

a. Dog

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1: MetLysProLeuLeuGluThrLeuTyrLeuLeuGlyMetLeuValProGlyGlyLeuGly: 20
MetLysProLeuLeuGlyThrLeuTyrLeuLeuGlyIleLeuLeuProGluGlyLeuGly
5052: ATGAAGCCTCTGCTGGGACCCCTTGCTCTTTGGGAGCTCTGATTCCTGAGGGCTGGGA: 5109

21: TyrASP[Ar] >>>> Target Intron 1 >>>> {g}SerLeuAlaGlnHisArg: 29
||||| 10329 bp |||||
TyrASP[G]++ ++{y}SerLeuAlaGlnProArg
5110: TATGAT{GG}gt.....ag{A}TCCTAGCACAACCCAGA: 15465

30: GlnGluIleValAspLysSerValSerProTrp<<<<SerLeuGluThrTyrSerTyrAsn: 48
:::|||||:::
rPmetIleGlnIleValGluGluThrGlySerProTrpGlnSerLeuAspThrTyrSerThr
15486: CTGGAGGTTGTGGAAGAGACAGGAGACCCCTGGCAGAGCCTGGACACCTATCTCATACC: 15525

49: IleTyrHisProMetMetGlyGlu >>>> Target Intron 2 >>>> IleTyrGluT: 59
||||| 2067 bp |||||
ArgTyrHisProMetMetGlyGlu++ ++IleTyrGlnT
15526: AGATATCACCCATGGAAGGAggt.....agATCTATCAGT: 17625

60: rPmetArgGluIleSerGluLysTyrLysGluValValThrGlnHisPheLeuGlyValTr: 79
|||||:::
rPmetIleGlnIleValGluGluLysTyrAlaGlyValAlaThrGlnHisPheLeuGlyMetT
17626: GGATGATCCAGATAAERGATGAGAAGTACCGAGAGCTGGCCACACAGCATTCCTAGGCATGA: 17685

80: hTyrGluThrHisProMetTyrTyrTyrLeuLys >>>> Target Intron 3 >>>>: 90
||||| 1296 bp |||||
hTyrGluThrArgProMetTyrTyrTyrLeuLys++ +
17686: CCTATGAGACCCGGCCCATGTATATTTTGAAGgt.....a: 19012

91: IleSerGlnProSerGlyAsnProLysLysIleIleTrpMetAspCysGlyIleHisAl: 109
|||||:::
+IleSerGlnProSerAspAsnProLysLysIleIleIleTrpMetAspCysGlyIleHisAl
19013: gATCAGCAGCAGCATCGATAACCCAGAAGATCATTTTGATGGACTGTGGAATTCATGC: 19071

110: aargGluTrpIleAlaProAlaPheCysGlnTrpPheValLysGlu >>>> Target: 125
||||| 87 |||||
aargGluTrpIleAlaProAlaPheCysGlnTrpPheValLysGlu++
19072: CAGGGAATGGATTGCCCACTTTTTGCCAATGGTTTGTGAAAGAAgt.....: 19121

126: Intron 4 >>>> IleLeuGlnAsnHisLysAspAsnSerSerIleArgLysLeuLeu: 139
||||| 1 bp |||||
++IleLeuGlnAsnTyrLysAspAsnProArgIleGlyArgPheLeu
19122: .....agATTCTACAAACATAAAGACAACCCAGGATAGGAAGATCTTC: 20032

140: ArgAsnLeuAspPheTyrValLeuProValLeuAsnIleAspGlyTyrIleTyrThrTrp: 159
|||||:::
ArgAsnLeuAspPheTyrValLeuProValLeuAsnIleAspGlyTyrIleTyrThrTrp
20033: AGAAACCTGGACTCTATGTGCTCCAGTCTCTAATATAGATGGTTATATCTATACTGG: 20092

160: ThrThr >>>> Target Intron 5 >>>> AspArgLeuTrpArgLysSerArgS: 170
||||| 1124 bp |||||
ThrThr++ ++AspArgLeuTrpArgLysSerArgS
20093: ACAACTgt.....agATAGGCTTTGAGGAAATCTCGTT: 21249

171: erProHisAsnAsnGlyThrCysPheGlyThrAspLeuAsnArgAsnPheAsnAlaSerT: 190
|||||:::
erSerHisAsnAsnGlyThrCysPheGlyThrAspLeuAsnArgAsnPheAsnValSerT
21250: CATCCCAATAATACGGCAGCATGTTTGGGACAGATCTCAATCGAAATTTCAAGGTTTCT: 21309

191: rPCys{S} >>>> Target Intron 6 >>>> {er}IleGlyAlaSerArgAsnC: 199
||||| {|||} 1142 bp ||||| {|||}
rPCys{S}++ ++{er}IleGlyAlaSerArgAsnC
21310: GGTGT{A}gt.....ag{GT}ATTGGCGCATCGAAAACT: 22478

200: ysgGlnAspGlnThrPheCysGlyThrGlyProValSerGluProGluThrLysAlaValA: 219
|||||:::
ysgGlnAspIleThrPheCysGlySerGlyProValSerGluProGluThrLysAlaValS
22479: GCCAGGATATAACATCTCTGTGCTCAGGACCATGTGCAGAACCAGAGACTAAGCCGTTT: 22538

220: lAserPheIleGluSerLysLysAspAspIleLeuCysPheLeuThrMethiSSerTyrG: 239
|||||:::
erSerPheValGluSerLysLysAspAspIleValGluThrMethiSSerTyrG
22539: CCAGCTTTGTGGAGAGCAAGGAGGAGCATCGTGTGCTCTCGACCATGCATCCTACG: 22598

240: lYglnLeuIleLeuThrProTyrGlyTyrThrLysAsnLysSerSerAsnHisSProGluM: 259
|||||:::
lYglnLeuIleLeuThrProTyrGlyTyrThrLysAsnLysSerSerAsnHisSgluGluL
22599: GGCAGCTCATCTCCTCAGCCTTATGGCTACAGAAAATAAGTCAGTAACCAAGAGGAAC: 22658

260: et >>>> Target Intron 7 >>>> IleGlnValGlyGlnLysAlaAlaAsnAl: 269
||| 5765 bp |||
eu++ ++IleGlnValGlyGlnLysAlaAlaAsnAl
22659: TGgt.....agATCAAGTTGGACAGAAGGCAGCAATGC: 28453

270: aLeuLysAlaLysTyrGlyThrAsnTyrArgValGlySerSerAlaAspIleLeu{T}: 288
||||| {|||}:::
aLeuLysLysLysHisGlyThrAsnTyrArgValGlySerSerAlaAspIleLeu{T}++
28454: ATTGAAAAAAGCATGGAACCAATTATAGAGTTGGATCGAGTGAGATATTTTA{T}gt: 28511

289: >>>> Target Intron 8 >>>> {yr}AlaSerSerGlySerSerArgAspTrpAl: 298
||||| 863 bp ||||| {|||}
++{yr}AlaThrSerSerArgAspTrpAl
28512: .....ag{AT}GCCACATCAGGCTCTCAAGAGACTGGGC: 29403

299: aArgAspIleGlyIleProPheSerTyrThrPheGluLeuArgAspSerGlyThrTyrGl: 318
|||||:::
aArgAspIleGlyIleProPheSerTyrThrPheGluLeuArgAspAsnGlyThrTyrGl
29404: TCGGACATTGGGATCCCCCTTCTCATACACATTTGAGCTCGGGGCAATGGTACATATGG: 29463

319: yPheValLeuProGluAlaGlnIleGlnProThrCysGluGluThrMetGluAlaValLe: 338
|||||:::
yIleLeuProGluAlaGlnIleGlnAlaThrCysGluGluThrMetGluAlaValLe
29464: ATTTATTTGGCAGACAGTCAGATTGAGGCCCATCGGAGAGACCATCTGAGGCGTGTCT: 29523

339: uSerValLeuAspAspValTyrAlaLysHisTrpHisSerAspSeraAglyArgValTh: 358
|||||:::
uSerValLeuAspAspValTyrGluLysTyrTrpAsnSerAspSeraAglyLysValTh
29524: CTGGCTCTGGATGATGTATATGAGAAATACTGGAATTCAGACAGTGTCTGGCAAGGTGAC: 29583

359: rSerAlaThr: 361
|||||
rProAlaThr
29584: ACCTGCCACG: 29594

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b. Mouse

[illegible]

c. Rat

[illegible]