasa_area	sasa_volume	disp_area	disp_volume	disp_p_int	disp_p_max	disp_p_min	ip	ea	homo	lumo	electrophilicity	nucleophilicity	electrofugality	nucleofugality	dipole_x	dipole_y	dipole_z	mass	radius	charge
206	652.440	1174.105	505.929	591.325	20.352	52.546	9.323	9.976	2.146	-0.269	-0.156	0.094	-5.130	5.225	2.794	2.448	8.324	0.167	467.640	6.172	0
207	652.058	1068.953	488.741	483.513	19.165	43.779	8.801	12.227	4.566	-0.368	-0.241	0.823	-7.381	8.204	1.103	0.297	2.519	1.070	376.447	6.971	0
208	672.747	1148.519	525.065	544.756	19.369	48.283	8.864	12.227	4.385	-0.369	-0.233	0.763	-7.381	8.145	1.224	-0.903	0.140	-2.035	404.540	6.932	0
209	616.348	982.436	435.207	427.277	19.409	48.978	8.603	12.531	8.757	-0.401	-0.398	4.454	-7.684	12.138	0.543	-5.857	0.471	2.434	355.431	7.966	-1
210	609.626	1105.240	499.187	541.620	20.405	52.816	9.506	12.430	8.523	-0.367	-0.394	4.057	-7.585	11.642	0.380	-0.504	-1.677	-0.831	423.520	6.047	-1
211	520.630	839.530	369.733	366.323	18.972	46.033	9.561	7.425	3.066	-0.357	-0.191	0.018	-2.579	2.597	1.798	6.770	3.612	0.025	330.334	5.226	1
212	462.749	749.435	324.496	324.033	19.293	50.943	8.628	13.213	5.077	-0.394	-0.276	1.136	-8.367	9.502	0.905	-0.372	-0.603	1.439	306.271	5.369	0
213	553.396	910.013	398.426	405.472	19.543	45.019	9.626	12.073	7.948	-0.377	-0.375	3.233	-7.227	10.460	0.131	5.516	3.227	2.006	360.360	6.500	-1
214	641.646	1051.029	458.566	461.587	20.404	54.841	9.329	12.276	8.394	-0.396	-0.390	3.880	-7.430	11.311	0.332	-1.645	-2.633	-1.700	434.873	8.310	-1
215	583.897	934.674	406.443	394.618	20.085	51.130	9.507	13.151	5.931	-0.411	-0.296	1.527	-8.305	9.832	0.441	-2.591	2.154	1.251	381.372	5.408	0
216	476.279	788.103	349.215	368.663	19.282	50.015	8.615	6.689	2.023	-0.306	-0.159	0.026	-1.843	1.869	2.849	5.547	-2.383	-1.699	300.372	5.390	1
217	667.119	1195.706	512.772	581.809	20.912	47.843	9.265	12.351	6.105	-0.379	-0.289	1.537	-7.505	9.043	0.278	0.320	-1.371	-1.032	521.430	6.512	0
218	533.806	864.276	377.810	376.915	19.235	46.665	9.442	12.345	7.931	-0.388	-0.383	3.173	-7.499	10.672	0.087	-4.832	1.927	-3.709	330.334	5.977	-1
219	353.397	532.940	237.938	230.330	16.170	38.959	9.279	13.615	8.064	-0.411	-0.407	3.236	-8.769	12.004	0.018	2.054	0.836	0.822	158.218	3.634	-1
220	507.510	832.634	374.102	389.629	18.450	45.867	8.362	11.739	2.705	-0.337	-0.208	0.312	-6.893	7.205	2.453	-0.616	-0.622	-0.632	277.402	5.606	0
221	476.239	759.404	323.097	324.935	20.550	48.435	9.662	12.746	8.390	-0.404	-0.392	3.758	-7.900	11.658	0.214	1.267	1.426	-0.803	320.150	4.735	-1
222	642.128	1063.705	459.254	467.510	20.207	45.766	9.421	12.445	7.836	-0.386	-0.388	3.041	-7.603	10.644	0.051	1.487	-1.009	-0.357	408.417	7.246	-1
223	502.659	804.770	365.197	354.488	19.504	46.661	9.551	12.435	8.313	-0.383	-0.380	3.707	-7.589	11.266	0.240	-0.002	-0.004	0.006	266.334	6.053	-2
224	267.408	370.025	150.445	134.004	16.871	37.371	8.560	14.911	9.037	-0.442	-0.440	4.325	-10.065	14.390	0.134	0.303	-0.307	0.016	134.096	2.989	-2
225	514.718	842.613	368.835	376.751	19.693	49.538	9.475	12.925	8.555	-0.412	-0.404	3.975	-8.079	12.055	0.266	0.439	-2.016	-0.203	333.382	6.024	-1
226	555.005	923.902	394.215	402.075	19.314	46.049	9.418	9.424	5.158	-0.389	-0.262	0.701	-4.578	5.278	0.388	0.815	-3.226	0.228	408.322	5.871	1
227	527.773	853.679	387.541	386.438	19.544	48.701	9.291	11.817	4.227	-0.347	-0.236	0.664	-6.971	7.635	1.284	-0.077	0.139	0.502	277.403	5.791	0
228	391.621	592.524	263.789	252.150	18.926	45.516	9.401	8.247	3.455	-0.366	-0.215	0.105	-3.401	3.507	1.497	2.543	-0.410	0.313	231.102	4.579	1
229	758.119	1282.217	589.843	602.748	19.108	47.813	9.244	12.098	4.047	-0.382	-0.224	0.646	-7.252	7.886	1.446	-0.089	0.780	-0.027	432.593	8.598	0
230	519.490	825.490	375.278	370.567	18.092	44.513	8.284	12.030	7.506	-0.376	-0.371	2.678	-7.184	9.862	0.018	-0.314	0.964	0.475	262.371	6.821	-1
231	270.848	374.578	156.502	138.292	16.494	40.954	8.744	14.274	8.217	-0.440	-0.416	3.381	-9.428	12.809	0.010	-2.586	0.453	-0.174	122.101	3.014	-1
232	436.199	671.456	293.506	282.032	18.375	44.865	8.185	12.394	7.780	-0.402	-0.375	2.976	-7.548	10.524	0.043	2.955	-1.780	0.166	229.251	5.845	-1
233	486.888	830.556	359.449	373.878	20.791	68.653	9.721	12.902	8.588	-0.400	-0.399	4.033	-8.056	12.089	0.291	-0.520	1.321	1.496	368.354	4.550	-1
234	787.047	1285.688	575.343	568.477	19.786	46.148	9.103	12.315	9.288	-0.400	-0.400	5.858	-7.469	13.327	1.416	-1.382	-1.655	-1.653	491.988	9.370	-2
235	527.552	855.945	382.168	390.803	20.004	46.200	9.687	7.178	2.290	-0.180	-0.150	0.001	-2.332	2.333	2.557	10.077	-0.601	0.362	314.448	5.890	1
236	571.872	972.502	433.466	462.665	19.750	51.377	9.824	6.311	2.233	-0.312	-0.151	0.040	-1.465	1.505	2.653	-7.173	-2.431	0.242	326.466	5.700	2
237	567.948	900.281	407.248	396.902	18.449	44.983	9.226	11.909	5.061	-0.366	-0.264	0.967	-7.063	8.030	0.752	-3.800	-0.200	-1.463	314.404	6.608	0
238	525.326	833.642	370.630	363.142	20.118	47.045	8.784	9.042	4.683	-0.347	-0.244	0.466	-4.196	4.663	0.629	-6.098	-1.746	-0.631	338.453	6.996	1
239	613.700	1060.771	479.517	503.788	20.986	59.627	8.508	7.955	3.936	-0.335	-0.215	0.150	-3.109	3.259	1.060	-4.733	-0.561	0.924	415.526	7.162	1
240	452.631	713.803	319.408	318.622	18.342	43.806	9.703	9.023	3.584	-0.350	-0.231	0.195	-4.177	4.372	1.457	-4.989	0.877	-0.892	240.749	5.279	1
241	576.510	982.401	425.702	461.495	20.527	47.500	9.828	11.554	5.031	-0.329	-0.264	0.910	-6.708	7.618	0.726	-2.514	-2.397	-2.523	388.888	5.569	0
242	496.376	817.590	364.508	374.270	18.879	48.100	9.811	13.293	0.764	-0.411	-0.129	0.190	-8.447	8.637	4.272	-1.851	-1.137	1.190	339.362	5.270	0
243	520.508	850.226	377.801	383.750	18.785	42.789	9.343	7.748	3.221	-0.333	-0.196	0.045	-2.902	2.947	1.670	-6.691	-0.205	-0.198	325.344	6.463	1
244	604.899	989.724	441.699	440.004	19.725	48.609	9.470	7.150	3.566	-0.206	-0.195	0.037	-2.304	2.341	1.317	-16.380	-0.376	-1.009	391.832	7.363	3
245	414.307	620.089	272.094	252.539	17.297	39.374	8.679	12.781	3.882	-0.379	-0.242	0.682	-7.935	8.617	1.647	-0.291	3.218	0.864	225.205	4.946	0
246	575.914	933.798	398.657	401.613	20.552	45.734	8.955	12.406	6.471	-0.385	-0.309	1.777	-7.560	9.337	0.152	-0.081	-0.744	2.398	395.414	6.113	0

Substrate ID	sasa_area	sasa_volume	disp_area	disp_volume	disp_p_int	disp_p_max	disp_p_min	ip	ea	homo	lumo	electrophilicity	nucleophilicity	electrofugality	nucleofugality	dipole_x	dipole_y	dipole_z	mass	radius	charge
247	581.578	1037.231	466.898	514.500	20.394	59.932	9.668	12.123	8.354	-0.382	-0.379	3.858	-7.277	11.135	0.350	1.195	-0.657	0.804	423.975	5.310	-1
248	605.808	1034.388	464.539	476.436	20.297	55.960	8.701	12.078	8.038	-0.381	-0.378	3.362	-7.232	10.594	0.170	-1.413	0.926	-0.152	398.429	6.733	-1
249	489.219	772.167	344.424	341.624	17.924	45.849	9.608	12.534	7.911	-0.381	-0.388	3.126	-7.688	10.814	0.061	2.898	-1.381	0.654	249.325	5.596	-1
250	399.768	599.867	264.628	250.826	16.890	39.370	8.365	12.469	2.928	-0.364	-0.217	0.426	-7.623	8.049	2.345	-0.492	0.947	0.199	198.216	4.508	0
251	613.701	1090.956	491.523	527.949	21.632	66.135	9.955	12.414	5.217	-0.388	-0.265	1.095	-7.568	8.663	0.724	-0.320	-1.434	0.699	428.529	6.623	0
252	730.387	1190.759	534.395	522.089	19.751	47.332	9.081	12.341	9.153	-0.388	-0.397	5.460	-7.495	12.956	1.154	1.493	1.817	2.658	443.519	9.377	-2
253	522.551	838.750	377.796	381.943	18.849	47.910	9.227	7.564	2.630	-0.302	-0.187	0.006	-2.718	2.724	2.222	-3.805	-0.010	2.915	300.804	5.629	1
254	642.261	1085.056	483.113	495.343	20.767	58.878	8.879	12.407	8.294	-0.393	-0.393	3.683	-7.561	11.244	0.235	-1.678	2.260	1.250	421.903	7.243	-1
255	649.514	1084.402	485.642	502.447	20.501	48.377	9.403	11.622	4.543	-0.344	-0.237	0.740	-6.776	7.515	1.043	0.799	0.031	0.104	390.948	7.457	0
256	327.907	484.313	211.527	196.668	16.435	38.405	8.313	13.886	5.214	-0.404	-0.307	1.276	-9.040	10.316	0.908	1.856	1.882	-1.108	171.154	3.210	0
257	480.578	811.153	356.638	390.818	18.774	42.537	9.144	12.482	4.342	-0.377	-0.270	0.781	-7.636	8.417	1.285	1.936	0.020	0.648	288.424	5.752	0
258	508.650	817.823	372.893	367.881	18.518	44.817	8.880	11.901	3.807	-0.340	-0.236	0.559	-7.055	7.614	1.598	-0.076	1.322	0.131	260.374	5.789	0
259	666.359	1099.641	488.454	500.565	19.503	43.602	9.474	11.993	5.528	-0.351	-0.275	1.185	-7.147	8.332	0.503	-2.523	-0.143	0.422	410.484	8.837	0
260	589.709	958.886	425.996	428.128	19.844	47.687	9.763	10.173	4.626	-0.270	-0.253	0.588	-5.327	5.915	0.808	-10.281	3.734	-4.349	337.412	5.518	0
261	605.426	1021.405	454.129	466.465	19.864	53.117	9.719	9.965	4.336	-0.262	-0.243	0.472	-5.119	5.591	0.982	15.431	-5.814	7.495	401.431	6.870	0
262	451.581	707.333	319.099	315.461	18.170	45.265	8.627	7.495	2.366	-0.347	-0.180	0.001	-2.649	2.649	2.481	-3.499	0.527	-0.606	234.314	4.692	1
263	616.662	1012.641	458.666	468.516	19.317	47.133	9.197	6.887	3.329	-0.188	-0.186	0.010	-2.041	2.050	1.527	0.518	-2.171	-2.390	338.486	7.868	2
264	457.780	937.262	426.731	456.549	18.415	48.474	9.183	5.887	0.577	-0.304	-0.110	0.245	-1.041	1.286	4.515	5.253	-0.910	-0.292	310.495	5.862	-1
265	489.863	789.847	364.054	358.186	19.143	51.420	9.075	12.194	3.843	-0.359	-0.223	0.603	-7.348	7.951	1.605	-0.513	-0.410	0.380	255.355	5.074	0
266	664.590	1045.847	487.721	465.836	17.470	41.748	9.040	5.603	1.436	-0.293	-0.125	0.211	-0.757	0.968	3.621	8.218	-0.556	-1.190	326.451	9.765	1
267	649.469	1110.987	494.738	522.529	19.785	48.016	8.806	12.360	4.422	-0.379	-0.246	0.792	-7.514	8.305	1.215	0.821	-0.210	-2.730	416.511	5.955	0
268	486.100	772.731	335.884	334.458	19.999	50.429	9.549	12.515	5.553	-0.379	-0.287	1.260	-7.669	8.929	0.553	-0.396	1.154	-0.188	300.740	4.892	0
269	345.572	520.225	236.379	229.475	17.158	44.309	9.348	6.719	1.233	-0.312	-0.139	0.069	-1.873	1.942	3.682	-5.014	0.834	0.554	150.241	4.077	1
270	719.449	1205.376	542.625	544.774	19.996	46.178	9.003	12.313	8.238	-0.395	-0.390	3.617	-7.467	11.064	0.225	-1.388	1.406	-1.581	437.508	7.946	-1
271	650.398	1145.001	494.497	546.328	21.116	52.297	9.126	10.877	4.680	-0.300	-0.257	0.694	-6.031	6.725	0.860	5.645	2.752	-0.880	474.576	6.537	0
272	501.672	816.005	358.647	366.903	19.390	54.169	8.926	12.079	4.814	-0.365	-0.267	0.892	-7.233	8.125	0.924	-1.901	1.996	0.515	293.363	6.427	0
273	565.508	926.895	424.240	426.344	18.260	49.658	8.573	12.513	4.688	-0.382	-0.279	0.901	-7.667	8.567	1.058	0.816	-1.427	1.214	312.405	5.844	0
274	728.713	1177.702	512.384	497.043	19.576	42.738	8.999	12.424	9.322	-0.404	-0.402	5.856	-7.578	13.434	1.380	-9.352	-1.288	-0.310	451.415	9.931	-3
275	748.829	1244.242	553.736	554.984	20.352	51.794	9.076	10.390	6.892	-0.321	-0.319	2.059	-5.544	7.603	0.013	15.145	-0.081	-0.682	471.511	10.578	0
276	632.356	1103.866	481.975	534.595	19.793	51.387	8.911	12.416	5.763	-0.378	-0.287	1.353	-7.570	8.923	0.436	0.919	1.413	-0.760	430.534	6.335	0
277	669.840	1139.174	505.771	520.078	20.684	59.313	8.630	8.638	4.672	-0.342	-0.235	0.413	-3.792	4.204	0.587	0.101	1.205	1.495	452.483	7.589	1
278	477.339	780.876	350.021	366.493	18.506	45.306	9.796	12.141	4.575	-0.362	-0.272	0.815	-7.295	8.110	1.086	0.463	2.629	-0.378	263.375	4.690	0
279	940.918	1838.074	816.424	980.946	21.379	57.742	10.168	5.917	2.310	-0.295	-0.146	0.074	-1.071	1.146	2.610	8.558	4.327	8.892	748.961	7.979	1
280	645.609	1072.938	482.995	496.785	19.126	44.686	9.223	11.518	5.073	-0.339	-0.265	0.923	-6.672	7.595	0.696	-1.264	-0.921	-0.227	385.503	9.238	0
281	588.499	1022.900	451.225	500.416	19.351	47.274	10.206	12.182	7.298	-0.385	-0.377	2.452	-7.336	9.788	0.000	2.225	-0.956	0.929	371.536	7.215	-1
282	577.071	987.330	450.979	470.100	20.481	52.955	9.806	6.260	2.427	-0.157	-0.155	0.033	-1.414	1.447	2.452	9.812	-0.508	1.163	364.481	6.574	2
283	788.611	1331.918	598.400	618.073	20.254	53.784	8.924	8.705	4.876	-0.362	-0.236	0.494	-3.859	4.352	0.464	5.159	-0.230	-0.362	532.439	10.088	1
284	547.122	912.332	406.666	425.467	19.769	51.698	9.579	11.909	4.344	-0.338	-0.249	0.711	-7.063	7.774	1.213	3.205	-0.470	0.459	309.445	5.006	0
285	629.334	1095.838	472.181	507.811	20.696	56.259	9.193	12.336	8.998	-0.395	-0.392	5.075	-7.490	12.564	0.923	3.205	-6.811	-0.507	454.443	6.711	-3
286	421.382	629.340	278.607	259.271	18.426	43.252	8.873	11.403	5.374	-0.318	-0.284	1.041	-6.557	7.598	0.513	-1.299	-0.132	0.383	213.239	5.959	0
287	604.726	1059.529	457.189	515.038	20.312	48.061	9.799	12.591	5.428	-0.389	-0.284	1.210	-7.745	8.955	0.628	-0.040	0.057	-1.956	416.573	6.461	0

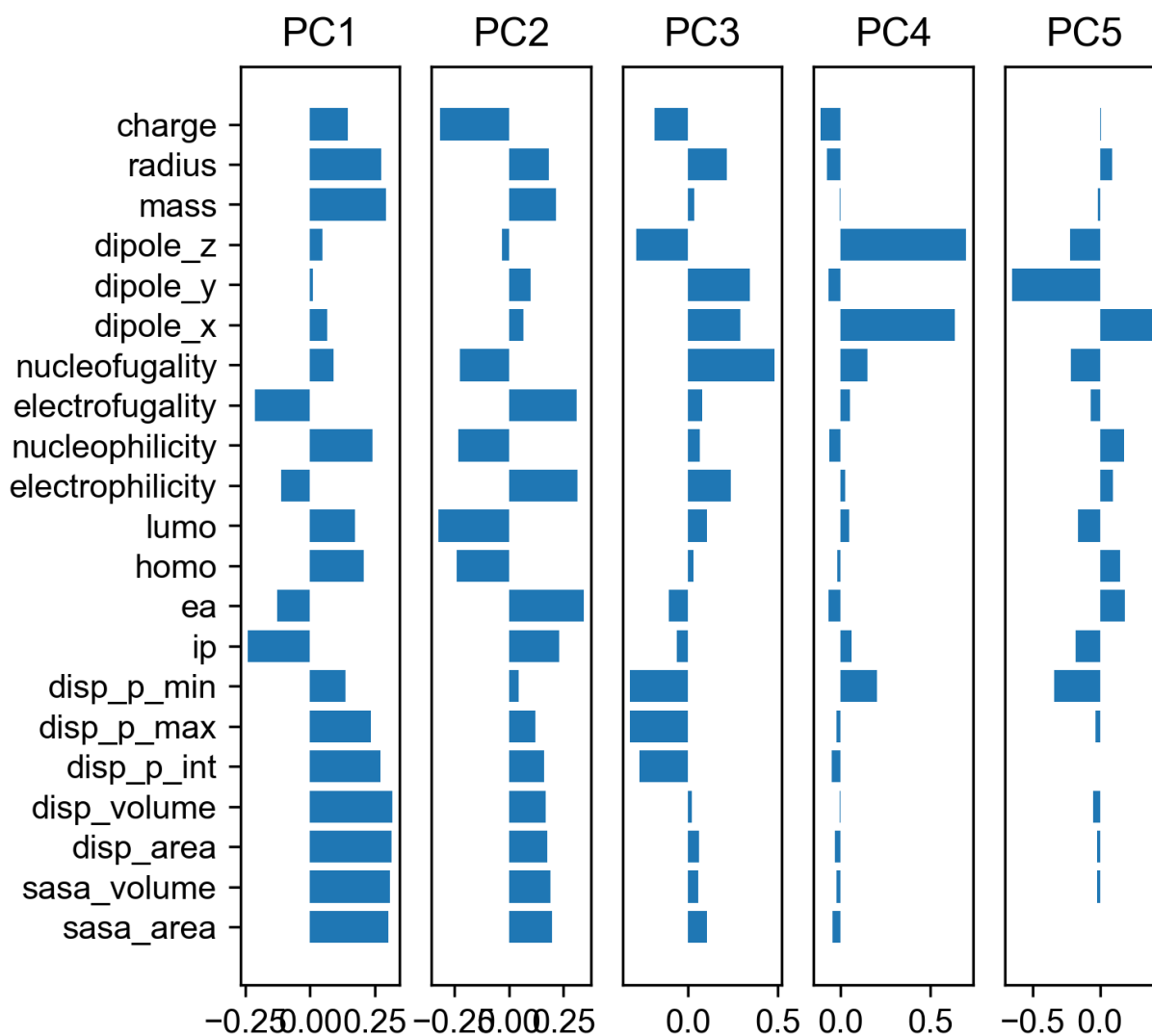
Substrate ID	sasa_area	sasa_volume	disp_area	disp_volume	disp_p_int	disp_p_max	disp_p_min	ip	ea	homo	lumo	electrophilicity	nucleophilicity	electrofugality	nucleofugality	dipole_x	dipole_y	dipole_z	mass	radius	charge
288																					
289	550.907	972.270	416.859	477.512	20.065	55.460	10.516	12.432	5.856	-0.375	-0.296	1.404	-7.586	8.990	0.395	2.658	0.424	-1.585	410.907	6.156	0
290	351.328	516.834	234.651	217.398	15.699	41.557	8.398	13.683	7.793	-0.440	-0.405	2.947	-8.837	11.784	0.000	-0.591	2.172	0.511	143.204	3.982	-1
291	698.095	1223.939	520.862	572.946	20.106	45.906	9.913	12.676	5.967	-0.387	-0.298	1.493	-7.830	9.323	0.372	0.768	0.472	-1.920	528.530	8.448	0
292	511.413	817.601	373.447	368.338	19.453	50.224	8.593	6.852	2.659	-0.308	-0.172	0.001	-2.006	2.007	2.188	8.179	-1.085	2.503	264.385	5.873	1
293	1050.718	1753.139	805.498	810.948	18.423	44.071	8.252	11.369	4.243	-0.364	-0.252	0.615	-6.523	7.137	1.218	-2.701	-1.537	0.046	603.742	13.293	0
294	551.319	868.597	380.385	370.164	19.106	43.692	9.169	13.090	4.597	-0.413	-0.410	4.003	-8.244	12.248	0.252	3.480	-1.859	1.711	315.367	7.346	-1
295	406.460	619.039	270.051	260.588	19.474	45.165	8.746	12.008	4.968	-0.340	-0.270	0.942	-7.162	8.104	0.820	0.886	0.896	-1.857	256.091	4.934	0
296	617.049	979.682	425.783	411.454	19.412	45.059	8.793	12.840	8.878	-0.410	-0.406	4.562	-7.994	12.556	0.530	0.384	0.645	0.326	402.200	6.974	-1
297	539.560	918.976	416.890	428.379	20.693	67.798	8.318	12.231	4.829	-0.374	-0.258	0.917	-7.385	8.302	0.934	-0.075	-0.987	-2.242	359.443	5.792	0
298	452.301	701.673	314.483	302.869	18.411	48.736	8.219	12.136	4.696	-0.363	-0.254	0.857	-7.290	8.147	1.007	-0.143	0.387	0.607	228.286	5.729	0
299	537.499	884.146	391.533	394.522	19.645	47.954	8.913	12.110	5.727	-0.364	-0.288	1.299	-7.264	8.564	0.418	2.107	0.452	-3.871	346.335	5.632	0
300	398.694	594.267	248.544	230.642	17.843	37.649	9.703	14.169	9.434	-0.438	-0.456	5.108	-9.323	14.431	0.521	-1.120	0.326	2.230	237.149	5.069	-1
301	282.183	396.701	170.697	150.631	14.490	33.332	8.229	14.584	4.891	-0.432	-0.329	1.234	-9.738	10.973	1.189	0.538	-0.599	0.093	137.091	2.685	0
302	621.361	1051.192	488.591	493.287	19.593	47.850	8.857	11.943	3.984	-0.348	-0.240	0.610	-7.097	7.707	1.473	0.448	-0.063	-0.311	357.486	7.410	0
303	588.258	980.897	435.604	443.182	20.483	54.048	9.002	8.945	4.344	-0.353	-0.227	0.352	-4.099	4.451	0.853	0.232	1.893	0.087	390.412	6.172	1
304	542.544	947.780	405.074	457.420	19.593	53.455	10.139	12.599	5.837	-0.379	-0.293	1.413	-7.753	9.167	0.422	1.184	0.187	1.810	394.434	6.238	0
305	490.852	779.884	357.296	349.849	18.157	49.241	8.779	6.960	2.013	-0.322	-0.161	0.013	-2.114	2.127	2.846	-2.369	2.954	0.483	251.345	5.094	1
306	482.538	826.778	364.349	372.823	21.134	64.879	9.497	12.817	8.415	-0.396	-0.365	3.782	-7.971	11.753	0.213	2.085	0.479	1.095	368.354	5.022	-1
307	649.202	1046.546	452.997	440.174	19.512	49.516	8.499	13.081	9.649	-0.422	-0.420	6.191	-8.235	14.426	1.388	3.041	1.833	-0.444	422.369	7.678	-2
308	447.098	686.067	300.124	284.822	17.555	43.932	8.332	12.892	8.298	-0.400	-0.399	3.598	-8.046	11.644	0.145	-3.276	-0.038	0.159	240.233	5.439	-1
309	803.116	1344.559	595.821	608.669	18.941	52.215	9.165	12.371	4.882	-0.397	-0.253	0.954	-7.525	8.479	0.918	2.575	-1.610	1.140	500.548	10.226	0
310																					
311	637.419	1037.664	466.190	467.864	19.206	46.093	8.529	8.604	4.182	-0.330	-0.225	0.271	-3.758	4.029	0.935	1.488	-1.417	1.268	388.441	8.214	1
312	457.249	771.745	341.507	360.859	20.141	54.477	10.107	11.930	3.961	-0.350	-0.242	0.603	-7.084	7.687	1.488	-1.185	-1.624	-2.473	295.400	4.363	0
313	696.108	1202.672	526.617	551.803	21.367	55.473	9.988	11.923	8.308	-0.373	-0.368	3.841	-7.077	10.918	0.379	3.887	-0.813	0.030	471.567	8.105	-2
314	457.083	738.267	326.139	336.949	19.660	47.480	9.617	11.461	3.896	-0.340	-0.225	0.530	-6.615	7.146	1.481	0.213	-0.674	-0.252	265.353	4.972	0
315	518.533	873.571	392.956	413.716	20.016	51.281	9.670	6.766	2.316	-0.328	-0.165	0.010	-1.920	1.930	2.541	6.604	-1.302	-0.753	308.437	5.408	1
316	396.488	616.201	278.633	264.651	18.290	55.344	8.860	12.818	3.900	-0.372	-0.238	0.692	-7.972	8.664	1.638	-0.773	-0.199	0.308	213.661	3.916	0
317	320.461	469.001	202.925	191.262	18.015	43.279	9.351	12.374	4.775	-0.342	-0.273	0.915	-7.528	8.442	0.986	0.638	-1.815	0.468	160.176	3.593	1
318	478.312	776.023	352.874	353.936	19.046	47.715	9.549	7.111	2.191	-0.285	-0.167	0.004	-2.265	2.269	2.659	-7.338	-1.306	0.351	260.331	5.033	0
319	841.343	1425.593	647.435	664.244	18.498	44.556	9.313	12.281	7.985	-0.400	-0.366	3.253	-7.435	10.688	0.114	6.719	-0.150	-0.455	499.614	10.660	-1
320	390.101	602.039	269.344	263.548	18.791	45.523	9.141	8.440	3.273	-0.269	-0.214	0.099	-3.594	3.693	1.672	-6.607	-0.113	-0.836	212.270	4.561	1
321	747.881	1291.464	579.678	609.573	19.878	49.131	8.553	11.102	4.122	-0.340	-0.225	0.548	-6.256	6.804	1.272	-1.138	1.051	-0.338	454.602	8.448	0
322	524.413	879.877	383.017	402.678	21.325	54.262	9.747	12.459	4.766	-0.367	-0.249	0.922	-7.613	8.535	1.002	0.562	0.229	-1.805	344.837	4.771	0
323	435.829	682.708	292.370	289.312	19.609	44.649	9.512	13.085	8.436	-0.407	-0.399	3.762	-8.239	12.001	0.172	0.297	3.023	-1.716	251.260	4.771	-1
324	324.821	478.008	216.378	205.360	16.962	44.564	9.308	6.782	1.234	-0.314	-0.141	0.063	-1.936	2.000	3.675	-4.691	-1.406	-1.105	136.214	3.551	1
325	422.110	643.432	293.706	285.292	17.865	44.389	8.573	6.610	1.320	-0.273	-0.139	0.073	-1.764	1.837	3.599	-4.601	-1.410	-1.926	212.335	4.916	1
326	780.187	1306.821	584.973	581.730	20.072	50.633	8.952	12.277	5.687	-0.381	-0.283	1.298	-7.431	8.729	0.457	1.172	1.071	0.621	522.568	8.248	0
327	454.669	725.728	313.215	311.307	20.344	49.693	9.708	12.443	8.131	-0.399	-0.380	3.433	-7.597	11.031	0.148	1.421	2.519	-0.027	295.141	4.772	-1
328	496.368	842.468	373.011	408.978	19.088	44.583	9.766	7.358	1.750	-0.169	-0.158	0.008	-2.512	2.520	3.103	-3.176	0.109	-0.735	317.426	5.581	2

Substrate ID	sasa_area	sasa_volume	disp_area	disp_volume	disp_p_int	disp_p_max	disp_p_min	ip	ea	homo	lumo	electrophilicity	nucleophilicity	electrofugality	nucleofugality	dipole_x	dipole_y	dipole_z	mass	radius	charge
329	938.078	1678.625	741.790	783.317	21.589	54.099	9.485	11.735	5.887	-0.351	-0.282	1.344	-6.889	8.233	0.303	2.644	1.553	1.051	693.720	9.756	0
330	407.821	618.625	269.679	261.784	19.720	48.063	9.331	9.458	4.917	-0.354	-0.263	0.604	-4.612	5.216	0.533	4.085	-0.190	-1.074	254.719	4.683	1
331	356.469	536.728	233.589	219.581	17.396	41.380	9.060	13.193	4.410	-0.389	-0.264	0.891	-8.347	9.237	1.327	1.507	0.434	-0.114	194.191	3.759	0
332	418.207	623.525	287.952	267.610	16.025	42.000	8.401	13.377	7.968	-0.424	-0.417	3.138	-8.531	11.669	0.016	-0.953	-1.675	0.890	171.257	5.156	-1
333	460.855	717.529	296.548	288.382	19.325	40.722	9.171	13.529	9.332	-0.427	-0.424	5.166	-8.683	13.849	0.679	0.349	0.445	0.152	283.212	5.757	-3
334	1018.435	1717.719	779.022	808.237	19.469	49.558	10.106	10.241	6.279	-0.326	-0.283	1.471	-5.395	6.885	0.038	-0.063	0.093	-0.242	536.873	14.114	0
335	343.887	515.611	221.737	210.061	17.462	43.377	8.688	13.521	8.313	-0.415	-0.404	3.538	-8.675	12.213	0.071	0.642	-0.042	0.430	181.165	3.501	-1
336	407.259	619.005	271.720	257.455	17.967	47.209	8.385	12.659	7.698	-0.379	-0.377	2.866	-7.813	10.679	0.014	0.301	3.476	0.053	219.213	4.632	-1
337	371.531	549.141	248.992	231.891	16.879	45.897	8.369	12.377	2.741	-0.363	-0.206	0.382	-7.531	7.913	2.487	0.393	0.629	-0.150	166.217	4.330	0
338	321.590	460.094	206.401	186.280	16.425	44.409	8.040	13.100	3.115	-0.381	-0.227	0.533	-8.254	8.787	2.264	-0.792	-0.037	0.194	138.164	4.053	0
339	388.237	572.400	242.531	225.404	17.321	41.963	8.223	13.220	8.113	-0.406	-0.403	3.317	-8.374	11.691	0.050	-2.966	-1.700	0.052	193.176	4.849	-1
340	351.320	519.306	234.493	220.381	16.878	43.203	9.222	12.866	2.853	-0.379	-0.298	1.371	-7.660	9.032	0.440	-1.936	1.276	-1.146	272.296	5.479	0
341	467.899	748.399	332.818	327.911	18.895	50.393	8.895	12.506	5.778	-0.372	-0.298	1.371	-7.660	9.032	0.440	-1.936	1.276	-1.146	272.296	5.479	0
342	551.000	960.447	419.499	457.052	21.470	57.700	10.576	12.034	5.847	-0.370	-0.291	1.355	-7.188	8.543	0.354	-1.237	-1.811	0.688	387.494	5.445	0
343	341.717	509.751	216.137	206.765	17.472	42.186	9.533	13.085	7.949	-0.399	-0.389	3.130	-8.239	11.370	0.028	-1.286	1.920	0.183	181.165	3.440	-1
344	346.361	503.964	227.293	209.354	16.579	42.393	8.087	12.337	2.825	-0.357	-0.215	0.393	-7.491	7.884	2.414	0.150	0.835	0.114	152.190	4.564	0
345	397.081	652.032	289.294	314.687	17.921	61.073	10.231	12.290	2.617	-0.364	-0.197	0.351	-7.444	7.796	2.581	-0.102	0.161	-0.055	204.351	4.106	0
346	340.488	500.890	211.319	198.586	17.810	41.302	9.579	13.494	8.246	-0.413	-0.400	3.458	-8.648	12.106	0.057	-1.201	-2.454	0.213	175.161	3.747	-1
347	406.308	615.386	282.525	265.586	16.749	36.843	8.288	6.890	1.675	-0.340	-0.157	0.030	-2.044	2.074	3.202	-2.950	1.396	-0.757	205.235	4.999	1
348	374.208	548.318	248.250	226.638	16.036	35.005	8.037	7.864	2.292	-0.381	-0.187	0.005	-3.018	3.023	2.559	0.496	-0.298	-1.999	176.190	5.141	1
349	415.172	628.877	286.379	269.114	17.530	43.743	8.696	12.304	3.201	-0.365	-0.210	0.464	-7.458	7.922	2.109	-0.819	0.428	0.185	192.254	4.370	0
350	413.980	620.565	282.811	261.388	16.856	41.693	8.490	13.059	3.079	-0.390	-0.218	0.520	-8.213	8.733	2.287	0.108	-0.011	-0.964	197.231	5.148	0
351	514.198	866.207	382.733	415.064	18.938	44.422	9.487	12.213	7.724	-0.378	-0.376	2.922	-7.367	10.289	0.045	2.619	1.726	1.862	301.443	5.942	-1
352	320.021	453.996	197.377	178.100	17.122	39.902	9.131	13.526	5.611	-0.397	-0.305	1.409	-8.680	10.088	0.644	-1.843	-0.454	0.223	132.159	4.300	0
353	329.741	483.631	207.091	194.961	18.468	43.254	9.342	12.860	5.017	-0.382	-0.279	1.068	-8.014	9.082	0.897	-1.257	-2.523	0.153	179.603	3.894	0
354	393.971	631.762	284.701	301.117	17.481	43.554	9.650	12.560	1.534	-0.370	-0.181	0.220	-7.714	7.934	3.532	0.036	-0.116	-0.047	192.340	4.104	0
355	425.490	698.265	315.609	339.608	18.030	48.003	10.028	3.863	-1.455	-0.325	-0.042	1.247	0.983	0.264	7.548	0.298	-0.548	-0.381	235.388	4.305	1
356	252.147	338.612	142.321	121.922	15.795	37.517	8.847	14.586	4.321	-0.419	-0.280	1.034	-9.740	10.774	1.559	-1.091	1.450	0.082	112.087	2.552	0
357	409.132	672.208	300.490	322.418	17.898	55.717	10.169	12.251	2.934	-0.365	-0.202	0.405	-7.405	7.810	2.317	0.002	-0.073	0.010	204.351	4.078	0
358	593.301	970.159	442.089	449.105	18.832	47.838	8.574	11.863	3.412	-0.358	-0.214	0.461	-7.017	7.478	1.895	1.305	-0.006	0.021	314.462	7.166	0
359	536.500	869.312	394.904	393.434	18.892	49.660	8.647	12.212	7.817	-0.372	-0.371	3.038	-7.366	10.405	0.068	0.015	-0.147	0.771	284.393	6.241	-2
360	577.871	931.236	420.186	418.838	18.913	45.714	8.544	12.006	7.325	-0.375	-0.359	2.481	-7.160	9.641	0.002	-0.172	1.296	0.024	309.422	7.535	-1
361	633.920	1025.333	468.901	465.714	18.384	49.352	8.644	11.747	7.179	-0.367	-0.360	2.334	-6.901	9.235	0.000	0.105	-0.993	2.093	315.470	8.215	-1
362	615.221	994.392	458.694	454.140	18.495	45.089	8.439	11.742	4.082	-0.355	-0.238	0.614	-6.896	7.510	1.378	-0.202	-0.417	0.074	314.462	8.207	0
363	558.711	923.162	424.009	436.663	18.794	49.961	8.577	12.157	3.014	-0.365	-0.210	0.410	-7.311	7.721	2.243	-0.879	0.219	0.248	314.462	6.617	0
364	570.010	939.473	434.708	441.391	18.769	48.009	8.678	12.085	3.008	-0.364	-0.209	0.402	-7.239	7.640	2.240	0.185	-0.105	-0.372	314.462	6.111	0
365	338.670	509.625	230.707	220.100	16.971	39.732	9.504	13.000	4.238	-0.382	-0.272	0.812	-8.154	8.966	1.421	-0.205	-0.658	-1.197	150.218	3.577	0
366	344.241	509.805	234.486	221.679	16.470	36.331	9.266	12.670	2.485	-0.372	-0.180	0.366	-7.824	8.190	2.728	-0.151	-0.167	0.085	136.234	4.169	0
367	432.032	663.550	303.783	290.743	17.517	46.603	8.758	12.269	2.852	-0.364	-0.208	0.391	-7.423	7.814	2.385	-0.801	-0.006	-0.335	206.281	4.649	0
368	281.617	388.160	163.839	142.545	15.949	37.262	8.695	14.575	8.423	-0.429	-0.428	3.598	-9.729	13.327	0.020	1.585	0.518	-0.089	125.102	2.928	-1
369	332.387	485.320	204.125	188.827	17.786	42.616	8.600	13.401	5.090	-0.398	-0.283	1.164	-8.555	9.719	0.921	2.235	-0.069	1.474	178.142	3.969	0

Substrate ID	sasa_area	sasa_volume	disp_area	disp_volume	disp_p_int	disp_p_max	disp_p_min	ip	ea	homo	lumo	electrophilicity	nucleophilicity	electrofugality	nucleofugality	dipole_x	dipole_y	dipole_z	mass	radius	charge
370	305.300	436.612	184.791	169.228	17.558	41.919	9.213	13.865	5.361	-0.410	-0.297	1.336	-9.019	10.355	0.821	-1.555	-1.542	-0.111	146.143	3.621	0
371	433.460	709.354	322.812	346.814	17.909	38.727	9.925	3.207	-1.675	-0.036	-0.020	1.705	1.639	0.066	8.226	0.280	-0.064	-0.244	236.396	5.188	2
372	318.613	462.800	203.845	189.582	17.761	43.217	9.237	12.784	4.677	-0.361	-0.270	0.930	-7.938	8.868	1.100	0.174	-0.456	-0.057	143.185	3.554	0
373	296.672	421.910	187.758	172.483	16.557	40.405	9.044	12.434	2.816	-0.349	-0.215	0.402	-7.588	7.990	2.431	-1.913	-0.341	-0.269	122.168	3.312	0
374	272.551	372.731	166.351	144.354	15.953	36.623	8.835	13.034	4.016	-0.371	-0.271	0.750	-8.188	8.939	1.581	-1.059	-0.111	0.419	109.129	2.950	0
375	312.818	441.549	194.324	173.594	16.155	40.483	8.332	13.528	4.356	-0.390	-0.271	0.914	-8.680	9.594	1.404	0.532	2.828	0.503	140.137	3.554	0
376	369.537	544.664	246.453	227.916	16.193	34.626	8.332	8.488	2.794	-0.364	-0.206	0.056	-3.642	3.698	2.107	1.932	-0.406	-0.432	172.202	4.537	1
377	285.098	394.956	169.408	148.945	16.102	39.080	8.658	13.794	7.639	-0.397	-0.397	2.799	-8.948	11.747	0.007	-0.850	-2.510	-0.274	124.117	2.901	-1
378	405.590	619.943	267.900	257.043	18.485	44.842	8.669	12.435	5.002	-0.374	-0.272	1.009	-7.589	8.597	0.853	0.576	0.419	-1.106	230.216	4.978	0
379	467.230	738.094	328.990	327.533	18.929	47.924	8.461	9.332	4.533	-0.352	-0.249	0.453	-4.486	4.939	0.767	-0.492	1.046	0.255	265.355	5.639	1
380	334.079	499.132	223.582	208.002	16.737	41.265	8.505	13.361	7.657	-0.397	-0.396	2.811	-8.515	11.326	0.000	0.580	-0.250	-0.194	168.173	3.589	-1
381	346.059	507.802	232.430	217.230	15.795	46.565	8.281	6.572	-0.315	-0.304	-0.098	0.214	-1.726	1.940	5.375	-1.836	3.340	2.171	146.207	4.204	1
382	368.998	567.721	252.021	243.882	17.843	56.929	9.158	11.334	5.497	-0.323	-0.299	1.092	-6.488	7.580	0.440	-3.946	-3.008	-0.047	195.215	4.161	0
383	372.528	547.345	252.720	234.001	15.814	38.172	8.197	12.550	2.413	-0.360	-0.236	0.343	-7.704	8.046	2.776	1.132	0.214	-0.767	160.214	4.639	0
384	419.618	620.140	286.208	262.951	16.395	38.086	8.216	5.689	0.686	-0.117	-0.116	0.275	-0.843	1.118	4.435	-2.557	-0.448	-0.778	190.243	5.862	2
385	273.559	372.727	170.321	145.783	14.375	30.691	7.984	13.706	2.275	-0.374	-0.234	0.432	-8.860	9.292	3.004	0.552	0.564	-0.254	103.120	3.002	0
386	350.429	517.725	235.948	218.402	16.478	41.819	8.220	12.491	3.484	-0.355	-0.242	0.548	-7.645	8.193	1.910	-1.407	0.421	-0.347	163.238	4.144	0
387	343.845	497.590	221.366	198.328	15.763	32.571	8.291	13.987	8.226	-0.422	-0.418	3.402	-9.141	12.543	0.022	-1.765	-1.652	-0.285	160.148	3.667	-1
388	336.839	497.992	230.022	215.689	15.773	36.460	8.358	13.289	2.263	-0.372	-0.229	0.389	-8.443	8.832	2.973	-0.190	-1.080	0.323	145.200	3.914	0
389	401.870	629.937	285.585	275.612	18.424	49.678	9.280	12.185	3.815	-0.359	-0.227	0.594	-7.339	7.933	1.625	0.264	-0.552	0.372	218.252	4.440	0
390	316.319	456.457	208.423	190.305	15.341	37.328	8.270	13.371	2.298	-0.371	-0.232	0.403	-8.525	8.928	2.951	0.447	0.211	0.817	131.173	3.783	0
391	296.456	425.944	185.857	168.275	15.364	33.911	8.075	14.351	8.848	-0.438	-0.431	4.144	-9.505	13.649	0.142	0.531	-1.320	-0.569	146.121	2.980	-1
392	618.600	1068.509	476.809	519.708	19.940	48.733	8.596	11.763	4.879	-0.362	-0.269	0.877	-6.917	7.794	0.844	1.245	0.100	-1.538	382.536	6.785	0
393	439.062	698.568	315.655	317.156	18.956	44.157	9.730	8.793	3.658	-0.343	-0.216	0.185	-3.947	4.133	1.373	-0.304	-0.910	0.246	239.335	4.837	1
394	484.933	762.198	324.172	315.578	19.129	44.509	9.361	13.055	8.897	-0.409	-0.408	4.518	-8.209	12.727	0.468	-3.005	-0.626	0.483	302.236	5.992	-2
395	457.556	712.383	305.129	297.287	19.167	45.681	8.764	12.952	8.418	-0.406	-0.402	3.760	-8.106	11.866	0.188	2.550	-0.054	-0.346	271.245	5.851	-1
396	466.016	733.286	313.241	307.074	19.153	45.924	8.782	12.762	8.350	-0.398	-0.396	3.694	-7.916	11.610	0.191	0.739	1.736	0.430	287.244	6.099	-1
397	472.734	737.792	311.066	301.764	18.986	41.871	9.048	13.256	9.357	-0.416	-0.416	5.352	-8.410	13.762	0.841	2.715	-1.376	-1.173	285.228	5.825	-3
398	469.594	733.040	308.265	299.227	19.112	41.876	9.894	13.360	9.442	-0.420	-0.420	5.484	-8.514	13.998	0.887	2.072	0.524	0.246	285.228	5.793	-3
399	486.752	761.033	319.702	322.536	19.091	45.027	9.954	14.053	7.862	-0.392	-0.387	6.991	-9.207	16.199	1.596	0.819	0.147	-0.263	299.212	5.875	-5
400	476.364	757.827	320.662	302.538	19.223	45.372	8.912	12.542	7.862	-0.392	-0.387	3.064	-7.696	10.760	0.049	0.551	0.342	-1.058	305.260	5.875	-1
401	475.099	776.739	342.504	353.019	19.599	52.812	8.687	11.830	7.187	-0.365	-0.359	2.341	-6.984	9.325	0.000	-1.392	-2.126	-0.529	296.340	4.897	-1
402	566.776	1011.411	430.997	492.766	20.204	50.524	9.637	12.497	7.776	-0.389	-0.384	2.964	-7.651	10.616	0.034	0.047	-2.496	-1.276	413.483	6.100	-1
403	605.196	1108.259	477.617	548.512	20.766	56.100	9.481	12.532	7.861	-0.392	-0.387	3.064	-7.686	10.750	0.049	-0.753	-1.678	-0.595	471.520	6.119	-1
404	603.348	1107.367	475.796	555.787	20.308	54.553	9.714	12.458	5.448	-0.394	-0.293	1.203	-7.612	8.816	0.601	1.705	-1.220	-0.739	460.560	5.536	0
405	609.317	1106.472	476.590	549.859	20.281	50.051	9.804	12.582	5.733	-0.398	-0.297	1.357	-7.736	9.093	0.470	2.553	-0.252	1.176	458.544	6.142	0
406	522.060	837.720	367.878	363.228	19.842	47.162	8.293	12.275	5.335	-0.377	-0.273	1.129	-7.429	8.559	0.640	0.615	-1.417	0.456	308.331	6.314	0
407	297.707	424.735	191.341	173.646	15.613	38.388	8.954	13.565	1.992	-0.385	-0.225	0.372	-8.719	9.090	3.225	-1.617	0.220	-1.678	129.157	3.032	0
408	394.106	590.925	259.435	243.120	17.427	38.166	9.650	12.837	7.408	-0.396	-0.381	2.564	-7.991	10.555	0.002	-0.828	-2.195	-1.183	194.207	4.796	-1
409	943.029	1750.563	777.509	866.008	20.952	63.969	10.063	12.684	10.169	-0.421	-0.420	8.608	-7.838	16.446	3.285	5.725	1.251	-1.838	701.799	9.529	-4
410	664.709	1180.583	516.313	578.690	20.523	49.954	10.090	10.363	4.497	-0.292	-0.266	0.569	-5.517	6.086	0.918	6.786	-4.830	-0.607	477.595	8.010	0

Substrate ID	sasa_area	sasa_volume	disp_area	disp_volume	disp_p_int	disp_p_max	disp_p_min	ip	ea	homo	lumo	electrophilicity	nucleophilicity	electrofugality	nucleofugality	dipole_x	dipole_y	dipole_z	mass	radius	charge
411	321.436	472.091	209.156	197.761	15.672	42.280	8.582	13.493	2.266	-0.402	-0.234	0.410	-8.647	9.057	2.990	-0.790	1.474	1.041	147.172	3.267	0
412	284.076	396.398	162.529	143.654	16.677	39.339	9.255	15.086	9.351	-0.454	-0.446	4.739	-10.240	14.979	0.234	-0.802	0.555	0.130	137.093	3.151	-2
413	499.254	858.976	374.199	395.032	19.650	47.772	8.878	12.453	4.404	-0.375	-0.258	0.797	-7.607	8.405	1.240	-1.279	0.478	0.547	373.312	4.612	0
414	303.218	435.757	194.150	181.975	16.726	38.408	9.343	11.838	2.134	-0.307	-0.194	0.236	-6.992	7.228	2.948	-6.192	0.101	0.597	146.211	3.033	0
415	596.503	998.660	442.103	456.487	18.818	49.453	9.601	12.475	3.610	-0.392	-0.240	0.576	-7.629	8.206	1.812	0.966	0.944	0.111	389.398	7.031	0
416	596.035	973.240	437.379	443.721	18.303	42.872	8.684	12.022	2.983	-0.363	-0.217	0.390	-7.176	7.566	2.254	-1.243	-0.218	0.345	371.382	7.360	0
417	646.985	1071.194	479.691	488.236	18.776	51.074	8.929	7.201	2.724	-0.341	-0.181	0.002	-2.355	2.357	2.123	2.089	-2.714	0.488	414.427	7.772	1
418	538.842	886.083	370.262	381.846	20.550	46.455	8.915	13.215	9.635	-0.422	-0.421	6.044	-8.369	14.413	1.256	0.365	-1.826	0.501	382.300	6.920	-3
419	318.919	470.469	219.118	208.025	16.118	40.364	9.511	12.614	-3.042	-0.346	0.017	0.000	-7.768	7.768	7.888	0.298	-0.722	0.011	141.211	3.280	0
420	336.557	509.719	231.144	226.283	16.206	36.514	9.091	12.481	-2.718	-0.346	0.008	0.000	-7.635	7.635	7.564	-2.128	-0.570	-0.228	173.210	3.282	0
421	502.853	853.767	375.932	404.875	20.038	47.916	9.338	12.029	3.894	-0.356	-0.224	0.597	-7.183	7.780	1.549	0.501	0.297	-0.293	372.546	5.139	0
422	563.953	1007.060	442.242	500.935	20.941	53.276	10.272	11.711	3.946	-0.350	-0.222	0.573	-6.865	7.438	1.473	0.501	0.297	-0.293	372.546	5.139	0
423	520.794	877.084	394.827	411.139	20.052	51.409	9.134	11.907	3.941	-0.352	-0.223	0.595	-7.061	7.655	1.499	-0.215	-0.817	-1.567	304.429	5.476	0
424	530.134	890.690	394.624	413.323	19.975	53.552	9.256	12.072	4.083	-0.361	-0.229	0.654	-7.226	7.880	1.417	-0.524	0.615	0.164	304.429	5.196	0
425	569.923	1027.450	449.446	508.374	20.958	56.635	9.841	11.904	4.057	-0.358	-0.228	0.626	-7.058	7.684	1.415	0.582	0.115	1.418	388.545	5.482	0
426	556.982	1001.956	431.964	497.413	21.031	53.994	10.291	11.926	4.037	-0.357	-0.226	0.623	-7.080	7.703	1.432	-0.432	-0.991	0.328	402.529	5.225	0
427	559.973	998.552	434.944	497.073	20.899	50.819	9.676	11.910	4.209	-0.357	-0.226	0.671	-7.064	7.735	1.307	-0.857	0.977	0.618	386.529	5.902	0
428	237.627	314.606	137.937	115.820	13.928	32.863	8.359	14.397	7.750	-0.444	-0.409	2.917	-9.551	12.465	0.013	-1.139	1.389	-0.028	88.085	2.112	-1
429	278.557	395.272	176.135	161.120	15.171	36.486	8.784	13.877	7.762	-0.436	-0.403	2.918	-9.031	11.948	0.002	0.089	1.549	-0.982	116.138	2.686	-1
430	326.177	469.851	208.961	193.413	16.315	36.504	8.844	12.816	3.552	-0.364	-0.235	0.601	-7.970	8.572	1.895	0.018	1.447	-0.552	149.211	3.964	0
431	249.595	337.188	144.456	124.546	14.275	32.899	9.261	14.713	8.165	-0.448	-0.425	3.320	-9.867	13.187	0.000	0.870	1.268	0.105	104.085	2.364	-1
432	273.506	383.115	169.050	152.187	14.864	36.896	8.598	13.893	2.259	-0.400	-0.236	0.448	-9.047	9.495	3.035	-0.692	-1.554	-0.431	119.119	2.856	0
433	296.675	399.658	171.456	151.646	15.544	35.294	8.388	14.121	8.273	-0.439	-0.415	3.449	-9.275	12.724	0.022	1.388	1.685	0.569	131.110	3.048	-1
434	259.437	356.842	153.159	137.805	16.070	36.892	9.531	13.890	8.375	-0.413	-0.410	3.583	-9.044	12.627	0.054	-0.287	-1.511	-0.723	120.150	2.369	-1
435	211.696	267.793	113.835	91.753	13.207	27.486	8.122	14.933	7.899	-0.451	-0.420	3.068	-10.087	13.155	0.015	-1.643	-0.544	-0.231	74.059	1.940	-1
436	314.648	466.248	209.129	204.159	16.070	35.743	8.947	6.614	-0.307	-0.306	-0.102	0.207	-1.768	1.975	5.360	2.455	1.084	0.622	147.196	3.406	1
437	280.643	390.255	162.278	142.059	15.285	35.558	9.585	15.693	9.577	-0.462	-0.456	4.960	-10.847	15.808	0.229	0.031	0.376	0.173	131.087	2.788	-2
438	313.933	445.777	192.381	170.935	15.691	37.587	8.861	14.311	8.431	-0.437	-0.430	3.620	-9.465	13.085	0.035	-1.772	1.472	0.235	146.121	3.400	-1
439	502.562	825.965	370.778	381.748	19.067	42.486	9.508	12.108	3.492	-0.363	-0.228	0.507	-7.262	7.769	1.860	-0.376	0.623	-0.283	297.391	6.117	0
440	453.821	713.031	321.678	317.594	18.624	42.713	9.406	12.249	3.518	-0.364	-0.229	0.528	-7.403	7.932	1.856	-0.346	-0.310	0.804	255.312	5.920	0
441	527.512	870.045	392.078	402.446	19.029	41.755	9.513	12.305	4.314	-0.375	-0.252	0.750	-7.459	8.209	1.283	-0.030	1.551	0.995	299.407	6.137	0
442	564.012	977.566	430.675	475.459	20.023	47.110	9.665	12.144	4.300	-0.376	-0.249	0.726	-7.298	8.025	1.273	0.903	0.060	0.388	365.508	6.737	0
443	510.032	808.465	362.075	360.778	18.603	44.520	9.426	11.843	4.290	-0.348	-0.251	0.687	-6.997	7.683	1.242	-0.221	1.229	1.580	284.353	6.640	0
444	452.537	702.258	294.416	286.610	19.178	44.311	8.742	12.701	7.953	-0.387	-0.387	3.164	-7.855	11.019	0.057	-2.774	3.195	-0.673	269.229	5.837	-1
445	586.690	1013.846	441.313	490.019	19.961	60.639	10.476	11.899	4.909	-0.368	-0.271	0.906	-7.053	7.959	0.843	-1.235	2.282	0.786	368.509	6.230	0
446	338.900	507.955	238.095	229.431	16.841	47.094	9.468	7.431	0.698	-0.340	-0.150	0.045	-2.585	2.630	4.194	0.339	0.135	-0.085	153.243	3.694	1
447	417.801	636.818	286.954	273.486	18.220	39.640	8.191	11.852	4.925	-0.353	-0.254	0.762	-7.006	7.768	1.083	0.836	1.005	-0.480	214.293	5.369	0
448	281.395	388.310	163.952	142.716	15.489	37.764	9.132	15.027	9.135	-0.447	-0.442	4.442	-10.181	14.624	0.153	-1.337	-1.658	0.673	127.098	2.815	-2
449	451.182	728.261	323.364	332.406	19.427	48.322	9.624	12.433	3.795	-0.371	-0.221	0.618	-7.587	8.205	1.669	1.073	-0.249	-0.370	253.339	4.746	0
450	293.637	419.430	188.739	174.366	15.641	34.963	9.341	13.538	2.165	-0.388	-0.231	0.397	-8.692	9.089	3.079	-2.047	0.471	-0.077	129.157	3.044	0
451	499.192	801.218	354.455	358.487	20.009	47.179	9.676	10.682	3.985	-0.297	-0.239	0.462	-5.836	6.299	1.323	-2.112	-9.522	1.210	332.235	4.791	0

452	Substrate ID
369.910	sasa_area
553.558	sasa_volume
249.078	disp_area
237.611	disp_volume
17.476	disp_p_int
45.184	disp_p_max
9.014	disp_p_min
11.591	ip
2.639	ea
-0.332	homo
-0.209	lumo
0.288	electrophilicity
-6.745	nucleophilicity
7.033	electrofugality
2.494	nucleofugality
0.875	dipole_x
0.057	dipole_y
-0.289	dipole_z
178.231	mass
4.599	radius
0	charge



Supplemental Figure S30. Contribution of MORFEUS features (shown in Supplemental Table S6) to PC1-PC5 for all substrates (shown in Supplemental Table S5).

18. Substrate-to-enzyme model

Initially, we built a simple enzyme prediction ranking formula which weighed the distance in chemical space and the distance in protein sequence space linearly, to use as a baseline model. This model was able to enrich the predictions ranked in the top 10 positions with enzymes compatible with each substrate more than 4-fold better than would be observed by randomly sampling aKGLib1 (Supplemental Table S8). To further minimize the experimental burden associated with enzyme screening, a model that rewards populating the enzyme prediction list with compatible enzymes at a low k was needed. Consequently, the YetiRank loss function⁴⁹ was used to train a gradient boosted decision tree ensemble (GBM).⁵⁰ This model offers an advantage in arbitrarily complex relationships and is relatively robust to overfitting with proper hyperparameters.⁵¹ The number of trees and their depth were optimized using a grid search procedure,⁵¹ yielding a relatively small model of 50 trees with a depth of 2 (Fig. 4C, right).

The performance of the GBM was compared to that of the baseline linear model. The GBM has higher nDCG than the baseline model at all values of k (Fig. 4D, left). Furthermore, the top 10 predicted enzymes are greater than 7-fold more likely to be compatible with the input substrate than through random sampling of aKGLib1 (Fig. 4D, right). Precision and recall were plotted at various points (k) within the enzyme prediction list. For both models, precision decreases as the number of enzymes in the rank list increases, and recall steadily increases as k increases (Fig. 4D, left). At low values of k ($k < 20$), the GBM outperforms the baseline model, indicating that the GBM is most well-suited for the curation of a focused enzyme prediction list (Supplemental Table S7). Given this performance, we used a gradient boosted decision tree ensemble model to build the final workflow. Analysis of feature importance revealed that principal component 3 (PC3), which is mostly comprised of two dipole moments and nucleofugality has the greatest weight on the model, followed by principal component 1 (PC1, most heavily comprised of dispersion descriptors, solvent-accessible surface area, and volume), and the alignment score percent (Fig. 4D).

Supplemental Table S8. Metrics for linear and gradient boosted model. Precision, recall, nDCG, and enrichment are calculated as shown in Fig. 4B. Values are graphed in Fig. 4D.

	GBM	Baseline			GBM	Baseline
precision	0.0199	0.0199		precision@26	0.0213	0.0231
recall	0.7032	0.7032		recall@26	0.2998	0.3180
ndcg	0.2643	0.2454		ndcg@26	0.1991	0.1704
enrichment	2.6997	2.6997		enrichment@26	3.6205	3.8404
precision@2	0.0692	0.0462		precision@27	0.0205	0.0222
recall@2	0.0689	0.0582		recall@27	0.2998	0.3180
ndcg@2	0.1117	0.0769		ndcg@27	0.1991	0.1704
enrichment@2	10.8238	9.1440		enrichment@27	3.4864	3.6982
precision@3	0.0615	0.0359		precision@28	0.0198	0.0220
recall@3	0.1016	0.0634		recall@28	0.2998	0.3334
ndcg@3	0.1348	0.0846		ndcg@28	0.1991	0.1735
enrichment@3	10.6377	6.6327		enrichment@28	3.3619	3.7387
precision@4	0.0500	0.0308		precision@29	0.0191	0.0223
recall@4	0.1021	0.0685		recall@29	0.2998	0.3493
ndcg@4	0.1414	0.0857		ndcg@29	0.1991	0.1770
enrichment@4	8.0172	5.3771		enrichment@29	3.2460	3.7817
precision@5	0.0492	0.0308		precision@30	0.0195	0.0231
recall@5	0.1406	0.0916		recall@30	0.3177	0.3659
ndcg@5	0.1510	0.0894		ndcg@30	0.2053	0.1835
enrichment@5	8.8292	5.7509		enrichment@30	3.3256	3.8299
precision@6	0.0436	0.0282		precision@31	0.0189	0.0228
recall@6	0.1560	0.0947		recall@31	0.3177	0.3664
ndcg@6	0.1565	0.0948		ndcg@31	0.2053	0.1838
enrichment@6	8.1628	4.9535		enrichment@31	3.2184	3.7114
precision@7	0.0396	0.0264		precision@32	0.0192	0.0221
recall@7	0.1611	0.0951		recall@32	0.3350	0.3664
ndcg@7	0.1616	0.1000		ndcg@32	0.2084	0.1838
enrichment@7	7.2267	4.2681		enrichment@32	3.2876	3.5954
precision@8	0.0365	0.0269		precision@33	0.0186	0.0219
recall@8	0.1765	0.1182		recall@33	0.3350	0.3683
ndcg@8	0.1665	0.1097		ndcg@33	0.2084	0.1868
enrichment@8	6.9272	4.6403		enrichment@33	3.1880	3.5047
precision@9	0.0359	0.0239		precision@34	0.0181	0.0217

recall@9	0.1938	0.1182		recall@34	0.3350	0.3688
ndcg@9	0.1757	0.1097		ndcg@34	0.2084	0.1870
enrichment@9	6.7614	4.1247		enrichment@34	3.0942	3.4063
precision@10	0.0354	0.0246		precision@35	0.0180	0.0211
recall@10	0.2246	0.1358		recall@35	0.3504	0.3688
ndcg@10	0.1846	0.1186		ndcg@35	0.2114	0.1870
enrichment@10	7.0514	4.2644		enrichment@35	3.1438	3.3089
precision@11	0.0322	0.0252		precision@36	0.0179	0.0205
recall@11	0.2246	0.1666		recall@36	0.3512	0.3688
ndcg@11	0.1846	0.1271		ndcg@36	0.2073	0.1870
enrichment@11	6.4103	4.7550		enrichment@36	3.0636	3.2170
precision@12	0.0308	0.0269		precision@37	0.0179	0.0200
recall@12	0.2268	0.1721		recall@37	0.3517	0.3688
ndcg@12	0.1830	0.1338		ndcg@37	0.2072	0.1870
enrichment@12	5.9337	4.5046		enrichment@37	2.9850	3.1301
precision@13	0.0284	0.0284		precision@38	0.0174	0.0198
recall@13	0.2268	0.1814		recall@38	0.3517	0.3693
ndcg@13	0.1830	0.1412		ndcg@38	0.2072	0.1872
enrichment@13	5.4772	4.3814		enrichment@38	2.9064	3.0518
precision@14	0.0286	0.0275		precision@39	0.0174	0.0193
recall@14	0.2312	0.1968		recall@39	0.3522	0.3693
ndcg@14	0.1862	0.1451		ndcg@39	0.2073	0.1872
enrichment@14	5.1846	4.4135		enrichment@39	2.8359	2.9735
precision@15	0.0287	0.0267		precision@40	0.0173	0.0192
recall@15	0.2487	0.2122		recall@40	0.3527	0.3712
ndcg@15	0.1896	0.1489		ndcg@40	0.2074	0.1874
enrichment@15	5.2070	4.4414		enrichment@40	2.7689	2.9143
precision@16	0.0279	0.0269		precision@41	0.0173	0.0191
recall@16	0.2509	0.2166		recall@41	0.3681	0.3866
ndcg@16	0.1894	0.1491		ndcg@41	0.2103	0.1903
enrichment@16	4.9247	4.2500		enrichment@41	2.8192	2.9610
precision@17	0.0262	0.0271		precision@42	0.0187	0.0190
recall@17	0.2509	0.2341		recall@42	0.3970	0.3918
ndcg@17	0.1894	0.1525		ndcg@42	0.2113	0.1931
enrichment@17	4.6350	4.3248		enrichment@42	2.9677	2.9289
precision@18	0.0256	0.0265		precision@43	0.0190	0.0186
recall@18	0.2561	0.2495		recall@43	0.4000	0.3918
ndcg@18	0.1930	0.1562		ndcg@43	0.2120	0.1931
enrichment@18	4.4670	4.3529		enrichment@43	2.9211	2.8608

precision@19	0.0259	0.0267		precision@44	0.0185	0.0185
recall@19	0.2588	0.2803		recall@44	0.4000	0.3940
ndcg@19	0.1911	0.1633		ndcg@44	0.2120	0.1959
enrichment@19	4.2764	4.6323		enrichment@44	2.8547	2.8114
precision@20	0.0254	0.0262		precision@45	0.0188	0.0188
recall@20	0.2639	0.2957		recall@45	0.4176	0.3967
ndcg@20	0.1918	0.1668		ndcg@45	0.2146	0.1962
enrichment@20	4.1431	4.6422		enrichment@45	2.9139	2.7678
precision@21	0.0249	0.0249		precision@46	0.0184	0.0184
recall@21	0.2690	0.2957		recall@46	0.4176	0.3967
ndcg@21	0.1924	0.1668		ndcg@46	0.2146	0.1962
enrichment@21	4.0225	4.4212		enrichment@46	2.8526	2.7096
precision@22	0.0245	0.0245		precision@47	0.0187	0.0181
recall@22	0.2844	0.2962		recall@47	0.4203	0.3967
ndcg@22	0.1958	0.1669		ndcg@47	0.2148	0.1962
enrichment@22	4.0592	4.2273		enrichment@47	2.8119	2.6539
precision@23	0.0234	0.0241		precision@48	0.0184	0.0178
recall@23	0.2844	0.2970		recall@48	0.4203	0.3967
ndcg@23	0.1958	0.1673		ndcg@48	0.2148	0.1962
enrichment@23	3.8827	4.0545		enrichment@48	2.7552	2.6005
precision@24	0.0231	0.0231		precision@49	0.0187	0.0178
recall@24	0.2998	0.2970		recall@49	0.4216	0.3997
ndcg@24	0.1991	0.1673		ndcg@49	0.2176	0.1958
enrichment@24	3.9222	3.8856		enrichment@49	2.7110	2.5711
precision@25	0.0222	0.0234		precision@50	0.0190	0.0178
recall@25	0.2998	0.3175		recall@50	0.4272	0.4019
ndcg@25	0.1991	0.1701		ndcg@50	0.2205	0.1963
enrichment@25	3.7653	3.9878		enrichment@50	2.6960	2.5373

Supplemental Table S9. Metrics from hyperparameter optimization step (difference from baseline). Values at nDCG@10 graphed in Fig. 4C.

ndcg	precision@5	recall@5	ndcg@5	enrichment@5	iterations	depth
-0.016	0.000	-0.012	0.001	-0.740	10	1
0.007	0.009	0.036	0.031	2.231	10	2
0.007	0.003	0.014	0.026	0.853	10	3

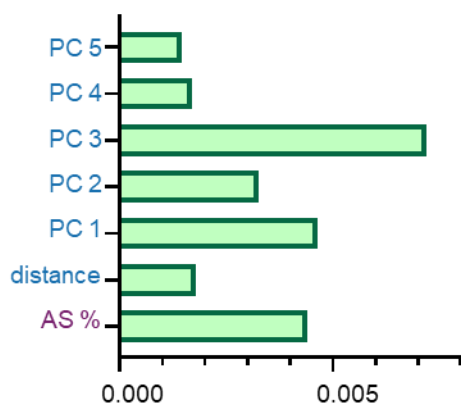
-0.004	0.006	0.034	0.020	2.124	10	4
-0.013	0.003	-0.010	-0.010	-0.613	10	5
-0.016	-0.006	-0.010	-0.011	-0.644	25	1
0.028	0.012	0.036	0.060	2.282	25	2
-0.013	0.003	-0.009	0.021	-0.588	25	3
-0.016	0.003	0.016	0.003	0.997	25	4
0.006	0.015	0.049	0.040	3.078	25	5
-0.011	-0.003	-0.021	-0.004	-1.334	50	1
0.019	0.018	0.049	0.062	3.078	50	2
-0.001	0.009	0.039	0.024	2.424	50	3
-0.004	0.006	0.003	0.013	0.197	50	4
0.006	0.012	0.031	0.019	1.923	50	5
0.004	0.003	0.015	0.016	0.943	75	1
0.015	0.006	-0.018	0.039	-1.149	75	2
-0.002	0.009	0.031	0.012	1.940	75	3
0.000	0.003	0.021	-0.001	1.339	75	4
0.002	0.003	0.001	0.007	0.059	75	5
0.000	0.009	0.031	0.021	1.940	100	1
0.000	-0.003	-0.017	0.001	-1.076	100	2
0.006	0.009	0.021	0.010	1.319	100	3
0.008	0.012	0.026	0.031	1.629	100	4
0.020	0.022	0.071	0.048	4.445	100	5
	precision@10	recall@10	ndcg@10	enrichment@10	iterations	depth
	0.002	0.025	0.002	0.794	10	1
	0.005	0.042	0.027	1.321	10	2
	0.002	-0.018	0.011	-0.563	10	3
	0.002	0.031	0.009	0.967	10	4
	0.006	0.024	-0.015	0.755	10	5
	0.000	0.019	-0.011	0.608	25	1
	0.006	0.056	0.061	1.760	25	2
	0.002	0.018	0.007	0.560	25	3
	0.008	0.049	0.006	1.532	25	4
	0.008	0.058	0.031	1.821	25	5
	0.003	0.027	0.001	0.838	50	1
	0.011	0.089	0.066	2.787	50	2
	0.008	0.034	0.017	1.056	50	3
	0.008	0.053	0.017	1.657	50	4
	0.015	0.091	0.031	2.865	50	5

	0.009	0.091	0.034	2.871	75	1
	0.011	0.068	0.053	2.143	75	2
	0.015	0.091	0.021	2.863	75	3
	0.014	0.065	0.025	2.055	75	4
	0.014	0.084	0.035	2.650	75	5
	0.014	0.100	0.041	3.153	100	1
	0.009	0.060	0.025	1.898	100	2
	0.017	0.092	0.032	2.889	100	3
	0.015	0.086	0.044	2.692	100	4
	0.015	0.076	0.045	2.389	100	5
	precision@20	recall@20	ndcg@20	enrichment@20	iterations	depth
	-0.005	-0.078	-0.033	-1.230	10	1
	-0.002	-0.030	-0.001	-0.466	10	2
	-0.004	-0.063	-0.005	-0.986	10	3
	-0.004	-0.040	-0.022	-0.631	10	4
	-0.003	-0.060	-0.035	-0.949	10	5
	-0.002	-0.074	-0.033	-1.162	25	1
	-0.001	-0.030	0.027	-0.475	25	2
	-0.002	-0.060	-0.023	-0.938	25	3
	0.002	-0.024	-0.020	-0.373	25	4
	-0.003	-0.057	-0.009	-0.902	25	5
	-0.001	-0.042	-0.019	-0.659	50	1
	-0.001	-0.032	0.025	-0.499	50	2
	-0.002	-0.042	-0.011	-0.663	50	3
	0.002	-0.028	-0.012	-0.436	50	4
	0.001	-0.011	0.003	-0.177	50	5
	-0.003	-0.046	-0.008	-0.715	75	1
	0.000	-0.027	0.017	-0.419	75	2
	-0.002	-0.029	-0.016	-0.462	75	3
	0.002	-0.022	-0.007	-0.350	75	4
	0.002	-0.010	-0.001	-0.164	75	5
	-0.002	-0.045	-0.011	-0.707	100	1
	-0.003	-0.055	-0.007	-0.856	100	2
	0.000	-0.027	-0.001	-0.419	100	3
	0.002	-0.009	0.014	-0.143	100	4
	0.002	0.003	0.015	0.043	100	5

Supplemental Table S10. Feature importance values for the substrate-to-enzyme gradient boosted model.

Feature	Importance
f_AS %	0.00441
f_distance	0.00180
f_neighbor_pca_1	0.00465
f_neighbor_pca_2	0.00325
f_neighbor_pca_3	0.00719
f_neighbor_pca_4	0.00171
f_neighbor_pca_5	0.00145

Supplemental Figure S31. Feature importance values for the substrate-to-enzyme gradient boosted model.



Supplemental Table S11. Feature importance values for substrate-to-enzyme model during hyperparameter optimization.

f_AS %	f_distance	f_neighbor_pca_0	f_neighbor_pca_1	f_neighbor_pca_2	f_neighbor_pca_3	f_neighbor_pca_4	iterations	depth
0.0010	0.0000	0.0007	0.0000	0.0000	0.0000	0.0000	10	1
0.0042	0.0000	0.0006	0.0006	0.0003	0.0001	0.0020	10	2
0.0026	0.0000	0.0015	0.0015	0.0033	-0.0005	0.0000	10	3
0.0043	0.0022	0.0005	0.0005	0.0035	0.0014	0.0007	10	4
0.0055	0.0003	0.0027	0.0044	0.0014	0.0015	0.0005	10	5
0.0047	0.0000	0.0005	0.0000	0.0013	0.0007	0.0000	25	1

0.0006	0.0000	0.0038	0.0022	0.0026	0.0019	0.0033	25	2
0.0030	-0.0002	0.0035	0.0025	0.0080	0.0012	0.0007	25	3
0.0083	0.0042	0.0019	0.0041	0.0078	0.0025	0.0025	25	4
0.0090	0.0025	0.0047	0.0113	0.0089	0.0039	0.0032	25	5
0.0023	0.0000	0.0020	0.0006	0.0054	0.0007	0.0020	50	1
0.0044	0.0018	0.0046	0.0032	0.0072	0.0017	0.0015	50	2
0.0078	0.0017	0.0052	0.0089	0.0126	0.0016	0.0018	50	3
0.0124	0.0050	0.0062	0.0107	0.0145	0.0064	0.0035	50	4
0.0211	0.0029	0.0080	0.0173	0.0166	0.0065	0.0048	50	5
0.0015	0.0008	0.0028	0.0010	0.0072	0.0019	0.0029	75	1
0.0061	0.0044	0.0063	0.0063	0.0097	0.0024	0.0017	75	2
0.0095	0.0046	0.0099	0.0103	0.0166	0.0022	0.0026	75	3
0.0203	0.0072	0.0074	0.0121	0.0192	0.0080	0.0052	75	4
0.0239	0.0030	0.0150	0.0195	0.0157	0.0074	0.0075	75	5
-0.0010	0.0015	0.0065	0.0014	0.0151	0.0024	0.0030	100	1
0.0070	0.0036	0.0093	0.0069	0.0135	0.0020	0.0017	100	2
0.0129	0.0048	0.0140	0.0142	0.0192	0.0027	0.0027	100	3
0.0234	0.0073	0.0121	0.0156	0.0219	0.0098	0.0049	100	4
0.0276	0.0038	0.0181	0.0217	0.0199	0.0088	0.0076	100	5

19. Enzyme-to-substrate model

We built a simple substrate prediction ranking formula which weighed the distance in chemical space and the distance in protein sequence space linearly, to use as a baseline model. To further minimize the experimental burden associated with reaction screening, a model that rewards populating the substrate prediction list with compatible substrates at a low k was needed. Consequently, the YetiRank loss function was used to train a gradient boosted decision tree ensemble (GBM). The number of trees and their depth were optimized using a grid search procedure.

The performance of the GBM was compared to that of the baseline linear model.

Supplemental Table S12. Hyperparameter optimization for the enzyme-to-substrate model with nDCG@10.

n_trees	depth	ndcg@10_delta
10	1	-0.095368959
10	2	-0.225681395
10	3	-0.01670759
10	4	0.011745548
10	5	-0.048657234
10	6	-0.107523213
25	1	-0.042546671
25	2	-0.103592727
25	3	-0.035281302
25	4	-0.041688486
25	5	-0.050823991
25	6	-0.05697125
50	1	-0.047741393
50	2	-0.070059611
50	3	-0.033610681
50	4	-0.032416249
50	5	-0.06508972
50	6	0.017112127
75	1	0.00622788
75	2	-0.036691841
75	3	-0.027322892
75	4	-0.042977004
75	5	-0.016546675

75	6	0.023212081
100	1	0.009175696
100	2	-0.030088061
100	3	-0.046653653
100	4	-0.018312601
100	5	-0.004520572
100	6	0.017968848

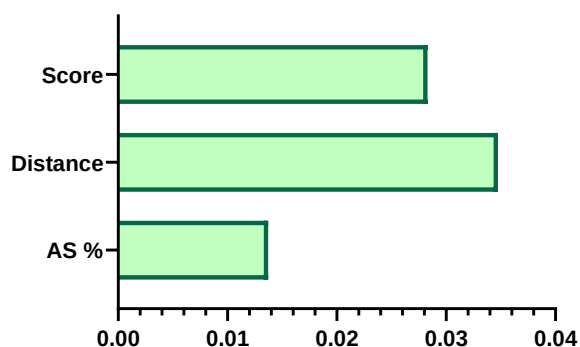
Supplemental Table S13. Metrics for linear and gradient boosted model for the enzyme-to-substrate model. Precision, recall, nDCG, and enrichment are calculated as shown in Fig. 4B. Values are graphed in Fig. 4D.

metric	k	GBM	baseline		metric	k	GBM	baseline
precision	2	0.262931	0.25		precision	26	0.061576	0.064655
recall	2	0.37227	0.37227		recall	26	0.808477	0.866954
ndcg	2	0.576264	0.59426		ndcg	26	0.629919	0.631447
enrichment	2	11.10417	11.12773		enrichment	26	2.449733	2.581014
precision	3	0.217241	0.206897		precision	27	0.061237	0.062426
recall	3	0.49181	0.477443		recall	27	0.819253	0.875575
ndcg	3	0.576625	0.591261		ndcg	27	0.63676	0.631447
enrichment	3	9.052989	9.078908		enrichment	27	2.449733	2.492013
precision	4	0.189655	0.186782		precision	28	0.05977	0.06092
recall	4	0.541667	0.542816		recall	28	0.836494	0.881322
ndcg	4	0.57015	0.586753		ndcg	28	0.636608	0.631399
enrichment	4	7.809243	7.854406		enrichment	28	2.369674	2.413659
precision	5	0.169951	0.169951		precision	29	0.057842	0.059511
recall	5	0.552011	0.553592		recall	29	0.86408	0.881322
ndcg	5	0.57058	0.586456		ndcg	29	0.636608	0.631255
enrichment	5	6.806404	7.068966		enrichment	29	2.293233	2.3434
precision	6	0.157328	0.155172		precision	30	0.056034	0.057651
recall	6	0.571408	0.574713		recall	30	0.866954	0.883046
ndcg	6	0.572864	0.588661		ndcg	30	0.636608	0.631255
enrichment	6	6.172091	6.379741		enrichment	30	2.22157	2.270169
precision	7	0.149425	0.141762		precision	31	0.055381	0.055904
recall	7	0.581034	0.603448		recall	31	0.866954	0.88592
ndcg	7	0.587039	0.585403		ndcg	31	0.640688	0.631255
enrichment	7	5.879023	5.775607		enrichment	31	2.197092	2.201376
precision	8	0.139655	0.131034		precision	32	0.05426	0.05426
recall	8	0.602155	0.622414		recall	32	0.866954	0.88592
ndcg	8	0.60199	0.584022		ndcg	32	0.640538	0.631255
enrichment	8	5.573879	5.286408		enrichment	32	2.136629	2.136629

precision	9	0.128527	0.12069		precision	33	0.052709	0.052709
recall	9	0.645259	0.633908		recall	33	0.884195	0.88592
ndcg	9	0.601604	0.584061		ndcg	33	0.640538	0.631255
enrichment	9	5.131426	4.818678		enrichment	33	2.075583	2.075583
precision	10	0.119253	0.114943		precision	34	0.052709	0.052709
recall	10	0.679741	0.644684		recall	34	0.88592	0.88592
ndcg	10	0.602533	0.593477		ndcg	34	0.640538	0.631255
enrichment	10	4.762716	4.605627		enrichment	34	2.075583	2.075583
precision	11	0.112732	0.107427		precision	35	0.052709	0.052709
recall	11	0.688362	0.646408		recall	35	0.88592	0.88592
ndcg	11	0.60783	0.593581		ndcg	35	0.640538	0.631255
enrichment	11	4.486981	4.269474		enrichment	35	2.075583	2.075583
precision	12	0.109606	0.100985		precision	36	0.052709	0.052709
recall	12	0.696983	0.673994		recall	36	0.88592	0.88592
ndcg	12	0.614929	0.597994		ndcg	36	0.640538	0.631255
enrichment	12	4.385283	3.998173		enrichment	36	2.075583	2.075583
precision	13	0.102299	0.095402		precision	37	0.052709	0.052709
recall	13	0.711351	0.676868		recall	37	0.88592	0.88592
ndcg	13	0.614929	0.602305		ndcg	37	0.640538	0.631255
enrichment	13	4.092931	3.825881		enrichment	37	2.075583	2.075583
precision	14	0.09806	0.08944		precision	38	0.052709	0.052709
recall	14	0.748707	0.682615		recall	38	0.88592	0.88592
ndcg	14	0.619065	0.602305		ndcg	38	0.640538	0.631255
enrichment	14	3.934321	3.586764		enrichment	38	2.075583	2.075583
precision	15	0.092292	0.085193		precision	39	0.052709	0.052709
recall	15	0.748707	0.699856		recall	39	0.88592	0.88592
ndcg	15	0.619065	0.606439		ndcg	39	0.640538	0.631255
enrichment	15	3.70289	3.41736		enrichment	39	2.075583	2.075583
precision	16	0.088123	0.082375		precision	40	0.052709	0.052709
recall	16	0.767672	0.699856		recall	40	0.88592	0.88592
ndcg	16	0.623124	0.614557		ndcg	40	0.640538	0.631255
enrichment	16	3.536446	3.30605		enrichment	40	2.075583	2.075583
precision	17	0.084392	0.080762		precision	41	0.052709	0.052709
recall	17	0.767672	0.708477		recall	41	0.88592	0.88592
ndcg	17	0.623862	0.618092		ndcg	41	0.640538	0.631255
enrichment	17	3.387523	3.238702		enrichment	41	2.075583	2.075583
precision	18	0.080172	0.07931		precision	42	0.052709	0.052709
recall	18	0.776293	0.725718		recall	42	0.88592	0.88592
ndcg	18	0.623862	0.619851		ndcg	42	0.640538	0.631255
enrichment	18	3.218147	3.156293		enrichment	42	2.075583	2.075583
precision	19	0.077176	0.077997		precision	43	0.052709	0.052709
recall	19	0.784914	0.750431		recall	43	0.88592	0.88592
ndcg	19	0.623683	0.623217		ndcg	43	0.640538	0.631255

enrichment	19	3.076122	3.113711		enrichment	43	2.075583	2.075583
precision	20	0.073668	0.076019		precision	44	0.052709	0.052709
recall	20	0.784914	0.769828		recall	44	0.88592	0.88592
ndcg	20	0.623683	0.619651		ndcg	44	0.640538	0.631255
enrichment	20	2.936298	3.017163		enrichment	44	2.075583	2.075583
precision	21	0.071964	0.074213		precision	45	0.052709	0.052709
recall	21	0.787787	0.797414		recall	45	0.88592	0.88592
ndcg	21	0.619521	0.619975		ndcg	45	0.640538	0.631255
enrichment	21	2.851662	2.937206		enrichment	45	2.075583	2.075583
precision	22	0.069684	0.072557		precision	46	0.052709	0.052709
recall	22	0.787787	0.809483		recall	46	0.88592	0.88592
ndcg	22	0.623233	0.620056		ndcg	46	0.640538	0.631255
enrichment	22	2.762296	2.873731		enrichment	46	2.075583	2.075583
precision	23	0.066897	0.071034		precision	47	0.052709	0.052709
recall	23	0.799856	0.823851		recall	47	0.88592	0.88592
ndcg	23	0.623233	0.627392		ndcg	47	0.640538	0.631255
enrichment	23	2.651805	2.843609		enrichment	47	2.075583	2.075583
precision	24	0.064324	0.068302		precision	48	0.052709	0.052709
recall	24	0.808477	0.841092		recall	48	0.88592	0.88592
ndcg	24	0.623233	0.627392		ndcg	48	0.640538	0.631255
enrichment	24	2.549812	2.73424		enrichment	48	2.075583	2.075583
precision	25	0.063218	0.066411					
recall	25	0.808477	0.866954					
ndcg	25	0.62637	0.630978					
enrichment	25	2.488101	2.659153					

Supplemental Figure S32. Feature importance values for the substrate-to-enzyme gradient boosted model.



20. CATNIP tutorial for biocatalytic reaction discovery

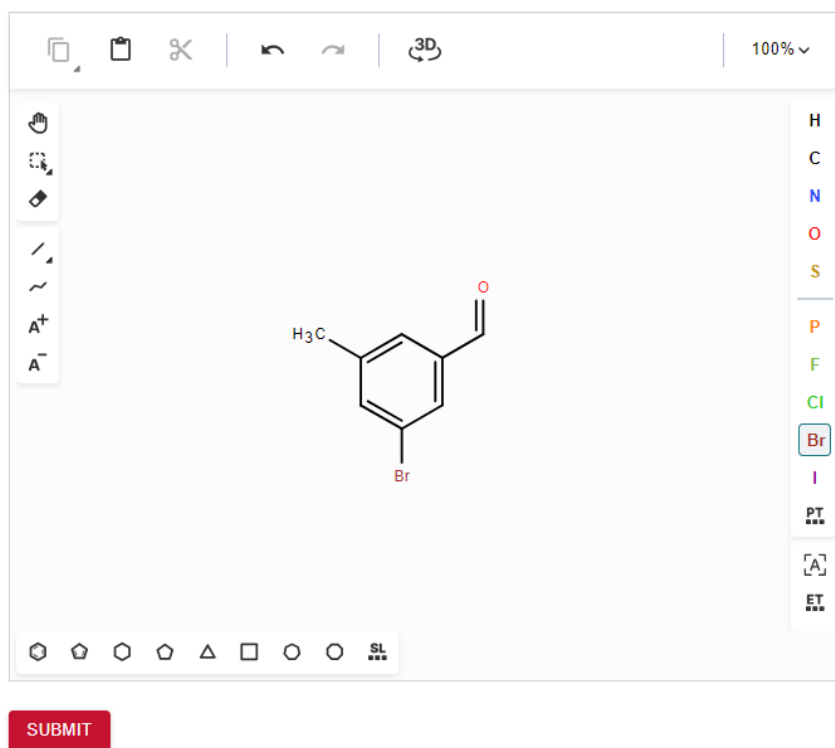
The generated machine learning models were modified to include all reactions in the reaction table to yield the best possible prediction rank list.

Supplemental Tutorial S1. How to use CATNIP to generate substrate-oriented compatible enzyme prediction rank lists.

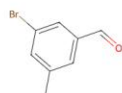
This expanded model was used to create the tool 'CATNIP', a web-based platform to predict which enzyme within our library will perform biocatalytic transformations on a user's substrate of interest. The recommended workflow for this application is as follows:

1. Enter substrate of interest into CATNIP web app (available at catnip.cheme.cmu.edu) and submit

Draw your substrate



2. Protonation state, 3D geometry optimization and MORFEUS descriptors will be generated for the provided substrate.

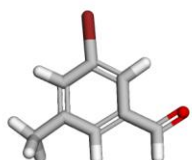


81eb42f9-883e-4aa4-bb88-9bea56bc60ae

Note that the results will be stored only for 7 days. Please save the run ID to access the results later.

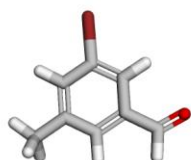
Step 1

Generating 3D geometry



Step 2

Optimizing molecular geometry



Step 3

Calculating MORFEUS descriptors

Feature	Value
mass	199.04457999999999
radius	3.46340975688701
charge	0
sasa_area	329.5914016911451
sasa_volume	475.02744202347117
disp_area	206.96701778916747
disp_volume	190.80345922795513
disp_p_int	18.00060260130867

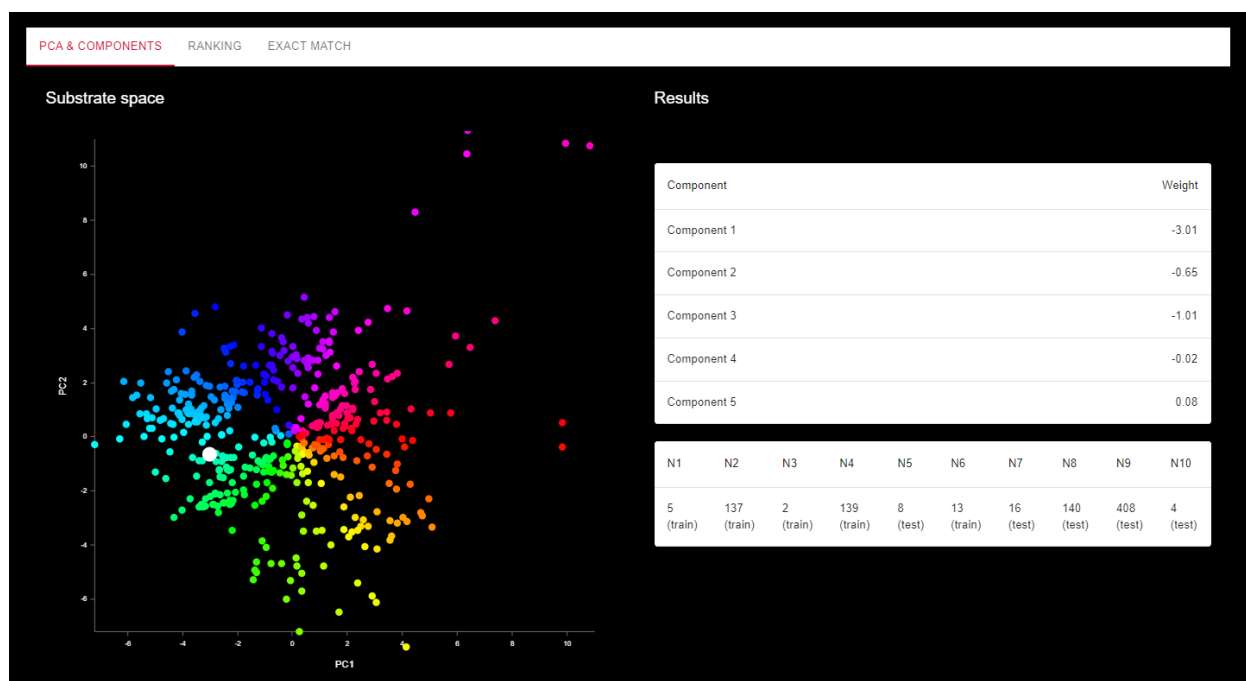
EXPAND

Step 4

Wrapping up

DOWNLOAD CSV

3. Below this, a two-dimensional representation of the chemical space used in the model is given. The user-entered substrate is mapped as a white circle, whereas all other substrates are mapped as colored circles. One can scroll over each point to show the corresponding chemical structure. On the right, the coordinates of the user entered substrate in 5 dimensions (component 1–5) are given. Below this, the ten nearest substrates in chemical space (N1-N10) with train or test affiliation are listed. All substrate numbers correspond to their substrate ID in the substrate table (Supplemental Table S6).



- Under the 'RANKING' tab, the enzyme rank list predicted to be compatible with the query substrate is given. This includes the rank number, enzyme ID as corresponding with the enzyme table (Supplemental Table S3), score, enzyme name if it has been coined, organism of source, and amino acid sequence.

PCA & COMPONENTS RANKING EXACT MATCH					
Ranking					
#	Enzyme ID	Score	Enzyme Name	Organism	AA Sequence
1	102	0.5107025506	scopoletin-8-hydroxylase	Arabidopsis thaliana	MGINFEDQTTLFNFVVRREGNGVKGIMIDSGLSVPRPFVQPLSERIPTQKALTCEATQPIDLSNLDGPDQHKVEAKQIVEAAETLGGFFQVNVHGV
2	66	0.5070272209	NCS1	Coptis japonica	MSKNLTGVGSLPVENVQVLGAGKELKNLPNRYRPELEHDDVVPIDNSLEIPVIDLSRLDDQQYACDELAKFHSACLDWGGFFQLINHGVRREEV
3	311	0.5070272209	ANC3		MTTETAPEIPTVDISAWLSPNASEEAKQQVVEAMRHACTTYGFFYLVGHGVSPEEQQKALDCTKLFALPMEERMEVWIGKSMGKSFRGYEF
4	1	0.5070272209	CitB		MPISTKSSFYLPVDISPYLQDPNSDAARKVIDDVRAACTSTGFFQLLGHGISPALQQSVFAAAKFFALPSDVKSRCRNVGFRGYDPMASQS
5	2	0.5070272209	ClaD		MPVLSNPSFYLPVDITPFLNPHGAAQDVIESVRTACKSTGFFQIKGHQVPLRLQKSVFEASARFFALPLKNKLELDSRKTGFRGYDVMET
6	6	0.5070272209			MPVPTKSSFYLPVDISPYLQDPNSDGARKVINDVRAACTSTGFFQLLGHGISPALQQSVFAAAKFFALPTDVKSRCRNVGFRGYDPMASQS
7	15	0.5070272209			MSSTTDRSPHQKFYIPQVNIIEFLKDPDSATSKIIEVRAACRSTGFFEITGHGIPKSLQKEVFGAASQFFKLSFDEKKRLDASKQIGRGYD
8	313	0.5070272209	ANC5		MGTTSATAIPTVDISAFLSPTASEAARQQVVEAMSHACTTYGFFNLVGHGIPQALQQAFCNKMFFALPQEKMEVWIGKSLGRSFRGYEF
9	18	0.5070272209			MASSATSSPYIPVDITPFLNPGTAAQVVDNVRACMSTGFFLMKGHGISPALQNSVFQASAKFFALPHEAKLSLDARKNVGFRGYDVM
10	5	0.5070272209	SxtS		MVA AVLTLWRDDPLNPLDCEGKEMLTVEQKQAYVNDGYFTVEETVPKALIEIRHEVELITEQKRGVLAGDYEWWSDHTIPDIRYQKIQR
11	123	0.5070272209		Acremonium sp.	MGSLEVPCIDLSENDTSIVVKELLDACKNWGVFSLKNHGIPLDEIDRTFKLADKFFDIPVEEKQKYLKGGRLHSGYTGHFGEKLDMEHQSRLG
12	22	0.5070272209			MHSSFYLPVDITPFLDDPSSPAQQVIDDVRRACRSTGFFQMKGHGVPLKLQKSILAAAKFFALPTETKLALDARKNVGFRGYDVMETQSY

- This enzyme rank list is intended to provide a starting point for initial reaction hit discovery. We recommend initially performing analytical-scale reactions to identify the best enzyme for a query substrate and then performing preparative-scale biocatalytic reactions for isolable product formation and characterization.

Supplemental Tutorial S2. How to use CATNIP to generate enzyme-oriented substrate enzyme prediction rank lists.

- On the landing page (catnip.cheme.cmu.edu) select 'ENZYME TO SUBSTRATE'. Paste the protein sequence directly into the box and click 'SUBMIT'.

SUBSTRATE TO ENZYME

ENZYME TO SUBSTRATE

Enter your enzyme sequence

```
MCAPLEKDDIRRLSQAHRFGIVTVTELIEPHTRKLVRAEADRLLDQYAERRDLRLATTD  
YTRRSMSVVPSETIAANSELVTGLYAHRELLAPLEAIAGERLHPCPKADEEFLITRQEQR  
GDTHGWHWGDFFSALIWWLQAPPIDVGGLQCVPHTTWDKASPQINRYLVENPIDTYH  
FESGDVYFLRTDTTLHRTIPLREDTTRIILNMTWAGERDLSRKLAADDRWWDNAEVSAA  
RAIKD
```

SUBMIT

- Wait while the program iterates through the model. This should not take more than 1-2 minutes.

CATNIP Carnegie Mellon University & University of Michigan

Enzyme Sequence Analysis

MCAPLEKDDIRRLSQAHRFGIVTVTELIEPHTRKLVRAEADRLLDQYAERRDLRLATTDYTRRSMSVVPSETIAANSELVTGLYAHRELLAPLEAIAGERLHPCPKADEEFLITRQEQR
GDTHGWHWGDFFSALIWWLQAPPIDVGGLQCVPHTTWDKASPQINRYLVENPIDTYH
FESGDVYFLRTDTTLHRTIPLREDTTRIILNMTWAGERDLSRKLAADDRWWDNAEVSAA
RAIKD

Run ID:

78525f9c-6726-41bc-9fe9-12562384b9fc

Note that the results will be stored only for 7 days. Please save the run ID to access the results later.

Step 1
Multiple Sequence Alignment

Step 2
Initial retrieval

Step 3
Reranking

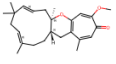
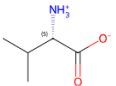
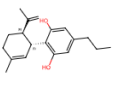
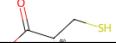
Step 4
Final results

DOWNLOAD RESULTS (CSV)

- Under 'SUBSTRATE PREDICTIONS' you will find a list of the ten best ranked substrates and their SMILES string.

SUBSTRATE PREDICTIONS

Predicted Compatible Substrates

Structure	SMILES	Enzyme Neighbor	Substrate	Score
	<chem>O=C(C(OC)=C1)C=C(C)C2=C1O[C@@]3(C)[C@@](C2)([H])CC/C(C)=C/CC(C)C=C-C/C3</chem>	NHI191	392	0.8911052237666883
	<chem>[NH3+][C@@H](C(C)C)C([O-])=O</chem>	NHI178	429	0.8911052237666883
	<chem>OC1=C([C@@H]2C=C(C)CC[C@H]2C(C)=C)C(O)=CC(CCC)=C1</chem>	NHI072	359	0.8857703300608406
	<chem>[NH3+][C@@H](CS)C([O-])=O</chem>	NHI178	434	0.68018629224602

21. Application of CATNIP for novel biocatalytic reaction discovery

General procedure for focused library screening: Enzymes were generated from plate growth and expression as detailed above. Reactions were performed at a total volume of 50 μ L in 2 mL 96-well plates. The top 10 ranked enzymes were chosen to profile in analytical-scale.

Stock solutions of substrate (50 mM) was prepared by dissolving the substrate in DMSO, MeOH, or H₂O, depending on substrate solubility. Stock solutions of α -ketoglutaric acid (α -KG) (100 mM), ferrous sulfate heptahydrate (FeSO₄) (10 mM) and L-ascorbic acid sodium salt (NaAsc) (100 mM) were freshly dissolved in milli-Q water before each use. 96-well plates containing cell pellets with the overexpressed NHI libraries were removed from storage at -78 °C and allowed to thaw at room temperature for 15 to 30 min prior to reaction setup.

A master mix containing 30 μ L of 1M TES buffer pH 7.5, 240 μ L of milli-Q water, 12 μ L of α -KG stock solution, 6 μ L of NaAsc stock solution, 6 μ L of FeSO₄ stock solution, and 6 μ L of substrate stock solution was prepared. 25 μ L of the stock solution was added to 12 wells. Individual wells within plates containing thawed cell pellet were for the enzymes of interest were resuspended in 100 μ L of 50 mM TES buffer pH 7.5 and 20 μ L of the suspension was added to the reaction plate. This was repeated until all ten enzymes and an empty vector control were added to the reaction plate. 5 μ L of toluene was added to each well before sealing with a breathable thin film. Plates were shaken at 30 °C and 300 rpm (4 mM orbital plate shaker) for 4 h before being quenched by the addition of 3 volume of acetonitrile containing 1 mM pentamethyl benzene as an internal standard. Each well was filtered through a 0.45 μ m syringe filter and supernatant was analyzed by LC-MS.

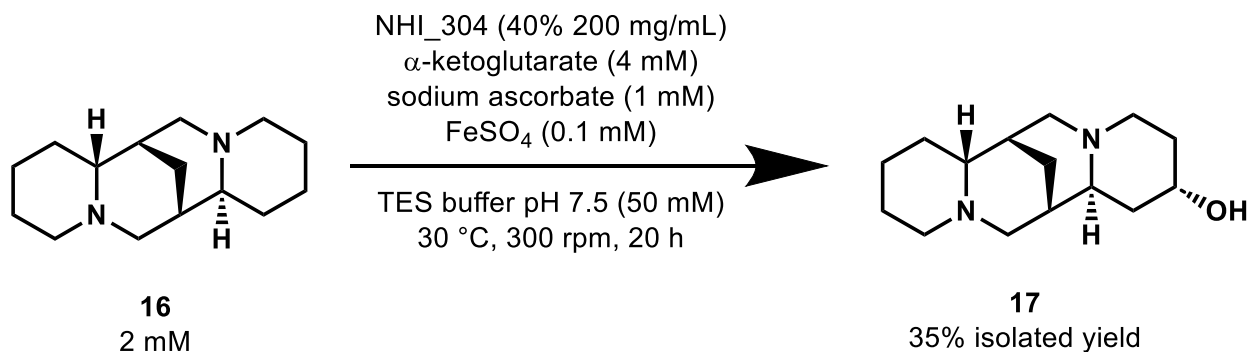
The enzyme identified to produce the greatest quantity / selectivity of product were chosen for preparative-scale reactions. A significant amount of protein was required for each reaction; therefore, enzymes were prepared in batch. Furthermore, preparative-scale whole cell biocatalytic reactions can be hindered by the presence of an abundance of cell material, making the isolation of product a difficult task. To overcome this, preparative-scale reactions were performed with clarified cell lysate and, consequently, toluene was not added to the reaction mixture.

General procedure for batch protein production: The plasmid corresponding to the enzyme of choice was used to transform chemically competent BL21(DE3) cells. Overexpression of each NHI enzyme was achieved using 4% glycerol (v/v) Terrific Broth (TB) in 2.8 L flasks. 750 mL portions of autoclaved media were inoculated with 7.5 mL of overnight culture prepared from a single colony in Lysogeny Broth (LB) and 50 µg/mL kanamycin (Gold Biotechnology). Cultures were grown at 37 °C and 200 rpm until the optical density (at 600 nm) reached 0.8. The culture was then cooled to 20 °C and protein expression was induced with 0.2 mM isopropyl-β-D-1-thiogalactopyranoside (IPTG, Gold Biotechnology). Expression was continued at 20 °C overnight (approx. 18 h) at 200 rpm. The typical yield for one 750 mL culture cell pellet (wet cell pellet) was ~35 g.

Preparation of clarified crude cell lysate: 10 g of cell pellet containing the enzyme of choice was resuspended to a volume of 200 mg/mL in lysis buffer containing 50 mM TES buffer (pH 7.4), 150 mM NaCl, and 10% glycerol. Cells were lysed by sonication on ice. Each cycle of sonication was 10 s sonication, followed by a 20 s rest period, for a total of 6 min at 60% power. The total cell lysate was centrifuged at 45,000 x g for 30 min and the supernatant was directly taken on to biocatalytic reaction.

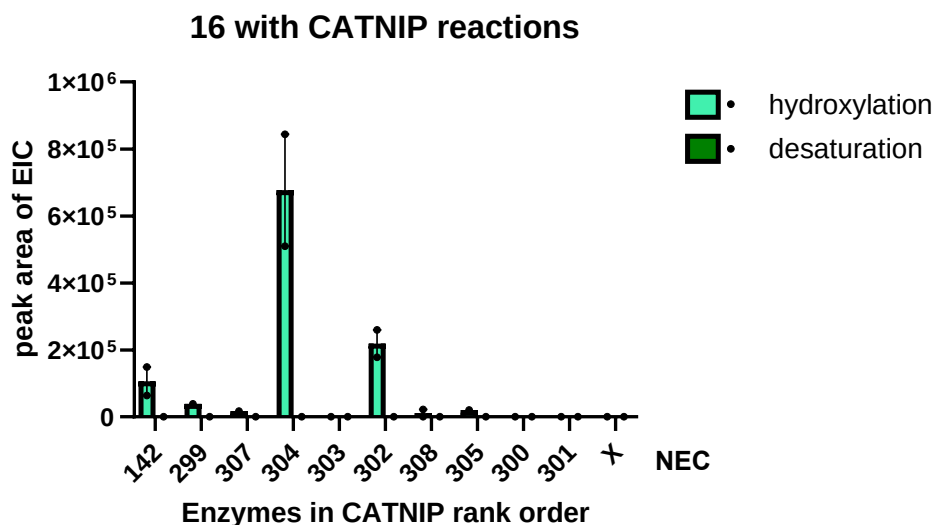
General procedure for preparative-scale biocatalytic reaction: Reactions were performed on 50 mg scale (100-200 mL total volume) using clarified cell lysate. Reactions were performed on 2 mM substrate concentration and DMSO was not added unless noted. A solution containing 50 mM TES buffer pH 7.5, 2 mM substrate (50 mg), 4 mM α-KG, 1 mM NaAsc, 0.1 mM FeSO₄, and 40% vol/vol of 200 mg/mL clarified cell lysate were added to a 2 L culture flask. The flask was sealed with a milk cloth and shaken at 30 °C and 200 rpm. Reactions were monitored by LC-MS before being quenched by the addition of 2 volumes of organic solvent. Products were isolated and characterized.

Biocatalytic hydroxylation of sparteine (16):



Sparteine (**16**) was entered to CATNIP web app and mapped to chemical space (1.05, -4.19, 2.13, 0.91, -2.26). The ten nearest neighbors are Substrate ID: 81, 64, 419, 420, 446, 63, 49, 355, 48, and 62 (Supplemental Table S6) The ten highest ranked enzymes are NHI_142, NHI_299, NHI_307, NHI_304, NHI_303, NHI_302, NHI_308, NHI_305, NHI_300, and NHI_301 (Supplemental Table S4). All ten enzymes and an empty vector control were used following the focused library screening protocol to identify which enzyme yields the most product formation.

Supplemental Figure S33. Relative formation of possible products of sparteine (**16**) with the ten best ranked enzymes and a no enzyme control (NEC). Shades of green represent different products identified by LC-MS. The y-axis represents the relative extracted ion count as normalized by an internal standard.



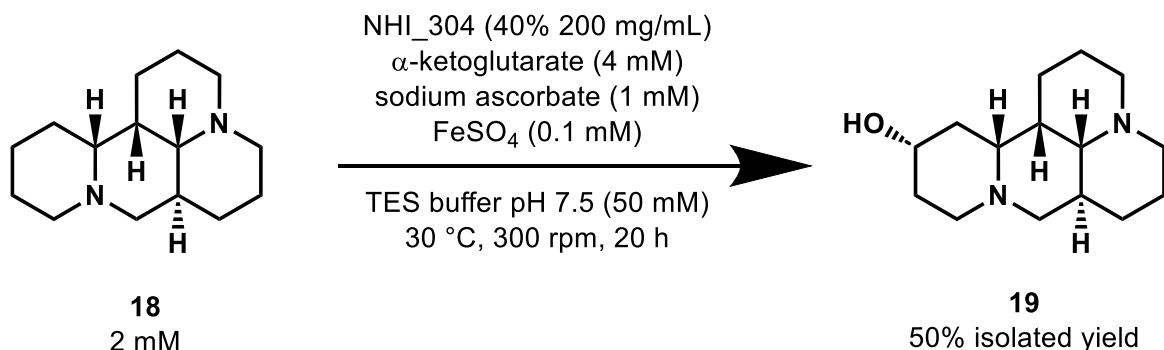
From this screen, the fourth ranked enzyme, NHI_304, was chosen to be used on preparative-scale. NHI_304 was grown in batch and lysed following the general protein preparation protocol above. A 50 mg sparteine reaction (2 mM) was prepared in 100 mL final volume. The 2.8 L flask containing 49 mL of milli-Q water, 5 mL of 1 M TES buffer pH 7.5, 4 mL of 100 mM α -KG stock solution, 1 mL of 100 mM NaAsc stock solution, 1 mL of 10 mM FeSO₄ stock solution, 50 mg of sparteine, and 40 mL of freshly prepared NHI_304 clarified cell lysate (200 mg/mL in 50 mM TES buffer pH 7.5) was shaken at 30 °C and 200 rpm for 20 h. The reaction was then quenched by the addition of 240 mL of acetone and the precipitated protein was pelleted by centrifugation at 2000 rpm for 15 min. The supernatant was decanted and acetone was removed under reduced pressure. The resulting aqueous solution was added to a separatory funnel and 10 mL of 3 M NaOH was added to bring the pH >12. 20 mL of an 80% sat. solution of sodium sulfate was added, and the solution was extracted 3x with 50 mL *n*-butanol. The organic layer was dried under reduced pressure and azeotroped with toluene and let to dry under house vacuum, yielding tan crystals. The contents were then purified by prep TLC to yield 18 mg (35% yield) of tan amorphous crystals. NMR values matched those in the literature.⁹⁰

¹H-NMR (600 MHz, CDCl₃) δ 3.63 (m, 1H), 2.81 – 2.83 (m, 1H), 2.75 – 2.77 (m, 1H), 2.68 – 2.70 (m, 1H), 2.53 – 2.55 (m, 1H), 2.33 – 2.36 (m, 1H), 2.07 – 2.13 (m, 2H), 2.01 – 2.07 (m, 2H), 1.90 – 1.97 (m, 2H), 1.83 – 1.86 (m, 2H), 1.70 – 1.76 (m, 2H), 1.50 – 1.57 (m, 4H), 1.36 – 1.38 (m, 2H), 1.20 – 1.26 (m, 2H), 1.09 (m, 1H).

¹³C NMR (151 MHz, CDCl₃) δ 69.3, 66.5, 61.9, 61.7, 56.2, 52.8, 52.6, 43.6, 35.8, 35.2, 33.1, 29.4, 27.5, 25.9, 24.8.

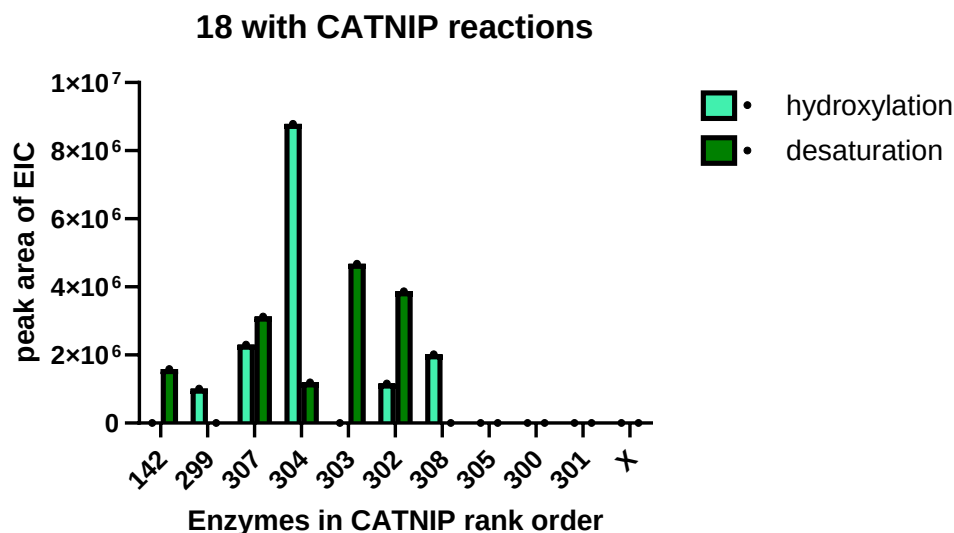
HRMS ESI: calculated for [M+H]⁺ : 251.2118; observed: 251.2115.

Biocatalytic hydroxylation of matridine (**18**):



Matridine (**18**) was entered to CATNIP web app and mapped to chemical space (0.73, -4.34, 2.29, 1.27, -2.22). The ten nearest neighbors are Substrate ID: 81, 64, 419, 420, 63, 446, 49, 355, 48, and 62 (Supplemental Table S6). The ten highest ranked enzymes are NHI_142, NHI_299, NHI_307, NHI_302, NHI_308, NHI_303, NHI_304, NHI_300, NHI_305, and NHI_306 (Supplemental Table S4). All ten enzymes and an empty vector control were used following the focused library screening protocol to identify which enzyme yields the most product formation.

Supplemental Figure S34. Relative formation of possible products of matridine (**18**) with the ten best ranked enzymes and a no enzyme control (X). Shades of green represent different products identified by LC-MS. The y-axis represents the relative extracted ion count as normalized by an internal standard.



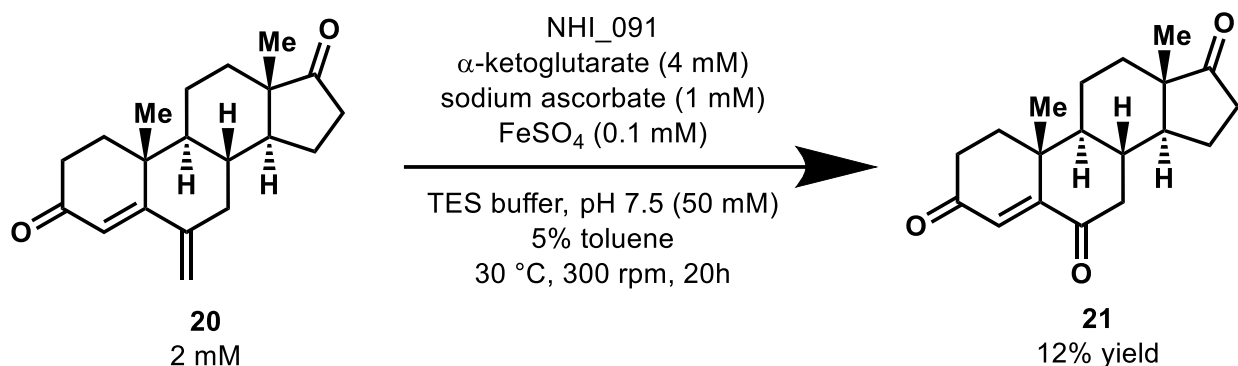
From this screen, the seventh ranked enzyme, NHI_304, was chosen to be used on preparative-scale. NHI_304 was grown in batch and lysed following the general protein preparation protocol above. A 50 mg matridine reaction (2 mM) was prepared in 100 mL final volume. The 2.8 L flask containing 49 mL of milli-Q water, 5 mL of 1 M TES buffer pH 7.5, 4 mL of 100 mM α -KG stock solution, 1 mL of 100 mM NaAsc stock solution, 1 mL of 10 mM FeSO₄ stock solution, 50 mg of matridine, 1 mL of DMSO, and 40 mL of freshly prepared NHI_304 clarified cell lysate (200 mg/mL in 50 mM TES buffer pH 7.5) was shaken at 30 °C and 200 rpm for 40 h. The reaction was then quenched by the addition of 200 mL of acetone and the precipitated protein was pelleted by centrifugation at 2000 rpm for 15 min. The supernatant was decanted and acetone was removed under reduced pressure. The resulting aqueous solution was added to a separatory funnel and 20 mL of 3 M NaOH was added to bring the pH >12. 50mL of an 80% sat. solution of sodium sulfate was added, and the solution was extracted 3x with 200 mL *n*-butanol. The organic layer was dried under reduced pressure and azeotroped with toluene and dry under house vacuum, yielding 27 mg of amorphous tan crystals in 50% yield.

¹H NMR (600 MHz, CDCl₃): 3.79 ppm (td, *J* = 11.4, 3.1 Hz, 1H), 3.15 – 3.00 (m, 4H), 2.79 (m, 2H), 2.71 – 2.63 (m, 3H), 2.37 (d, *J* = 11.5 Hz, 1H), 2.27 – 2.19 (m, 2H), 2.03 (m, 3H), 1.93 (d, *J* = 11.5 Hz, 1H), 1.91 – 1.31 (m, 6H), 1.09 (qd, *J* = 12.9, 4.2 Hz, 1H).

¹³C NMR (600 MHz, CDCl₃): 65.8, 63.5, 62.9, 57.0, 54.0, 45.5, 40.5, 29.8, 29.6, 29.5, 26.5, 25.8, 24.7, 19.7, 18.9.

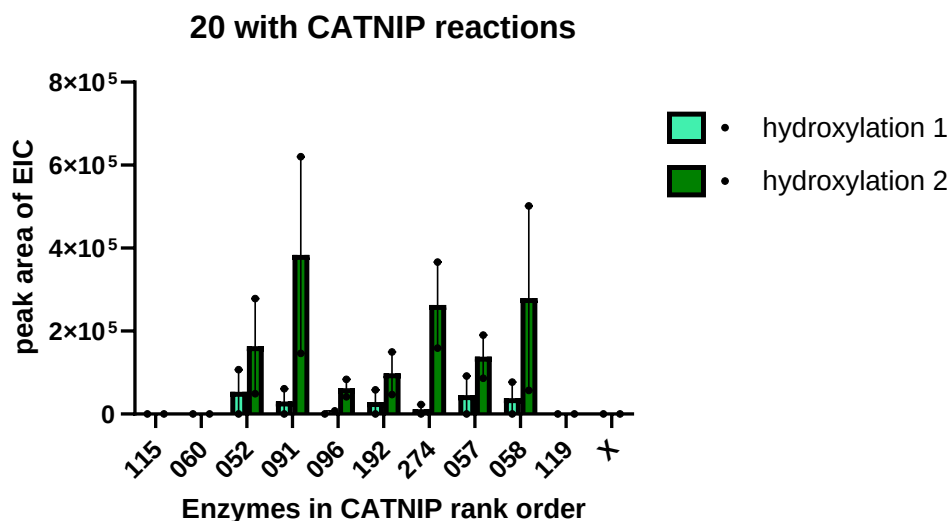
HRMS ESI: calculated for [M+H]⁺ : 251.2118; observed: 251.2130.

Biocatalytic oxidation of **20**:



6-Methyleneandrost-4-ene-3,17-dione (**20**) was entered to CATNIP web app and mapped to chemical space (0.09, 0.31, -1.21, 0.69, -1.32). The ten nearest neighbors are Substrate ID: 78, 413, 424, 77, 449, 357, 25, 427, 415, 22 (Supplemental Table S5). The ten highest ranked enzymes are NHI_115, NHI_060, NHI_052, NHI_091, NHI_096, NHI_192, NHI_274, NHI_057, NHI_058, and NHI_119 (Supplemental Table S3). All ten enzymes and an empty vector control were used following the focused library screening protocol to identify which enzyme yields the most product formation.

Supplemental Figure S35. Relative formation of possible products of 6-Methyleneandrost-4-ene-3,17-dione (**20**) with the ten best ranked enzymes and a no enzyme control (X). The y-axis represents the relative extracted ion count as normalized by an internal standard.



From this screen, the fourth ranked enzyme, NHI_091, was chosen to be used on preparative-scale. NHI_091 was grown in batch and lysed following the general protein preparation protocol above. A 60 mg reaction (2 mM) was prepared in 100 mL final volume. The 2.8 L flask containing 49 mL of milli-Q water, 5 mL of 1 M TES buffer pH 7.5, 4 mL of 100 mM α -KG stock solution, 1 mL of 100 mM NaAsc stock solution, 1 mL of 10 mM FeSO₄ stock solution, 60 mg of **20**, 5 mL of toluene, and 40 mL of freshly prepared NHI_091 clarified cell lysate (200 mg/mL in 50 mM TES buffer pH 7.5) was shaken at 30 °C and 200 rpm for 18 h. The reaction was then quenched by the addition of 200 mL of acetone and stirred at 4 °C for 2 h. Reaction mixture was filtered and concentrated under reduced pressure to remove acetone. Reaction mixture was then extracted with ethyl acetate 3 x 300 mL, washed with brine, dried over sodium sulfate, filtered and concentrated. Reaction was purified with column chromatography on silica to afford 7 mg of **21** in 12% yield, with characterization in agreement with literature values.^{91,92}

¹H NMR (600 MHz, CDCl₃) δ 6.22 (s, 1H), 2.81 (d, *J* = 11.8 Hz, 1H), 2.48 – 2.58 (m, 3H), 2.10 – 2.19 (m, 4H), 1.90 – 1.99 (m, 3H), 1.81 (dd, *J* = 13.3, 3.4 Hz, 1H), 1.47 – 1.61 (m, 4H), 1.38 (td, *J* = 13.1, 4.3 Hz, 1H), 1.20 (s, 3H), 0.93 (s, 3H).

¹³C NMR (151 MHz, CDCl₃) δ 219.34, 201.27, 199.22, 160.26, 126.12, 51.66, 51.10, 47.73, 45.57, 39.85, 35.73, 35.66, 34.06, 33.87, 31.07, 21.75, 20.37, 17.76, 13.82.

HRMS ESI: calculated for [M+H]⁺ : 301.1799; observed: 301.1784.

Supplemental Figure S36. AneA (NHI_058) substrate scope from Renata and coworkers with CATNIP predictions.⁹³



22. Enzyme to Substrate CATNIP Application

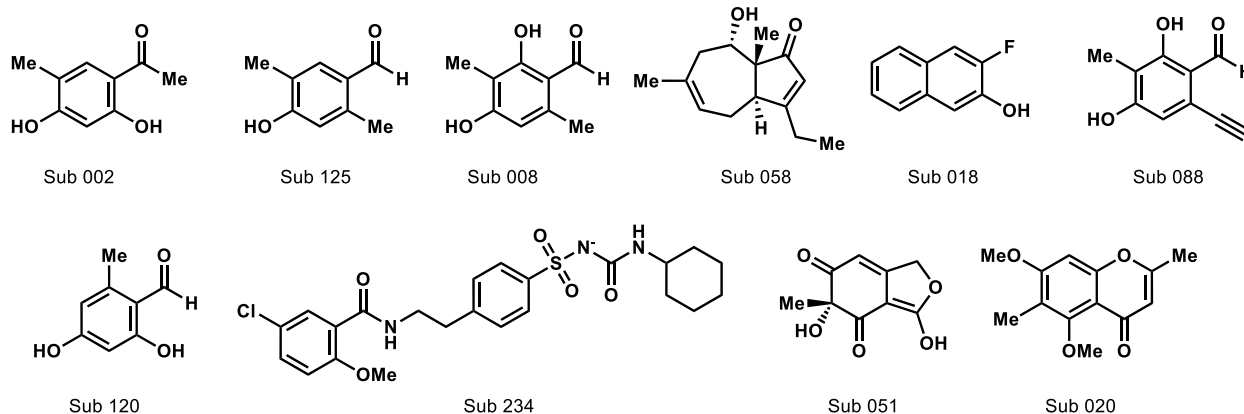
Test set example with NHI_123

The sequence for NHI_123, UniProt ID: Q7LL04) was submitted to the enzyme-to-substrate CATNIP model to predict compatible substrates. The ten most similar enzyme sequences were identified and are shown in the table below.

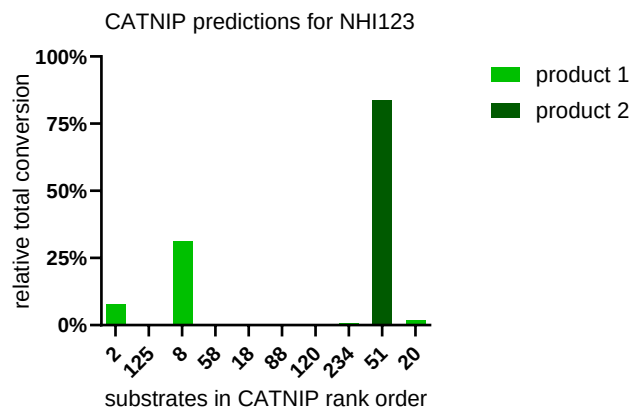
Enzyme1	Enzyme2	Percent_Similarity
USER	NHI123	100.0
USER	NHI062	86.23
USER	NHI055	85.65
USER	NHI143	85.54
USER	NHI103	85.38
USER	NHI078	85.33
USER	NHI122	85.33
USER	NHI079	85.27
USER	NHI104	84.95
USER	NHI116	84.85

The substrates most likely to be compatible with NHI_123 were identified and the top predictions, including scores are shown in the table below. Compatible substrate predictions are scored based on the lowest population for a given prediction.

Rank	Substrate ID	SMILES
1	2	<chem>OC1=C(C(C)=O)C=C(C)C(O)=C1C</chem>
2	125	<chem>OC1=C(C)C=C(C([H])=O)C(C)=C1</chem>
3	8	<chem>OC1=C(C)C(O)=C(C([H])=O)C(C)=C1</chem>
4	58	<chem>O=C(C=C1CC)[C@]2(C)[C@]1([H])CC=C(C)C[C@@H]2O</chem>
5	18	<chem>FC1=CC2=CC=CC=C2C=C1OC</chem>
6	88	<chem>OC1=C(C([H])=O)C(C#C)=CC([O-])=C1C</chem>
7	120	<chem>OC1=CC(O)=C(C([H])=O)C(C)=C1C</chem>
8	234	<chem>O=C([N-]S(=O)(C1=CC=C(CCNC(C2=C(OC)C=CC(Cl)=C2)=O)C=C1)=O)NC3CCCCC3</chem>
9	51	<chem>[O-]C1=C2C(CO1)=CC([C@](O)(C)C2=O)=O</chem>
10	20	<chem>O=C1C=C(C)OC2=CC(OC)=C(C)C(OC)=C21</chem>



NHI123 was screened against the substrate library as described in Section 18. Of the ten substrates highest ranked for compatibility with NHI123 and with reasonable available, the relative total conversion was calculated for all of the discovered reactions. Reaction traces can be found in the discovered reaction section (discovered reactions 12, 46, and 116).



Supplemental Figure S37. Relative conversion of NHI123 with the ten best ranked substrates.

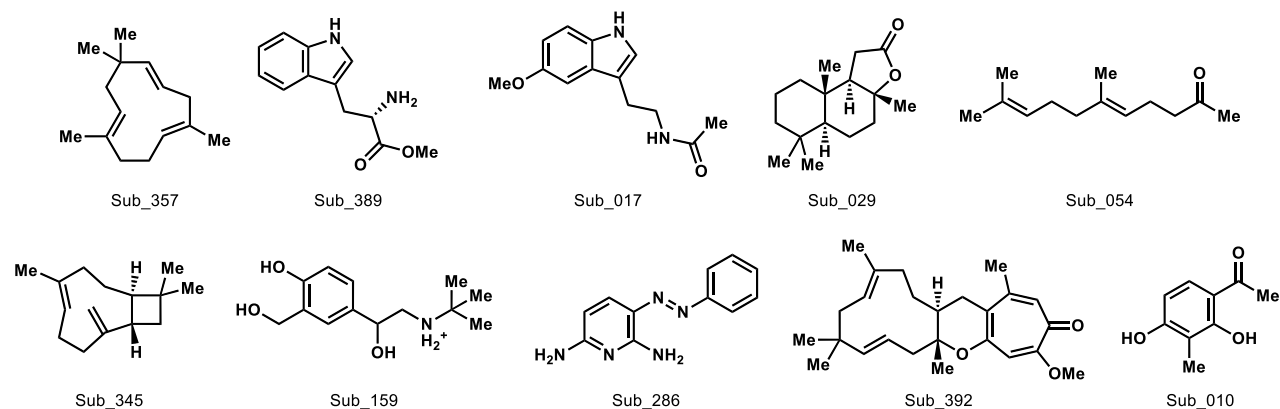
Test set example with NHI_177

The sequence for NHI_177, UniProt ID: A0A0F7LT18) was submitted to the enzyme-to-substrate CATNIP model to predict compatible substrates. The ten most similar enzyme sequences were identified and are shown in the table below.

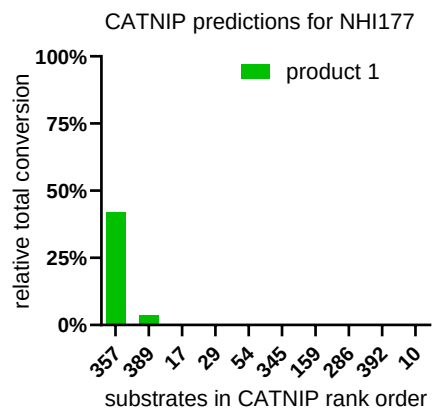
Enzyme1	Enzyme2	Percent_Similarity
USER	NHI177	100.0
USER	NHI196	80.18
USER	NHI193	79.67
USER	NHI005	79.56
USER	NHI189	79.34
USER	NHI134	79.28
USER	NHI137	79.0
USER	NHI053	78.94
USER	NHI095	78.89
USER	NHI050	78.83
USER	NHI091	78.83

The substrates most likely to be compatible with NHI_177. were identified and the top predictions, including scores are shown in the table below. Compatible substrate predictions are scored based on the lowest population for a given prediction.

Rank	Substrate ID	SMILES
1	357	<chem>C/C1=C\CC/C(C)=C/CC(C)(C)/C=C/C1</chem>
2	389	<chem>N[C@@H](CC1=CNC2=C1C=CC=C2)C(OC)=O</chem>
3	17	<chem>O=C(C)NCCC1=CNC2=CC=C(C=C12)OC</chem>
4	29	<chem>[H][C@]12C(C)(C)CCC[C@]1(C)[C@]3([H])[C@@](OC(C3)=O)(C)C2</chem>
5	54	<chem>CC(CC/C=C(C)/CCC=C(C)C)=O</chem>
6	345	<chem>C=C1CC/C=C(C)/CC[C@]2([H])[C@]1([H])CC2(C)C</chem>
7	159	<chem>CC([NH2+])CC(O)C1=CC(CO)=C(C=C1)O)(C)C</chem>
8	286	<chem>NC1=NC(N)=C(C=C1)/N=N/C2=CC=CC=C2</chem>
9	392	<chem>O=C(C(OC)=C1)C=C(C)C2=C1O[C@@]3(C)[C@@](C2)([H])CC/C(C)=C/CC(C)(C)/C=C/C3</chem>
10	10	<chem>OC1=C(C)C([O-])=C(C(C)=O)C=C1</chem>



NHI177 was screened against the substrate library as described in Section 18. Of the ten substrates highest ranked for compatibility with NHI177 and with reasonable available, the relative total conversion was calculated for all of the discovered reactions. Reaction traces can be found in the discovered reaction section (discovered reactions 160 and 177).



Supplemental Figure S38. Relative conversion of NHI177 with the ten best ranked substrates.

External validation with TqaL.

The sequence for TqaL *Streptomyces violaceusniger* (UniProt ID: A0A0X3VRU7) was submitted to the enzyme-to-substrate CATNIP model to predict compatible substrates. The ten most similar enzyme sequences were identified and are shown in the table below.

Supplemental Table S14. Percent similarity of the input enzyme, TqaL *S. vio.*, with all enzymes in the database. Filtered to show the ten most similar enzymes.

Enzyme1	Enzyme2	Percent_Similarity
USER	NHI177	86.57
USER	NHI202	85.59
USER	NHI073	85.18
USER	NHI207	84.47
USER	NHI137	81.24
USER	NHI193	80.8
USER	NHI196	80.62
USER	NHI232	80.39
USER	NHI171	80.35
USER	NHI134	80.3

The substrates most likely to be compatible with TqaL *S. vio.* were identified and the top predictions, including scores are shown in the table below. Compatible substrate predictions are scored based on the lowest population for a given prediction.

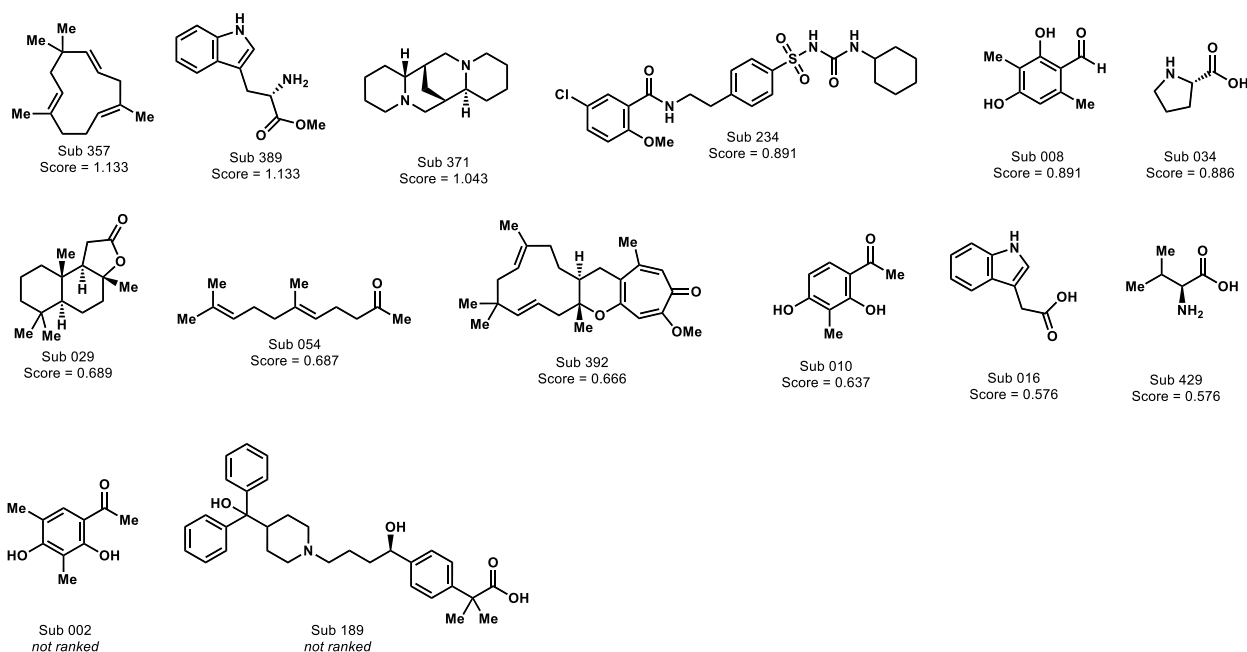
Supplemental Table S15. Top twenty predictions of compatible substrates for TqaL, ranked by score.

Index	Enzyme2	E2_Sub	Enzyme2_neighbor	Predicted
0	NHI177	357	357.0	1.133984
1	NHI177	389	389.0	1.133984
2	NHI177	389	17.0	1.043082
3	NHI073	8	125.0	0.891105
4	NHI207	371	371.0	0.891105
5	NHI202	234	234.0	0.885770
6	NHI073	8	8.0	0.878095
7	NHI073	34	34.0	0.878095
8	NHI177	389	29.0	0.687861
9	NHI177	389	54.0	0.687861
10	NHI137	392	392.0	0.666239
11	NHI193	10	10.0	0.637575
12	NHI193	10	88.0	0.637575

13	NHI137	392	267.0	0.633357
14	NHI196	359	359.0	0.616363
15	NHI193	10	117.0	0.604692
16	NHI193	10	120.0	0.604692
17	NHI177	357	345.0	0.594981
18	NHI171	16	16.0	0.576050
19	NHI134	429	429.0	0.576050

The predicted substrates that were available for experimental analysis were tested with TqaL following the analytical reaction protocol outlined in Supplementary Information section 8. The substrates were screened and their relative total conversion (RTC) to calculated as such:

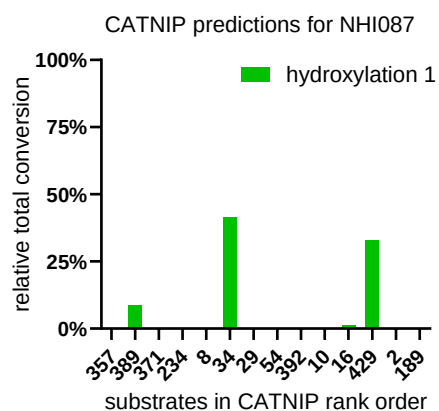
$$\text{RTC} = (\text{A}_{\text{hydrox}} + \text{A}_{\text{dihydrox}} + \text{A}_{\text{desat}} + \text{A}_{\text{chlor}} + \text{A}_{\text{ox/desat}}) / (\text{A}_{\text{hydrox}} + \text{A}_{\text{dihydrox}} + \text{A}_{\text{desat}} + \text{A}_{\text{chlor}} + \text{A}_{\text{ox/desat}} + \text{A}_{\text{sm}})$$



Of the twelve substrates highest ranked for compatibility with TqaL and with reasonable available, the relative total conversion was calculated for all of the discovered reactions. Notably, Sub429 has been reported in the literature to be the native substrate for a homologue of TqaL.

Supplemental Table S16. Discovered reactions and values associated with RTC.

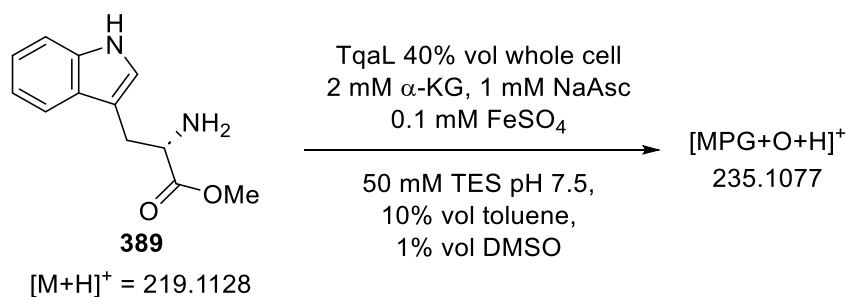
Substrate	RTC	Notes
357	0%	
389	8.61%	
371	0%	
234	0%	
8	0%	
34	41.55%	HILIC
29	0%	
54	0%	
392	0%	
10	0%	
16	1.29%	
429	33.07%	HILIC
2	0%	
189	0%	



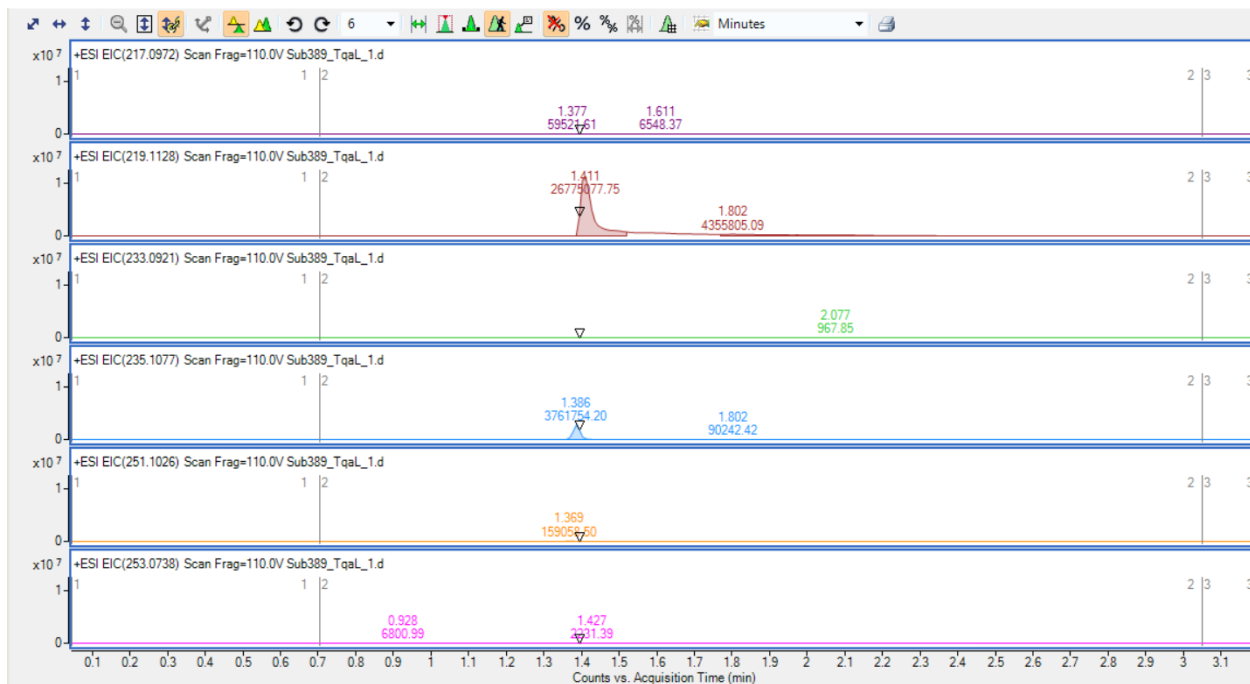
Supplemental Figure S39. Relative conversion of TqaL with the ten best ranked substrates.

Enzyme-oriented reaction discovery

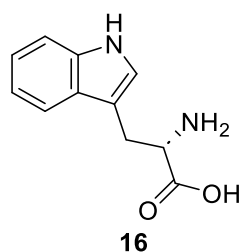
Discovered Reaction 216. Sub_389 + TqaL = hydroxylation



	Neutral	Positive	Negative
Desaturation	216.0899	217.0972	215.0826
Substrate	218.1055	219.1128	217.0982
oxidation/desaturation	232.0848	233.0921	231.0775
Hydroxylation	221.1900	222.1973	220.1827
Dihydroxylation	237.1849	238.1922	236.1776
Chlorination	239.1561	240.1634	238.1488



Discovered Reaction 217. Sub_016 + TqaL = hydroxylation



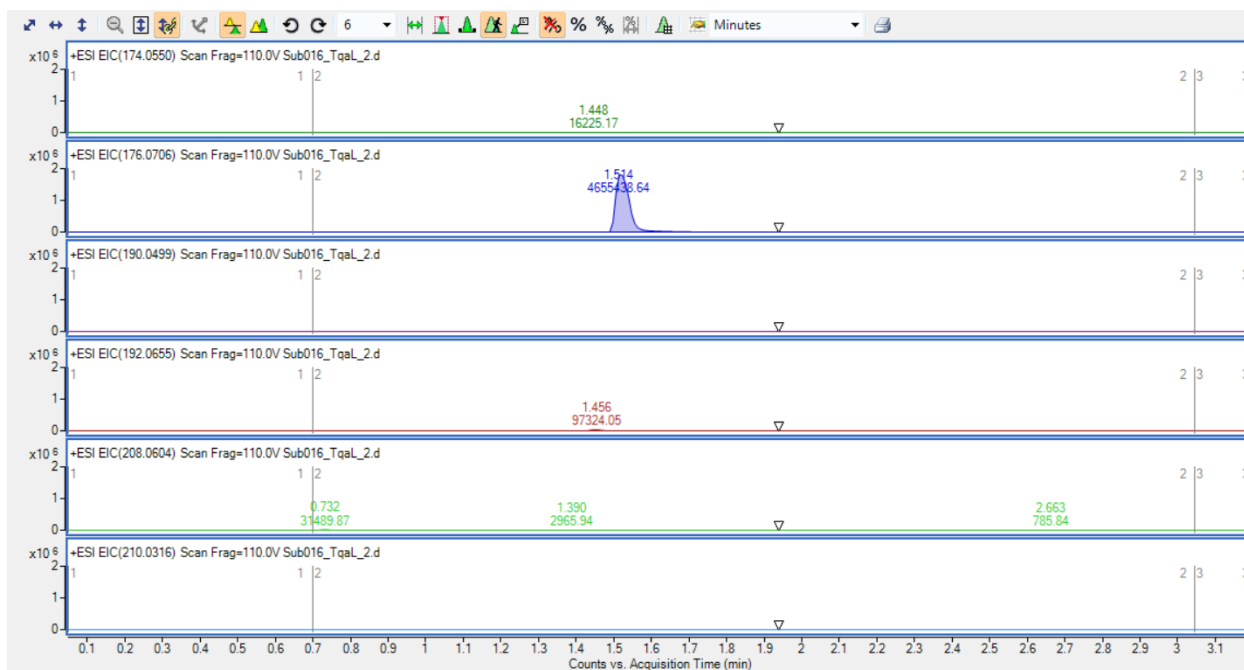
$[M+H]^+ = 176.0706$

TqaL 40% vol whole cell
2 mM α -KG, 1 mM NaAsc
0.1 mM FeSO₄

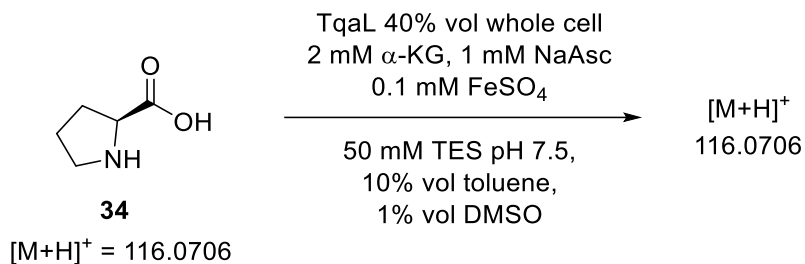
50 mM TES pH 7.5,
10% vol toluene,
1% vol DMSO

$[M+O+H]^+$
192.0655

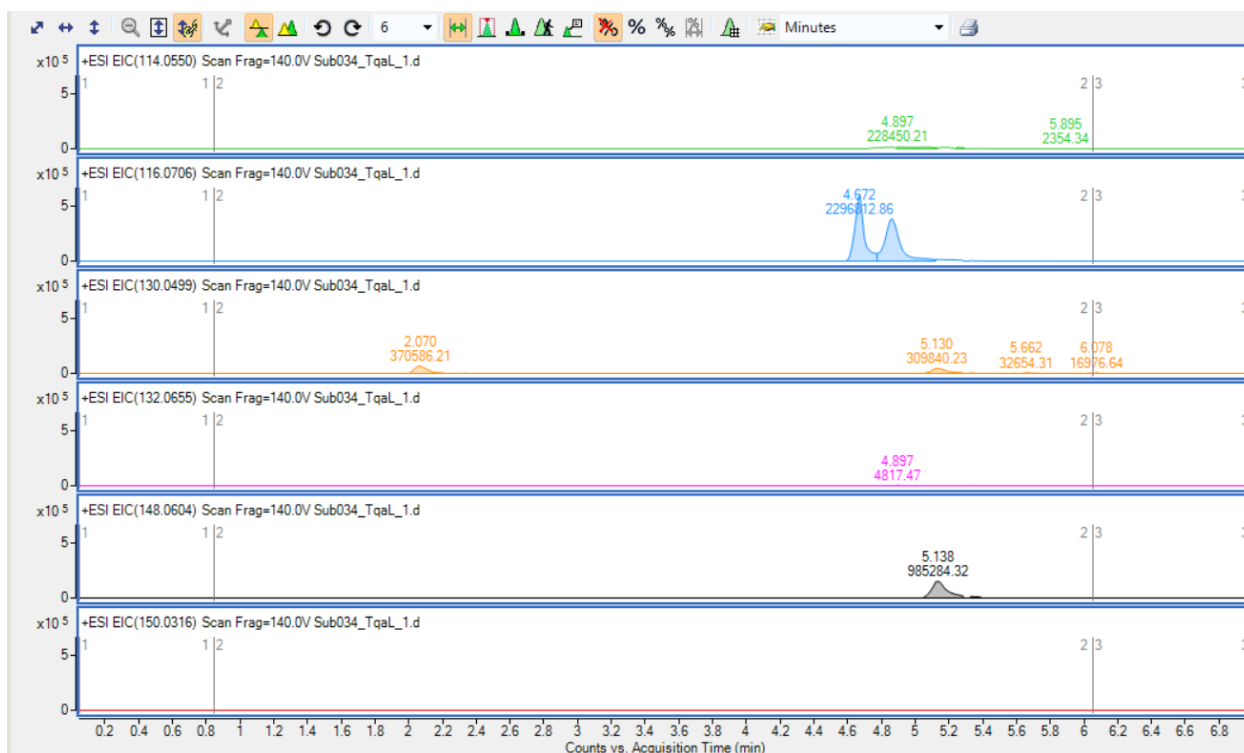
	Neutral	Positive	Negative
Desaturation	173.0477	174.0550	172.0404
Substrate	175.0633	176.0706	174.0560
oxidation/desaturation	189.0426	190.0499	188.0353
Hydroxylation	191.0582	192.0655	190.0509
Dihydroxylation	207.0531	208.0604	206.0458
Chlorination	209.0243	210.0316	208.0170



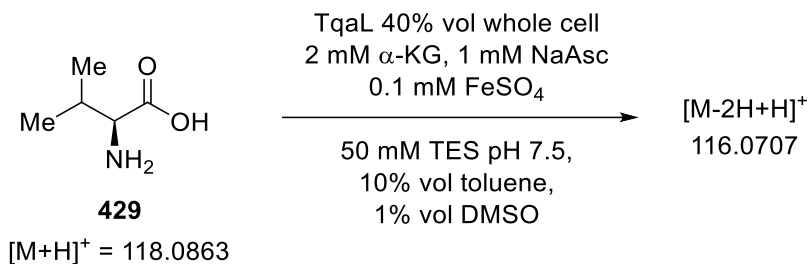
Discovered Reaction 218. Sub_034 + TqaL = rearrangement



	Neutral	Positive	Negative
Desaturation	113.0477	114.0550	112.0404
Substrate	115.0633	116.0706	114.0560
oxidation/desaturation	129.0426	130.0499	128.0353
Hydroxylation	131.0582	132.0655	130.0509
Dihydroxylation	147.0531	148.0604	146.0458
Chlorination	149.0243	150.0316	148.0170



Discovered Reaction 219. Sub_429 + TqaL = desaturation and hydroxylation



	Neutral	Positive	Negative
Desaturation	115.0634	116.0707	114.0561
Substrate	117.0790	118.0863	116.0717
oxidation/desaturation	131.0583	132.0656	130.0510
Hydroxylation	133.0739	134.0812	132.0666
Dihydroxylation	149.0688	150.0761	148.0615
Chlorination	151.0400	152.0473	150.0327



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