

Additional file 1

Positive samples:

>2JULA 256 NMR NA NA NA no Calsenilin <UNP CSEN_MOUSE> [MUS MUSCULUS]
MQRTKEAVKASDGNLLGDPGRIPLSKRESIKWQRPRFTRQALMRCCLIKWILSSAAPQGS
DSSDSELELSTVRHQPEGLDQLQAQTKFTKKELQSLYRGFKNECPTGLVDEDTFKLIYSQ
FFPQGDATTYAHFLNFAFDADGNGAIHFEDFVVGLSILLRGTVEKWKWAFNLYDINKDG
CITKEEMLAIMKSIYDMMGRHTYPILREDAPLEHVERFFQKMDRNQDGVVTIDEFLETCTQ
KDENIMNSMQLFENVI

>3P9AA 162 XRAY 1.75 0.178 0.216 no DNA-packaging protein gp3 <UNP TERM_BPP22> [ENTEROBACTERIA
PHAGE P22]
MAAPKGNRFWEARSSHGRNPKFESPEALWAACCEYFEWVEANPLWEMKAFSYQGEVIQEP
IAKMRAMTITGLTLFIDVTLETWRTYRLREDLSEVVTRAQVIYDQKFSGAAADLLNANI
IARDLGLKEQSQVEDVTPDKGDRDKRRSRIKELFNRTGTRDS

>4FJOA 97 XRAY 2.72 0.202 0.236 no DNA repair protein REV1 <UNP REV1_MOUSE> [MUS MUSCULUS]
AAPNLGAVEFSDVKTLLKEWITTISDPMEEIDLVVRYCTDLIEEKDLEKLDLVIKYMK
RLMQQSVESVWNMAFDLFDNVQVVLQQTGYSTLKV

>4FJOC 210 XRAY 2.72 0.202 0.236 no Mitotic spindle assembly checkpoint protein MAD2B <UNP
MD2L2_MOUSE> [MUS MUSCULUS]
MTTLTRQDLNFGQVADVLSSEFLEVAVHLILYVREVPVVGIFQKRKKYNVPVQMSCHPEL
NQYIQDTLHCVKPLLEKNDVEKVVVVILDKHRPVEKFVFEITQPPLLSINSDSLLSHVE
QLLAFFILKISVCDAVLDHNPFGCTFTVLVHTREAATRNMEKIQVIKDFPWILADEQDVH
MHDPRLIPLKMTSDILKMQLYVEERAHKN

>3U4VA 117 XRAY 1.80 0.182 0.200 no Telomerase-associated protein 82 <UNP D2CVN6_TETH>
[TETRAHYMENA THERMOPHILA]
NFNIGSLSDQLSKQTLLISQLQVGKNRFSFKFEGRVVYKSSTFQNNQDSKYFFITAQDAN
NQEINMSFWQKVDQSYQTLKVGQYYFIFGGEVKQFKNNLELKFQKFDYQIIPKETLS

>3U4ZA 109 XRAY 2.30 0.225 0.266 no Telomerase-associated protein 82 <UNP D2CVN6_TETH>
[TETRAHYMENA THERMOPHILA]
TLLISEVLKTSKQYLSVLAQVVDIQSSDKNIRLKICDNSCNQELKVVIFPDLCEWRDKF
SINKWYFYNEFVRQIYNDEVQLKNNIHSSIKESDDQRKVITYNQEQGVF

>208BB 1022 XRAY 2.75 0.245 0.281 no DNA mismatch repair protein MSH6 <UNP MSH6_HUMAN> [HOMO
SAPIENS]
MGSAPQNSSESAHVSGGGDDSSRPTVWYHETLEWLKEEKRRDEHRRRPDHPDFDASTLYV
PEDFLNSCTPGMRKWWQIKSQNFDLVICYKVGKIFYELYHMDALIGVSELGLVFMKGNWAH
SGFPEIAFGRYSDSLVQKGYKVARVEQTETPEMMEARCRKMAHISKYDRVVRREICRIIT
KGTQTVSVLEGDPSSENYSKYLLSLKEKEEDSSGHTRAYGVCVFDTSLGKFFIGQFSDDRH
CSRFRTLVAHYPPVQVLFEGNLSKETKTILKSSLSCSLQEGIPGSQFWDASKTLRLL
EEYFREKLSDGIGVMLPQVLKGMTSESDSIGLTPGEKSELALSALGGCVFYLKKCLIDQ
ELLSMANFEEYIPLSDTVSTTRSGAIFTKAYQRMVLDVATLNNLEIFLNGTNGSTEGTL
LERVDTCHTPFGKRLKQWLCAPLCNHYAINDRLDAIEDLMVVPDKISEVVELLKKLPDL
ERLLSKIHNVGSPLKSNHPDSRAIMYEETTYSKKKIIDFLSALEGFKVMCKIIGIMEEV
ADGFKSKILKQVISLQTKNPEGRFPDLTVELNRWDTAFDHEKARKTGLITPKAGFDSYD
QALADIRENEQSLLEYLEKQRNRIGCRTIVYWGIGRNRYQLEIPENFTTRNLPEEYELKS
TKKGCKRYWTKTIEKKLANLINAERRDVSLLKDCMRRLFYNFDKNYKDWQSAVECIAVLD
VLLCLANYSRGGDGPMPVILLPEDTPPFLELKGSRHPCITKTFFGDDFIPNDILIGCE

EEEQENGKAYCVLVTGPNMGGKSTLMRQAGLLAVMAQMGCVPAEVCRLTPIDRVFTRLG
 ASDRIMSGESTFFVELSETASILMHATAHSLVLVDELGRGTATFDGTAIANAVVKELAET
 IKCRTLFSTHYHSLVEDYSQNVAVRLGHMACMVENECEDEPSQETITFLYKFIKACPKSY
 GFNAARLANLPEEVIQKGRKAREFEKMNQSLRFLREVCLASERSTVDAEAVHKLLTLIK
 EL
 >3VW4A 128 XRAY 2.70 0.260 0.262 no Rep <UNP Q06B24_ECOLX> [ESCHERICHIA COLI]
 MGHHHHHHRNYHLFEKVRKWAYRAIRQGWPVFSQWLDAVIQVEMYNASLPVPLSPAECR
 AIGKSIKYYTHRKFSPEGFSAVQAARGRKGGTKSKRAAVPTSARSLKPWEALGISRATYY
 RKLKCDPD
 >1Q1VA 70 NMR NA NA NA no DEK protein <UNP DEK_HUMAN> [HOMO SAPIENS]
 DEPLIKLKKPPTDEELKETIKLLASANLEEVMTKQICKKVYENPTYDLTERKDFIKT
 TVKELISLEH
 >1R7JA 95 XRAY 1.47 0.232 0.244 no Conserved hypothetical protein Sso10a <UNP Q5W1E8_SULSO>
 [SULFOLOBUS SOLFATARICUS]
 AKKKSKLEIIQAILEACKSGSPKTRIMYGANLSYALTGRYIKMLMDLEIIRQEGKQYMLT
 KKGEELLEDIRKFNEMRKNMDQLKEKINSVLSIRQ
 >4DFCA 93 XRAY 2.80 0.240 0.282 no Transcription-repair-coupling factor <UNP MFD_ECOLI>
 [ESCHERICHIA COLI]
 GPHMASALVMKKGQRLSRDALRTQLDSAGYRHVDQVMEHGEYATRGALLDLFPMGSELPY
 RLDFDDEIDSLRVFDVDSQRTLEEVEAINLLP
 >1SFUA 75 XRAY 2.00 0.237 0.270 no 34L protein <UNP Q9DHS8_YLDV> [YABA-LIKE DISEASE VIRUS]
 MDLLSCTVNDAEIFSLVKKEVLSLNTNDYTTAISLSNRLKINKKKINQQLYKLQKEDTVK
 MVPSNPPKWFKNYNC
 >2FE3A 145 XRAY 1.75 0.172 0.229 no Peroxide operon regulator <UNP PERR_BACSU> [BACILLUS
 SUBTILIS]
 MAAHELKEALETKETGVRITPQRHAILEYLVNSMAHPTADDIYKALEGKFPNMSVATVY
 NNLRVFRESGLVKELTYGDASSRFDVTS DHYHAICENCGKIVDFHYPGLDEVEQLAAHV
 TGFKVSHHRLEIYVCQECSSKENH
 >4FE7A 412 XRAY 2.90 0.222 0.279 no Xylose operon regulatory protein <UNP XYLR_ECOLI>
 [ESCHERICHIA COLI]
 MGS SHHHHHSSGLVPRGSHMFTKRHRITLLFNANKAYDRQVVEGVGEYLQASQSEWDIF
 IEEDFRARIDKIKDWLGDGVIADFDKQIEQALADVDVPIVGVGGSYHLAESYPPVHYIA
 TDNYALVESAFHLHKEKGVNRFAFYGLPESSGKRWATEREYAFRQLVAEEKYRGVVYQGL
 ETAPENWQHAQNLADWLQTLPPQTGIIAVTDARARHILQVCEHLHIPVPEKLCVIGIDN
 EELTRYLSRVALSSVAQGARQMGYQAAKLLHRLDKEEMPLQRILVPPVRVIERSTDYR
 SLTDPAVIQAMHYIRNHACKGIKVDQVLDAVGISRSNLEKRFKEEVGETIHAMIHAEKLE
 KARSLLISTTSLINEISQMGYPSLQYFYSVFKKAYDTPKEYRDVNSEVML
 >3G1CA 104 XRAY 2.20 0.206 0.237 no The TrpR like protein from Eubacterium eligens ATCC
 27750 <PDB 3G1C> [EUBACTERIUM ELIGENS]
 MNNKLTQAVEQLFQAILSLKDLDEAYDFEDVCTINEILSLSQRFEVAKMLREHRTYLD
 IAEKTGASTATISRVNRSNLNYGNDGYDRVFERLGMLEKESDNK
 >1PH6B 217 XRAY 2.10 0.245 0.276 no Telomere-binding protein beta subunit <UNP TEBB_OXYNO>
 [STERKIELLA NOVA]
 PQQQSAFKQLYTELFNNEGDFSKVSSNLKKPLKCYVKESYPHFLVTDGYFFVAPYFTKEA
 VNEFHAKFPNVNIVDLTDKVIIVNNWSLELRRVNSAEVFTSYANLEARLIVHSFKPNLQE
 RLNPTRYPVNLFRDDEFKTTIQHFRHTALQAAINKTVKGDNLVDISKVADAAGKKGKVDA
 GIVKASASKGDEFSDFSFKEGNTATLKIADIFVQKEG
 >2LLHA 74 NMR NA NA NA no Nucleophosmin <UNP NPM_HUMAN> [HOMO SAPIENS]
 GSHMQESFKKQEKTPKTPKGPSSVEDIKAKMQASIEKGGSLPKVEAKFINYVKNCFRMTD

QEAIQDLWQWRKSL
>3PVVA 101 XRAY 2.00 0.252 0.271 no Chromosomal replication initiator protein dnaA <UNP DNAA_MYCTA> [MYCOBACTERIUM TUBERCULOSIS]
GPHMISAATIMAATAEYFDDTVEELRGPGKTRALAQSRQIAMYLCRELTDLSLPKIGQAF
GRDHTTVMYAQRKILSEMAERREVFHDVKELTTRIRQRSKR
>3IVPA 126 XRAY 2.02 0.202 0.235 no Putative transposon-related DNA-binding protein <UNP Q180H4_CLOD6> [CLOSTRIDIUM DIFFICILE]
MRKKEDKYDFRALGLAIKEARKKQGLTREQVGAMIEIDPRYLTNIENKGQHPSLQVLYDL
VSLNVSDEFFLPASSQVKSTKRRQLENKIDNFTDADLVIMESVADGIVKSKEVGEMAG
ENLYFQ
>3AXJA 249 XRAY 2.10 0.210 0.238 no GM27569p <UNP Q7JVK6_DROME> [DROSOPHILA MELANOGASTER]
MGSSHHHHHSQDPMNFVNLDFSNYQKYIDNEQEVRENIRIVREIEHLSKEAQIKLQ
IIHSDLSQISAACGLARKQVELCAQKYQKLAELVPAGQYYRYSDHWTFTITQRLIFIIALV
IYLEAGFLVTRETVAEMLGLKISQSEGFHLDVEDYLLGILQLASELSRFATNSVTMGDYE
RPLNISHFIDGLNTGFRLLNLKNDGLRKRFDALKYDVKKIEVVYDVSIRGLSSKEKDQQ
EPAVPATE
>3AXJB 298 XRAY 2.10 0.210 0.238 no Translin associated factor X, isoform B <UNP Q8INE1_DROME> [DROSOPHILA MELANOGASTER]
MPKNGGAGHRNTAPKRQIPAAQLDEDSPIVQQFRIYSNELIMKHDRHERIVKLSRDITI
ESKRIFLLHSIDSRKQNKQKVLLEEARQRLNKLIAVNFRAVALELRDQDVYQFRSSYSPG
LQEFIQAYTYMEYLCHEDAEGENETKSVSDWQAIQAVMQYVEESSQPKEEPTEGEDVQAI
AQVESPKKFQFFVDPTHEYILGLSDLTGELMRRCINSLGSGDITDCLDTCKALQHFYSGYI
SLNCQRARELWRKITTMKQSVLKAENVVCYNVVRGGEAAKWGATFDQKPADEVDEGFY
>3KOSA 799 XRAY 2.20 0.188 0.246 no DNA mismatch repair protein mutS <UNP MUTS_ECOLI> [ESCHERICHIA COLI]
SAIENFDAHTPMMQQLRLKAQHPEILLFYRMGDFYELFYDDAKRASQLLDISLTKRGAS
AGEPIPMAGIPYHAVENYLAKLVNQGESVAICEQIGDPATSKGPVERKVVRIVTPGTISD
EALLQERQDNLLAAIWQDSKGFYATLDISSGRFRLSEPADRETMAAELQRTNPAELLYA
EDFAEMSLIEGRRGLRRRPLWEFEIDTARQQLNLQFGTRDLVGFVENAPRGLCAAGCLL
QYAKDTQRTTLPHIRSITMEREQDSIIMDAATTRNLEITQNLAGGAENTLASVLDCTVTP
MGSRLKRWLHMPVRDTRVLLERQQTIGALQDFTAGLQPVLRQVGDLERILARLALRTAR
PRDLARMRHAQQQLPELRAQLETVD SAPVQALREKMGEFAELRDLLERAIIDTPPVLRD
GGVIASGYNEELDEWRALADGATDYLERLEVRERERTGLDTLKVGFNAVHGYYIQISRGQ
SHLAPINYMRRQTLKNAERYIIPELKEYEDKVLTSKGKALALEKQLYEELFDLLLPHLEA
LQQSASALAEALDVLNLAERAYTLNYTCPTFIDKPGIRITEGRHPVVEQVLNEPFIANPL
NLSPQRRMLIITGPNMGKSTYMRQTALIALMAYIGSYVPAQKVEIGPIDRIFTRVGAAD
DLASGRSTFMVEMTETANILHNATEYSLVLMNEIGRTSTYDGLSLAWACAENLANKIKA
LTLFATHYFELTQLPEKMEGVANVHLDALHGDITAFMHSVQDGAASKSYGLAVALAGV
PKEVIKRARQKLRELEIS
>1UKLA 876 XRAY 3.00 0.239 0.297 no Importin beta-1 subunit <UNP IMB1_MOUSE> [MUS MUSCULUS]
MELITILEKTVSPDRLELEAAQKFLERA AVENLPTFLVELSRVLANPGNSQVARVAAGLQ
IKNSLTSKDPDIKAQYQQRWLAI DANARREVKNYVLQTLGTETYPSSASQCVAGIACAE
IPVSQWPELIPQLVANVTNPSTEHMKESTLEAIGYICQDIDPEQLQDKSNEILTAIQG
MRKEEPSNNVKLAATNALLNSLEFTKANFDKESERHFIMQVVCEATQCPDTRVRVAALQN
LVKIMSLYYQYMETYMGPALFAITIEAMKSDIDEVALQGIEFWSNVCDEEMDLAIEASEA
AEQGRPPEHTSKFYAKGALQYLVPILTQTLTKQDENDDDDWNPCAAGVCLMLLSTCCE
DDIVPHVLPFIKEHIKNPDWRYRDAAVMAFGSILEGPEPNQLKPLVIQAMPTLIELMKDP
SVVVRDTTAWTVGRICELLPEAAINDVYLAPLLQCLIEGLSAEPRVASNVCWAFSSLAEA

AYEADVADDQEEPATYCLSSSFELIVQKLETTDRPDGHQNNLRSSAYESLMEIVKNSA
 KDCYPAVQKTTLVIMERLQQVLQMESHIQSTSDRIQFNDLQSLLCATLQNVLRKVQHQA
 LQISDVVMASLLRMFQSTAGSGGVQEDALMAVSTLVEVLGGEFLKYMEAFKPFLGIGLKN
 YAEYQVCLAAGVLVDLCRALQSNILPFCDEVMLLENLGNENVHRSVKPQILSVFGDI
 ALAIGGEFKKYLEVVLNTLQQASQAQVDKSDFDMDVYLNELRESCLEAYTGIVQGLKGDQ
 ENVHPDVMLVQPRVEFILSFIDHIAGDEDHTDGVVACAAGLIGDLCTAFGKDVLKLVEAR
 PMIHELLTEGRRSKTNKAKTLATWATKELRKLKNQA
 >1T23A 93 NMR NA NA NA no Chromosomal protein MC1 <UNP HMC1_METTE>
 [METHANOSARCINA THERMOPHILA]
 SNTRNFVLRDEGDNEHGVFTGKQPRQAALKAANRSGGTKANPDIIRLRERGTTKVVHVFKA
 WKEIVDAPKNRPAWMPEKISKPFVKKERIEKLE
 >2GMGA 105 NMR NA NA NA no hypothetical protein Pf0610 <UNP Q8U362_PYRFU> [PYROCOCUS
 FURIOSUS]
 AHHHHHHGSATREKIIELLEGDYSPSELARILDMRGKSGKKVILEDLKVISKIAKREG
 MVLLIKPAQCRKCGFVFKAEINIPSRCPKCKSEWIEEPRFKLERK
 >1I11A 81 NMR NA NA NA no TRANSCRIPTION FACTOR SOX-5 <UNP SOX5_MOUSE> [MUS MUSCULUS]
 GSPHIKRPMAFMVWAKDERRKILQAFPMHNSNISKILGSRWKAMTNLEKQPYEEQAR
 LSKQHLEKYPDYKYKPRPKRT
 >4I1KA 146 XRAY 1.60 0.120 0.166 no B3 domain-containing transcription factor VRN1 <UNP
 VRN1_ARATH> [ARABIDOPSIS THALIANA]
 MRGSHHHHHHGSRSKFYESASARKRTVTAEERERAINAAKTFEPTNPFFRVVLRPSYLYR
 GCIMYLPSPGFAEKYLSGISGFIKVQLAEKQWPVRCLYKAGRAKFSQGWYEFTLENNLGEG
 DVCVFELLRTRDFVLKVTAFRVNEYV
 >2JMPA 107 NMR NA NA NA no Chromosomal replication initiator protein dnaA <UNP DNAA_MYCGE>
 [MYCOPLASMA GENITALIUM]
 MGGGGGMEQFNAFKSLLKKHYEKTIGFHDKYIKDINRFVFKNNVLLILLENEFARNSLN
 DNSEIIHLAESLYEGIKSVNFVNEQDFFNLAKLENSRDTLYQNSG
 >3U50C 172 XRAY 2.50 0.218 0.253 no Telomerase-associated protein 82 <UNP D2CVN6_TETH>
 [TETRAHYMENA THERMOPHILA]
 QRIYSSIEEIIQQAQASEIGQKKEFYVYGNLVSIMKNKLYYRCTCQGKSVLKYHGDSF
 FCESCQQFINPQVHMLRAFVQDSTGTIPVMIFDQSSQLINQIDPSIHVQEAQYVKNC
 IENGQEEIIRQLFSKLDFAFIFEIFEQFENKEFNNEQEIAYKVLKIEKENIKE
 >2WYQA 85 XRAY 1.65 0.126 0.160 no UV EXCISION REPAIR PROTEIN RAD23 HOMOLOG A <UNP
 RD23A_HUMAN> [HOMO SAPIENS]
 GIPMAVTITLTKLQQQTFKIRMEPDETIVKVLKEKIEAEKGRDAFPVAGQKLIYAGKILSD
 DVPIRDYRIDEKNFVVVMVTKTKAG
 >2XJ3A 66 XRAY 1.23 0.148 0.184 no CYLR2 SYNONYM CYTOLYSIN REPRESSOR 2 <UNP Q8VL32_ENTFA>
 [ENTEROCOCCUS FAECALIS]
 MIINNKLIREKKKISQSELAALLEVSRQTINGIEKNKYNPSLQLALKIAYYLNCPLEDI
 FQWQPE
 >2YVAA 196 XRAY 1.85 0.183 0.214 no DnaA initiator-associating protein diaA <UNP
 DIAA_ECOLI> [ESCHERICHIA COLI]
 MQERIKACFTESIQTQIAAAEALPDASRAAMTLVQSLLNGNKILCCGNGTSAANAQHFA
 ASMINRFETERPSLPAIALNTDNVLTAIANDRLHDEVYAKQVRALGHAGDVLLAISTRG
 NSRDIVKAVEAAVTRDMTIVALTYDGGELAGLLGPQDVEIRIPSHRSARIQEMHMLTVN
 CLCDLIDNTLFPHQDD
 >2REBA 352 XRAY 2.30 0.210 NA no REC A <UNP RECA_ECOLI> [ESCHERICHIA COLI]
 AIDENKQKALAAALGQIEKQFGKGSIMRLGEDRSMDETISTGSLSLDIALGAGGLPMGR
 IVEIYGPESSGKTTTLTQVIAAAQREGKTCAFIDAHALDPIYARKLGVDIDNLLCSQPD

TGEQALEICDALARSGAVDIVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKL
 NLKQSNLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLDIRRIGAVKEGENVVGS
 ETRVKVVKNKIAAPFKQAEFQILYGEINFYGELVDLGVKEKLEKAGAWYSYKGEKIGQ
 GKANATAWLKDNPETAKEIEKKVRELLSNPNSTPDFSVDDSEGVAETNEDF
 >4NDHA 182 XRAY 1.85 0.164 0.196 no Aprataxin <UNP APTX_HUMAN> [HOMO SAPIENS]
 GSHMGHWSQGLKISMQDPKMVYKDEQVVVIKDKYPKARYHWLVLPWTSISSLKAVAREH
 LELLKHMHTVGEKIVDFAGSSKLRFLGYHAIPSMHVHLHVISQDFDSPCLKNKKHWN
 SFNTEYFLESQAVIEMVQEAGRVTVRDGMPPELLKLPLRCHECQQLPSIPQLKEHLRKHW
 TQ
 >2LFHA 68 NMR NA NA NA no DNA-binding protein inhibitor ID-3 <UNP ID3_HUMAN> [HOMO SAPIENS]
 MGHSHHHHSHMGGGKGPAAEEPLSLDDMNHCSRLRELVPVPRGTQLSQVEILQRVID
 YILDQVV
 >2A1IA 146 XRAY 1.90 0.218 0.248 no DNA excision repair protein ERCC-1 <UNP ERCC1_HUMAN> [HOMO SAPIENS]
 MGS SHHHHHSQDPAKSNSIIIVSPRQGNPVLKFVRNVPWEFGDVIPDYVLGQSTCALFL
 SLRYHNLHPDYIHGRLQSLGKNFALRVLLVQVDVKDPQALKELAKMCILADCTLILAWS
 PEEAGRYLETYKAYEQKPADLLMEKL
 >2A1JA 63 XRAY 2.70 0.250 0.275 no DNA repair endonuclease XPF <UNP ERCC4_HUMAN> [HOMO SAPIENS]
 MPQDFLLKMPGVNAKNCRLMHVKNIAELAALSQDELTSILGNAANAKQLYDFIHTSFA
 EVV
 >2A1JB 91 XRAY 2.70 0.250 0.275 no DNA excision repair protein ERCC-1 <UNP ERCC1_HUMAN> [HOMO SAPIENS]
 MGS SHHHHHSQD PADLLMEKLEQDFVSRVTECLTTVKSVNKTDSTLLTTFGSLEQLIA
 ASREDLALCPGLGPQKARRLFDVLHEPFLKV
 >2A1KA 233 XRAY 2.00 0.243 0.259 no gp32 single stranded DNA binding protein <UNP Q7Y265_BPR69> [ENTEROBACTERIA PHAGE RB69]
 KGFSSSEDKGEWKLKDASNGGQAVIRFLPAKTDDALPFAILVNHGFKKNGKWIETCSST
 HGDYDSCPCQYISKNDLYNTNKTEYSQLKRKTSYWANILVVKDPQAPDNEGKVFKYRFG
 KKIWDKINAMIAVDTEMGETPVDVTCPWEGANFVLKVKQVSGFSNYDESKFLNQSAIPNI
 DDES FQKELFEQMVDLSEMTSKDKFKSFEELNTKFNQVLGTAALGGAAAAAAS
 >4A11B 408 XRAY 3.31 0.178 0.233 no DNA EXCISION REPAIR PROTEIN ERCC-8 <UNP ERCC8_HUMAN> [HOMO SAPIENS]
 MLGFLSARQTGLEDPRLRLRAESTRRVLGLELNKDRDVERIHGGGINTLDIEPVEGRYML
 SGGSDGVIVLYDLENSRQSYTCKAVCSIGRDHPDVHRYSVETVQWYPHDTGMFTSSSF
 DKTLLKVDNTLQTADVFNFETVYSHHSPVSTKHCLVAVGTRGPKVQLCDLKS GSCSH
 ILQGHRQEILAVSWSPRYDYILATASADSRVKLWDVRRASGLITLDQHNGKKSQAVESA
 NTAHNGKVNGLCFTSDGLHLLTVGTDNRMRLWNSSNGENTLVNYGKVCNNSKKGLKFTVS
 CGCSSEFVFPYGSTIAVYTVYSGEQITMLKGHYKTVDCVFQSNFQELYSGSRDCNILA
 WVP SLYEPVPDDDETTKSQLNPAFEDAWSSSDEEGGTS AW SHPQFEK
 >3VH5T 111 XRAY 2.40 0.194 0.244 no CENP-T <UNP F1NPG5_CHICK> [GALLUS GALLUS]
 GSTREPEIASSLIKQIFSHYKTPVTRDAYKIVEKASERYFKQISSDLEAYSQHAGRKTV
 EMADVELLMRRQGLVTDKMPHLVVERHLPLEYRKLIIPIAVSGNKVIPAK
 >3BRGC 427 XRAY 2.20 0.221 0.255 no Recombining binding protein suppressor of hairless <UNP SUH_MOUSE> [MUS MUSCULUS]
 GPLGSPPKRLTREAMRNYLKERGDQTVLILHAKVAQKSYGNEKRFFCPPPCVYLMGSGWK
 KKKEQMERDGCSEQSQPCAFIGIGNSDQEMQQLNLEGKNYCTAKTLYISDS DKRKH FML
 SVKMFYGN SDDIGVFLSKRIKIVISKPSKKKQSLKNADLCIASGTKVALFNRLRSQTVSTR
 YLHVEGGNFHASSQQWGA FYIHLLDDDESEGE EFTVRDGYIHYGQTVKLVCSVTGMALPR
 LIIRKVDKQTALLDADDPVSQLHKCAFYLK DTERMYLCLSQERIIQFQATPCPKEQNKEM

INDGASWTIISTDKAEYTFYEGMGPVLAPVTPVPVVESLQLNGGGDVAMLELTGQNFTPN
LRVWFGDVEAETMYRCGESMLCVVPDISAFREGWRWVRQPVPVTLVRNDGVIYSTSLT
FTYTPEP

>1RIFA 282 XRAY 2.00 0.221 0.246 no DNA helicase uvsW <UNP UVSU_BPT4> [ENTEROBACTERIA PHAGE
T4]

MDIKVHFHDFSHVRIDCEESTFHELDRFFSFEADGYRFNPRFRYGNWDGRIRLLDYNRL
PFGLVGQIKKFCDFGYKAWIDPQINEKEELSRKDFDEWLSKLEIYSGNKRIEPHWYQKD
AVFEGLVNRRLNLPTSAGRSLLIALLARYYLENYEGKILIIVPTTALTTQMADDFVDY
RLFSHAMIKKIGGGASKDDKYKNDAPVVVGTVVVKQPKWFSSQFGMMNDECHLATGK
SISSIISGLNNCMFKFGLSGSLRDGKANIMQYVGMFGEIFKP

>2QHBA 86 XRAY 2.40 0.251 0.264 no Telomere binding protein TBP1 <UNP
Q84ZU4_NICGU> [NICOTIANA GLUTINOSA]

RRIRRPFSVAEVEALVEAHLGTGRWRDVKMRAFDNADHRTYVDLKDQKTLVHTASIA
PQQRGEPPVQDLDRVLAHAYWSQ

>2DGZA 113 NMR NA NA NA no Werner syndrome protein variant <UNP WRN_HUMAN> [HOMO SAPIENS]
GSSGSSGSSQPVISAEQETQIVLYGKLVEARQKHANKMDVPAILATNKILVDMAKMRP
TTVENVKRIDGVSEGAAMLAPLWEVIKHFCQTNVQTDLFSSSTKPSGSSG

>1IN4A 334 XRAY 1.60 0.236 0.253 no HOLLIDAY JUNCTION DNA HELICASE RUVB <UNP RUVB_THEMEA>
[THERMOTOGA MARITIMA]

MSEFLTPTERTVYDSGVQFLRPKSLDEFIQENVKKLSLALEAAKMRGEVLDHVLLAGPP
GLGKTTLAHIIASELQTNIHVTSGPVLVKQGDMAAILTSLERGDVLFIDEIHRNLKAVEE
LLYSAIEDFQIDIMIGKGPSAKSIRIDIQPFITLVGATTSGLSSPLRSRFGIILELDFY
TVKELKEIIKRAASLMDVEIEDAAAEMIAKRSRGTPIAIRLTKRVRDMLTVVKADRINT
DIVLKTMEVLNIDDEGLDEFDRKILKTIIEIYRGGPVGLNALAASLGVEADTLSEVYEPY
LLQAGFLARTPRGRIVTEKAYKHLKYEVNENRF

>2INGX 213 XRAY 3.60 0.251 0.302 no Breast cancer type 1 susceptibility protein <UNP
BRCA1_HUMAN>
[HOMO SAPIENS]

GPRMSMVVSGLTPEEFMLVYKFARKHHITLTNLITEETTHVVMKTDAEFVCERTLKYFLG
IAGGKWVVSFYFWVTQSIKERKMLNEHDFEVRGDVVNGRNHQGPKRARESQRKIFRGLEI
CCYGPFTNKPTDQLEWMVQLCGASVVKELSSFTLGTGVHPIVVVQPDWTEGNGFHAIGQ
MCEAPVVTREWVLDVALYQCQELDTYLIPQIP

>2OBPA 96 XRAY 1.70 0.188 0.219 no Putative DNA-binding protein <UNP Q46TT3_RALEJ> [RALSTONIA
EUTROPHA]

GMSDPGNEQNGDIDPAIVEVLLVLREAGIENGATPWSLPKIAKRAQLPMSVLRRVLTQL
QAAGLADVSEADGRGHASLTQEGAALAAQLFPDPF

>3TUOA 105 XRAY 1.70 0.161 0.218 no DNA-binding protein SATB1 <UNP SATB1_HUMAN> [HOMO SAPIENS]
GPGSGTMLPVFCVVEHYENAIEYDCKEEHAEFVLVRKDMFLNQLIEMALLSLGYSHSSAA
QAKGLIQVGKWNVPLSYVTDAPDATVADMLQDVYHVVTLLKILH

>3V20A 293 XRAY 2.35 0.246 0.293 no Endonuclease Bse634IR <UNP Q8RT53_GEOSE> [GEOBACILLUS
STEAROTHERMOPHILUS]

MTNLTSNSCVEEYKENGKTKIRIKPFNALIELYHHQTPTGSIKENLDKLENYVKDVVKA
KGLAIPTSAGFSNTRGTWFEVMIAIQSWNYRVKRELNDYLIKMPNVKTFDFRKIFDNET
REKLHLQLEKSLTHKQVRLITSNPDLIIIRQKDLKSEYNLPINKLTHENIDVALTLFK
DIEGCKWDSLAVAGVGLKTSRDPDRRLQLVHEGNILKSLFAHLKMAWNPKAEFKYYGAS
SEPVSKADDDALQTAATHTIVNVNSTPERAVDDIFSLTSFEDIDKMLDQIIKK

>4E1PA 61 XRAY 1.73 0.161 0.185 no Protein lsr2 <UNP LSR2_MYCTU> [MYCOBACTERIUM TUBERCULOSIS]
MAKKVTVTLVDDFDGSGAADETVEFGLDGVTYEIDLSTKNATKLRGDLKQWVAAGRRVGG

R

>1WH5A 80 NMR NA NA NA no ZF-HD homeobox family protein <UNP Y5541_ARATH> [ARABIDOPSIS THALIANA]
GSSGSSGSSAEAGGGIRKRRHTKFTAEQKERMLALAERIGWRIQRQDDEVIQRFQETGV
PRQVLKVLHNNKHS GPSSG
>3II2A 157 XRAY 2.00 0.173 0.237 no Putative uncharacterized protein <UNP Q70LE6_AFV1>
[ACIDIANUSFILAMENTOUS VIRUS 1]
GSEMSVVEYEVVSKNLTSMKSHLLFSVKKRWFVKPFRHQRQLGKLHYKLLPGNYIKFGL
YVLKNQDYARFEIAWVHVDKGKIEERTVYSIETYWHIFIDIENDLNCYPVLAKFIEMRP
EFHKTAWVEESNYSIAEDDIQMVESIKRYLERKIASD
>3II6A 203 XRAY 2.40 0.240 0.280 no DNA repair protein XRCC4 <UNP XRCC4_HUMAN> [HOMO SAPIENS]
MERKISRHLVSEPSITHFLQVSWEKTLES GFVITLTDGHS AWGTGTSESEISQEADDME
MEKGKYVGELRKALLSGAGPADVYTFNFSKESCYFFFEKNLKDVSFRLGSFNLEKVENPA
EVIRELICyclDTTAENQAKNEHLQKENERLLRDWNDVQGRFEKCVSAKEALETDLKRF
ILVLNEKKTIRSLHNKLLNAAQ
>4KOPA 177 XRAY 1.75 0.185 0.220 no Single-stranded DNA-binding protein WHY2, mitochondrial
<UNP
WHY2_ARATH> [ARABIDOPSIS THALIANA]
MKDAAKPSGRLFAPYSIFKGAALSVEPVLPSFTEIDSGNLRIDRRGSLMMTFMPAIGER
KYDWEKKQKFALSPTEVGLISMGSKDSSEFFHDPMSKSSNAGQVRKSLSVKPHADGSGY
FISLSVNNLSILKTDYFVVPVTKAEFAVMKTAFSFALPHIMGNRLTGHEHHHHHHH
>3KOJA 108 XRAY 1.90 0.202 0.218 no uncharacterized protein ycf41 <UNP Q5N255_SYNP6>
[SYNECHOCOCCUS ELONGATUS PCC 6301]
MGHHHHHHSHMNSCILQATVVEAPQLRYAQDNQTPVAEMVVQFPGLSSKDAPARLKVVGW
GAVAQELQDRCRLNDEVVLEGRRLINSLKPDGNREKQTELTVTRVHH
>2PKHA 148 XRAY 1.95 0.222 0.277 no Histidine utilization repressor <UNP Q87UX0_PSESM>
[PSEUDOMONAS SYRINGAE PV. TOMATO]
SNAARGHRHTCKVMVLKEEAAGSERALALDMREGQRV FHS LIVHFENDIPVQIEDRFVNA
QVAPDYLKQDFTLQTPYAYLSQVAPLTEGEHVVEAILAEADECKLLQIDAGEPCLLIRRR
TWSGRQPVTAA RLHPGSRHRLEGRFTK
>2RH3A 121 XRAY 1.70 0.184 0.209 no Protein virC2 <UNP VIRC2_AGR5> [AGROBACTERIUM
TUMEFACIENS]
IQVFLSARPPAPEVSKIYDNLILQYSPSKSLQMILRRALGDFENMLADGSFRAAPKSYPI
PHTAFEKSIIVQTSRMFPVSLIEARNHFDPLGLETA R AFGHKLATAALACFFAREKATN
S
>1RH6A 55 XRAY 1.70 0.193 0.226 no Excisionase <UNP VXIS_LAMB> [ENTEROBACTERIA PHAGE LAMBDA]
MYLTLEWNA RRRPSLETVRRWVRESRIFPPPVKDGREYLFHESAVKVDLNR
>1F6VA 91 NMR NA NA NA no DNA TRANSPOSITION PROTEIN <UNP VPB_BPMU> [ENTEROBACTERIA PHAGE
MU]
GSRIAKRTAINTKKADVKA IADAWQINGEKELELLQQAQKPGALRI LNHSLRLAAMTA
HGKGERVNEDYLRQAFRELDLDV DISTLLRN
>3F6CA 134 XRAY 1.45 0.212 0.256 no Positive transcription regulator evgA <UNP
EVGA_ECOLI> [ESCHERICHIA COLI K-12]
SLNAIIIDDHPLAIAAIRNLLIKNDIEILAELTEGGS AVQ RVETLKP DIVIIDVDIPGVN
GIQVLETLRKRQYSGIIIIIVSAKNDFYKGHCADAGANGFVSKKEGMNIIAAIEAAKNG
YCYFPFSLNRFVGS
>4F6MA 133 XRAY 2.40 0.223 0.240 no Transcriptional regulator Kaiso <UNP KAISO_HUMAN> [HOMO
SAPIENS]
ANKRMKVKHDDHYELIVDGRVYYICIVCKRSYVCLTSLRRHFNIHSWEKKYPCRYCEKVF
PLAEYRTKHEIHHTGERRYQCLACGKSFINYQFMSSHIKSVHSQDPSGDSKLYRLHPCRS

LQIRQYAYLSDRS
>4NE3A 93 XRAY 1.80 0.232 0.252 no Centromere protein S <UNP CENPS_HUMAN> [HOMO SAPIENS]
SYQQRLKAAVHYTVGLCEEVALDKAMQFSKQTIAAISELTFRCENFAKDLEMFARHAK
RTTINTEDVKLLARRSNSLLKYITDKSEEIAQA

>1GDTA 183 XRAY 3.00 0.235 NA no GAMMA DELTA RESOLVASE <UNP TNR1_ECOLI> [ESCHERICHIA COLI]
MRLFGYARVSTSQQSLDIQVRALKDAGVKANRIFTDKASGSSSDRKGLDLLRMKVEEGDV
ILVKKLDRLGRDTADMIQLIKEFDAQGV SIRFIDDGISTDGEMGKMVVTILSAVAQAERQ
RILERTNEGRQEAMAKGVVFGRRKIDRDAVLNMWQQGLGASHISKTMNIARSTVYKVIN
ESN

>2AN7A 83 NMR NA NA NA no Protein parD <UNP PARD4_ECOLI> [ESCHERICHIA COLI]
MSRLTIDMTDQQHQS LKALAALQGKTIKQYALERLFPGDADADQAWQELKTMLGNRINDG
LAGKVSTKSVGEILDEELSGDRA

>1ZZKA 82 XRAY 0.95 0.124 0.127 no Heterogeneous nuclear ribonucleoprotein K <UNP HNRPK_HUMAN> [HOMO SAPIENS]
GAMGPIITTQVTIPKDLAGSIIGKGGRIKQIRHESGASIKIDEPLEGSEDRIITITGTQ
DQIQNAQYLLQNSVKQYSGKFF

>2RRDA 101 NMR NA NA NA no HRDC domain from Bloom syndrome protein <UNP BLM_HUMAN> [HOMO SAPIENS]
GIPEFKQKALVAKVSQREEMVKKCLGELTEVCKSLGKVFVGHYFNIFNTVTLKKLAESLS
SDPEVLLQIDGVTEDKLEKYGAEIVSLQKYSEWTS PAEDS

>2L49A 99 NMR NA NA NA no C protein <UNP Q83VS7_BPP2> [ENTEROBACTERIA PHAGE P2]
MSNTISEKIVLMRKSEYLSRQQLADLTGVPYGTLSYYESGRSTPPTDVMNILQTPQFTK
YTLWFMNTQIAPESGQIAPALAHFGQNETTSPHSGQKTG

>4E45E 137 XRAY 2.00 0.202 0.245 no Fanconi anemia group M protein <UNP FANCM_HUMAN> [HOMO SAPIENS]
GAMDPMRQSSLKKDWFLSEEEFKLWNRLYRLRDSDEIKEITLPQVQFSSLQNEENKPAQE
STTGIHQLSLSEWRLWQDHLPLTHQVDHSDRCRHF IGLMQMIEGMRHEEGECSYELEVES
YLQMEDVTSTFIAPRNE

>3GYDA 187 XRAY 1.79 0.170 0.212 no Cyclic nucleotide-binding domain <UNP Q1GZZ4_METFK> [METHYLOBACILLUS FLAGELLATUS KT]
MGSDKIH HHHHHENLYFQGMYPDLVHLGGADKYFEEILEIVNKIKLFGDFSNEEVRYLCS
YMQCYAAPRDCQLLTEGDPGYDLLILTGEVNVIKDIPNKG IQTIAKVGAGAIIGEMSMI
DGMPRSASCVASLPTDFAVLSRDALYQLLANMPKLGKVLIRLLQLLTARFRESYDRILP
KTLGELI

>2CXYA 125 XRAY 1.60 0.186 0.203 no BAF250b subunit <UNP ARI1B_HUMAN> [HOMO SAPIENS]
GSSGSSGEKITKVYELGNPERKLWDRYLT FMEERGSPVSSLPVGGKKPLDLFRLYVCV
KEIGGLAQVNKNKKWRELATNLNVGTSSSAASSLKKQYIQYLF AFECKIERGEEPPPEVF
STGDT

>1KNOA 212 XRAY 2.85 0.286 0.297 no Rad52 <UNP RAD52_HUMAN> [HOMO SAPIENS]
MSGTEEAILGGRD SHPAAGGGSVLCFGQCQYTAEEYQAIQKALRQRLGPEYISSRMAGGG
QKVCYIEGHRVINLANEMFGYNGWAHSITQQNVDFVDLNNKFYVGVCAFVRVQLKDGSY
HEDVGYGVSEGLSKALSLEKARKEAVTDGLKRALRSFGNALGNCILDKDYLRSLNKLPR
QLPLEVDLTAKRQDLEPSVEEARYNSCRPNM

>2KNGA 55 NMR NA NA NA no Protein lsr2 <UNP LSR2_MYCTU> [MYCOBACTERIUM TUBERCULOSIS]
SGSGRGRGAIDREQSAAIREWARRNGHNVSTRGRIPADVIDAYHAATLEHHHHHH

>2QSFA 533 XRAY 2.35 0.226 0.245 no DNA repair protein RAD4 <UNP RAD4_YEAST> [SACCHAROMYCES CEREVISIAE]
MGNEVAGVEDISVEIKPSSKRNSDARRTSRNVCSNEERKRRKYFHMLYL VCLMVHGFIRN
EWINSKRLSRKLSNLVPEKVFELLHPQKDEELPLRSTRKLLDGLKKCMELWQKHWKITKK

YDNEGLYMRTWKEIEMSANNKRKFKTLKRSDFLRAVSKGHGDPDISVQGFVAMLRACNVN
 ARLIMSCQPPDFTNMKIDTSLNGNNAYKDMVKYPIFWCEVWDKFSKKWITVDPVNLKTIE
 QVRLHSLKAPKGVACCERNMLRYVIAIDRKYGCRDVTRRYAQWMNSKVRKRITKDDFGE
 KWFRKVITALHHRKRTKIDDYEDQYFFQRDESEGIPDSVQDLKNHPYYVLEQDIKQTQIV
 KPGCKECCGYLKVHGVKGVKLVYAKRDIADLKSARQWYMNGRILKTGSRCKKVIKRTVGR
 PKGEAEEEDERLYSFEDTELYIPPLASASGEITKNTFGNIEVFAPTMIPGNCCLVENPVA
 IKAARFLGVFAPAVTSFKFERGSTVKPVLGIVVAKWLREAIETAIDGIEFI
 >2QSFX 171 XRAY 2.35 0.226 0.245 no UV excision repair protein RAD23 <UNP RAD23_YEAST>
 [SACCHAROMYCES CEREVISIAE]
 GSGNASSGALGTTGGATDAAQGGPPGSIGLTVEDLLSLRQVSGNPEALAPLENISARY
 PQLREHIMANPEVFSMLLEAVGDNMQDVMGADDMEGEDIEVTGEAAAAAGLQGEGEG
 SFQVDYTPEDDQAISRLCELGFERDLVIQVYFACDKNEEAAAANILFSDHAD
 >1WJVA 79 NMR NA NA NA no Cell growth regulating nucleolar protein LYAR <UNP LYAR_MOUSE> [MUS
 MUSCULUS]
 GSSGSSGMVFFTCNACGESVKKIQVEKHVSNCRNCECLSCIDCGKDFWGDDYKSHVKCIS
 EGQKYGGKGYEAKSGPSSG
 >1WJ2A 78 NMR NA NA NA no Probable WRKY transcription factor 4 <UNP WRKY4_ARATH> [ARABIDOPSIS
 THALIANA]
 GSSGSSGVQTTSEVDLLDDGYRWRYGQKVVGKNPYPRSYKCTTPGCGVRKHVERAATD
 PKAVVTTYEGKHNHDLPA
 >30LCX 298 XRAY 2.40 0.223 0.258 no DNA topoisomerase 2-binding protein 1 <UNP TOPB1_HUMAN>
 [HOMO SAPIENS]
 MSRNDEKPEFFVKFLKSSDNSKCFKALESIKEFQSEYLIITEEEEALKIKENDRSLYIC
 DPFSGVVFHLLKGLCRIVGPQVIFCMHHQRCVPRAEHPVYNMMSDVTISCTSLEKEK
 REEVHKYVQMMGGRVYRDLNVSVTHLIAGEVGSKKYLVAANLKKPILLPSWIKTLWEKSQ
 EKKITRYTDINMEDFKCPIFLGCIICVTGLCGLDRKEVQQLTVKHGGQYMGQLKMNETH
 LIVQEPKGQKYECAKRWNVHCVTQWFFDSIEKGFCQDESIYKTEPRPEALEHHHHHH
 >2KI2A 90 NMR NA NA NA no Ss-DNA binding protein 12RNP2 <UNP O25501_HELPY> [HELICOBACTER
 PYLORI]
 MRNIYVGNLVYSATSEQVKELFSQFGKVFNVKLIYDRETKPKGFGFVEMQEEVSSEAIA
 KLDNTDFMGRTIRVTEANPKKSLEHHHHHH
 >2KIWA 111 NMR NA NA NA no Int protein <UNP Q4L7R3_STAHJ> [STAPHYLOCOCCUS HAEMOLYTICUS
 JCSC1435]
 TFKQVADDWLKQYANDVKVSSVRAREKAIQHAIERFNTKPIQTIKKHDYQRFVDDISAQY
 SKNYVDSIVASTNMIFKYAYDTRLIKAMPSEGIKRPKKKVSVELEHHHHHH
 >3W3WB 69 XRAY 2.20 0.217 0.256 no Protein STE12 <UNP STE12_YEAST> [SACCHAROMYCES CEREVISIAE]
 PRRRTVGMKSSQGNVPTGNKQSVGKSAKISKPLHIKTSAYQKQYKINLETARPASAGED
 SAHPDKNKE
 >3GVAA 116 XRAY 2.00 0.221 0.265 no Alkyltransferase-like protein 1 <UNP ATL1_SCHPO>
 [SCHIZOSACCHAROMYCES POMBE]
 MRMDEFYTKVYDAVCEIPYGVSTYGEIARYVGMPSYARQVGQAMKHLHPETHVPWHRVI
 NSRGTISKRDISAGEQRQKDRLEEVEIYQTSLEGEYKLNLPYMWKPGSHHHHHH
 >3GV6A 58 XRAY 1.76 0.214 0.266 no Chromobox protein homolog 6 <UNP CBX6_HUMAN> [HOMO SAPIENS]
 ERVFAAESIIKRRIRKGRIEYLVKWKGAIKYSTWEPEENILDSRLIAAFEQKERERE
 >30MYA 52 XRAY 1.30 0.151 0.173 no Protein traM <UNP TRAM8_ECOLX> [ESCHERICHIA COLI]
 MPKIQTYYNNVYEQITDLVTIRKQEGIEEASLSNVSSMLLEGLRVYMIQQ
 >4H9NC 212 XRAY 1.95 0.209 0.209 no Death domain-associated protein 6 <UNP DAXX_HUMAN> [HOMO
 SAPIENS]
 SPRTGRSRRQIQRLLEQLLALYVAEIRRLQEKELDLSELDDPD SAYLQEARLKRKLIRLFG

RLCELKDCSSLTGRVIEQRIPYRGTRYPEVNRRIERLINKPGPDTFPDYGDVLRAVEKAA
 ARHSLGLPRQQLQMAQDAFRDVGIRLQERRHLDLIYNFGCHLTDDYRPGVDPALSDPVL
 ARRLRENRLSAMSRLDEVISKYAMLQDKSEEG
 >3FHW 115 XRAY 1.90 0.276 0.289 no Primosomal replication protein n <UNP PRIB_BORPA>
 [BORDETELLA PARAPERTUSSIS]
 MNTLELSARVLECGAMRHTPAGLPALELLLVHESEVVEAGHPRRVELTISAVAGDLALL
 LADTPLGTEMQVQGFAPARKDSVKVHLHLQQARRIAGSMGRDPLVGLEHHHHHH
 >3RCOA 89 XRAY 1.80 0.178 0.230 no Tudor domain-containing protein 7 <UNP TDRD7_HUMAN> [HOMO
 SAPIENS]
 ENLYFQGMLEGLVSKMLRAVLQSHKNGVALPRLQGEYRSLTGDWIPFKQLGFPTLEAYL
 RSVPAVVRIETSRSGEITCYAMACTETAR
 >1ZP7A 206 XRAY 2.25 0.219 0.269 no Recombination protein U <UNP RECU_BACSU> [BACILLUS SUBTILIS]
 MIRYPNGKTFQPKHSVSSQNSQKRAPSYSNRGMTLEDDLNETNKYYLTNQIAVIHKKPTP
 VQIVNVHYPKRSAAVIKEAYFKQSSTTDYNGIYKGRYIDFEAKETKNKTSFPLQNFHDHQ
 IEHMKQVKAQDGICFVIISAFDQVYFLEADKLFYFWRKEKNGRKSIRKDELEETAYPIS
 LGYAPRIDYISIIIEQLYFSPSSGAKG
 >2F2EA 146 XRAY 1.85 0.181 0.251 no PA1607 <UNP Q9I3B4_PSEAE> [PSEUDOMONAS AERUGINOSA]
 MVKRTSHKQASCPVARPLDVIGDWSMLIVRDAFEGLTRFGEFQKSLGLAKNILAARLRN
 LVEHGMVAVPAESGSHQEYRLTDKGRALFPLLVAIRQWGEDYFFAPDESHVRLVERDSG QVPVRLQVRAGDGSPLAEDTRVSRD
 >1F2RI 100 NMR NA NA NA no INHIBITOR OF CASPASE-ACTIVATED DNASE <UNP DFFA_MOUSE> [MUS
 MUSCULUS]
 MELSRGASAPDDVRPLKPCLLRRNHSRDQHGVAASSLEELRSKACELLAIDKSLTPIT
 LVLAEDGTIVDDDDYFLCLPSNTKFVALACNEKWYNDSD
 >4JLXA 366 XRAY 2.00 0.189 0.215 no Uncharacterized protein <UNP I3LM39_PIG> [SUS SCROFA]
 GAMGAWKLQTVLEKVRSLRHEISEAAEVNWNVVEHLLRRLQGGSEFEKGVALLRTGSYYE
 RVKISAPNEFDVMFKLEVPRIQLEEYCNSGAHYFVKFRNPGGNPLEQFLEKEILSASKM
 LSKFRKIIKEEIKNIEDTGVTVRKRGRSPAVTLLISKPKESISVDIILALESKSSWPAST
 QKGLPISQWLGAQVKNLKRQPFYLVPHAKEGSGFQEETWRLSFSHIEKDILKNHGQSK
 TCCEIDGVKCCRKECLKMKYLLQLKKKFGNRRELAKFCSYHVKTAFHVCTQDPHDNQ
 WHLKNLECCFDNCVAYFLQCLKTEQLANYFIPGVNLFSRDLIDKPSKEFLSKQIEYERNN
 GPPVFW
 >2JD3A 130 XRAY 2.80 0.239 0.277 no STBB PROTEIN <UNP Q9S101_ECOLI> [ESCHERICHIA
 COLI]
 MDDERKRKKYTLYLHPEKAADFQTLAIESVPRSERGELFRNAFISGMALHQLDPRLPVL
 LTAILSEEFSAQVVTLLSQTTGWKPSQADIRAVLTELGASQSVEKMPPSATDSVQEAMN
 DVRLKMKKLF
 >3KZ5A 52 XRAY 1.58 0.198 0.234 no Protein sopB <UNP SOPB_ECOLI> [ESCHERICHIA COLI]
 GSHMSSRHQFAPGATVLYKGDKMVLNDRSRVPTCEIEKIEAILKELEKPAP
 >4JW3A 120 XRAY 2.60 0.226 0.264 no Neocarzinostatin <UNP NCZS_STRML> [STREPTOMYCES
 MALAYENSIS]
 AAPTATVTPSSGLSDGTVVKVAGAGLQAGTAYWVAQWARVDTGVWAYNPADNSSVTADAN
 GSASTSLTVRRSFEGLFDGTRWGTVDCTTAACQVGLSDAAGNGPEGVAISFAHHHHHHH
 >1DMLA 319 XRAY 2.70 0.230 0.281 no DNA POLYMERASE PROCESSIVITY FACTOR <UNP VPAP_HHV11>
 [HUMAN HERPESVIRUS 1]
 MTDSPGGVAPASVEDASDASLGQPEEGAPCQVVLQGAELNGILQAFAPLRTSLDSSLV
 MGDGRGILIHNTIFGEQVFLPLEHSQFSRYRWRGPTAAFLSLVDQKRSLLSVFRANQYPDL
 RRVELAITGQAPFRTLQRIWTTTSDGEAVELASETLMKRELTSFVVLVPQGTPDVQLRL
 TRPQLTKVLNATGADSATPTTFELGVNGKFSVFTTSTCVTFAAAREEGVSSSTSTQVQILS
 NALTKAGQAAANAKTVYGENTHRTFSVVDDCSMRAVLRRLQVGGGTLKFFLTTPVPSLC

VTATGPNASAVFLLKPQK
>3BTPA 556 XRAY 2.30 0.212 0.256 no Single-strand DNA-binding protein <UNP VIRE2_AGR5>
[AGROBACTERIUM TUMEFACIENS STR.]
MDPKAEGNGENITETAAGNVETSDFVNLKRQKREGVNSTGMSEIDMTGSQETPEHNMHGS
PTHTDDLGPRLDADMLDSQSSHVSSAQGNRSEVENELSNLFAKMALPGHDRRTDEYILV
RQTGQDKFAGTTKCNLDHLPTKAEFNASCLYRDGVGNYPPLAFERIDLPEQLAAQLH
NLEPREQSKQCFQYKLEVWNRHAEMGITGTDIFYQTDKNIKLDRNYKLRPEDRYIQTEK
YGRREIQKRYEHQFQAGSLLPDILIKTPQNDIHFSYRFAGDAYANKRFEEFERAIKTKYG
SDTEIKLKS KSGIMHDSKYLESWERGSADIRFAEFAGENRAHNKQFPAATVNMGRQPDGQ
GGMTRDRHVSVDYLLQNLNPSFWTQALKEGKLWDRVQVLARDGNRYMSPSRLEYSDEPHF
TQLMDQVGLPVSMGRQSHANSVKFEQFDRQAAVIVADGPNLREVPLSPEKLQQLSQKDV
LIADRNEKGQRTGTYNVVEYERLMMKLPSDAAQLLAEPSDRYSRAFVRPEPALPPISDS
RRTYESRPRGPTVNSL
>3BTPB 63 XRAY 2.30 0.212 0.256 no Protein virE1 <UNP VIRE1_AGR5> [AGROBACTERIUM TUMEFACIENS
STR.]
MVIKLNANKNMPVLAVEKPQEIHKELSDHHQSNGFTSLDLEMIELNFVLHCPLPEEN
LAG
>1YUAA 122 NMR NA NA NA no TOPOISOMERASE I <UNP TOP1_ECOLI> [ESCHERICHIA COLI]
MNGEVAPPKEDPVPLPELPCEKSDAYFVLRDGAAGVFLAANTFPKSRETRAPLVEELYRF
RDLRLEKRLYLADAPQQDPEGKTMVRFSRKTKQQYVSSEKDGKATGWSAFYVDGKWVEG
KK
>1YUIA 54 NMR NA NA NA no GAGA-FACTOR <UNP GAGA_DROME> [DROSOPHILA MELANOGASTER]
PKAKRAKHPPGTEKPRSRSSQSEQPATCPICYAVIRQSRNLRHLELRHFAKPGV
>3V6TA 499 XRAY 1.85 0.206 0.222 no dHax3 <PDB 3V6T> [XANTHOMONAS]
LEHHHHHHQWSGARALEALLTVAGELRGPLQLDTGQLLKIARKGGVTAVEAVHAWRNAL
TGAPLNLTPQVVAIASHDGKKQALETVQRLLPVLCQAHGLTPQQVVAIASHDGKKQALE
TVQRLLPVLCQAHGLTPEQVVAIASHDGKKQALETVQALLPVLCQAHGLTPEQVVAIASN
GGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPQ
QVVAIASNNGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLC
QAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPQQVVAIASHDGKKQALETV
QRLLPVLCQAHGLTPEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDG
GKQALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKPALESIVAQLSRPDALAALTNDH
LVALACLGGPALDAVKKL
>1V63A 101 NMR NA NA NA no Nucleolar transcription factor 1 <UNP UBF1_MOUSE> [MUS MUSCULUS]
GSSGSSGPKPPMNGYQKFSQELLSNGELNHLPLKERMVEIGSRWQRISQSQKEHYKKLA
EEQQRQYKVHLDLWVKSLSPPQDRAAYKEYISNKRKSGPSSG
>3V68A 252 XRAY 1.56 0.199 0.225 no Putative uncharacterized protein <UNP Q8TZE5_PYRFU>
[PYROCOCUS FURIOSUS]
MIERILEFTAKHEEWIVGENVEDFTNENIAMFLSRVSNTVSSKIPGYLGEKIDVNGLLSI
KIEGSLEELKALISPKVSRQIGRLVMEDDKLKLKLLVEVAKAVLTREILKNELPIEFPG
GKIEGLKIQPRYEEDHINFRTARYGSWIVVKRMIIDEKTPLLDIARLLASINETAVNKKID
FADVDDKKIVEYFGGFKVKKEEIKEIVQLFREFKGFNEFEVRYAAREMLSKLGLKVDVP
SKNLEKYLEKAG
>3V62C 69 XRAY 2.90 0.187 0.237 no ATP-dependent DNA helicase SRS2 <UNP SRS2_YEAST>
[SACCHAROMYCES CEREVISIAE]
SHNPDDTTVDNRPIISNAKFLADAAMKKTQKFSKKVKNEPASSQMDIFSQLSRAKKKSKL
NNGEIIVID
>2FUFA 134 XRAY 1.45 0.170 0.189 no Large T antigen <UNP TALA_SV40> [SIMIAN VIRUS]

40] GSKVEDPKDFPSELLSFLSHAVFSNRTLACFAIYTTKEKAALLYKKIMEKYSVTFISRHN
SYNHNILFFLTTPHRRVSAINNYAQKLCTFSFLICKGVNKEYLMYSALTRDPFVSIEESL
PGGLKEHDFNPES

>4GFA 196 XRAY 1.95 0.212 0.239 no Nucleoid occlusion factor SlmA <UNP SLMA_VIBCH> [VIBRIO
CHOLERA 01 BIOVAR EL TOR]
MAGNKKINRREEILQALAEMLESNEGASRITTAKLAKQGVSEAAALYRHFPSKTRMFEG
IEFIEESLSMRINRIFDEEKDTLNRIRLVMQLLLAFAERNPGLTRILSGHALMFENERLR
DRINQLFERIETSLRQILRERKLREGKSFPVDENILAAQLLGQVEGSLNRFVRSDFKYLP
TANFDEYWALLSAQIK

>2GFUA 134 NMR NA NA NA no DNA mismatch repair protein MSH6 <UNP MSH6_HUMAN> [HOMO
SAPIENS]
KAKNLNGGLRRSVAPAAPTSSDFSPGDLVWAKMEGYPPWPSLVYNHPFDGTFIREKGKSV
RVHVQFFDDSPTRGWVSKRLLKPYTGSKSKEAQKGGHFYSAPKPEILRAMQRADEALNKDK
IKRLELAVSDEPSE

>2YRQA 173 NMR NA NA NA no High mobility group protein B1 <UNP HMGB1_HUMAN> [HOMO SAPIENS]
GSSGSSGMKGDPKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMS
AKEKGKFEDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLCSEYRPKI
KGEHPGLSIGDVAKKLGEMWNNTAADKQPYEKAAKLKEYEKDIAAYRAKG

>4EOGA 480 XRAY 2.30 0.227 0.250 no Putative uncharacterized protein <PDB 4EOG> [PYROCOCCUS
FURIOSUS]
MGMRLVTTWGNPFQWEPITYEYRGIVKSRNTLPILVKTLEPERILILVADTMANYYDS
GKNKPEIEEKSFSSYSEVVEDTKERILWHIKEEVIEELREEDPELAKKIENMLKDERITI
EVLPGVGVGFNITVEGEMLDFFYYATYKLAEWLPVQNNLEVYLDLTHGINFMPTFTYRAL
RNLLGLLAYLYNVKFEIVNSEPYPLGVSQEIREDTILHIREIGGVVRPRPQYSPVEGKL
YWNAFISSVANGFPLVFASFYPNIRDVEDYLNKKLEEFVGVGEREDGKPYVKREKAL
DRSFKNASKLYALRVFNTKFQNPKEVPIDEEIMEISKIFESLPRIGIILERQVEWLRN
LVYGRWYENGEQKIKKGLLEIIKDKKDKRKEAEALKKGKTISLAAAKLTRIFSPSPGER
IETIESPNVVRNFIAHSGFEYNIVYKYDRLSDRLYFFYKDKKAAANLAYEALLYRGEKE

>3P7NA 258 XRAY 2.10 0.266 0.329 no Sensor histidine kinase <UNP Q2NB98_ERYLH> [ERYTHROBACTER
LITORALIS]
MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDHPTMGQDRPIDGSGAPGADDTRVEVQP
PAQWVLDLIEASPIASVSDPRLADNPLIAINQAFTDLTGYSSEECVGRNCRFLAGSGTE
PWLTDKIRQGVREHKPVLVEILNYKKDGTFFRNAVVLVAPIYDDDELLYFLGSQVEVDDD
QPNMGMARREAAEMLKTLSPRQLEVTTLVASGLRNKEVAARLGLSEKTVKMRGLVMEK
LNLKTSADLVRIAVEAGI

>4K2JA 140 XRAY 2.05 0.184 0.226 no KSHV (HHV-8) latency-associated nuclear antigen (LANA)
<UNP Q9DUNO_HHV8> [HUMAN HERPESVIRUS 8]
SHPRYQQPPVPYRQIDDCPAKARPQHIFYRRFLGKDGRDPKCQWKFAVIFWGNDPYGLK
KLSQAFQFGGVKAGPVSLPHPGPDQSPITYCVYVYCQNKDTSKKVQMARLAWEASHPLA
GNLQSSIVKFKKPLPLTQPG

>3K2AA 67 XRAY 1.95 0.216 0.239 no Homeobox protein Meis2 <UNP MEIS2_HUMAN> [HOMO SAPIENS]
GSGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQDTGLTILQVNNWFNARRRIVQPM
IDQSNRA

>4DAMA 128 XRAY 1.70 0.155 0.192 no Single-stranded DNA-binding protein 1 <UNP SSB1_STRCO>
[STREPTOMYCES COELICOLOR] MRGSHHHHHHGSMEIMICAVGNVATTPVFRDLANGPSVRFRLAVTARYWDREKNAWTDG
HTNFFTWWANRQLATNASGSLAVGDPVVVQGRLKVRTDVREGQRTSADIDAVAIGHDLA
RGTAAFRR

>4I99A 354 XRAY 2.30 0.221 0.236 no Chromosome partition protein Smc <UNP SMC_PYRFU>

[PYROCOCUS FURIOSUS]
 MPYIEKLELKGFSYGNKKVIVPFSKGFATVGVANGSGKSNIGDAILFVLGGLSAKAMRA
 SRISDLIFAGSKNEPPAKYAEVAIYFNEDRGFPIDEDEVVIRRRVYPDGRSSYWLNGRR
 ATRSEILDILTAAMISPDGYNIVLQGDITKFIKMSPLERRLLIDDISGIAEYDSKKEKAL
 EEEKEKKNVFMRTFEAISRNFSFIFAKLSPGGSARLILENPDPFSGGLEIEAKPAGKDV
 KRIEAMSGGEKALTALAFVFAIQKFKPAPFYLFDEIDAHLLDANVKRVADLIKESSESQ
 FIVITLDRVMMANADKIIGVSMRDGVSKVVSLSEKAMKILEEIRKKQGWHEGN
 >4I99C 87 XRAY 2.30 0.221 0.236 no Putative uncharacterized protein <UNP Q8TZY3_PYRFU>
 [PYROCOCUS FURIOSUS]
 KKVEIDEEIFVIDDFRVDIEKYVEELYKVVKIYEKTGTPIKFWDLVPDVEPKIIARTFL
 YLLFLENMGRVEIIQEEPFGIILVVP
 >4GNXA 114 XRAY 2.80 0.222 0.278 no Putative uncharacterized protein <UNP Q4P6U8_USTMA>
 [USTILAGO MAYDIS]
 MEKPTPLINSSMLGQYVGQTVRIVGKVHKVTGNTLLMQTSDLG NVEIAMTPDSVSSSTF
 VEVTKGVSDAGSSFAQNIREFTTVDCGHDVDTLVENVVQISAAFPNLFSDST
 >4GNXB 136 XRAY 2.80 0.222 0.278 no Putative uncharacterized protein <UNP
 Q4PBD4_USTMA> [USTILAGO MAYDIS]
 GKKAGNNTLRPVTIRQILNAEQPHPD AEFILDGAELGQLTFVAVVRNISR NATNVAYSVE
 DGTGQIEVRQWLDSSSDSSKASEIRNNVYVRVLGTLKSFQNRRISSGHMRPVIDYNEV
 MFHRLEAVHAHLQVTR
 >4GNXC 444 XRAY 2.80 0.222 0.278 no Putative uncharacterized protein <UNP Q4P407_USTMA>
 [USTILAGO MAYDIS]
 MPIYPIEGLSPYQNRWTIKARVTSKSDIRHWSNQRGEGKLFSVNLDDSGEIKATGFNDA
 VDRFYPLLQENHVYLISKARVNIKKQFSNLQNEYEITFENSTEIEECTDATDVPEVKYE
 FVRINELESVEANQQCDVIGILDSYGELSEIVSKASQRPVQKRELTLVDQGNRSVKLTW
 GKTAETFPNTAGVDEKPVLA FKGVKVGDFGGRSLSMFSSSTMLINPDITESHVLRGWYDN
 DGAHAQFQPYTNGVG GGGAMGGGAGANMAERRTIVQVKDENLGMSEKPDYFNVRATVVY
 IKQENLYYTACASEGNKKVNL DHENNRCEKCDRSYATPEYRYILSTNVADATGQMWLS
 GFNEDATQLIGMSAGELHKLREESEFS AALHRAANRMYMFNCRAKMDTFNDTARVRYT ISRAAPVDFAKAGMELVD AIRAYM
 >3C1YA 377 XRAY 2.10 0.223 0.257 no DNA integrity scanning protein disA <UNP
 DISA_THEME> [THERMOTOGA MARITIMA]
 MGSSHHHHHHSSGLVPRGSHMGVKS LVPQELIEKIKLISPGTELKALDDIINANFGALI
 FLVDDPKKYEDVIQGGFWLDTDFSAEKL YELSKMDGAIVLSEDITKIYYANVHLVPDPTI
 PTGETGTRHRTAERLAKQTGKVVI AVSRRRNIIISLYYKNKYVNVQVDFLISKVTQAIST
 LEKYKDNFNKLLSELEVL ELENRVTLADVVRTLAKGFELLRIVEEIRPYIVELGEEGLA
 RMQLRELTEDVDDLVL LMDYSSEEVEEETAQNILQDFITRREPSPISISRVLG YDVQQ
 AAQLDDVLVSARGYRLKTVARIPLSIGYNVVMFKTLDQISKASVEDLKKVEGIGEKRA
 RAISESISSLKHKRTSE
 >1C1KA 217 XRAY 1.45 0.205 0.253 no BPT4 GENE 59 HELICASE ASSEMBLY PROTEIN <UNP VG59_BPT4>
 [ENTEROBACTERIA PHAGE T4]
 MIKLMPAGGERYIDGKSVYKLYLMIKQH MNGKYDVIKYNWCMRVSDAAYQKRRDKYFFQ
 KLSEKYKLKELALIFISNLVANQDAWIGDISDADALVFYREYIGRLKQIKFKFEEDIRNI
 YYFSKKVEVSFAKEIFEYNPKVQSSYIFKLLQSNII SFETFILLDSFLNIIDKHDEQTDN
 LVWNNYSIKLKAYRKILNIDSQKAKNVFIETVKSCKY
 >3C1DA 159 XRAY 1.80 0.182 0.223 no Regulatory protein recX <UNP RECX_EC057> [ESCHERICHIA COLI]
 GPAYARLLDRAVRILAVRDHSEQELRRKLAAPIMGKNGPEEIDATAEDYERVI AWCHEHG
 YLDDSRFVARFIASRSRKGYPARIRQELNQKGISREATEKAMREADIDWAALARDQATR
 KYGEPLPTVFSEKVKIQRFLLYRGYLMEDIQDIWRNFAD

>2QLCA 126 XRAY 2.30 0.219 0.274 no DNA repair protein radC homolog <UNP RADC_CHLTE> [CHLOROBIVUM TEPIDUM TLS]
MNLKVKGARDVFEYMKGRIPDETKEHLFVFLSTKNQILRHETITIGTLTASLIHPREIF
KAAIRESAHSIILVHNHPSGDVQPSNADKQVTSILKKAGDLLQIELLDHVIVGNNDWFSF
RDHALL

>1TZYB 126 XRAY 1.90 0.190 0.222 no Histone H2B <UNP H2B_CHICK> [GALLUS GALLUS]
MPEPAKSAPAPKKGSKKAVTKTQKKGDKKRKKSRKESYSIYVYKVLKQVHPDTGISSKAM
GIMNSFVNDIFERIAAGEASRLAHYNKRSTITSREIQTAVRLLLPGELAKHAVSEGKAVT
KYTSSK

>1MOJA 182 XRAY 1.90 0.151 0.182 no Dps-like ferritin <UNP DPSA_HALN1> [HALOBACTERIUM SALINARUM]
MSTQKNARATAGEVEGSDALRMDADRAEQCVDALNADLANVYVLYHQLKKHHWNVEGAEF
RDLHLFLGEAAETAEEVADELAERVQALGGVPHASPETLQAEASVDVEDEDVYDIRTSLA
NDMAIYGDIIETATREHTELAENLGDHATAHMLREGLIELEDDAHHIEHYLEDDTLVTQGA
LE

>3BS3A 76 XRAY 1.65 0.185 0.219 no Putative DNA-binding protein <UNP Q5LGD2_BACFN> [BACTEROIDES FRAGILIS]
SNAMSNNQMMNLRIKVVLAQKQRTNRWLAEQMGKSENTISRWCNKSQPSLDMLVKVAE
LLNVDPRLINGIKI

>3EYIA 72 XRAY 1.45 0.157 0.194 no Z-DNA-binding protein 1 <UNP ZBP1_HUMAN> [HOMO SAPIENS]
HMASPQFSQQREEDIYRFLKDNQPQALVIAQALGMRTAKDVNRDLYRMKSRHLLDMDEQ
SKAWTIYRWTIY

>3VZHA 244 XRAY 1.70 0.185 0.226 no Putative uncharacterized protein <UNP Q99YS3_STRP1> [STREPTOCOCCUS PYOGENES SEROTYPE M1]
GHMYRSRDFYVRVSGQALFTNPATKGGSERSSYSVPTRQALNGIVDAIYKPTFTNIVT
EVKVINQIQTELQGVALLHDYSADLSYVSYSLSVYLIKHFHVWNEGRKDLNSDRLPK
HEAIMERSIRKGGRRDVLGTRCLGLVDDISQEEYETTVSYNGVNIDLGIMFHSFAYP
KDKKTPLKSYFTKTMKNGVITFKAQSECDIVNTLSSYAFKAPEEIKSVNDECMEYDAME
KGEN

>3MU6A 71 XRAY 2.43 0.231 0.251 no Myocyte-specific enhancer factor 2A <UNP MEF2A_HUMAN> [HOMO SAPIENS]
GRKKIQITRIMDERNRQVTFTRKRFGLMKKAYELSVLCDCEIALIIFNSSNKLQYASTD
MDKVLLKYTAY

>2D9HA 78 NMR NA NA NA no Zinc finger protein 692 <GB NP_060335> [HOMO SAPIENS]
GSSGSSGLQCEICGFTCRQKASLNWHQRKHAETVAALRFPCEFCGKRFEKPDVAAHRSK
SHPALLAPQESSGPSSG

>3VKOA 114 XRAY 1.88 0.184 0.230 no Transcriptional regulator <UNP Q7DDD9_NEIMB> [NEISSERIA MENINGITIDIS]
MMGNKLTLPALPDEQDLRAVLAYNMRLFRVNGWSQEELARQCGLDRTYVSAVERKRW
IALSNIEKMAAALGVAAYQLLPPQERLKLMTNSADTRQMPSESILEHHHHH

>3VEAA 151 XRAY 2.55 0.222 0.250 no Macrodomein Ter protein <UNP MATP_YERPE> [YERSINIA PESTIS]
MKYQQLENLESGWKWAYLVKKHREGEAITRHIENSAAQDAVEQLMKLENEPVKVQEWIDA
HMNVNLATRMKQTIARRKRHFNAEHQHTRKKSIDLEFLVWQRLAVLARRRGNTLSDTV
QLIEDAERKEKYASQMSSLKQDLKDILDKEV

>3V9RA 90 XRAY 2.40 0.242 0.290 no Uncharacterized protein YOL086W-A <UNP Y0086_YEAST> [SACCHAROMYCES CEREVISIAE]
MNDDEDRAQLKARLWIRVEERLQQVLSSEDIKYTPRFINSLELAYLQLGEMGSDLQAF

RHAGRGVVKSDMLMLYLKQPDQERVTTQE
>1P4EA 429 XRAY 2.70 0.236 0.275 no Recombinase FLP protein <UNP FLP_YEAST> [SACCHAROMYCES CEREVISIAE]
SQFDILCKTPPKVLVRQFVERFERPSGEKIASCAAELTYLCWMITHNGTAIKRATFMSYN
TIISNSLSFDIVNKSQFKYKTQKATILEASLKKLIPAWFTIIPYNGQKHQSDITDIVS
SLQLQFESSEADKGNSSHKKMLKALLSEGESIWEITEKILNSFEYTSRFTKTKTLVQFL
FLATFINCGRFSDIKNVDPKSFKLVLQNKYLGVI IQCLVTETKTSVSRHIYFFSARGRIDP
LVYLDEFRLRNSEPVLRVNRGTGNSSSNKQEQYQLLKDNLVRSYNKALKKNAPYPIFAIKNG
PKSHIGRHLMTSFLSMKGLTELTVVGNFSDKRASAVARTTYTHQITAIPDHYFALVSRY
YAYDPISKEMIALKDETNPIEEWQHIEQLKGSAGSIRYPANGIISQEVLDYLSSYINR
RIGHHHHHH
>4ABXA 175 XRAY 2.04 0.203 0.250 no DNA REPAIR PROTEIN REC N <UNP REC_N_DEIRA> [DEINOCOCCUS RADIODURANS]
GIDPFTQQRERARQIDLLAFQVQEISEVSPDPGEEGLNTELSRLSNLHTIAQAAAGGVEL
LSDGDLNAAGLIGEAVRALNAGAKYDETMQLQNELRAALESVQAIAGELRDVAEGSAAD
PEALDRVEARLSALSCLKNKYGTLEDVVEFGAAAEELAGLEEDERDAGSLQAD
>3GIOA 186 XRAY 2.40 0.233 0.241 no Putative uncharacterized protein <UNP 025318_HELPY> [HELICOBACTER PYLORI]
MGSSHHHHHSSGLVPRGSHMPNTSQRNSFLQDVPYWMQNRSEYITQGVDSHIVDGKK
TEEIEKIATKRATIRVAQNIVHKLKEAYLSKTNRIKQKITNEMFIQMTQPIYDSL MNVDR
LGIYINPNNEEVFALVRARGFDKDALSEGLHKMSLDNQAVSILVAKVEEIFKDSVNYGDV
KVPIAM
>2KWQA 92 NMR NA NA NA no Protein MCM10 homolog <UNP MCM10_XENLA> [XENOPUS LAEVIS]
GPMGMQSIREQSCRVTCTCKYTHFKPKETCVSENHDFHWHNGVKRFFKCPCGNRTISL
DRLPKKHCTCGLFKWERVGMLEKGTGPKLGG
>2KW3A 68 NMR NA NA NA no DNA-binding protein RFX5 <UNP RFX5_HUMAN> [HOMO SAPIENS]
GAGEPTTLLQRLRGITISKAVQNKVEGILQDVQKFSNDKLYLYLQLPSGPTTGDKSSEPS
TLSNEEYM
>2KW3C 62 NMR NA NA NA no Regulatory factor X-associated protein <UNP RFXAP_HUMAN> [HOMO SAPIENS]
GHGTSGFGRPARPTLLEQVLNQKRLSLLRSPEVVQFLQKQQQLLNQQVLEQRQQQFPGT
SM
>1KW4A 89 XRAY 1.75 0.220 0.234 no Polyhomeotic <UNP PHP_DROME> [DROSOPHILA MELANOGASTER]
METKRVNGTDRPPISWSVDDVSNFIRELPGCQDYVDDFIQQEIDGQALLRLKEKHLVNA
MGMKLGPAKIVAKVESIKEVRDHHHHHH
>1KU9A 152 XRAY 2.80 0.245 0.280 no hypothetical protein MJ223 <UNP Y1563_METJA> [METHANOCALDOCOCUS JANNASCHII]
MIIMEEAKKLIIELFSELAKIHGLNKS VGAVYAILYLSDKPLTISDIMEELKISKGNVSM
SLKKLEELGFVRKVVWIKGERKNYYEAVDGFSSIKDIAKRKHDLIAKTYEDLKKLEECNE
EEKEFIKQKIKGIERMKKISEKILEALNDLDN
>2AQLA 173 XRAY 2.30 0.273 0.273 no Mortality factor 4-like protein 1 <UNP M04L1_HUMAN> [HOMO SAPIENS]
MNRVEVKVKIPEELKPWLVDWDLITRQKQLFYLPKKNVDSILEDYANYKKS RGN TDNK
EYAVNEVVAGIKEYFNVLGTQLLYKFERPQYAEILADHPDAPMSQVYGAPHLRL FVRI
GAMLAYTPLDEKSLALLLNLYLHDFLKYLA KNSATLFSASDYEVAPPEYHRKAV
>2L1PA 83 NMR NA NA NA no DNA-binding protein SATB1 <UNP SATB1_HUMAN> [HOMO SAPIENS]
MGHHHHHHSHMLPPEQWSHTTVRNALKDLLKDMNQSSLAKECPLSQSMISSIVNSTYYAN
VSAAKCQEFGRWYKHFKKTKDMM
>2NOGA 173 XRAY 2.00 0.216 0.274 no ISWI protein <UNP Q6DFM0_XENLA> [XENOPUS LAEVIS]

MVSEPKVPKAPRPPKQPNVQDFQFFPPRLFELLEKEILYYRKTIGYKVP RNPDL PNSAQV
 QKEEQLKIDEAEPLNDEELEEKEKLLTQGFTNWNKRDFNQFIKANEKWGRDDIENIAREV
 EGKTPEEVIEYSVFWERCNELQDIEKTMQUIERGEARIQRRISILEHHHHH
 >3N07A 80 XRAY 1.40 0.198 0.212 no Putative plasmid related protein <UNP Q6EEF9_LEIXC>
 [LEIFSONIA
 XYLI SUBSP. CYNODONTIS]
 GPEASARSEVKMTVTVGEERRARLTAYTLTHLQEGHRTFSGFIAAALDAEVQRLEQRYN
 EGRRFENAERGVTRGRPLGS
 >3KDEC 77 XRAY 1.74 0.179 0.216 no Transposable element P transposase <UNP PELET_DROME>
 [DROSOPHILA MELANOGASTER]
 MKYCKFCCKAVTGKLIHVPKCAIKRKLWEQSLGCSLGENSQICDTHFNDSQWKAAPAKG
 QTFKRRRLNADAVPSKV
 >2DQBA 376 XRAY 2.20 0.223 0.286 no Deoxyguanosinetriphosphate triphosphohydrolase, putative
 <UNP
 Q5SL81_THET8> [THERMUS THERMOPHILUS]
 MRFSREALLELEASRLAPYAQKARDTRGRAHPEPESLYRTPYQKDRDRILHTTAFFRRELY
 KTQVLPGWAGDYRTRLTHTLEVAQVSRSIARALGLNEDLTEAIALSHDLGHPPFGHTGE
 HVLNALMQDHGGFEHNAQALRILTHLEVRYPGFRGLNTYEVLEGIATHEAAYSPGFKPL
 YEGQGTLEAQVVDLSDAIAYAHDLDGFRAGLLHPEELKEVELLQALALEEGLDLLRLP
 ELDRRLVLRQLLGYFITAAIEATHRRVEEAGVQSAEAVRRHPSRLAALGEEAEKALKALK
 AFLMERFYRHPEVLRRERRKAEAVLEGLFAAYTRYPELLPREVQAKIPEEGLERAVCDYIA
 GMTDRFALEYRRLSP
 >4BJIA 215 XRAY 1.45 0.152 0.170 no TRANSCRIPTION FACTOR TAU SUBUNIT SFC1 <UNP SFC1_SCHPO>
 [SCHIZOSACCHAROMYCES POMBE]
 GAMGKGQCRVWIITNMGVESVPTCRHSLGEPSTIQEVIEALKPLFEKRPVWTRALL
 NHLDPSTHYLKFALPYLSYLWTSGPFRDITYTRFGYDPRKDSNAAAYQALFFKLKLNKGK
 KGTKTHVFDGKTLFPTNRVYQVCDIVDPTIAPLLKDTQLRSECHRTGWYRSGRYKVRD
 LMREKLFALIEGEMPSEVAVNMILNAEEVEESDRY
 >4BJ1A 319 XRAY 2.94 0.199 0.229 no PROTEIN RIF2 <UNP RIF2_YEAST> [SACCHAROMYCES CEREVISIAE]
 GGGRDVHVYQKFKSMALQELGTNYLSISYVPSLSKFLSKNLRS MKNCIVFFDKVEHIHQ
 YAGIDRAVSETLSLVDINVIIEMNDYLMKEGIQSSKSKECIESMGQASYSGQLDFEASE
 KPSNHTSDLMMVMRKINDESIDHIVYFKFEQLDKLSTSTIIEPSKLTEFINVLSVLEK
 SNNIAFKVLIYSNNVSISSLLSTSLKKLNTKYTVFEMPILTCAQEQEYLKKMIKFTFDS
 GSKLLQSYNSLVTCLNNKESNLAIFFEFLKVFPHPFTYLFNAYTEIIVQSRTFDELLDK
 IRNRLTIKNYPHSAYNFKK
 >4OUOA 73 XRAY 1.40 0.199 0.238 no Replication protein A 32 kDa subunit <UNP RFA2_HUMAN>
 [HOMO SAPIENS]
 GPGSANGLTVAQNQVLNLKAXPRPEGLNFQDLKNQLKHMVS SSIKQAVDFLSNEGHIYS
 TVDDHFKSTDAE
 >1IGNA 246 XRAY 2.25 0.219 0.294 no RAP1 <PDB 1IGN> [SACCHAROMYCES CEREVISIAE]
 GALPSHNKASFTDEEDEFILDVVRKNPTRRTTHTLYDEISHYVPNHTGNSIRHRFRVYLS
 KRLEYVVEVDKFGKLVRRDDGNLIKTKVLPPSIKRKFSADEDYTLAIAVKKQFYRDLFQI
 DPDTGRSLITDEDTPTAIARRNMTMDPNHVPGSEPNFAAYRTQSRRGPIAREFFKHFAEE
 HAAHTENAWRDRFRKFLAYGIDDYISYYEAEKAQNREPEPMKNLTNRPKRPGVPTPGNY
 NSAAKR
 >2L93A 55 NMR NA NA NA no DNA-binding protein H-NS <UNP HNS_SALTY> [SALMONELLA TYPHIMURIUM]
 AARPAKYSYVDENGETKTWTGQGRTPAVIKKAMEEQGKQLEDFLIKELEHHHHH
 >3SJMA 64 XRAY 1.35 0.174 0.208 no Telomeric repeat-binding factor 2 <UNP TERF2_HUMAN> [HOMO
 SAPIENS] GSHMTNITKKQKWTVEESEWVKAGVQKYGEGNWAATSKNYPFVNRTAVMIKDRWRMTMKR

LGMN
 >1UD9A 245 XRAY 1.68 0.202 0.238 no DNA polymerase sliding clamp A <UNP PCNA1_SULTO>
 [SULFOLOBUS TOKODAII]
 AHIVYDDVRLKAI IQALLKLVD EALFDIKPEGIQLVAIDKAHISLIKIELPKEMFKEYD
 VPEEFKFGFNTQYMSKLLKAAKRKEEIIIDADSPEVVKLTLSGALNRVFNVNNIEVLPPE
 VPEVNLEFDIKATINASGLKNAIGEIAEVADTLLISGNEEKVVVKGEENKVEVEFSKDT
 GSLADIEFNKESSAYDVEYLNDIISLTKLSDYVKVAFADQKPMQLEFNMEGGGKVITYLL
 APKLS
 >3EUSA 86 XRAY 1.80 0.204 0.254 no DNA-binding protein <UNP Q5LU41_SILPO> [SILICIBACTER
 POMEROYI]
 QAMTKTLRTPEHVYLCQRLRQARLDAGLTQADLAERLDKPSFVAKVETRERRLDVIEFA
 KWMAACEGLDVVSEIVATIAEGRAQA
 >3VU9A 245 XRAY 1.75 0.185 0.231 no Platinum sensitivity protein 3 <UNP PSY3_YEAST>
 [SACCHAROMYCES
 CEREVISIAE]
 GSHMEVLKNIRIYPLSNFITSTKNYINLPNELRNLISEEQESKLGLHIIESDFKPSVAL
 QKLVNCTTGDEKILIIDIVSIWSQQKQRQHGAITYMNSLSCINITGLIVFLELLYDSPMDA
 LRRQCVDNFNFLRGIVIDNLSFLNFESDKNYDVINLSKFEKLFKILRKLREFLGCIIT
 KSFTPDFYNGIENTLVDKWSIKRSGVTLYPTKLPSYMKGMDLIYREVVDGRPQYRRI
 AALEE
 >3VU9B 213 XRAY 1.75 0.185 0.231 no Chromosome segregation in meiosis protein 2 <UNP
 CSM2_YEAST> [SACCHAROMYCES CEREVISIAE]
 MEYEDLELITIWPSTKNKLCQFIKQNSKEHVVTQLFFIDATSSFPLSQFQKLVPTLP
 ENVRIYENIRINTCLDLEELSAITVKLLQILSMNKINAQRGTEDAVTEPLKIILYINGLE
 VMFRNSQFKSSPQRSHELLRDTLKLKRVMGNDENENASIRTLLEFPKEQLLDYYLKKNN
 TRTSSVRSKRRRIKNGDSLAEYIWKYYADSLFE
 >1D4UA 111 NMR NA NA NA no NUCLEOTIDE EXCISION REPAIR PROTEIN XPA (XPA-MBD) <UNP
 XPA_HUMAN> [HOMO SAPIENS]
 MEFDYVICEECGFEMDSYLMDFDLPTCDDCRDADDKHKLITKTEAKQEYLLKDCDLEK
 REPPLKFIVKKNPHHSQWGMKLYLKLQIVKRSLEVWGSQEAL EEAKEVRQ
 >4JJNK 382 XRAY 3.09 0.233 0.255 no Regulatory protein SIR3 <UNP SIR3_YEAST>
 [SACCHAROMYCES CEREVISIAE]
 SAKTLKDLDGWQVIITDDQGRVIDDNNRRRSRKRGGENVFLKRISDGLSFGKGESVIFND
 NVTETYSVYLIHEIRLNTLNNVVEIWVFSYLRWFELKPKLYEQFRPDLIKEDHPLEFYK
 DKFFNEVNKSELYLTAELSEIWLKDFIAGQILPESQWNDSSIDKIEDRDFLVRYACEPT
 AEKFVPIDIFQIIRRVKEMEPKQSNEYLKRVSVVPSGQKTNRQVMHKMGVERSSKRLAKK
 PSMKKIKIEPSADDDVNNGNIPSRGTSTHGSISPQEEVSPNISSASPSALTSPDSS
 KILQKRSISKELIVSEEIPINSSEQESDYEPNNETSVLSSKPGSKPEKTSTELVDGREN
 VYANNPEVSDDGGLEEETDEVS
 >3V72A 335 XRAY 2.49 0.299 0.291 no DNA polymerase beta <UNP DPOLB_RAT> [RATTUS NORVEGICUS]
 MSKRKAPQETLNGGITDMLVELANFEKNVSQAIHKYNAYRKAASVIAKYPHKIKSGAEAK
 KLPVGVTKIAEKIDEFLATGKLRKLEKIRQDDTSSSINFLTRVTGIGPSAARKLVDEGIK
 TLEDLRKNEDKLNHHQRIGLYKFEDFEKRIPREMLQMQDIVLNEVKKLDPEYIATVCGS
 FRRGAESSGDMVLLTHPNFTSESSQPKLLHRVVEQLQKVRFITDTLSKGETKFMGVCQ
 LPSENDENEYPHRRIDIRLIPKDQYYCGVLYFTGSDIFNKNMRAHALEKGFTINKYTIRP
 LGVTGVAGEPLPVDSEQDIFDYIQWRYREPKDRSE
 >1XVPB 246 XRAY 2.60 0.180 0.234 no Orphan nuclear receptor NR1I3 <UNP NR1I3_HUMAN> [HOMO
 SAPIENS]
 PVQLSKEQEELIRTLGATHRMGMTMEQFVQFRPPAHLFIHHQPLPTLAPVLPLVTHFA

DINTFMVLQVIKFTKDLPVFRSLPIEDQISLLKGAIVEICHIVLNTTFCLQTQNFLCGPL
 RYTIEDGARVGFQVEFLELLHFHFGTLRKLQLQEPEYVLLAAMALFSPDRPGVTQRDEID
 QLQEEMALTLSYIKGQRRPRDRFLYAKLLGLLAELRSINEAYGYQIQHIQGLSAMMPL
 LQEICS
 >2LUA 52 NMR NA NA no Protein male-specific lethal-2 <UNP MSL2_DROME> [DROSOPHILA
 MELANOGASTER]
 SPPKPKCRCGISGSSNTLTTCRNSRCPCYKSYNSCAGCHCVGCKNPHKEDYV
 >2LUYA 97 NMR NA NA no Meiotic chromosome segregation protein P8B7.28c <UNP YORS_SCHPO>
 [SCHIZOSACCHAROMYCES POMBE]
 HMGKNDNDALIMCRCKVKGIDSYSTQWSKTFTFVRGRTVSVDPKVICRTCQPKQHD
 SIWCTACQQTGKINEFSKAQRHVLDPRCQICVHSQRN
 >1B8ZA 90 XRAY 1.60 0.215 0.236 no HISTONELIKE PROTEIN HU <UNP DBH_THEMA> [THERMOTOGA
 MARITIMA]
 MNKKELIDRVAKKAGAKKKDKVLILDITILETITEALAKGEKVQIVGFGSFEVRKAAARKG
 VNPQTRKPITIPERKVPKFKPGKALKEKVK
 >1WIJA 140 NMR NA NA no ETHYLENE-INSENSITIVE3-like 3 protein <UNP EIL3_ARATH> [ARABIDOPSIS
 THALIANA]
 GSSGSSGSQFVLQDLQDATLGSLLSSLMQHCDPPQRKYPLEKGTTPPWPTGNEEWWVKL
 GLPKSQSPPYRKPHDLKMMWVGVLTAVINHMLPDIAKIKRHVRQSKCLQDKMTAKESAI
 WLAVLNQEESLIQQSGPSSG
 >1Q87A 221 XRAY 2.32 0.220 0.274 no 39 kDa initiator binding protein <UNP Q95VR4_TRIVA>
 [TRICHOMONAS VAGINALIS] PVNTKRSNGTKRVEFPTTKSMCIGNSTPNEQETFRKVDIWFRLTQKTDGTVMRDFLI
 EKAAEYFKQPEQPKQNAIEVISAIMAPQEEQTKSKADLYKFLAMFGPYETIMLKIASLLL
 ISNNKGHWLTFDPQAEKNANNQRDSISGWFQNEPNCLILKTPTGIRKIWNKPLIEATGQ
 YLMDENGEKYDSWDKYFEMKPIETYLTAIPTFAPMHHHHHH
 >2HGVA 164 XRAY 2.30 0.168 0.244 no GTP-sensing transcriptional pleiotropic repressor codY
 <UNP CODY_BACSU> [BACILLUS SUBTILIS]
 GSSHHHHHMHALLQKTRIINSMQLAAAGKPVNFKEMAETLRDVIDSNIFVVSRRGKLLGY
 SINQQIENDRMKMLEDRQFPPEYTKNLFNVPETSSNLDINSEYTAFPVENRDLFQAGLT
 TIVPIIGGGERLGLTILSRLQDQFNDDDLILAEGATVVGMEIL
 >2OXOA 103 XRAY 2.00 0.234 0.289 no Integrase <UNP VINT_LAMBD> [UNIDENTIFIED PHAGE]
 MTLHSWLDREYKILASRGIKQKTLINYSKIKAIRRGLPDAPLEDITTKEIAAMLNGYID
 EGKAASAKLIRSTLSDAFREIAIEGHITTNHVAATRAAKSEVR
 >3LHKA 154 XRAY 2.20 0.206 0.249 no putative DNA binding protein MJ0014 <UNP Y014_METJA>
 [METHANOCALDOCOCUS JANNASCHII]
 SNAKIIIGYARVSFNAQKDDLERQIQLIKSYAEENGWDIQLKDIGSGLNEKRKNYKLLK
 MVMNRKVEKVIIAYPDRLTRFGFETLKEFFKSYGTEIVIIINKKHKTPQEELVEDLITIVS
 HFAGKLYGMHSHKYKLTKTVEIVREEDAKEKE
 >1JE5A 206 XRAY 1.90 0.221 0.268 no HELIX-DESTABILIZING PROTEIN <UNP VHED_BPT7>
 [ENTEROBACTERIA PHAGE T7]
 MAKKIFTSALGTAEPYAIYIAKPDYGNEERGFGNPRGVYKVDLTIPNKDPRCQRMVDEIVK
 CHEEYAAAAVEEYANPPAVARGKKPLKPYEGDMPFFDNGDGTTFKFKCYASFQDKKTK
 ETKHINLVVVDSSGKKMEDVPIIGGSKLKVKYSLVPYKWNTAVGASVKLQLESVLMVEL
 ATFGGEDDWADEVEENGYVASGSAK
 >1JEYA 609 XRAY 2.50 0.220 0.280 no Ku70 <UNP KU70_HUMAN> [HOMO SAPIENS]
 MSGWESYKTEGDEEAEQEEENLEASGDYKYSGRDSLIFLVDASKAMFESQSEDELTPF
 DMSIQCIQSVYISKIISDRDLLAVVFGTEKDKNVNFKNIIYVLQELDNPGAKRILELD
 QFKGQQGQKRFQDMMGHGSDYSLSEVLWVCANLFSVDVQFKMSHKRIMLFTNEDNPHGND

AKASRARTKAGDLRDTGIFLDMHLKKPGGFDISLFYRDIISIAEDEDLRVHFEESKLE
DLLRKVRKETRKRLSRLKLKLNKDIVISVGIYNLVQKALKPPPIKLYRETNEPVKTKT
RTFNTSTGGLLLPSDTKRSQIYGSRQIILEKEETEELKRFDDPGLMLMGFKPLVLLKKHH
YLRPSLFVYPEESLVIGSSTLFSALLIKCLEKEVAALCRYTPRRNIPPYFVALVPQEEEL
DDQKIQTTPPGFQLVFLPFADDKRKMPFTEKIMATPEQVGKMKAIVEKLRTYRSDSFEN
PVLQQHFRNLEALALDLMEPEQAVDLTLPKVEAMNKRLGSLVDEFKELVYPPDYNPEGKV
TKRKHDNEGSGSKRPKVEYSEEELKTHISKGTLGKFTVPMLKEACRAYGLKSGLKKQELL
EALTKEHFQD

>1JEYB 565 XRAY 2.50 0.220 0.280 no Ku80 <UNP KU86_HUMAN> [HOMO SAPIENS]

MVRSGNKAADVLCMDVGFTMSNSIPGIESPFQAKKVITMFVQRQVFAENKDEIALVLF
TDGTDNPLSGGDQYQNTVHRHMLPDFDLEDIESKIQPGSQADFLDALIVSMDVIQH
ETIGKKFEKRHIEIFTDLSSRFSKSQLDIIHSLKKCDISLQFFLPFSLGKEDGSGDRGD
GPFRLGGHGPSFPLKGITEQQKEGLEIVKMVMISLEGEDGLDEIYSFSESLRKLCVFKKI
ERHSIHWPCLRTIGSNLSIRIAAYKSILQERVKKTWTVVDAKTLKKEDIQKETVYCLNDD
DETEVLKEDIIQGFYRGSDIVPFSKVDEEQMKYKSEGKCFSVLGFCKSSQVQRRFFMGNG
VLKVFAARDDEAAVALSSLIHALDDLMDVAIVRYAYDKRANPQVGVAFPKHNIECLV
YVQLPFMEDLRQYMFSSLKNSKKYAPTEAQLNAVDALIDSMSLAKKDEKTDLTLEDLFTT
KIPNPRFQRLFQCLLHRALHPREPLPIQQHIWNMLNPPAEVTTKSIPLSKIKTLFPLI
EAKKQDQVTAQEIFQDNHEDGPTAK

>1QZQA 483 XRAY 2.40 0.185 0.234 no tyrosyl-DNA phosphodiesterase 1 <UNP TYDP1_HUMAN> [HOMO SAPIENS]

MEEYMPTEHHHHHENLYFQGTSGEGQDIWMLDKGNPFQFYLTRVSGVKPKYNSGALHI
KDILSPLFGTLVSSAQFNICYFDVDWLKQYPPEFRKKPILLVHGDKREKAHLHAQAKPY
ENISLCQAKLDIAFGTHHTKMMLLLYEEGLRVVIHTSNLIHADWHQKTQGIWLSPLYPRI
ADGTHKSGESPTFKADLISYLMAYNAPSLKEWIDVIHKHDLSETNVYLIGSTPGRFQGS
QKDNWGHFRLLKLDHASSMPNAESWPVVGQFSSVGLGADESKWLCSEFKESMLTLGK
ESKTPGKSSVPLYLIYPSVENVRTSLEGYPAGGSLPYSIQTAEKQNLHSHYFKWSAETS
GRSNAMPHIKTYMRPSPDFSKIAWFLVTSANLSKAAWGALEKNGTQLMIRSYELGVLFLP
SAFGLDSFKVKQKFFAGSQEPMATFPVPYDLPELYGSKDRPWIWNIPYVKAPDTHGNMW
VPS

>1N1JB 97 XRAY 1.67 0.181 0.206 no NF- κ B <UNP NFYC_HUMAN> [HOMO SAPIENS]

GSHMEEIRNLTVKDFRVQELPLARIKKIMKLEDEVKMISAEAPVLFAKAAQIFITELTLR
AWIHTEDNKRRTLQRNDIAMAITKFDQDFDLIDIVPR

>2LTTA 80 NMR NA NA NA no Putative uncharacterized protein ydbC <UNP Q9CIP3_LACLA> [LACTOCOCCUS LACTIS SUBSP. LACTIS]

MADKLKFEIIEELIVLSENAKGWRKELNRVSWNDAEPKYDIRTWSPDHEKMKGITLSEE
EFGVLLKELGNKLEHHHHHH

>4ICGC 75 XRAY 2.92 0.283 0.332 no Hemolysin expression-modulating protein <UNP F5ZMH5_SALTU> [SALMONELLA ENTERICA SUBSP. ENTERICA SEROVAR TYPHIMURIUM]

GSHMSDKPLTKTDYLMRLRRCQTIDTLERVIEKNKYELSDNELAVFYSAADHRLAELTMN
KLYDKIPSSVWKFIR

>2M8EA 57 NMR NA NA NA no SLEEPING BEAUTY TRANSPOSASE <PDB 2M8E> [SYNTHETIC CONSTRUCT]

ASMGKSKEISQDLRKKIVDLHKSGLGAISKRLKVRSSVQTIVRKYKHHGTTQHH

>3M8EA 124 XRAY 2.00 0.240 0.270 no Putative DNA-binding protein <UNP Q8KNP2_BACTI> [BACILLUS THURINGIENSIS]

MGSSHHHHHSSGLVPRGSHMNRDHFYTLNIAEIAERIGNDDCAYQVLMAFINENGEAQM
LNKTAVAEMIQLSKPTVFATVNSFYCAGYIDETRVGRSKIYTLSDLGVEIVECFKQKAME
MRNL

>1SD4A 126 XRAY 2.00 0.210 0.237 no PENICILLINASE REPRESSOR <UNP Q6UB84_STAUA>

[STAPHYLOCOCCUS AUREUS]
MTNKQVEISMAEWDVMNIIWDKKSVSANEIVVEIQKYKEVSDKTIRTTLITRLYKKEIIKR
YKSENIYFYSSNIKEDDIKMTAKTFLNKLYGGDMKSLVLFNAKNEELNNKEIEELRDIL
NDISKK
>2F7NA 207 XRAY 2.00 0.200 0.220 no DNA-binding stress response protein, Dps family <GB
NP_295984> [DEINOCOCCUS RADIODURANS]
MTKKSTKSEAASKTKKSGVPETGAQGVRAGGADHADAHLGTVNNALVNHYLEEKEFQT
VAETLQRNLATTISLYLKFKKYHWDIRGRFFRDLHLAYDEFIAEIFPSIDEQAERLVALG
GSPLAAPADLARYSTVQVPQETVRDARTQVADLVQDLRVGKGYRDDSQCDEANDPVTA
DMYNGYAATIDKIRWMLQAIMDDERLD
>2LVSA 105 NMR NA NA NA no Putative uncharacterized protein <UNP A2BLH2_HYPBU> [HYPERTHERMUS
BUTYLICUS]
MPSVNSLDIVEKLYKDGVPVKEIAKRSNNSMSTVYKALEKLEAMGRIKRRKGGRYRQHRR
LTEEELATIRELYLK GATVYEIARQLGRPESTIYYALKKLGLKLE
>4G63A 470 XRAY 2.70 0.225 0.258 no Cytosolic IMP-GMP specific 5'-nucleotidase <UNP
Q5ZZB6_LEGPH> [LEGIONELLA PNEUMOPHILA SUBSP. PNEUMOPHILA]
MDTHKVFVNRIINMRKIKLIGLDMHTLIRYNSKNFESLVYDLVKERLAESFHYP E E I K K
FKFNFDDAIRGLVIDSKNGNILKLSRYGAIRLSYHGTKQISFSDQKKIYRSIYVDLGDPN
YMAIDTSFSIAFCILYQGLVDLKDTPDKMP SYQAIAQDVQYCVDKVHSDGTLKNI I I K N
LK KYVIREKEVVEGLKHFI RY GKKIFILTNSEYSYSKLLLDYALSPFLDKGEHWQGLFEF
VITLANKPRFFYDNL RFLSVNPENGTMTNVHGPIVPGVYQGGNAKKFTEDLG VGGDEILY
IGDHIYG DILRLKKDCNWR TALVVEELGEEIASQIRALPIEKKIGEAMAIKKELEQKYVD
LCTRSIDESSQQYDQEI HDLQLQISTVDLQISRLQEQNSFYNP KWERVFRAGAEESYFA
YQVDRFACIYMEKLSDLLEHSPMTYFRANRRLLAHDIDIAAALEHHHHHH
>4G6DA 73 XRAY 2.00 0.206 0.243 no RNA polymerase sigma factor rpoD <UNP RPOD_STAA8>
[STAPHYLOCOCCUS AUREUS SUBSP. AUREUS]
MKEQLEDVLDTLTDREENVLRLRFLGLDDGRTRTLEEVGKVFGVTRERIRQIEAKALRKLR
HPSRSKRLKDFMD
>4G6DB 198 XRAY 2.00 0.206 0.243 no ORF067 <UNP Q4Z9Y5_9CAUD> [STAPHYLOCOCCUS PHAGE G1]
MKLKILDKDNATLNVFHRNKEHKTIDNVPTANLVDWYPLSNAYEYKLSRNGEYLELKRRL
STLPSSYGLDDNNQDIIRDNNHRCKIGYWYNPAVRKDNLKIIEKAKQYGLPIITEEYDAN
TVEQGFRDIGVIFQSLKTI VTRYLEGKTEEELRIFNMKSEESQLNEALKESDFSVDLTY
SDLGQIYNM LLLMKKISK
>4E0GA 462 XRAY 2.20 0.196 0.238 no Protelomerase <UNP Q7CWV1_AGRT5> [AGROBACTERIUM
TUMEFACIENS]
MGSSHHHHHSSGLVPRGSHMLAAKRKTKTPVLVERIDQFVGQIKEAMKSDDASRNKIR
DLWDAEVRYHF DNGRTEKTLELYIMKYRNALKA EFGPKSTPLAICNMKKLRERLNTYIAR
GDYPKTG VATSIVEKIERAEFN TAGRKPTVLLRIADFIAMNGMDAKQDMQALWDAEIAI
MNGRAQT TII SYITKYRNAIREAFGDDHPMLKIATGDAAMYDEARRVKMEKIANKHGALI
TFENYRQVLKICEDCLKSSDPLMIGLIGMTGRRPYEVFTQAEFSPAPYKGKVS KWSIL
FNGQAKTKQGE GTFGITYEIPVLT RSETVLAAYKRLRESGQGLWHGMSIDDFSSETRL
LLRDTVFNL FEDVWPKEELPKPYGLRHLYAEVAYHNFAPPHVTKN SYFAAILGHNNNDLE
TSLSYMTYTL PEDRDNALARKRTNERTLQQMATIAPVSRKG
>2KKVA 121 NMR NA NA NA no Integrase <UNP Q5PJ5_SALPA> [SALMONELLA ENTERICA SUBSP. ENTERICA
SEROVAR PARATYPHI A]
MENS GAYTFETIAREWHESNKRWSEDHRSRVLRYLELYIFPHIGSSDIRQLKTS HLLAPI
KEVDTS GKH DVAQR LQQRVTAIMRYAVQNDYIDSNPASDMAGALSTTKARHYPLEHHHHH
H

>2KKOA 108 NMR NA NA NA no POSSIBLE TRANSCRIPTIONAL REGULATORY PROTEIN (POSSIBLY ARSR- FAMILY)
<UNP Q7U294_MYCBO> [MYCOBACTERIUM BOVIS]
MAQSDRKAALLDQVARVGKALANGRRLLQILDLLAQGERAVEAATATGMNLTASANLQ
ALKSGGLVEARREGTRQYYRIAGEDVARLFALVQVVADEHLEHHHHH

>1C8CA 64 XRAY 1.45 0.229 0.287 no DNA-BINDING PROTEIN 7A <UNP DN72_SULSO> [SULFOLOBUS
SOLFATARICUS]
MATVKFKYKGEEKQVDISKIKKVVWRVGKMISFTYDEGGGKTGRGAVSEKDAPKELLQMLA
KQKK

>1C6VX 81 XRAY 3.00 0.203 0.362 no SIU89134 <UNP Q87706_SIVCZ> [SIMIAN IMMUNODEFICIENCY VIRUS]
QQSKNSKFKNFRVYYREGDQLWKGPCELLWKGEAVLLKVGTDIKVPPRRKAKI IKDYG
GGKEVDSSSHMEDTGEAREVA

>1YSEA 141 NMR NA NA NA no DNA-binding protein SATB1 <UNP SATB1_HUMAN> [HOMO SAPIENS]
GSHVSRSMNKPQQVSTNTEVSSEIYQWVRDELKRAGISQAVFARVAFNRTQGLLSEIL
RKEEDPKTASQSLVLNLRAMQNFLQLPEAERDRIYQDERERSLNAASAMGPAPLISTPPS
RPPQVKTATIATERNKGPENN

>2RT6A 98 NMR NA NA NA no Primosomal replication protein N' <UNP PRIC_ECOLI> [ESCHERICHIA COLI]
MKTALLLEKLEGQLATLRQRCAPVSQFATLSARFDRHLFQTRATTQLACLDEAGDNLAAL
RHAVEQQQLPQVAWLAHLAAQLEAIAREASAWSLEW

>3BOSA 242 XRAY 1.75 0.168 0.201 no Putative DNA replication factor <UNP A1S6W5_SHEAM>
[SHEWANELLA AMAZONENSIS]
GMRSNRVTQHPPLQLSLPVLHPDDETFTSYPPAAGNDELIGALKSAASGDGVQAIYLGWP
VKSGRTHLIHAACARANELERRSFYIPLGIHASISTALLEGLEQFDLICIDDDVAVAGHP
LWEEAIFDLYNRVAEQKRGSLIVSASASPMEAGFVLPDLVSRMHWGLTYQLQPMMDDEKL
AALQRRRAAMRGLQLPEDVGRFLLNRMARDLRTLFDVLDRLDKASMVHQKRLTIPFVKEML
RL

>1NGNA 155 XRAY 2.10 0.213 0.263 no methyl-CpG binding protein MBD4 <UNP MBD4_MOUSE> [MUS
MUSCULUS]
ALSPPRRKSFKKWTTPRSPFNLVQEILFHDPPWKLIIATIFLNRTSGKMAIPVLWEFLEKY
PSAEVARAADWRDVSSELLKPLGLYDLRAKTI IKFSDEYLTQWRYPIELHGIGKYGNDYS
RIFCVNEWKQVHPEDHKL NKYHDWLWENHEKLSLS

>3FDQA 170 XRAY 1.75 0.217 0.232 no Motility gene repressor mogR <UNP MOGR_LISMO> [LISTERIA
MONOCYTOGENES]
MPKSEIRKLLQEIKKQVDNPGNSSTTEIKKMASEAGIDEQTAEIYHLLTEFYQAVEEHG
GIEKYMHSNISWLKIELELLSACYQIAILEDMMKVLDISEMLSLNDLRIFPKTPSQLQNTY
YKLKKELIQVEDIPKNKPGKRKRTQKNTKKEKTNIFGKVVPALHHHHHH

>2FZ4A 237 XRAY 2.40 0.243 0.265 no DNA repair protein RAD25 <UNP O29889_ARCFU> [ARCHAEOGLOBUS
FULGIDUS]
MGSSHHHHHSSGLVPRGSHMQMIAEIYERGTIVVKGAHVPHAKFDSRSGTYRALAFR
YRDIIEYFESNGIEFVDNAADPIPTPYFDAEISLRDYQEKALERWLVDKRGCIVLPTGSG
KTHVAMAANELSTPTLIVVPTLALAEQWKERLGIFGEEYVGEFSGRIKELKPLTVSTYD
SAYVNAEKLGNRFMLLIFDEVHHLPAESYVQIAQMSIAPFRLGLTATFEREDGRHEI

>1X3CA 73 NMR NA NA NA no Zinc finger protein 292 <UNP ZN292_HUMAN> [HOMO SAPIENS]
GSSGSSGRKKPVQSLEFPTRYSPYRRCVHQGCFAFTIQQNLILHYQAVHKSDLPAF
SAEVEEESGPSSG

>4ATHA 83 XRAY 1.95 0.196 0.228 no MICROPHthalmia-ASSOCIATED TRANSCRIPTION FACTOR <UNP
MITF_MOUSE> [MUS MUSCULUS]
GAMRFNINDRIKELGTLIPKSNPDPMRWNGKITLKASVDYIRKLQREQQRAKDLENRQKK
LEHANRHLLLRVQELQMARAHG

>1ZAEA 70 NMR NA NA NA no Early protein GP16.7 <UNP VG167_BPPH2> [BACILLUS PHAGE PHI29]
HMDKTVNLSACEVAVLDLYEQSNIRIPSDIIEDLVNQRLQSEQEVLYNIETQRTYWKLEN
QKKLYRGSLK

>2QPYA 251 XRAY 2.50 0.269 0.269 no Androgen receptor <UNP ANDR_MOUSE> [MUS MUSCULUS]
CQPIFLNVLEAIEPGVVCAGHDNNQPDFAALLSSLNELGERQLVHVVKWAKALPGFRNL
HVDDQMAVIQYSWMGLMVFAMGWSFTNVNSRMLYFAPDLVFNEYRMHKSRYMQCVRMR
HLSQEFQWLQITPQEFCLMKALLFSIIPVDGLKNQKFFDELRMNYIKELDRIIACKRKN
PTSCSRRFYQLTKLLDSVQPIARELHQFTFDLLIKSHMVSVDFPEMMAEIIISVQVPKILS
GKVKPIYFHTQ

>1G5HA 454 XRAY 1.95 0.183 0.224 no MITOCHONDRIAL DNA POLYMERASE ACCESSORY SUBUNIT <UNP
DPOG2_MOUSE> [MUS MUSCULUS]
WLSGYAGPADGTQQDAPEHAVAREALVDLCRRRHFLSGTPQQQLSTAALLSGCHARFGPL
GVELRKNLASQWWSSMVVFREQVFAVDSLHQEPGSSQPRDSAFRLVSPESIREILQDREP
SKEQLVAFLENLLKTSGLKRLATLLHGALEHYVNCLDLVNRKLPFGLAQIGVCFHPVSNSN
QTPSSVTRVGEKTEASLVWFTPTRTSSQWLDLWLRHLLWWRKFAMSPSNFSSADCQDEL
GRKGSKLYYSFPWGKEPIETLWNLGDQELLHTYPGNVSTIQGRDGRKNVPCVLSVSGDV
DLGTLAYLYDSFQLAENSFARKKSLQRKVLKLHPCLAPIKVALDVGKGPTVELRQVCQGL
LNELLENGISVWPVGYSETVHSSLEQLHSKYDEMSVLSVLVTETLENGLIQLRSRDTM
KEMMHISKLRDFLVKYLASASNVAALDHHHHHH

>2XE0A 152 XRAY 2.31 0.215 0.256 no I-CREI V2V3 VARIANT <PDB 2XE0> [CHLAMYDOMONAS REINHARDTII]
NTKYNKEFLLYLAGFVDGDSIIAQINPNASSKFKHRLRLTFYVTQKTQRRWFCLKLVDE
IGVGYVRDSGSVSQYVLSEIAPLHNFLTQLQPFLLKQKQANLVLKIIIEQLPSAKASPAA
FLEVCTWVDQIAALNDSATRKTTSETVAAVLD

>4M6WA 221 XRAY 2.90 0.257 0.299 no Fanconi anemia group M protein <UNP FANCM_HUMAN> [HOMO
SAPIENS]
MGQEGKGTICILVGGHEITSGLEVISSLRAIHGLQVEVCPLNGCDYIVSNRMVVERRSQSE
MLNSVNKNKFIEQIQHLQSMFERICVIVEKDREKTGDTSRMFRRTKSYDSLTTLIGAGI
RILFSSCQEETADLLKELSLVEQRKNVGIVPTVVNSNKSEALQFYLSIPNISYITALNM
CHQFSSVKRMANSLSQEISMYAQVTHQKAEIYRYIHYVFD

>4M6WB 208 XRAY 2.90 0.257 0.299 no Fanconi anemia-associated protein of 24 kDa <UNP FAP24_HUMAN>
[HOMO SAPIENS]
MGHIVANEKWRGSQLAQEMQKGKIKLIFEDGLTPDFYLSNRCCILYVTEADLVAGNGYRKR
LVRVRNSNNLKGIVVEKTRMSEQYFPALQKFTVLDLGMVLLPVASQMEASCLVIQLVQE
QTKEPSKNPLLKGRALLSEPSLLRTVQQIPGVGKVKAPLLLQKFPSIQQLSNASIGEL
EQVVGQAVAQQIHAFFTQPRLEHHHHHH

>2ADLA 72 NMR NA NA NA no CcdA <UNP Q9S0Z5_ECOLI> [ESCHERICHIA COLI]
MKQRITVTVDSDSYQLLKAYDVNISGLVSTTMQNEARRLRAERWKVENQEGMVEVARFIE
MNGSFADENKDW

>1WEUA 91 NMR NA NA NA no inhibitor of growth family, member 4 <UNP ING4_MOUSE> [MUS
MUSCULUS]
GSSGSSGSPEYGMPSVTFGSVHPSDVLDPVDPNEPTYCLCHQVSYGEMIGCDNPDCSIE
WFHFACVGLTTKPRGKWFCPRCSQESGPSSG

>1WE0A 93 NMR NA NA NA no cellulose synthase, catalytic subunit (IRX3) <UNP CESA7_ARATH>
[ARABIDOPSIS THALIANA]
GSSGSSGPKPLKNLDGQFCEICGDQIGLTVEGDLFVACNECGFPACRCPYEYERREGTQN
CPQCKTRYKRLRGS PRVEGDEDEEDIDSGPSSG

>3WE2A 147 XRAY 2.70 0.237 0.271 no Bloom syndrome protein <UNP BLM_HUMAN> [HOMO SAPIENS]
GPLGSKTKDYKTRDVTDDVKSIVRFVQEHSSSQGMRNKHKVGPGRFTMNLVDIFLGSK

SAKIQSGIFGKGSAYSRHNAERLFKKLILDKILDEDLYINANDQAIAYVMLGNKAQTVLN
GNLKVDFMETENSSSVKKQKALVAKVS
>2P2UA 171 XRAY 2.75 0.245 0.290 no Host-nuclease inhibitor protein Gam, putative <UNP
Q72CZ5_DESVH> [DESULFOVIBRIO VULGARIS]
SLSRRKPNPVIVADIRQAEGALAEIATIDRKVGEIEAQMNEAIDAAKARASQKSAPLLAR
RKELEDGVATFATLNKTEMFKDRKSLDLGFGTIGFRLSTQIVQMSKITKDMTLERLRQFG
ISEGIRIKEDVNKEAMQGWPDERLEMVGLKRRTTDAFYIEINREEVADTAA
>2LW1A 89 NMR NA NA NA no ABC transporter ATP-binding protein uup <UNP UUP_ECOLI> [ESCHERICHIA
COLI]
GSHMKAETVKRSSKLSYKLQRELEQLPQLLEDLEAKLEALQTQVADASFFSQPHEQTQK
VLADMAAAEQELEQAFAERWEYLEALKNGG
>3THOA 382 XRAY 2.61 0.206 0.242 no Probable DNA double-strand break repair Rad50 ATPase <UNP
RAD50_THEMA> [THERMOTOGA MARITIMA]
HHHHHHSSGENLYFQGHMRPERLTVRNFLGLKNVDIEFQSGITVVEGPNAGKSSLF EAI
SFALFGNGIRYPNSYDVNNAVDGTARLVFQFERGGKRYEII REINALQRKHNAKLSEI
LENGKKAATAAKPTSVKQVEVEKILGIEHRTFIRTVFLPQGEIDKLLISPSEITEIISDV
FQSKETLEKLEKLLKEKMKKLENEISSGGAGGAGGSLEKKLKEMSDEYNNLDLLRKYLF
KSNFSRYFTGRVLEAVLKRTKAYLDILTNGRFDIDFDEKGGFIKDWGIERPARGLSGG
ERALISISLAMSLAEVASGRDLDAFFIDEGFSSLCTENKEIASVLKELERLNKVIVFITC
DREFSEAFDRKLRTGGVVVNE
>3THXA 934 XRAY 2.70 0.212 0.273 no DNA mismatch repair protein Msh2 <UNP MSH2_HUMAN> [HOMO
SAPIENS]
MAVQPKETLQLESAAEVGFVRFFQGMPEKPTTTVRLFDRGDFYTAHGEDALLAAREVFKT
QGVIKYMGPAGAKNLQSVVLSKMNFEFVKDLLLRQYRVEVYKNRAGNKASKENDWYLA
YKASPGNLSQFEDILFGNNDMSASIGVVGKMSAVDQQRQVGVYVDSIQRKLGCEFPD
NDQFSNLEALLIQIGPKCEVLPGETAGDMGKLRQIIQRGGILITERKKADFSTKDIYQD
LNRLKGGKGEQMNSAVLPENQVAVSSLSAVIKFLELLSDDSNGGFELTTFDFSQYM
KLDIAAVRALNLFQGSVEDTTGSQSLAALLNKCKTPQGQRLVNQWIKQPLMDKNRIEERL
NLVEAFVEDAELRQTLQEDLLRRFPDLNRLAKKFQRQAANLQDCYRLYQGINQLPNVIQA
LEKHGKHQKLLAVFVTPLTDLRSDFSKFQEMIETLMDQVENHEFLVKPSFDPNLSE
LREIMNDLEKKMSTLISAARDLGLDPGKQIKLDSSAQFGYYFRVTCKEEVLRNNKNFS
TVDIQKNGVKFTNSKLTSLNEEYTKNKTEYEEAQDAIVKEIVNISSGYVEPMQTLNDVLA
QLDAVVSFAHVSNGAPVPYVRPAILEKGQGRIILKASRHACVEVQDEIAFIPNDVYFEKD
KQMFHIIITGPNMGKSTYIRQTVIVLMAQIGCFVPCESAESIVDCILARVGAGDSQLK
GVSTFMAEMLETASILRSATKDSLIIIDELGRGTSTYDGFGLAWAISEYIATKIGAFCMF
ATHFHELTALANQIPTVNNLHVLTALTTEETLTMLYQVKKGVCDQSFGIHVAELANFPKHV
IECAKQKALELEEFQYIGESQGYDIMEPAAKKCYLEREQGEKIIQEFLSKVKQMPFTEMS
EENITIKLKQLKAEVIAKNNFSVNEIISRIKVT
>3THXB 918 XRAY 2.70 0.212 0.273 no DNA mismatch repair protein Msh3 <GB EAW95862> [HOMO
SAPIENS]
GPKSANKRSKSIYTPLELQYIEMKQHKDAVLCVECGYKYRFFGEDAEIAARELNIYCHL
DHNFMASIPTHRLFVHVRRLVAKGYKGVVKQTETAALKAIGDNRSSLFSRKLTALYTK
STLIGEDVNPLIKLDDAVNVDEIMTDTSTSYLLCISENKENVRDKKKGNIFIGIVGVQPA
TGEVVFDSFQDSASRSELETRMSSLQPVELLPSALSEQTEALIHRA TSVSVQDDRIRVE
RMDNIYFEYSHAFQAVTEFYAKDTV DIKGSQIIISGIVNLEKPVICSLAAIIKYLKEFNLE
KMLSKPENFKQLSSKMEFMTINGTTLRNLEILQNQTMKTGSLWLDHTKTSFGRRKL
KKWVTQPLLKREINARLDAVSEVLHSESVFGQIENHLRKLPIERGLCSYHKKCSTQ
EFFLIVKTLYHLKSEFQAIIPAVNSHIQSDLLRTVILEIPELLSPVEHYLKILNEQAQV

GDKTELFKDLSDFLIKKRKDEIQGVIDEIRMLQEIIRKILKNPSAQYVTVSGQEFMIEI
KNSAVSCIPTDWWKVGSTKAVSRFHSPFIVENYRHLNQLREQLVLDCSAEWLDFLEKFSE
HYHSLCKAVHHLATVDCIFSLAKVAKQGDYCRPTVQEERKIVIKNGRHPVIDVLLGEQDQ
YVPNNTDLSERVMIIITGPNMGKSSYIKQVALITIMAQIGSYVPAEEATIGIVDGIF
TRMGAADNIYKGRSTFMEELTDTAETIRKATSQSLVILDELGRGTSTHDGIAIAYATLEY
FIRDVKSLLTFVTHYPPVCELEKNYSHQVGNHMGFLVSEDESKLDPGAAEQVPDFVTFL
YQITRGIAARSYGLNVAKLADVPEILKKAHKSKELEGLINTKRKRLKYFAKLWTMHNA
QDLQKWTEEFNMEETQTS

>4H7AA 168 XRAY 2.60 0.176 0.230 no CRISPR-associated protein Cse2 <UNP CSE2_THET8> [THERMUS
THERMOPHILUS]
MSRGHHHHHSGMSPPGERFLDWLRLQGQKAWTAARAAFRRLAFPPGAYPRAMPYVEPF
LAKGDWRQEEREAHYLVAAALYALKDGDHQVGRTLARALWEKAQGSASVEKRFLALLEADR
DQIAFRLRQAVALEGGIDFARLLDLLRWFSRPERHVQARWAREYYGA

>4H79A 216 XRAY 1.90 0.150 0.196 no CRISPR-associated protein, Cse2 family <UNP Q47PI5_THEFY>
[THERMOBIFIDA FUSCA]
GSMTTETPKTISLTWVGTFVDQRVREIQEGYRLDNPRAVATLARLRGAGKEIGDTPDL
WGLILDDRFDYADAPPLKEKMEVAENSAHIALTYAIHQSSRRDDRMHQRGWGLGEAVRR
LMPSSIDEPLRKRFRVQGVHAVTYKALAQRLREIVTLLRRDAIPLDYGLLADQLYQFRTP
QGAQVRVTAWGRGFHAYRPKTTQNPSTTTTEKDNS

>1K99A 99 NMR NA NA NA no Upstream binding factor 1 <UNP UBF1_HUMAN> [HOMO SAPIENS]
MKKLLKHPDFPKPLTPYFRFFMEKRAKYAKLHPMSNLDLTKILSKKYKELPEKKMKY
IQDFQREKQEFERNLARFREDHPDLIQNAKKLEHHHHHH

>2HKVA 149 XRAY 1.70 0.185 0.227 no Hypothetical protein <UNP Q41IB9_9BACI> [EXIGUOBACTERIUM
SIBIRICUM]
GMTDWQQALDRHVGVGVRTTRDLIRLIQPEDWDRPISGKRSVYEVAVHLAVLLEADLRI
ATGATADEMAQFYAVPVLPEQLVDRLDQSWQYYQDRLMADFSTETTYWGVTDSTTGWLE
AAVHLYHHRSQLLDYLNLLGYDIKLDLFE

>1HKQA 132 XRAY 2.75 0.238 0.272 no REPLICATION PROTEIN <UNP Q52546> [PSEUDOMONAS SYRINGAE
PV. SAVASTANOI]
MVDNKVTQSNKLISSHTLTNEKRLVCAASLIDSRKPLPKDGYLTIRADTFAEVFGID
VKHAYALDDAATKLFNRDIRRYVKGKVVVERMRWVFHVKYREGQGCVELGFSPTIIPHIL
MLHKEFTSYQLK

>1JKOC 52 XRAY 2.24 0.244 0.306 no DNA-INVERTASE HIN <UNP HIN_SALTY> [SALMONELLA TYPHIMURIUM
LT2]
GRPRANKHEQEIQISRLLEKGHPRQQLAIIFGIGVSTLYRYFPASSIKKRMN

>1OY3D 282 XRAY 2.05 0.219 0.247 no transcription factor inhibitor I-kappa-B-beta <UNP
IKBB_MOUSE> [MUS MUSCULUS]
VFGYVTEGDGTALHLAVIHQHEPFLDFLLGFSAGHEYLDLQNDLGQTALHLAAILGEAST
VEKLYAAGAGVLVAERGGHTALHLACRVRAHTCACVLLQPRPSHPRDASDTYLTQSQDCT
PDTSHAPAAVDSQPNPENEEPRDEDWRLQLEAENYDGHPTPLHVAVIHKDAEMVRLLRDA
GADLNKPEPTCGRTPLHLAVEAQAASVLELLLKAGADPTARMYGGRTPLGSALLRPNPIL
ARLLRAHGAPEPEDGGDKLSPCSSSGSDSDNRDEGDEYDD

>3OD8A 116 XRAY 2.40 0.194 0.241 no Poly [ADP-ribose] polymerase 1 <UNP PARP1_HUMAN> [HOMO
SAPIENS]
MGSSHHHHHSSGLVPRGSHMAESSDKLYRVEYAKSGRASCKKCSSEIPKDSLRLMAIMVQ
SPMFDGKVPWHYHFSFVKVGHHSIRHPDVEVDGFSSELRWDDQKVKKTAEAGGVTG

>2D8MA 129 NMR NA NA NA no DNA-repair protein XRCC1 <UNP XRCC1_HUMAN> [HOMO SAPIENS]
GSSGSSGEPRRPRAGPEELGKILQGVVVLSGFQNPFRSELRDKALELGAKYRPDWTRDS
THLICAFANTPKYSQVLGLGGRIVRKEWVLDCHRMRRRLPSQRYLMAGPGSSSEDEASH

SGSGPSSG

>1D8BA 81 NMR NA NA NA no SGS1 RECQ HELICASE <UNP SGS1_YEAST> [SACCHAROMYCES CEREVISIAE]
ELNNLRMTYERLRELSNLGNRMVPPVGNFMPDSILKKMAAILPMNDSAFATLGTVEDKY
RRRFKYFKATIADLSKKRSSE

>2L3NA 104 NMR NA NA NA no DNA-binding protein rap1, Telomere length regulator taz1 <UNP
TAZ1_SCHPO> [SCHIZOSACCHAROMYCES POMBE, SYNTHETIC]
SVSILRSSVNHREVDEAIDNILRYTNSTEQQFLEAMESTGGRVRIAIKLLSKQTSGGSG
GSKLGGSGSRKDL SVKGMLYDSDSQQILNRLRERVSGSTAQSA

>2L3RA 162 NMR NA NA NA no E3 ubiquitin-protein ligase UHRF1 <UNP UHRF1_HUMAN> [HOMO SAPIENS]
GGMWDETELGLYKVNEYVDARDTNMGAWFEAQVVRVTRKAPSRDEPCSSTSRPALEEDVI
YHVKYDDYPENGVVQMNSRDVRARARTIIKWQDLEVGVVMLNYPDNPKERGFWDYDAEI
SRKRETRTARELYANVVLGDDSLNDCRIIFVDEVFKIERPGE

>3BU8A 235 XRAY 2.15 0.238 0.256 no Telomeric repeat-binding factor 2 <UNP TERF2_HUMAN>
[HOMO SAPIENS]

GAGEARLEEAVNRWVLKFYFHEALRAFGRSGRYGDFRQIRDIMQALLVRPLGKEHTVSRL
RVMQCLSRIEEGENLDCSFDMEALTPLESAINVLEMIKTEFTL TEAVESSRKLVEAA
VIICIKNEFEKASKILKKHMSKDPTTQKLRNDLLNIIREKNLAHPVIQNSYETFQQKM
LRFLESHLDDAEPLYLTMAKKALKSESAASSTGKEDKQAPGPVEKPPREPARQL

>3GZ5A 240 XRAY 2.20 0.223 0.273 no MutT/nudix family protein <UNP Q8EFJ3_SHEON> [SHEWANELLA
ONEIDENSIS]

GSHMTEAEYLANYPKAFKAQLLTVDVLFYHDQQLKVLLVQRSNHPFLGLWGLPGGFI
DETCDESLEQTVLRKLAECTAVVPPYIEQLCTVGNNSRDARGWSVTVCYTALMSYQACQI
QIASVSVDVKKWPLADVLQMPPLAFDHLQLIEQARERLTQKALYSLVPGFALSEPFTLPELQ
HVHEVLLGKPIQGKSFRRRVEQADLLIDTGLKRTGRANLYCLKPDTASYRFLRNLEC

>2FMYA 220 XRAY 2.20 0.209 0.247 no carbon monoxide oxidation system transcription regulator
CooA-1

<GB ABB15035> [CARBOXYDOTHERMUS HYDROGENOFORMANS]

ATQMRLTDTNLLVLNSEEYSGVLKEFREQRYSKKAILYTPNTERNLVFLVKSGRVRYVL
AYEDKEFTLAILEAGDIFCTHTRAFIQAMEDTTILYTDIRNFQNIIVVEFPFASLNMVKVL
GDLLKNSLTIINGLVFKDARLRLAEFLVQAAMDTGLKVPQGIKLELGLNTEEIALMLGTT
RQTVSVLLNDFKKMGILERVNQRTLLLDLQKLKEFSSGV

>3FMYA 73 XRAY 1.40 0.157 0.182 no HTH-type transcriptional regulator MQSA (ygiT/b3021) <UNP
YGIT_ECOLI> [ESCHERICHIA COLI K-12]

GHMASVNAETVAPEFIVKVRKKLSLTQKEASEIFGGGVNAFSRYEKGXPHSTIKLLR
VLDKHPELLNEIR

>4DHXA 75 XRAY 2.10 0.224 0.250 no 80 kDa MCM3-associated protein <UNP MCM3A_HUMAN> [HOMO
SAPIENS]

GSLVLSLSQGLAVELMERVMMEFVRETCSQELKNAVETDQVRVARCCEDVCAHLVDLF
LVEEIFQTAKETLQE

>4DHXB 101 XRAY 2.10 0.224 0.250 no Enhancer of yellow 2 transcription factor homolog <UNP
ENY2_HUMAN> [HOMO SAPIENS]

MVVSKMNKDAQMRAAINQKLIETGERERLKELLRAKLIIECGWKDQLKAHCKEVIKEKGLE
HVTVDLVAEITPKGRALVPDSVKELLQRI RTFLAQHASL

>1UL1X 379 XRAY 2.90 0.220 0.284 no Flap endonuclease-1 <UNP FEN1_HUMAN> [HOMO SAPIENS]

GIQGLAKLIADVAPSAIRENDIKSYFGRKVAIDASMSIYQFLIAVRQGGDVLQNEEGETT
SHLMGMFYRTIRMMENGIKPVYVFDGKPPQLKSGELAKRSERRAEAEKQLQQAQAAGAEQ
EVEKFTKRLVKVTKQHNDCKHLLSLMGIPYLDAPSEAEASCAALVKAGKVYAAATEDMD
CLTFGSPVLMRHLTASEAKKLP IQEFHLSRILQELGLNQEQQFVLDLCILLGSDYCESIRGI
GPKRAVDLIQKHKSIEEIVRRDPNKYPVPENWLHKEAHQLFLEPEVLDPESVELKWSEP

NEELIKFMCGEKQFSEERIRSGVKRLSKSRQGSTQGRLLDDFFKVTGSLSSAKRKEPEPK GSTKKKAKTGAAGKFKRGRK
>1UL4A 94 NMR NA NA NA no squamosa promoter binding protein-like 4 <UNP SPL4_ARATH>
[ARABIDOPSIS THALIANA]
GSSGSSGLRLCQVDRCADMKEAKLYHRRHKVCEVHAKASSVFLSGLNQRFCCQCSRFDH
LQEFDEAKRSCRRRLAGHNERRRKSSGESGPSSG
>3ULXA 174 XRAY 2.60 0.229 0.276 no Stress-induced transcription factor NAC1 <UNP Q27JE5_ORYSJ>
[ORYZA SATIVA SUBSP. JAPONICA]
MGMRRERDAEAEELNPPGFRFHPTDDELVEHYLCRKAAGQRLPVPIIAEVDLYKFDPWDL
PERALFGAREWYFFTPDRKYPNGSRPNRAAGNGYWKATGADKPVAPRGRTLGIKKALVF
YAGKAPRGVKTDWIMHEYRLADAGRAAAGAKKGSRLDDWVLCRLYNKKNEWK
>3ULJA 90 XRAY 1.06 0.121 0.139 no Lin28b, DNA-binding protein <UNP B4F6IO_XENTR> [XENOPUS
(SILURANA) TROPICALIS]
GSDPQVLRGSGHCKWFNVRMGFGFISMTSREGSPLENPVDVVFVHQSKLYMEGFRSLKEGE
PVEFTFKKSSKGFESLRVTGPGGNPCLGNE
>3F1ZA 133 XRAY 2.46 0.194 0.228 no putative nucleic acid-binding lipoprotein <UNP
A6TEE6_KLEP7> [KLEBSIELLA PNEUMONIAE SUBSP. PNEUMONIAE MGH 78578]
GASKAFYSAGDKLFQPGDDAVASMQTYSVAQFLQPFITLPAKASSDYLKGWVKVRGVIVD
IRRKSGIAGSYFIVTMRDEQNKTDKRLTFNFGSHNSADVEALSNGSVATIVGQVHVQVQD
STIPTLQNPVKVK
>1F1EA 154 XRAY 1.37 0.166 0.206 no HISTONE FOLD PROTEIN <UNP 093641_METKA> [METHANOPYRUS
KANDLERI]
MAVELPKAAIERIFRQGIGERRLSQDAKDTIYDFVPTMAEYVANAASVLDASGKKTLM
EHLKALADVLMVEGVEDYDGLFGRATVRRILKRAGIERASSDAVDLYNKLICRATEELG
EKAAEYADEDGKRTVQGEDVEKAITYSMPKGEL
>1IXCA 294 XRAY 2.20 0.219 0.245 no LysR-type regulatory protein <UNP Q9WXC7_ALCEU>
[CUPRIIVIDUS NECATOR]
MEFRQLKYFIAVAEAGNMAAAAKRLHVSQPPITRQMMALEADLGVVLLERSHRGIELTAA
GHAFLEDARRILELAGRSGDRSRAAARGDVGELSVAYFGTPIYRSLPLLLRAFLTSTPTA
TVSLTHMTKDEQVEGLLAGTIHVGFSRFFPRHPGIEIVNIAQEDLYLAVHRSQSGKFGKT
CKLADLRAVELTLFPRGGRPSFADEVIGLFKHAGIEPRIARVVEDATAALALTMAGAASS
IVPASVAAIRWPDIAFARIVGTRVKVPISCIFRKEKQPPILARFVEHVRRSAKD
>4IX7A 115 XRAY 1.58 0.191 0.216 no RE55538p <UNP Q8SYK5_DROME> [DROSOPHILA MELANOGASTER]
DNVMVSGPNNCTVPASVFENINWSVCSLATRKLLVTIFDRETLATHSVTGKPSPAFKDQ
DKPLKRMLDPGKIQDIIFAVTHKCNASEKEVRNAITTKCADENKMMKIQNVKRRS
>2KEBA 101 NMR NA NA NA no DNA polymerase subunit alpha B <UNP DPOA2_HUMAN> [HOMO SAPIENS]
MGSSHHHHHHGSSLEVLFGQPGSMSASAAQLAEELQIFGLDCEEALIEKLVELCVQYQGN
EEGMVGELIAFCTSTHKVGLTSEILNSFEHEFLSKRLSKAR
>1057A 291 XRAY 2.20 0.100 0.237 no PUR OPERON REPRESSOR <UNP PURR_BACSU> [BACILLUS SUBTILIS]
MKFRRSGRLVDLTNYLLTHPELIPLTFFSERYESAKSSISEDLTIIKQTFEQQIGITLL
TVPGAAGGVKYPKMKQAEAEFVQTLGQSLANPERILPGGYVYLTIDLGKPSVLSKVVK
LFASVFAEREIDVVMVTATKGIPLAYAAASYLNVPVIVRKDNKVTEGSTVSINYVSGSS
NRIQTMSLAKRSMKTGSNVLIIIDDFMKAGGTINGMINLLDEFNANVAGIGVLVEAGVDE
RLVDEYMSLLTLSTINMKEKSEIQNGNFLRFFKDNLLKNGETESHHHHHH
>20ZEA 298 XRAY 1.83 0.192 0.218 no Orf delta <UNP Q57280_STRPY> [STREPTOCOCCUS PYOGENES]
MIQYYYTKKEWGVMEKEELKILEELRRILSNKNEAIVILNNYFKGGVGSKSLSTMFAYL
TDKLNKVLMLDKDLQATLTKDLAKTFKVELPRVNFYEGLKNGNLASSIVHLTDNLDLIP
GTFDLMLLPKLTRSWTFENESRLATLLAPLKSVDYDLIIIDTVPTPSVYTNNIVASDYV
MIPLQAEESTNNIQQYISYIDLQEQFNPGLDMIGFVYPYLVDTDSATIKSNLEELYKQH
KEDNLVFQNIKRSNKVSTWSKNGITEHKGDKKVLKMYKNVFFEMLERIIQLENEKE

>4HQBA 148 XRAY 2.30 0.193 0.246 no Single-stranded DNA-binding protein DdrB <UNP DDRB_DEIRA>
 [DEINOCOCCUS RADIODURANS] DPFTMLQIEFITDLGARVTVNVEHESRLLDVQRHYGRLGWTSGEIPSGGYQFPIENEADF
 DWSLIGARKWKSPEGEELVIHRGHAYRRRELEAVDSRKLKLPAAIKYSRGAKVSDPQHVR
 EKADGDIEYVSLAIFRGGKRQERYAVPG

>2BKYA 97 XRAY 1.70 0.172 0.205 no DNA/RNA-BINDING PROTEIN ALBA 1 <UNP ALBA1_SULSO>
 [SULFOLOBUS SOLFATARICUS] MSSGTPTPSNVVLIGKKPVMNYVLAALTLLNQGVSEIVIKARGRAISKAVDTVEIVRNR
 LPDKIEIKEIRVGSQVVTSDGRQSRVSTIEIAIRKK

>2FC7A 82 NMR NA NA NA no ZZZ3 protein <GB AAH35079> [HOMO SAPIENS]
 GSSGSSGQQMAESGFVQHVGFKCDNCGIEPIQGVWRHCQDCPPEMSLDFCDSCSDCLHE
 TDIHKEDHQLLEPIYRSSGPSSG

>10SVA 230 XRAY 2.50 0.242 0.276 no Bile acid receptor <UNP NR1H4_RAT> [RATTUS NORVEGICUS]
 AELTVDQQTLDDYIMDSYSKQRMPEITNKILKEEFSAEENFLILTEMATSHVQILVEFT
 KRLPGFQTLDHEDQIALLKGSAAVEAMFLRSAEIFNKKLPAGHADLLEERIRKSGISDEYI
 TPMFSFYKSVGELKMTQEEYALLTAIVILSPDRQYIKDREAVEKLQEPLLDVLQKLCKIY
 QPENPQHFACLLGRTELRTFNHHAEMLSWRVNDHKFTPLLCEIWDVQ

>3RWRD 230 XRAY 3.94 0.274 0.326 no Non-homologous end-joining factor 1 <UNP NHEJ1_HUMAN> [HOMO SAPIENS]
 MEELEQGLLMQPWAWLQLAENSLAKVFITKQGYALLVSDLQQVWHEQVDTSVVSQRAKE
 LNKRLTAPPAFLCHLDNLLRPLLKDAHPSEATFSCDCVADALILVRSELGLPFYWN
 FHCMLASPSLVSQLIRPLMGMSLALQCCVRELATLLHMKDLEIQDYQESGATLIRDRLK
 TEPFEENSFLEQFMIEKLPEACSIGDGKPFVMNLQDLYMAVTTQHHHHHH

>4IBYA 200 XRAY 1.45 0.171 0.200 no Cellular tumor antigen p53 <UNP P53_HUMAN> [HOMO SAPIENS]
 SSSVPSQKTYQGSYGFRLGFLHSGTAKSVTCTYSPALNKMFCQLAKTCPVQLWVDSTPPP
 GTRVRAMAIYKQSQHMTVEVRRCPHHERCSDSDGLAPPQHLIRVEGNLVEYLLDDRNTFR
 HSVVVPYEPPEVGSDCTTIHYNMCMNRSCMGMNRRPILTIITLEDSSGNLLGRNSFEVH
 VCACPRDRRTEENLRKKG

>3TEDA 271 XRAY 2.00 0.195 0.249 no Chromo domain-containing protein 1 <UNP CHD1_YEAST>
 [SACCHAROMYCES CEREVISIAE] GPDMSIGESEVRALYKAILKFGNLKEILDELIADGTLPVKSFEKYGETYDEMMEAADKDC
 VHEEEKNRKEILEKLEKHATAYRAKLKSGEIKAENQPKDNPLTRLSLKKREKKAVLNFNK
 GVKSLNAESLLSRVEDLKYLKNLINSNYKDDPLKFSLGNNTPKPVQNWSSNWTKEEDEKL
 LIGVFKYGYGSWTQIRDDPFLGITDKIFLNEVHNPAKKSASSSDTTPTPSKKGKITGS
 SKKVPGAIHLLGRRVDYLLSFLRGGLNTKSPS

>3TEKA 148 XRAY 2.00 0.207 0.255 no ThermoDBP-single stranded DNA binding protein <PDB 3TEK>
 [THERMOPROTEUS TENAX] MGEELREEERGEVRSELITKGEKKVLIRWNTGKTSAGRLFGRYGPGGRPEFFKLLFGAV
 AGSLREQFGPDGENIFNRIRDSEKFRETSRELFGLKKWFFEEAVPRYNLERGDIFMIST
 ELVLDPDTGELLWNRDKTQLIYWIRSDR

>2BA3A 51 NMR NA NA NA no Nika <GB BAA78022> [PLASMID R64]
 SDSAVRKKSEVRQKTVVRTLRFSPVEDETIRKKAEDSGLTVSAYIRNAALN

>3EWAA 322 XRAY 2.00 0.223 0.255 no DNA repair and recombination protein radA <UNP RADA_METMP> [METHANOCOCCUS MARIPALUDIS]
 MADVLTLPVGPSTADKLEGGYLDPMKIATATIGELTDIEGISEKAAAKMIMAARDLC
 DLGFKSGVELLKQRQSVWRLSTGSTELDTVLAGGIESQSVTEFAGMFGSGKTQIMHQTCV
 NLQMREKIFADLEGVVEEELEAPKAVYIDTEGTFRPERVVQMAEGAGIDGQTVLDNTFVA
 RAYNSDMQMLFAEKIEDLIKGGNNIKLVIIDSLTSTFRNEFTGRGKLAERQQKLGRHMAT
 LNKLADLYNCIVLVTNQVAAKPDAYFGVAEQAIGGHVVGHAATFRFFLRKSKGDKRVAKL YDSPHLPDSEAVFRITEKGIQD

>2H6BA 250 XRAY 2.20 0.186 0.229 no ChloroPhenol Reduction gene K <UNP Q18R04_DESHD> [DESULFITOBACTERIUM HAFNIENSE]
 MSVEGLGKDFCGAIIIPDNFFPIEKLRYTQMGLIRDFAKGSVIMPGEEITSMIFLVEGK

IKLDIIFEDGSEKLLYYAGGNSLIGKLYPTGNNIYATAMEPTRTCWFSEKSLRTVFRTDE
DMIFEIFKNYLTKVAYYARQVAEMNTYNPTIRILRLFYELCSSQGKRVGDYEITMPLSQ
KSIGEITGVHHVTVSRVLACLKRENILDKKKNKIIVYNLDELKHLSEQTSYSDPNSSSV
DKLAAALDHH

>3B0DC 76 XRAY 2.20 0.208 0.261 no Centromere protein W <PDB 3B0D> [GALLUS GALLUS]
GRRTVPRGTLRKIIKKHKPHRLAANTDLLVHLSFLLFLHRLAEEARTNAFENKCKIIKP
EHTIAAAKVLKKSRLG

>3NFIA 237 XRAY 1.90 0.190 0.224 no DNA-directed RNA polymerase I subunit RPA49 <UNP
RPA49_YEAST>
[SACCHAROMYCES CEREVISIAE]
GSHMDLPTRAQMEITSNDRPTPLANIDATDVEQIYPIESIIIPKKELQFIRVSSILKEAD
KEKKLELFPYQNNKSKYVAKKLDLSTQPSQMTKLQMLYYLSLLGVYENRRVNNKTKLLER
LNSPPEILVDGILSRFTVIKPGQFGRSKDRSYFIDPQNEKILCYILAIIMHLDNFIVEI
TPLAHELNLKPSKVVSFLRVLGAIKVGATVAQAEAFGIPKSTAASYKIATMKVPFKL

>1Z4HA 66 NMR NA NA NA no Tor inhibition protein <UNP Q9AZ38_BPHK6> [ESCHERICHIA
COLI] MQHELQPDLSVDLKFIMADTGFGKTFIYDRIKSGDLPAKVIHGRARWLYRDHCEFNKL
LSRANG

>2Z4SA 440 XRAY 3.00 0.291 0.291 no Chromosomal replication initiator protein dnaA <UNP
DNAA_THEMA> [THERMOTOGA MARITIMA]
MKERILQEIKTRVNRKSWELWFSSFDVKSIEGNKVVFSVGNLFKEWLEKKYYSVLSKAV
KVVLGNDAFTEITYEAFEPHSSYSEPLVKKRAVLLTPLNPDYTFENFVVGPGNSFAYHAA
LEVAKHPGRYNPLFIYGGVGLGKTHLLQSIGNYVVQNEPDLRVMYITSEKFLNDLVDSMK
EGKLNFEFREKYRKVDILLIDDVQFLIGKTGVQTELFHTFNLHDSGKQIVICSDREPQK
LSEFQDRLVSRFQMGVLVAKLEPPDEETRKSIARKMLEIEHGELPEEVLNFVAENVDDNLR
RLRGAIKLLVYKETTGEVDLKEAIIILLKDFIKPNRVKAMPIDELIEIVAKVTGVPRE
EILSNSRNVKALTARRIGMYVAKNYLKSSLRTIAEKFNRSHPVVVDSVKKVKDSLKGK
QLKALIDEVIGEISRRALSG

>3EI3B 383 XRAY 2.30 0.210 0.251 no DNA damage-binding protein 2 <UNP Q2YDS1_DANRE> [DANIO
RERIO]
MHHHHHHVDENLYFQGGGRTGGQKKVGQTSILHYIYKSSLGQSIHAQLRQCLQEPFIRSL
KSYKLHRTASPFDRRVTSLEWHPTHTTAVGSKGGDIILWDYDVQNKTSFIQGMGPGDA
ITGMKFNQFNTNQLFVSSIRGATTLRDFSGSVIQVFAKTDSDWYWCYCDVSVSRQMLAT
GDSTGRLLLLGLDGHEIFKEKLHKAKVTHAEFNPRCDWLMATSSVDATVKLWDLRNIKDK
NSYIAEMPHEKPVNAAYFNPTDSTKLLTTDQRNEIRVYSSYDWSKPDQIIHPHRQFQHL
TPIKATWHPMYDLIVAGRYPDQLLLNDKRTIDIYDANSGLVHQLRDPNAAGIISLNKF
SPTGDLVLSGGMGNILIWNRDT

>1EIJA 80 NMR NA NA NA no HYPOTHETICAL PROTEIN MTH1615 <UNP DNB_P_METH>
[METHANOTHERMOBACTER THERMAUTOTROPHICUS]
MRQQLEMQKKQIMMQLTPEARSRLANLRLTRPDFVEQIELQLIQLAQMGVRVRSKITDEQ
LKELLKRVAGKKREIKISRK

>2HUEA 175 XRAY 1.70 0.209 0.239 no Anti-silencing protein 1 <UNP ASF1_YEAST> [SACCHAROMYCES
CEREVISIAE]
PLGSPNSSIVSLLGIKVLNPAKFTDPYEFETFECLSLKHDLEWKLYTVGSSRSLDHD
QELDSILVGPVPVGNKVFVSADPPSAELIPASELVSVTVILLSCSYDGREFVRVGYVYN
NEYDEEELRENPPAKVQVDHIVRNILAEKPRVTRFNIVWDNENEGDLYPPEQPGV

>2HUEB 77 XRAY 1.70 0.209 0.239 no Histone H3 <UNP Q92133_XENLA> [XENOPUS LAEVIS]
MALIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVALFEDTNLCAIHAKRVT
IMPKDIQLARRIGERA

>2HUEC 84 XRAY 1.70 0.209 0.239 no Histone H4 <UNP H4_XENLA> [XENOPUS LAEVIS]

MKVLRDNIQGITKPAIRRLARRGGVKRISGLIYEETRGLKVFLENVIRDAVITYTEHAKR
 KTVTAMDVVYALKRQGRTLYGFGG
 >3SSCA 170 XRAY 2.10 0.197 0.259 no 5-methylcytosine-specific restriction enzyme B <UNP
 MCRB_ECOLI> [ESCHERICHIA COLI]
 MESIQPWIEKFIKQAQQRSQSTKDYPSTYRNLRVKLSFGYGNFTSIPWFAFLGEGQEAS
 NGIYPVILYYKDFDELVLAYGISDTNEPHAQWQFSSDIPKTIAEYFQATSGVYPKKYGQS
 YYACSQKVSQGIDYTRFASMLDNIINDYKLIFNSGKSVIPPLEGHHHHHH
 >3GXQA 54 XRAY 2.35 0.237 0.261 no Putative regulator of transfer genes ArtA <UNP
 Q2FDC9_STAA3> [STAPHYLOCOCCUS AUREUS SUBSP. AUREUS USA300]
 ENSVFFGKKKVSLLHLLVDPDMKDEIIKYAQEKDFDNVSQAGREILKKGLEQIA
 >3TOCA 224 XRAY 2.20 0.217 0.258 no Putative uncharacterized protein <UNP Q99ZV9_STRP1>
 [STREPTOCOCCUS PYOGENES]
 GSFTMNLNFSLLDEPIPLRGGTILVLEDVCVFSKIVQYCYQEEDSELKFFDHMKMTIKE
 SEIMLVTDILGFDVNSSTILKLIHADLESQFNEKPEVKSMIDKLVAITELIVFECLENE
 LDLEYDEITILELIKSLGVKQVETQSDTIFEKCLEILQIFKYLTKKKLLIFVNSGAFITKD
 EVASLQEYISLTNLTVLFLPRELYDFPQYILDEDYFLITKNMV
 >2IJGX 526 XRAY 2.10 0.238 0.262 no Cryptochrome DASH, chloroplast/mitochondrial <UNP
 CRYD_ARATH> [ARABIDOPSIS THALIANA]
 MNDHIHRVPALTEEEIDSVAIKTFERYALPSSSSVKRKGKGVITLWFRNDRVLDNDALY
 KAWSSSDTILPVYCLDPRLFHTTHFFNFPKTGALRGGFLMECLVDLRKNLMKRGLNLLIR
 SGKPEEILPSLAKDFGARTVFAHKETCSEEVDERLVNQGLKRVGNSTKLELIWGSTMVH
 KDDLPGDVFDPDVTQFRKSVEAKCSIRSSTRIPSLGPTPSVDDWGDVPTLEKLGVEP
 QEVTRGMRVFGGESAGVGRVFEYFWKKDLLKVYKETRNGMLGPDYSTKFSPLAFGCISP
 RFIYEEVQRYEKERVANNSTYVWLFELIWRDYFRFLSIKCGNSLFHLGGPRNVQGWKSD
 QKLFESWRDAKTGYPLIDANMKELSTTGFMNSNRGRQIVCSFLVRDMGLDWRMGAEWFTC
 LLDYDPCSNYGNWYTGAGVGNPDREDRYFSIPKQAQNYDPEGEYVAFWLQQLRRLPKER
 HWPGRMLMYMDTVVPLKHGNGPMAGGSKSGGGFRGSHSGRRSRHNGP
 >4JQFA 179 XRAY 1.60 0.199 0.219 no CST complex subunit STN1 <UNP STN1_HUMAN> [HOMO SAPIENS]
 AEALSNPGALDPLSLTLLSEKAKEFLMENRVQSFYQQELEMVESLLSLANQPVIHSASS
 DQVNFKKDTSKAIHSIFKNAIQLLQEKGLVFQKDDGFDNLYVVTREDKDLHRKIHRITQ
 QDCQKPNHMEKGCHFLHILACARLSIRPGLSEAVLQQVLELLEDQSDIVSTMEHYTAF
 >3QOEA 302 XRAY 3.00 0.183 0.247 no Heterocyst differentiation protein <UNP
 Q2ACK9_9CYAN> [FISCHERELLA THERMALIS]
 SNAMSDVDLIKRLGPSAMDQIMLYLAFSAMRTSGHRHGAFLDAAATAAKCAIYMTYLEQ
 GQNLRTMTHLHLEPKRVKAIVEEVQALTEGKLLKMLGSQEPYLIQFPYVWMEKYPWR
 PGRSRIPGTSLTSEEKRIEQKLPSNLPDAHLITSFEFLELIEFLHKRSQEDLPKEHQMP
 LSEALAEHIKRRLLYSGTVTRIDSPWGMFPFYALTRPFYAPADDQERTYIMVEDTARFFRM
 MRDWAIEKRPNTMRVLEELDILPEKMQAKDELDEIRAWADKYHQDDGVPVVLQMVFGKK
 ED
 >3QRFF 82 XRAY 2.80 0.248 0.283 no Forkhead box protein P3 <UNP FOXP3_HUMAN> [HOMO SAPIENS]
 MRPPFTYATLIRWAILEAPEKQRTLNEIYHWFTRMFAFFRNHPATWKNAIRHNSLHKCF
 VRVESEKGAVWTVDELEFRKKR
 >2ECCA 76 NMR NA NA NA no Homeobox and leucine zipper protein Homez <UNP HOMEZ_HUMAN> [HOMO
 SAPIENS]
 GSSGSSGKRKTKEQAILKSFFLQCQWARREDYQKLEQITGLRPEIIQWFGDTRYALKH
 GQLKWFRDNASGPSSG
 >3M03A 95 XRAY 2.50 0.228 0.266 no Origin recognition complex subunit 6 <UNP ORC6_HUMAN> [HOMO
 SAPIENS]

MSNIGIRD LAVQFSCIEAVN MASKILKSYESSLPQTQQVDLDLSRPLFSAALLSACKIL
 KLVVDKNKMVATSGVKKAIFDRLCKQLEKIGQQVD
 >1UB4A 110 XRAY 1.70 0.251 0.232 no MazF protein <UNP CHPA_ECOLI> [ESCHERICHIA COLI]
 VSRYPVDMGDLIWVDFPTKGSEQAGHRPAVVLSPFMYNKTMCLCVPCTTQSKGYPFE
 VVLSGQERDGVADQVKSI AWRARGATKKGTV APEELQLIKAKINVLIG
 >1UB4C 85 XRAY 1.70 0.251 0.232 no MazE protein <UNP CHPR_ECOLI> [ESCHERICHIA COLI]
 GPHMIHSSVKRWGNSPAVRIPATLMQALN LNIDDEVKIDLDVGKLIIEPVRKEPVFTLAE
 LVNDITPENLHENIDWGEPKDKEVW
 >1MSZA 86 NMR NA NA NA no DNA-binding protein SMUBP-2 <UNP SMBP2_HUMAN> [HOMO SAPIENS]
 MGS LN GSGPEGVESQDGV DHFRAMIVEFMASKKMLEFP PSLNSHDRLRVHQIAEEHGLR
 HDSSGEGKRRFITVSKRAGSHHHHHH
 >4JOLA 64 XRAY 2.91 0.211 0.252 no Protein CBFA2T1 <UNP MTG8_HUMAN> [HOMO SAPIENS]
 SEEMIDHRLTDREWAEWKHL DHLN C IMDMVEKTRRSLTVLRRCQ EADREELNYWIRRY
 SDAE
 >4JOIA 166 XRAY 2.05 0.213 0.249 no CST complex subunit STN1 <UNP STN1_HUMAN> [HOMO SAPIENS]
 LDPVFLAFAKLYIRDILDMKESRQVPGVFLYNGHP IKQVDVLGT VIGVRERDAFYSYGVD
 DSTGVINCICWKKLNTESVSAAPSAARELSLTSQLKKLQETIEQKTKIEIGDTIRVRSI
 RTYREEREIHATTYYKVDDPVWNIQIARMLELPTIYRKVYDQPFHS
 >4JOIC 122 XRAY 2.05 0.213 0.249 no CST complex subunit TEN1 <UNP TEN1L_HUMAN> [HOMO SAPIENS]
 MLPKPGTYLLPWEVSAGQVPD GSTLR TFGRLCLYDMIQSRVTLMAQHGS DQHQLVCTKL
 VEPFHAQVGS LYIVLGELQHQQDRGS VVKARVLT C VEGMNLPLLEQAIREQRLYKQERGG
 SQ
 >2G99A 308 XRAY 1.90 0.212 0.243 no WD-repeat protein 5 <UNP WDR5_HUMAN> [HOMO SAPIENS]
 KPTPVKPNYALKFTLAGHTKAVSSVKFSPNGEWLASSADKLIKIWGAYDGKFEKTISGH
 KLGISDVAWSSDSNLLVSASDDKTLKIWDVSSGKCLKTLKGHSNYVFCCNFNPQSNLIVS
 GSFDESVR IWDVKTGKCLKTLP AHS DPVSAVHFNRD GSLIVSSSYDGLCRIWDTASGQCL
 KTLIDDDNPPVSFVKFSPNGKYILAATLDNTLKLWDYSKGKCLKTYTGHKNEKYCIFANF
 SVTGGKWIVSGSEDNLVYIWNLQTK EIVQKLQGH TDVVISTACHPTENI IASAALENDKT
 IKLWKS DC
 >2G9WA 138 XRAY 1.80 0.204 0.252 no conserved hypothetical protein <UNP P95163_MYCTU>
 [MYCOBACTERIUM TUBERCULOSIS]
 MAKLTRLGDLERAVMDHLWSRTEPQTVRQVHEALSARRDLAYTTVM AVLQRLAKKNLVLQ
 IRDDRAHRYAPVHGRDEL VAGLMVDALAQ AEDSGSRQAALVHFVERVGADEADALRRALA
 ELEAGHGNRPPAGAATET
 >3D6WA 111 XRAY 2.40 0.184 0.209 no Methyl-accepting/DNA response regulator <UNP Q73A38_BACC1>
 [BACILLUS CEREUS]
 GKS VVTLKTTD GWIPVPFSKVMYLEAKDKKTYVNAEELTGTHKYS LQEF EYLLPKDSFIR
 CHRSFIVNVNHIKAIYPDTHSTFLLSMDNGERVPSQSYASYFRKLLGFGS
 >1WG6A 127 NMR NA NA NA no HYPOTHETICAL PROTEIN (RIKEN cDNA 2810455B10) <GB XP_110852> [MUS
 MUSCULUS]
 GSSGSSGLKGEPDCYALSLESSEQLTLEIPLNDSGSAGLGVS LKGNKSRETGTDLGIFIK
 SIIHGGA AFKDGRLRMNDQLIAVNGETLLGKSNHEAMETLRRSMSMEGNIRGMIQLVILR
 RSGPSSG
 >1WG2A 64 NMR NA NA NA no zinc finger (AN1-like) family protein <UNP ZF2N3_ARATH> [ARABIDOPSIS
 THALIANA]
 GSSGSSGSPSRPVRPN NRCFSCNKKVGMGFKCKGSTFCGSHRYPEKHECSFDFKEVGSG
 PSSG
 >2ZTDA 212 XRAY 2.40 0.204 0.268 no Holliday junction ATP-dependent DNA helicase ruvA <UNP
 RUVA_MYCTU> [MYCOBACTERIUM TUBERCULOSIS]

MASMTGGQQMGRGSEFMIA SVRGEVLEVALDHVVEAAGVG YRVNATPATLATLRQGTEA
 RLITAMIVREDSMTLYGFPDGETRDLFLTLLSVSGVGPRLAMAALAVHDAPALRQVLADG
 NVAALTRVPGIGKRGAE RMVLELRDKVGVAATGGALSTNGHAVRSPVVEALVGLGFAAKQ
 AEEATDTVLAANH DATTSSALRSALSLLGKAR
 >1ZS3A 182 XRAY 2.70 0.209 0.258 no Lactococcus lactis MG1363 DpsA <PDB 1ZS3> [LACTOCOCCUS
 LACTIS]
 MITKLMIDEKYAKELDKAEIDHHKPTAGAMLGHVLSNLF IENIRLTQAGIYAKSPVKCEY
 LREIAQREVEYFFKISDLLLDENEIVPSTTEEF LKYHKFITEDPKAKYWTDEDLLESFIV
 DFQAQNMFITRAIKLANKEEFALAAAGVVELYGYNLQVIRNLAGDLGKSVADFHDEDEDN
 DN
 >2Q79A 93 XRAY 1.80 0.227 0.241 no Regulatory protein E2 <UNP VE2_HP V16> [HUMAN PAPILLOMAVIRUS
 TYPE 16]
 TTPIVHLKGDANTLKCLRYRFKKHCTLYTAVSSTWHWTGHN VKHKS AIVTLTYDSEWQRD
 QFLSQVKIPKTITVSTGFMSIGGGTGGGSGGGS
 >1EE8A 266 XRAY 1.90 0.214 0.258 no MUTM (FPG) PROTEIN <UNP FPG_THET8> [THERMUS
 THERMOPHILUS]
 PELPEVETRRRLRPLVLGQTLRQVVHRDPARYRNTALAEGRRILEVDRRGKFL LFALEG
 GVELVAHLGMTGGFRLEPTPHTRAALVLEGR TLYFHDPRRFGRLFGVRRGDYREIPLLLR
 LGPEPLSEAFAPFGFRGLKESARPLKALLDQRLAAGVGN IYADEALFRARLSPFRPAR
 SLTEEEARRLYRALREVLAEEVELGGSTLSDQSYRQPDGLPGGFQTRHAVYGREGLPCPA
 CGRPVERRRVAGRGTHFCPTCQGE GP
 >2OWYA 306 XRAY 2.50 0.234 0.279 no Recombination-associated protein rdgC <UNP RDGC_PSEAE>
 [PSEUDOMONAS AERUGINOSA]
 MWFRNLLVYRLTQDLQLDADSLEKALGEKSARPCASQELTTYGFTAPFGKGPDA PLVHVS
 QDFFLISARKEERILPGSVVRDALKEKVDEIEAQQMRKVYKKERDQLKDEIVQTLLPRAF
 IRRSSTFAAIAPSLGLILVDSASAKKAEDLLSTLREALGSLPVRPLSVKVAPTATLTDWV
 KTQEAAGDFHVLDEC ELRDTHEDGGVVRCKRQDLTSEEIQLHLTAGKLV TQLSLAWSDKL
 SFVLDDKLAVKRLRFEDLLQEQA EKDGGEDALGQLDASFTLMMLTFAEFLPALFEALGGE
 EIPQGV
 >1T0FC 54 XRAY 1.85 0.211 0.235 no Transposon Tn7 transposition protein tnsC <UNP TNSC_EC OL I>
 [ESCHERICHIA COLI]
 GSAIKVVKPSDWDSL PDTD LRYIYSQRQPEKTMHERLKGKG VIVDMASL FKQAG
 >1WOC A 103 XRAY 2.00 0.221 0.276 no Primosomal replication protein n <UNP PRIB_EC OL I>
 [ESCHERICHIA COLI]
 TNRLVLSGTVCRA PLRKVSPSGIPHCQFVLEHRSVQEEAGFHRQAWCMPVIVSGHENQA
 ITHSITVGSRITVQGFI SCHKAKNGLSKMVLHAEQIELIDSGD
 >2COBA 70 NMR NA NA no LCoR protein <UNP Q5VW16_HUMAN> [HOMO SAPIENS]
 GSSGSSGRGRYRQYNSEILEEAISVVM SGKMSVSKAQSIYGIPHSTLEYKVKERLGT LKN
 PPKKKMKLMR
 >2PI2E 142 XRAY 2.00 0.233 0.255 no Replication protein A 14 kDa subunit <UNP RFA3_HUMAN> [HOMO
 SAPIENS]
 MGHHHHHHHHHHSSGHIEGRHMVDMMDLPRSRINAGMLAQFIDKPVC FVGRLEKIHPTGK
 MFILSDGEGKNGTIELMEPLDEEISGIVEVVG RVTAKATILCTSYVQFKEDSHPFDLGLY
 NEAVKIIHDFPQFYPLGIVQHD

>1YDOA 96 XRAY 1.50 0.170 0.185 no UvrABC system protein C <UNP UVRC_THEMA> [THERMOTOGA MARITIMA]
MKEKIRKKILLAPEEPGVYIFKNKGVPYIYGKAKRLSNRLRSYLNQTEKVFRIGEEADE
LETIVVMNEREAFILEANLIKYPKYNVRLKDTDF

>1YDXA 406 XRAY 2.30 0.199 0.231 no type I restriction enzyme specificity protein MG438 <UNP T1SX_MYCGE> [MYCOPLASMA GENITALIUM]
MGHHHHHHHHHSSGHIDDDDKHMPKLLNNINWTKRTIDSLFDLKKGEMLEKELITP
EGKYEYFNGGVKNSGRDKNFTFKNTISVIVGGSCGYVRLADKNFFCGQSNCTLNLLDPL
ELDLKFAYYALKSQQERIEALAFGTTIQNIRISDLKELEIPFTSNKNEQHAIANTLSVFD
ERLENLASLIEINRKLREYAHKLFSLDEAFLSHWKLEALQSQMHEITLGEIFNFKSGKY
LKSEERLEEGKFPYYGAGIDNTGFVAEPNTEKDTISIIISNGYSLGNIRYHEIPWFNGTGS
IALEPMNNEIYVPPFYCALKYKQDIKERMKSDDSPFLSLKLAGEIKVPYVKSFLQQRKA
GKIVFLDDQKLDQYKKESSLTVIRDITLLKKLFPDMTERTKSIKY

>3TRBA 104 XRAY 2.00 0.201 0.243 no Virulence-associated protein I <UNP Q83BL4_COXBU> [COXIELLA BURNETII]
SNAMAANMRPIHPGEILAEELGFLDKMSANQLAKHLAIPNRTAILNGARSITADTAL
RLAKFFGTTFEFLNLQDAYDIKALKKSGKKIEKEVTPYDQAA

>1WPKA 146 NMR NA NA NA no ADA regulatory protein <UNP ADA_ECOLI> [ESCHERICHIA COLI]
MKKATCLTDDQRWQSVLARDPNADGEFVFAVRTTGIFCRPSCRARHALRENVSYANASE
ALAAGFRPCKRCQPEKANAAQHRLDKITHACRLLEQETPTVLEALADQVAMSPFHLHRLF KATTGMTPKAWQQAWRARRRLRESLAK

>2WPOA 180 XRAY 2.67 0.228 0.266 no HOBA <UNP O25828_HELPY> [HELICOBACTER PYLORI]
MKNFYDWIKEFIRDQGEFIAQQSGWLELERSYAKLIAQTISHVLNNGSLLVSADSSRHW
FLNYILSNLNPDKLKERPLLSVIDFNASSFYPKNDANLSLATIEMTYQNPMFHWVGKIEN
EGLKTILLSKIPSFLWLFEELKEDCLLLKEHDSLLDYKLLQLFKLFENALFSVLYNKVTL

>4IOOA 127 XRAY 1.25 0.150 0.167 no Bromodomain-containing protein 4 <UNP BRD4_HUMAN> [HOMO SAPIENS]
SMNPPPPETSNPNPKRQTNQLQYLLRVVLKTLWKHQFAWPFQQPVDVAVKLNLPDYKII
KTPMDMGTIKKRLNNYYWNAQECIQDFNTMFTNCYIYNKPGDDIVLMAEAEKLFQKI NELPTEE

>3IO5A 333 XRAY 2.40 0.212 0.248 no Recombination and repair protein <UNP UVSX_BPT4>
[ENTEROBACTERIA PHAGE T4]
GSHMDVVRTKIPMMNIALSGEITGGMQSGLLILAGPSKSFKNFGLTMVSSYMRQYPDAV
CLFYDSEFGITPAYLRSMGVDPERVIHTPVQSLEQLRIDMVNQLDAIERGEKVVFIDS
GNLASKKETEDALNEKVVSDMTRAKTMKSLFRIVTPYFSTKNIPICIAINHTYETQEMFSK
TVMGGGTGPMYSADTVFIIGKRQIKDGSIDLQGYQFVLNVEKSRTVKEKSKFFIDVKFDGG
IDPYSGLLDMALELGFVVKPKNGWYAREFLDEETGEMIREEKSWRAKDTNCTTFWGPLFK
HQPFPRDAIKRAYQLGAIDSNEIVEAEVDELINS

>3PGZA 193 XRAY 2.10 0.212 0.256 no Single-stranded DNA-binding protein <UNP Q6G302_BARHE>
[BARTONELLA HENSELAE] MAHHHHHMGTLAQTCGPGSMAGSLNKVILIGNLGADPEIRRLNSGDQVANLRIATSES
WRDRNTNERKERTWHNIVIFNENLVKVVEQYLKKGSKIYIEGQLQTRKWQDQNGNDRYT
TEIVLQKYRGELQMLDGRAAGGEQMQGANQSSGAYSSVGFGDNSANQRDVFGSNNSQLG
ESFSHKLDDDVPF

>3ZLJC 53 XRAY 3.10 0.229 0.263 no DNA MISMATCH REPAIR PROTEIN MUTS <UNP MUTS_ECOLI>
[ESCHERICHIA COLI K-12]
PNAAATQVDGTQMSLLSVPEETSPAWEALNDPRSLTPRQALEWIYRLKSLV

>1ZRJA 50 NMR NA NA NA no E1B-55kDa-associated protein 5 isoform c <UNP HNRL1_HUMAN> [HOMO SAPIENS]
GSSGSSGMDVRLKVNELREELQRRGLDTRGLKAELAERLQAALSGPSSG

>3POVA 488 XRAY 2.50 0.209 0.264 no ORF 37 <UNP P88925_HHV8> [HUMAN HERPESVIRUS 8 TYPE M]
GAMEATPTPADLFSEDYLVDTLDGLTVDDQQAVALASLSFSKFLKHAKVRDWCAQAKIQPS
MPALRMAYNYFLFSKVGFIGSEDVCNFFVDRVFGGVRLLDVASVYAACSQMAHQRHII

CCLVERATSSQSLNPVWDALRDGIISSSKFHWAVKQNTSKKIFSPWPITNNHFVAGPLA
 FGLRCEEVVKTLATLLHPDETNC LDYGMQSPQNGIFGVSLDFAANVKTDTEGRLQFDP
 NCKVYEIKCRFKYTFAKMECDPIYAAYQRLYEAPGKLALKDFFYSISKPAVEYVGLGKLP
 SESDYLVAYDQEWACPRKKRKLTPHLNIRECILHNSTTESDVYVLTDPQDTRGQISIK
 ARFKANLFVNRHSYFYQVLLQSSIVEEYIGLDGIPRLGSPKYYIATGFFRKRGYQDPV
 NCTIGGDALDPHVEIPTLLIVTPVYFPRGAKHRLHQAANFWSRS AKDTFPYIKWDFSYL
 SANVPHSP
 >3GA8A 78 XRAY 1.70 0.166 0.186 no HTH-type transcriptional regulator MqsA (YgiT/B3021) <UNP
 YGIT_ECOLI> [ESCHERICHIA COLI K-12]
 GHMKCPVCHQGEMVSGIKDIPYTFRGRKTVLKG IHGLYCVHCEESIMNKEESDAFMAQVK
 AFRASVNAETVAPEFIVK
 >3RLOA 204 XRAY 1.80 0.169 0.192 no Gamma-interferon-inducible protein 16 <UNP IF16_HUMAN> [HOMO
 SAPIENS]
 GSVDDSAQSDLKEVMVLNATESFVYEPKEQKKMFHATVATENEVFRVKVFNIDLKEKFTP
 KKIIAIAINYVCRNGFLEVYPFTLVADVNADRNM EIPKGLIRSASVTPKINQLCSQTKGSF
 VNGVFEVHKKNVRGEFTYIEIQDNTGKMEVVHGRLLTINCEEGLKLTCTFELAPKSGN
 TGELRSVIHSHIKV I KTRKNAAS
 >1Z91A 147 XRAY 2.50 0.223 0.305 no Organic hydroperoxide resistance transcriptional regulator <UNP
 OHRR_BACSU> [BACILLUS SUBTILIS] MENKFDHMKLENQLSFLLYASSREMTKQYKPLLDKLNITYPQYLALLLWEHETLTVKKM
 GEQLYLD SGTLPMLKRMEQQGLITRKRSEEDERSVLISLTEDGALLKEKAVDIPGTILG LSKQSGEDLKQLKSALYTLLETLHQKN
 >3TB6A 298 XRAY 2.21 0.188 0.231 no Arabinose metabolism transcriptional repressor <UNP ARAR_BACSU>
 [BACILLUS SUBTILIS]
 GIDPFTSAKSALHSNKTIGVLT TYISDYIFPSIIRGIESYLSEQGYSM LLTSTNNPNDE
 RRGLENLLSQHIDGLIVEPTKSALQTPNIGYYLNLEKNGIPFAMINASYAELAAPSFTLD
 DVKGGMMAAEHLLSLGHTHMMGIFKADDTQGVKRMNGFIQAHRERELFPSPDMI VTFTE
 EKESKLLKEVKATLEKNSKHMPTAILCYNDEIALKVIDMLREMDLKVPEDMSIVGYDDSH
 FAQISEVKLTSVKHPKSVLGKAAAKYVIDCLEHKKPKQEDVIFEPELIIRQSARKLNE
 >2099A 182 XRAY 1.70 0.207 0.261 no Acetate operon repressor <UNP ICLR_ECOLI> [ESCHERICHIA COLI]
 GHMSRNLLAIVHPILRNLMESGETVNMVLDQSDHEAIIIDQVQCTHLMRMSAPIGGKL
 PMHASGAGKAFLAQLSEEQVTKLLHRKGLHAYTHATLVSPVHLKEDLAQTRKRGYSFDDE
 EHALGLRCLAACIFDEHREPF AAISISGPISRITDDRVT EFGAMVIKAAKEVTLAYGGM R
 GS
 >2G70A 70 XRAY 1.40 0.195 0.224 no Protein traM <UNP TRAM1_ECOLI> [ESCHERICHIA COLI]
 ESAFNQTEFNKLLLECVVKTQSSVAKILGIESLSPHVSGNSKF EYANMVEDIREKVSSEM
 ERFFPKNDDE
 >3CNBA 143 XRAY 2.00 0.208 0.256 no DNA-binding response regulator, merR family <UNP Q47UF8_COLP3>
 [COLWELLIA PSYCHRERYTHRAEA] MSLNVKNDFSILIIEDDK EFADMLTQFLENLFPYAKIKIAYNPF DAGDLLHTVKPDVVML
 DLMVMGMDGFSICHRIKSTPATANIIVIAMTGALTD DNVSRIVALGAETCFGKPLNFTLL
 EKTIKQLVEQK KATSEGH HHHHH
 >1KGA 225 XRAY 1.50 0.181 0.210 no DNA BINDING RESPONSE REGULATOR D <UNP Q9WYNO_THEMA> [THERMOTOGA
 MARITIMA]
 MNVRVLVVEDERDLADLITEALKKEMFTVDVCYDGE EGYMALNEPFDVVIL DIMPVHD
 GWEILKSMRESGVNTPVLM LTALSDVEYRVKGLNMGADDYLPKPF DLRELIARV RALIRR
 KSESKSTKL VCGDLILDATKKAYRGSKEIDLTKKEYQILEYLMNKNRVVTKEELQEHL
 WSFDDDEVFSDVLRSHIKNL RKKVDKGFKKKI IHTVRGIGYVARDE
 >3RYPA 210 XRAY 1.60 0.209 0.234 no Catabolite gene activator <UNP CRP_ECOLI> [ESCHERICHIA COLI]
 MVLGKPQTDPTLEWFLSHCHIHKYP SKSTLIHQGEKAETLYYIVKGSVAVLIKDEEGKEM

ILSYLNQGDFIGELGLFEEGQERSAWVRKTACEVAEISYKKFRQLIQVNPDILMRLSAQ
 MARRLQVTSEKVGNLAFDVTGRIAQTLLNLAQPDAMTHPDGMQIKITRQEIGQIVGCS RETVGRILKMLEDNQLISAHGKTIVVYGT
 >3DSHA 246 XRAY 2.00 0.206 0.242 no Interferon regulatory factor 5 <UNP IRF5_HUMAN> [HOMO SAPIENS]
 EQLLPDLLISPHMLPLTDLEIKFYRGRPPRALTISNPHGCRLFYSQLQLEATQEQLVFGP
 ISLEQVRFPSPEDIPSDKQRFYTNQLLDVLDRLILQLQGQDLYAIRLCQCKVFWSGPCA
 SAHDSCPNPIQREVKTFLSLEHFLNELILFQKGQTNTPPPFIFFCFGEWPDRKPREK
 KLITVQVVPVAARLLLEMFSGELSWADDIRLQISNPDLKDRMVEQFKELHHIWQSQQRL
 QPVAQA
 >4BHA 94 XRAY 1.95 0.174 0.224 no PATERNALLY-EXPRESSED GENE 3 PROTEIN <UNP PEG3_HUMAN>
 [HOMO SAPIENS]
 GHMTDSEFFHQFRNLIYVEFVGPRKTLIKLRNLCLDWLQPETRTKEEIIELLVLEQYLT
 IIPKLPVVRRAKPPENCEKLVLTLENYKEMYQP
 >2GPEA 52 XRAY 1.90 0.205 0.249 no Bifunctional protein putA <UNP PUTA_ECOLI> [ESCHERICHIA COLI]
 MGTMTMGVKLDDATREIKSAATRDRTPHWLIKQAFSYLEQLENSDTLPE
 >1XD7A 145 XRAY 2.30 0.260 0.285 no ywnA <UNP P71036_BACSU> [BACILLUS SUBTILIS SUBSP. SUBTILIS]
 MSLINSRLAVAIHISLISMDEKTSSEIIADSVNTNPVVRRMISLLKKADILTSRAGVP
 GASLKKDPADISLLEVYRAVQKQELFAVHENPNPKCPVGKKIQNALDETFSVQRAMEN
 ELASKSLKDVNMHLFEGGSHHHHHH
 >3R4KA 260 XRAY 2.46 0.192 0.231 no Transcriptional regulator, IclR family <UNP
 Q1GKY2_SILST> [RUEGERIA SP. TM1040]
 MGTVSKALTLTYFNHGRLEIGLSDLTRLSGMNKATVYRLMSELQEAGFVEQVEGARSY
 RLGPQVRLAALREASVPILSASRRVRLRESEDTGETTHLSLLQGEQLASLSHAYSSRNA
 TKVMMEDAEVLTFHGTASGLAVLAYSEPSFVDAVLAAPLTARTPQTQTDPAAIRAEIAEV
 RRTGLAQSIGGFEEVSHAVPIFGPDAVLGALAVAAPTSRMTPDQKRTIPPALRAAGL SLTERIGGACPPEFPTDIAA
 >3AL2A 235 XRAY 2.00 0.172 0.204 no DNA topoisomerase 2-binding protein 1 <UNP TOPB1_HUMAN> [HOMO
 SAPIENS]
 GPLGSLKKQYIFQLSSLPQERIDYCHLIEKLGGLVIEKQCFDPTCTHIVVGHPLRNEKY
 LASVAAGKWVLRHSYLEACRTAGHFVQEEDYEWGSSSILDVLTGINVQRRLLALAAMRWR
 KKIQQRQESGIVEGAFSGWKVILHVDQSREAGFKRLQSGGAKVLPGHVSVPLFKEATHLF
 SDLNKLKPDSDGVNIAEAQAQNVYCLRTEYIADYLMQESPPHVENYCLPEAISFI
 >2ALCA 65 NMR NA NA NA no ETHANOL REGULON TRANSCRIPTIONAL ACTIVATOR <UNP ALCR_EMENT> [EMERICELLA
 NIDULANS]
 GSMADTRRRQNHSCDPCRKGKRRCDAPENRNEANENGWVSCSNCKRWKDCFTFNWLSQR
 SKNSS
 >1XNAA 183 NMR NA NA NA no DNA-REPAIR PROTEIN XRCC1 <UNP XRCC1_HUMAN> [HOMO SAPIENS]
 MPEIRLRHVVCSSQDSTHCAENLLKADTYRKWRAAKAGEKTSVVLQLEKEEQIHSVDI
 GNDGSFAFVEVLVGSSAGGAGEQDYEVLLVTSSFMSPSESRSRGNPNRVRMFGPDKLVRAA
 AEKRWDRVKIVCSQPYSKDSPFGLSFVRFHSPDKDEAEAPSQKVTVTKLGGFRVKEEEE
 SAN
 >3U61B 324 XRAY 3.20 0.244 0.305 no DNA polymerase accessory protein 44 <UNP DPA44_BPT4>
 [ENTEROBACTERIA PHAGE T4]
 GPGGSMITVNEKEHILEQKYRSTIDECLPAFDKETFKSITSKGKIPHIILHSPSPGTG
 KTTVAKALCHDVNADMMFVNGSDCKIDFVRGPLTNFASAASFDRQKVIIVIDEFDRSGLA
 ESQRHLRSFMEAYSSNCSIIITANNIDGIIKPLQSRCRVITFGQPTDEDKIEMMQMIRR
 LTEICKHEGIAIADMKVVAALVKKNFPDFRKTIGELDSYSSKGVLDAIILSLVTNDRGAI
 DDVLESLKNKDVQKRLRALAPKYAADYSWVFGKLAEEIYSRVTPQSIIRMYEIVGENNQYH
 GIAANTELHLAYLFIQLACEMQWK
 >3U61F 228 XRAY 3.20 0.244 0.305 no DNA polymerase processivity component <UNP DPA5_BPT4>

[ENTEROBACTERIA PHAGE T4]
 MKLSKDDTALLKNFATINSIGIMLKSGQFIMTRAVNGTTYAEANISDVIDFDVAIYDLNGF
 LGILSLVNDDAEISQSESGNIIKADARSTIFWPAADPSTVVAPNKPPIFPVASAVTEIKA
 EDLQQLLRVSRGLQIDTIAITVKEGKIVINGFNKVEDSALTRVKYSLTLGDYDGENTFNF
 IINMANMKMQPGNYKLLWAKGKQGAAKFEGEHANYVVALEADSTHDF
 >3N4PA 279 XRAY 2.15 0.222 0.272 no Terminase subunit UL89 protein <UNP TERL_HCMVA> [HUMAN HERPESVIRUS
 5]
 MGHHHHHHDYDIPTTENLYFQGGGTNKISQNTVLITDQSREEFDILRYSTLNTNAYDYFG
 KTLVYVLDPAFTTNRKASGTGVAAGVAYRHQFLIYGLEHFFLRDLSESSEVAIAECAAHM
 IISVLSLHPYLDLRIAVEGNTNQAADVRIACLIRQSVQSSTLIRVLFYHTPDQNHIEQP
 FYLMGRDKALAVEQFISRFNSGYIKASQELVSYTIKLSHDPIEYLLLEQIQNLHRVTLAEG
 TTARYSAKRQNRISDDLIIAVIMATYLCDDIHAIRFRVS
 >4LRVA 109 XRAY 2.50 0.203 0.242 no DNA sulfur modification protein DndE <UNP B3HI59_ECOLX>
 [ESCHERICHIA COLI]
 SMLPNRMALSRQTEDQLKKLKGYTGITPNIAARLAFFRSVESEFRYSPERDSKKLDGTLV
 LDKITWLGETLQATELVKMLYPQLEQKALIKAWAAHVEDGIAALRNHK
 >2P5KA 64 XRAY 1.00 0.139 0.160 no Arginine repressor <UNP ARGR_BACSU> [BACILLUS SUBTILIS]
 MNKGQRHIKIREIITSNEIETQDELVDMLKQDGYKVTQATVSRDIKELHLVKVPTNNGSY
 KYSL
 >1AKHB 83 XRAY 2.50 0.201 0.302 no MATING-TYPE PROTEIN ALPHA-2 <UNP MTAL2_YEAST> [SACCHAROMYCES
 CEREVISIAE] TKPYRGHRFTKENVRILESWFAKNIENPYLDTKGLENLMKNTSLSRQIKNWVSNRRRKE
 KTITIAPELADLLSGEPLAKKKE
 >3P83A 245 XRAY 3.05 0.188 0.216 no DNA polymerase sliding clamp <UNP PCNA_ARCFU>
 [ARCHAEOGLOBUS FULGIDUS]
 MIDVIMTGELLKTVTRAIVALVSEARHIFLEKGLHSRAVDPANVAMVIVDIPKDSFEVYN
 IDEEKTIGVMDRIFDISKSISTKDLVELIVEDESTLKVKGFSVEYKVALIDPSAIRKEP
 RIPELELPAKIVMDAGEFKKAAIAADKISDQVIFRSDKEGFRIEAKGDVDSIVFHMTE
 LIEFNGGEARSMFSVDYLKEFCKVAGSGDLLTIHLGTNYPVRLVFELVGGRKVEYILAP
 RIESE
 >3P83D 217 XRAY 3.05 0.188 0.216 no Ribonuclease HII <UNP RNH2_ARCFU> [ARCHAEOGLOBUS FULGIDUS]
 GPLGSPEFPGRMLKAGIDEAGKCVIGPLVAGVACSDERLRLKLGKDSKKLSQGRREE
 LAEEIRKICRTEVLKVPENLDERMAAKTINEILKECYAEIILRLKPEIAYVDSPDVIPE
 RLSRELEEITGLRVVAEHKADEKYPLVAAASIIAKVEREREIERLKEKFGDFGSGYASDP
 RTREVLKEWIASGRIPSCVRMRWKTVSNLRQKTLDDF
 >2D7LA 81 NMR NA NA NA no WD repeat and HMG-box DNA binding protein 1 <UNP WDHD1_HUMAN> [HOMO SAPIENS]
 GSSGSSGRPKTGFQMWLEENRSNLSNPDFSDEADIKEGMIRFVRLSTEERKVVWANKA
 KGETASEGTEAKKRKSGPSSG
 >1S6MA 293 XRAY 2.28 0.210 0.245 no TrwC <UNP Q47673_ECOLI> [ESCHERICHIA COLI]
 MLSHMVLTRQDIGRAASYEDGADDYYAKDGDASEWQKGAEELGSGEVDKSRFRELLA
 GNIGEGHRIMRSATRQDSKERIGLDLTFSAKPSVSLQALVAGDAEIIKAHRAVARTLEQ
 AEARAQARQKIQKGKTRIETTGNLVIGKFRHETSRRERDPQLHTHAVILNMTKRSQWAL
 KNDEIVKATRYLGAVYNAELAHELQKLGYYQLRYGKDGNFDLAHIDRQQIEGFSKRTEQIA
 EWYAARGLDPNVSLEQKQAAKVLRAKKTSDREALRAEWQATAKELGIDFS
 >3BQOA 211 XRAY 2.00 0.220 0.237 no Telomeric repeat-binding factor 1 <UNP TERF1_HUMAN> [HOMO
 SAPIENS]
 EEEEEAGLVAEAEVAAGWMLDFLCLSLCRAFRDGRSEDFRTRNSAEAIHGLSSLTA
 CQLRTIYICQLTRIAAGKTLDAQFENDERITPLESALMIWGSIEKEHDKLHEEIQNLK

IQAIAVCMENGNFKEAEEVFERIFGDPNSHMPFKSKLLMIISQKDTFHSFFQHFSYNHMM EKIksyVnYVLSEKSSTFLMKAaAKVVESKR
 >3VIBA 210 XRAY 2.40 0.212 0.256 no MtrR <UNP C0ITL7_NEIGO> [NEISSERIA GONORRHOAE]
 MRKTKTEALKTKHEHMLAALETfYRKGIARTSLNEIAQAAGVTRDALYWHFNKEDLFDA
 LFQRICDDIENCIAQDAADAEGGSWTVFRHTLLHFFERLQSNDIHYKFHNILFLKCEHTE
 QNAAVIAIARKHQAIWREKITAVL TEAVENQDLADDLDKETAVIFIKSTLDGLIWRWFSS GESFDLGKTAPRIIGIMDNLENHPCLRRK
 >3V4GA 180 XRAY 1.60 0.182 0.198 no Arginine repressor <UNP ARGR_VIBVY> [VIBRIO VULNIFICUS]
 MHHHHHSSGVDLGTENLYFQSNAMRPSEKQDNLVRAFKALLKEERFGSQGEIVEALKQE
 GFENINQSKVSRMLTKFGAVRTRNAKMEMVYCLPTELGVPTVSSSLRELVDVDHNQALV
 VIHTGPAAQLIARMLDSLKGSEGILGVVAGDDTIFITPTLTITTEQLFKSVCELFYAG
 >1JHGA 101 XRAY 1.30 0.127 0.172 no TRP OPERON REPRESSOR <UNP TRPR_ECOLI> [ESCHERICHIA COLI]
 SAAMAEQRHQEWLRFVDLLKNAYQNDLHPLLNMLTPDEREALGTRVRIIEELLRGEMS
 QRELKNELGAGIATITRGSNSLKAAPVELRQWLEEVLLKSD
 >2LJ6A 177 NMR NA NA NA no Probable ATP-dependent DNA ligase <UNP Q9I1X7_PSEAE> [PSEUDOMONAS
 AERUGINOSA]
 MPSSKPLAEYARKRDFRQTPEPSGRKPRKDSTGLLRYCVQKHDA SRLHYDFRLELDGTLK
 SWAVPKGPCLDPAVKRLAVQVEDHPLDYADFEQSIPQGHYGAGDVIVWDRGAWTPLDDPR
 EGLEKGHLSFALDGEKLSGRWHLIRTNLRGKQSQWFLVKAKDGEARSLDRFDVLKER
 >3MAJA 382 XRAY 2.05 0.187 0.232 no DNA processing chain A <UNP Q6N563_RHOPA>
 [RHODOPSEUDOMONAS PALUSTRIS]
 GHMDVGERSSDQGTTVL TEAQRIDWMRLIRAENVGPRTFRSLINHFGSARAALERLPELA
 RRGGAARAGRIPSEDEARREIEAGRRIGVELVAPGETGYPTLATIDDAPPLLGVHALPE
 ALAVMARPMIAIVGSRNASGAGLKFAGQLAADLGAAGFVVISGLARGIDQAAHRASLSSG
 TVAVLAGGHDKIYPAEHEDLLLDIIQTRGAAISEMPLGHVPRGKDFPRRNRLISGASVGV
 AVIEAAYRSGSLITARAADQGREVFVAVPGSPLDPRAAGTNDLIKQGATLITSASDIVEA
 VASILERPIELPGREPEHAPGEPDGTDRTRILALLGPSPVGIDDLIRLSGISPAVVRT ILLELELAGRLERHGGSLVSL
 >2MA1A 75 NMR NA NA NA no DNA helicase RecQ <UNP Q9RUU2_DEIRA> [DEINOCOCCUS RADIODURANS]
 HDAPLFEALRAWRLQKAKELSLPPYTI FHDTLKTIAELRPGSHATLGTVSGVGGRKLAA
 YGDEVLQVVRDSSGG
 >2WKDA 119 XRAY 2.10 0.240 0.256 no ORF34P2 <UNP Q09WL7_9CAUD> [LACTOCOCCUS PHAGE P2]
 GTIITVTAQANEKNTRTVSTAKGDKKIISVPLFEKEKGSNVKVAYGS AFMPDFIQMGDTV
 TVSGRVQAKESGEYVNYNFVPTVEKVFITNDSSQSQAQDLFGGSEPIEVNSEDLPF
 >1MP9A 198 XRAY 2.00 0.209 0.254 no TATA-binding protein <UNP TBP_SULAC> [SULFOLOBUS
 ACIDOCALDARIUS] YIIPDEIPYKAVNIENIVATVTLDTL DLYAMERSVPNVEYDPDQFPGLIFRLESPKIT
 SLIFKSGKMVVTGAKSTDELIAVKRIIKTLKKYGMQLTGKPKIQIQNIVASANLHVIVN
 LDKAAFLLENMYEPEQFPGLIYRMDEPRVLLIFSSGKMVITGAKREDEVHKAVKKIFD
 KLVELDCVKPVEEELEF
 >3EQXA 373 XRAY 1.60 0.170 0.197 no FIC DOMAIN CONTAINING TRANSCRIPTIONAL REGULATOR <UNP
 Q8E9K5_SHEON> [SHEWANELLA ONEIDENSIS]
 GMEWQAEQAYNHLPLPLDSKLAELAETLPILKACIPARAALAEKQAGELLPNQGLLIN
 LLPLLEAQGSSEIENIVTTDKLFQYAQEDSQADPMTKEALRYRTALYQCFTQLSNRPLC
 VTTALEICSTIKSVQMDVRKVPGTSLTNQATGEVIYTPPAGESVIRDLLSNWEAFLHNQD
 DVDPLIKMAMAHYQFEAIHPFIDNGRTGRVLNILYLIDQQLLSAPILYLSRYIVAHKQD
 YYRLLLNVTQEQEWQPWIIFILNAVEQTAKWTTHKIAAARELIAHTTEYVRQQLPKIYSH
 ELVQVIFEQPYCRIQNLVESGLAKRQTASVYLKQLCDIGVLEEVSQSGKEKLFVHPKFVTL
 MTKDSNQFSRYAL
 >1VJFA 180 XRAY 1.62 0.146 0.167 no DNA-binding protein, putative <UNP Q9ABV9_CAUCR>
 [CAULOBACTER CRESCENTUS CB15]

MGSDKIHIIHHHMKTRADLFAFFDAHGVHDHKTLDHPPVFRVEEGLEIKAAMPGGHTKNLF
 LKDAKGQLWLISALGETTIDLKKLHHVIGSGRLSFGPQEMMLETLGVTGPSVTAFGLIND
 TEKRVRFLVDKALADSDPVNFHPLKNDATTAVSQAGLRRFLAALGVEPMIVDFAAMEVVG
 >2EBIA 86 NMR NA NA NA no DNA binding protein GT-1 <UNP Q9FX53_ARATH> [ARABIDOPSIS THALIANA]
 KKRAETWVQDETRSLIMFRRGMDGLFNTSKSNKHLWEQISSKMREKGFDRSPDMCTDKWR
 NLLKEFKKAKHHDRNGSAKMSYYKE
 >3JRHA 98 XRAY 2.88 0.224 0.253 no DNA-binding protein fis <UNP FIS_ECOLI> [ESCHERICHIA COLI]
 MFEQRVNSDVLTVSTVNSQDQVTQKPLRDSVKQALKNYFAQLNGQDVNDLYELVLAEEVEQ
 PLLDMVMQYTRGNQTRAAALMMGINRGTLRKKLKKYGMN
 >2JR1A 79 NMR NA NA NA no Virulence regulator <UNP Q9PFC9_XYLFA> [XYLELLA FASTIDIOSA]
 FNVKQKSEITALVKEVTPPRKAPSKAKREAPIKYWLPHSGATWSGRGKIPKPFPAWIGTA
 AYTAWKAKHPDEKFPAPPG
 >4G4KA 103 XRAY 1.52 0.181 0.209 no Accessory gene regulator protein A <UNP AGRA_STAAU>
 [STAPHYLOCOCCUS AUREUS]
 MDNSVETIELKRGSSNSVYVQYDDIMFFESSTKSHRLIAHLNDRQIEFYGNLKELSQLDDR
 FFRCHNSFVVNRHNIESIDSKERIVYFKNKEHCYASVRNVKKI
 >3O27A 68 XRAY 2.80 0.252 0.289 no Putative uncharacterized protein <UNP Q9P9J8_SULIS> [SULFOLOBUS
 ISLANDICUS]
 MRPGIRKLVVLNPRAYKGGSGHTTFYLLIPKDIAEALDIKDDTFILNMEQKDGDIVLSY
 KRVKELKI
 >2KJ8A 118 NMR NA NA NA no Putative prophage CPS-53 integrase <UNP INTS_ECOLI> [ESCHERICHIA COLI-12]
 SSNNNSFSAIYKEWYEHKKQVWSVGATELAKMFDDDLPIIGGLEIQDIEPMQLLEVIR
 RFEDRGAMERANKARRRCGEVFRYAIVTGRAKYNPAPDLADAMGYRKKNEHHHHHH
 >3KJPA 299 XRAY 1.80 0.211 0.234 no Protection of telomeres protein 1 <UNP POTE1_HUMAN> [HOMO SAPIENS]
 MSLVPATNYIYTPLNQLKGGTIVNVYGVVKFFKPPYLSKGTDYCSVVTIVDQTNVKTCL
 LFSGNYEALPIIYKNGDIVRFHRLKIQVYKKEQGITSSGFASLTFEGLGAPIIPRTSS
 KYFNFTTEDHKMVEALRVWASTHMSPSWTLLKLCVQPMQYFDLTCQLLGKAEVDGASFL
 LKVDGTRTPFSPSWRLIQDLVLEGLDSHHLRLQNLIDILVYDNHVVHVARSLKVGSLR
 IYSLHTKLQSMNSENQTMLSLEFHLHGGTSYGRGIRVLPESNSDQVQLKKDLESANLTA
 >4NJYA 163 XRAY 1.32 0.139 0.164 no Histidine triad nucleotide-binding protein 2, mitochondrial
 <UNPHINT2_HUMAN> [HOMO SAPIENS]
 MAAAVVLAAGLRAARRAATGVRGGQVRGAAGVTDGNEVAKAQQATPGGAAPTIFSRIL
 DKSLPADILYEDQQCLVFRDVAPQAPVHFLVIPKKIPRISQAEEDQQLLGHLLLVAKQ
 TAKAEGLDGYRLVINDGKLGAQSVYHLHIHVLGGRQLQWPPG
 >3UFDA 82 XRAY 2.80 0.207 0.237 no Regulatory protein <UNP Q8GGHO_9ENTR> [ENTEROBACTER SP.
 RFL1396] GSHMESFLLSKVSFVIKKIRLEKGMTQEDLAYKSNLDRYISGIERNRNLTIKSLELIM
 KGLEVSDVVFEMLIKEILKHD
 >3MKWB 138 XRAY 2.99 0.234 0.268 no Protein sopB <UNP SOPB_ECOLI> [ESCHERICHIA COLI]
 MGSSHHHHHSSGLVPRGSHYRPTSAYERGQRYASRLQNEFAGNISALADAENISRKIIT
 RCINTAKLPKSVVALFSHPGELSARSGDALQKAFTDKEELLKQQASNLHEQKAGVIFEA
 DEVITLLTSVLKTSSASR
 >3FPNB 106 XRAY 1.80 0.231 0.248 no Geobacillus stearothermophilus UvrB interaction domain <PDB 3FPN>
 [GEOBACILLUS STEAROTHERMOPHILUS] GSHMGSPEEYRELVSRLVGMIEIERNALLRRLVDIQYDRNDIDFRGTFRVRGDVVEIFP
 ASRDEHCIRVEFFGDEIERIREVDALTGEVLGEREHVAIFPASHFV
 >2FPHX 165 XRAY 1.70 0.243 0.299 no ylmH <GB AAL00310> [STREPTOCOCCUS PNEUMONIAE]
 GIYQHFSIEDRPFLDKGMEWIKKVEDSYAPFLTPFINPHQEKLLKILAKTYGLACSSSGE
 FVSSEYVRVLLYPDYFQPEFSDFEISLQEIYVSNKFEYLTHAKILGTVINQLGIERKLF
 DILVDEERAQIMINQQFLLLFQDGLKKIGRIPVSLEERPFTTEKID

>304QA 150 XRAY 1.55 0.166 0.211 no integrase <UNP Q4ZJZ6_RSISR> [ROUS SARCOMA VIRUS]
 GSGRGLGPLQIWQTDFTLEPRMAPRSLAVTVDASSAIVVTQHGRVTSVAAQHHWATAI
 AVLGRPKAIKTDNGSCFTSKSTREWLARWGIAHTTGIPGNSQQQAMVERANRLKDKIRV LAEGDGFMKRIPTSKQGELLAKAMYALNHF

>3LX2A 259 XRAY 2.40 0.246 0.305 no DNA polymerase sliding clamp 2 <UNP PCNA2_PYRKO> [THERMOCOCCUS
 KODAKARENSIS] MTFEIVFDSAREFESLIATLEKFFDEAVFQVNMEGIQMRAIDPSRVVLVDLNLPEMLFSK
 YSVESEEIAAFDLKRFLKVLKLARSRDTLVRKGGNFLEVGLLDGENTWFKLPLIDANT
 PEIEIPSLPWTVKAVVLGALKRAVKAACLVSDSIYFMATPEKLTFAEGNDSEVRTVLT
 MEDPGLLDLEHKMTAKSAYGVAYLEDILRSLADAEVIRFGFDIPLLLKYMVRDAGEV SFLIAPRVEEGRSHHHHHH

>3KHKA 544 XRAY 2.55 0.214 0.242 no Type I restriction-modification system methylation subunit <UNP
 Q8PZR3_METMA> [METHANOSARCINA MAZEI] MSLDIEQQFLNDLDNLWRAADKLRSNLDAANYKHVVGLGLFLKYVSDAFEERQQELTEL
 FQKDDDDNIYYLPREDYDSDEAYQQAIAEELEIGDYYTEKNVFWVPKTARWNKLRDVITL
 PTGSVIWQDEQGEDVKLRVSWLIDNAFDDIEKANPKLKGILNRISQYQLDADKLIGLIN
 EFSLTSFNPEYNGEKNLKS KDILGHVYEFYLGQFALAEGKQGGQYTPKSIVTLIVEM
 LEPYKGRVYDPAMSGGGFFVSSDKFIEKHANVKHYNASEQKKQISVYGQESNPTTWKLAA
 MNMVIIRGIDFNFQKKNADSFLDDQHPDLRADFVMTNPPFNMKDWWHEKLADDPRTINTN
 GEKRILTPTGNANFAWMLHMLYHLAPTGSMAALLANGSMSNTNNEGEIRKTLVEQDLV
 ECMVALPGQLFTNTQIPACIWFLTKDKNAKNGKRRGQVLFIDARKLGYMKDRVLRDFK
 DEDIQKLADTFHNWQQEWSEENNAGFCFSADLALIRKNDFVLTPGRYVGAEAEDEGHH
 HHHH

>2M14A 119 NMR NA NA NA no RNA polymerase II transcription factor B subunit 1 <UNP TFB1_YEAST>
 [SACCHAROMYCES CEREVISIAE] PSHSGAAIFEKVSGIIAINEVDSPAELTWRSTDGDKVHTTVLSTIDKLQATPASSEKMMML
 RLIGKVDESKKRKNNEGNEVVPKQRMFSFNNRTVMDNIKMTLQQIISRYKDADGNSS

>2BNZA 53 XRAY 2.60 0.227 0.258 no ORF OMEGA <UNP Q57468_STRPY> [STREPTOCOCCUS PYOGENES]
 MAKKDIMGDKTVRVRADLHHIIKIETAKNGGNVKEVMDQALEEYIRKYLPDKL

>2Z3XA 63 XRAY 2.10 0.257 0.283 no Small, acid-soluble spore protein C <UNP SSPC_BACSU> [BACILLUS
 SUBTILIS]
 AKLLIPQAASAIEQMKLEIASSEFGVQLGAETTSRANGSVGGEITKRLVRLAQQNMGQGFH
 GQQ

>2JX3A 131 NMR NA NA NA no Protein DEK <UNP DEK_HUMAN> [HOMO APIENS]
 FTIAQGGKQKLCEIERIHFFLSKKKTDELRLNHLKLLYNRPQTVSSLKKNVGGQFSGFPFEK
 GSVQYKKKEEMLKKFRNAMLKSICEVLDLERSGVNSELVKRILNFLMHPKPSGKPLPKSK KTCSEKSGSKKER

>2NTIA 249 XRAY 2.50 0.211 0.251 no DNA polymerase sliding clamp B <UNP PCNA2_SULSO>
 [SULFOLOBUS SOLFATARICUS]
 MVKIVYPNAKDFFSFINSITNVTDSIILNFTEDGIFSRHLEDKVLMAIMRIPKDLSEY
 SIDSPTS VKLDVSSVKILSKASSKATIELTETDGLKIIIRDEKSGAKSTIYIKAKEG
 QVEQLTEPKVNLAVNFTTDESVLNVIAADVTLVGEEMRISTEEDKIKIEAGEEGKRYVAF
 LMKDKPLKELSIDTSASSSYSAEMFKDAVKGLRGFSAPTMSVSGENLPMKIDVEAVSGGH
 MIFWIAPRL

>3RH2A 212 XRAY 2.42 0.207 0.250 no Hypothetical TetR-like transcriptional
 regulator
 <UNP A1S1Q5_SHEAM> [SHEWANELLA AMAZONENSIS]
 GMKTRDKIIQASLELFNEHGERTITTNHIAAHLDISPGNLYYHFRNKEDIIRCIFDQYEQ
 HLLLGFKPYADQKVDLELLMSYFDAMFYTMWQFRFMYANLADILARDDTLKARYLKVQQA
 VLEQSI AVLNLKKGILQIEDERIADLDTIKMIIGFWISYKLTQSSIATISKASLYEG
 LLRVLMIFKAYSTPDSLAFDRLEQHFRSQSN

>2HQLA 110 XRAY 2.00 0.210 0.272 no Hypothetical protein MG376 homolog <UNP
 Y554_MYCPN> [MYCOPLASMA PNEUMONIAE]
 GGGGGMLNRVFLGEIESSCWSVKKTGFLVTIKQMRFFGERLFTDYYVIYANGQLAYEL

EKHTKKYKTISIEGILRTYLERKSEIWKTTIEIVKIFNPKNEIVIDYKEI
>1KNUA 274 XRAY 2.50 0.224 0.264 no PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR
GAMMA
<UNP PPAT_HUMAN> [HOMO SAPIENS]
LNPEADLRALAKHLYDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIK
FKHITPLQEQSKEVAIRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVH
EIIYTMLASLMNKDGLVISEGQGFMTREFLKSRLKPFQDFMEPKFEFAVKFNALELDDSD
LAIFIAVILSGDRPGLLNKPIEDIQDNLLQALELQLKLNHPSSQLFAKLLQKMTDLR
QIVTEHVQLLQVIKKTETDMSLHPLLQEIKDLY
>1UFIA 64 XRAY 1.65 0.236 0.309 no Major centromere autoantigen B <UNP CENPB_HUMAN>
[HOMO SAPIENS]
GSHMPVPSFGEMAYFAMVKRYLTSFPIDDRVQSHILHLEHDLVHVTRKNHARQAGVRGL
GHQS
>3Q8DA 242 XRAY 2.30 0.197 0.234 no DNA repair protein recO <UNP D5CXR1_ECOKI>
[ESCHERICHIA COLI]
MEGWQRAFLHSRPWSETSLMLDVFTEESGRVRLVAKGARSKRSTLKGALQPFTPLLLRF
GGRGEVKTLSAEAVSLALPLSGITLYSGLYINELLSRVLEYETRFSELEFFDYLCIQSL
AGVTGTPEPALRRFELALLGHLGYGVNFTHCAGSGEPVDDMTYRYREEKGFIASVVIDN
KTFTGRQLKALNAREFPDADTLRAAKRFRMALKPYLGGKPLKSRELFRQFMPKRTVKTH
YE
>2DIGA 68 NMR NA NA NA no Lamin-B receptor <UNP LBR_HUMAN> [HOMO SAPIENS]
GSSGSSGMPSRKFADGEVVRGRWPGSSLYEVEILSHDSTSQLYTVKYKDGTELELKEND
IKSGPSSG
>3PC6A 104 XRAY 1.90 0.182 0.227 no DNA repair protein XRCC1 <UNP XRCC1_MOUSE>
[MUS MUSCULUS]
MPELPDFFEKGHFFLYGEFFPGDERRRLIRYVTAFNGELEDYMNERVQFVITAQEWDPNFE
EALMENPSLAFVRPRWIYSCNEKQKLLPHQLYGVVPQAHHHHH
>3W3WA 1078 XRAY 2.20 0.217 0.256 no Importin subunit beta-3 <UNP IMB3_YEAST>
[SACCHAROMYCES CEREVISIAE]
MSALPEEVNRTLLQIVQAFASPDNQIRSVAEKALSEEWITENNIEYLLTFLAEQAQAFSQD
TTVAALSAVLFRKLALKAPITHIRKEVLAQIRSSLLKGFLSERADSIHKLSDAIAECVQ
DDLPAWPELLQALIESLKSNGPNFRESSFRILTTVPYLITAVDINSILPIFQSGFTDASD
NVKIAAVTAFVGYFKQLPKSEWSKLGILLPSLLNSLPRFLDDGKDDALASVFESLIELVE
LAPKLFKDMFDQIIQFTDMVIKNKDLEPPARTTALELLTVFSENAPQMCKSNQNYGQTLV
MYTLIMMTEVSIDDDDAAEWIESDDTDDEEEVTDHARQALDRVALKLGGEYLAAPLFQY
LQQMITSTEWREFAAMMALSSAAEGCADVLIGEIPKILDMVIPLINDPHPRVQYGCCNV
LGQISTDFSPFIQRTAHDRIPLALISKLTSECTSRVQTHAAAALVNFSEFASKDILEPYL
DSLLTNLLVLLQSNKLYVQEALTTIAFIAEAAKNKFIKYDTLMPLLLNLKVNNDNS
VLKKGKMECATLIGFAVGKEKFHEHSQELISILVALQNSDIDEDDALRSYLEQSWSRICR
ILGDDFVPLLPVIVPILLITAKATQDVGLIEEEAANFQQYPDWDVVQVQGHIAHTSV
LDDKVSAMELLQSYATLLRGQFAVYVKEVMEEIALPSLDFYLDHGVRAAGATLIPILLSC
LLAATGTQNEELVLLWHKASSKLIGGLMSEPMEITQVYHNSLVNGIKVMGDNCLSEDQL
AAFTKGVSANLTDTYERMQRHGDGEYNENIDEEEDFTDEDLLDEINKSIAAVLKTNG
HYLKNLENIWPMINTFLDNEPILVIFALVIGDLIQYGGEQTASMKNAPKPVTECLIS
PDARIRQAASYIIGVCAQYAPSTYADVCIPTLDTLVQIVDFPGSKLEENRSSTENASAAI
AKILYAYNSNIPNVDITYTANWFKTLPTITDKEAASFNYQFLSqliennSPIVCAQSNISA

VVDSVIQALNERSLTEREGQTVISSVKLLGFLPSSDAMAIFNRYPADIMEKVHKWFA
>1R5KA 261 XRAY 2.70 0.208 0.236 no Estrogen receptor <UNP ESR1_HUMAN> [HOMO SAPIENS] MDPMIKRSKNSLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRE LVHMINWAKRVPGFVDLTLHDQVHLLCAWLEILMIGLVWRSMHPGKLLFAPNLLDRN QGKCVEGMVEIFDMLLATSSRFRMMNLQGEEFVCLKSIIILLNSGVYTFLSSTLKSLEEKD HIHRVLDKITDTLIHLMAGLTLQQQHQLAQLLLILSHIRHMSNKGMEHLYSMCKNV VPLYDLLLEMLDAHRLHAPTS
>1U9NA 236 XRAY 2.30 0.208 0.231 no Transcriptional repressor EthR <UNP P96222_MYCTU> [MYCOBACTERIUM TUBERCULOSIS] MGSSHHHHHHSSGLVPRGSHVTTSAASQASLPRGRRTARPSGDDRELAILATAENLLEDR PLADISVDDLAKGAGISRPTFYFYFPSKEAVLLTLLDRVVNQADMALQTLAENPADTDRE NMWRTGINVFETFGSHKAVTRAGQAARATSVEVAELWSTFMQKWIAYTAAVIDAERDRG AAPRTLPAHELATALNLMNERTLFASFAGEQPSVPEARVLDLTVHIWVTSIYGENR
>3II6X 263 XRAY 2.40 0.240 0.280 no DNA ligase 4 <UNP DNLI4_HUMAN> [HOMO SAPIENS] GAMGSKISNIFEDVEFCVMSGTDSQPKPDLENRIAEFGGYIVQNPGPDYTCVIAGSENI R VKNIIILSNKHDVVKPAWLECFKTKSFVPWQPRFMIHMCPTKEHFAREYDCYGDSYFID TDLNQLKEVFSGIKNSNEQTPEEMASLIADLEYRYSWDCSPLSMFRRHVYLDYSYAVIND LSTKNEGTRLAIKALELRFHGAKVVSCLAEGVSHVIGEDHSRVADFKAFRRTFKRKFKI LKESWVTDSIDKCELQEEYLI
>2DA6A 102 NMR NA NA NA no Hepatocyte nuclear factor 1-beta <UNP HNF1B_HUMAN> [HOMO SAPIENS] GSSGSSGRNRFKWPASQQILYQAYDRQKNPSKEEREALVEECNRAECLQRGVSPSKAHG LGSNLVTEVRVYNWFANRRKEEAFRQKLAMDAYSSNSGPSSG
>3DPJA 194 XRAY 1.90 0.196 0.243 no Transcription regulator, TetR family <UNP Q5LS67_SILPO> [SILICIBACTER POMEROYI] SNAMVQAQTRDQIVAADELQYRQGAQTSFVDISAAGVSRGNFYHFKTKDEILAEVI RLRLARTAQLMADWQGTGDSRARIASFIDLMMNRKAITRYGCPVGSCLTELSKLDHAA QGQANGLFTLFRDWLQRQFAEAGCTTEAPALAMHLLARSQGAATLAQSFHDEGFLRSEVA DMHRWLDNTLPMTT
>1TC3C 51 XRAY 2.45 0.234 0.318 no TC3 TRANSPOSASE <UNP TC3A_CAEL> [CAENORHABDITIS ELEGANS] PRGSALSDTERAQLDVMKLLNVSLHEMSRKISRHRHCIRVYLKDPVSYGTS
>3EZ2A 398 XRAY 2.05 0.191 0.232 no Plasmid partition protein A <UNP PARA_ECOLX> [ESCHERICHIA COLI] MSDSSQLHKVAQRANRMLNVLTEQVQLQKDELHANEFYQVYAKAALAKPLLLTRANVDYA VSEMEEGYVFDKRPAGSSMKYAMSIQNIIDIYEHARGVPKYRDRYSEAYVIFISNLKGGV SKTVSTVSLAHAMRAHPHLLMEDLRILVIDLDPQSSATMFLSHKHSIGIVNATSAQAMLQ NVSREELLEEFIVPSVVPVGDVMPASIDDAFIASDWRELCNEHLPQQNIHAVLKENVIDK LKSDYDFILVDSGPHLDAFLKNALASANILFTPLPPATVDFHSSLKYVARLPELVKLISD EGCECQLATNIGFMSKLSNKADHKYCHSLAKEVFGGDMLDVFLPRLDGFERCGESFDTVI SANPATYVGSADALKNARIAAEDFAKAVFDRIEFIRSN
>2Q2KA 70 XRAY 3.00 0.258 0.297 no Hypothetical protein <UNP Q2FDA3_STAA3> [STAPHYLOCOCCUS AUREUS] MGSSHHHHHHSSGLVPGSHMDKKETKHLKIKKEDYPQIFDFLENVPRGKTAHIREALR RYIEEIGENP
>3GE4A 173 XRAY 1.70 0.145 0.179 no DNA PROTECTION DURING STARVATION PROTEIN <UNP

Q8YE98_BRUME> [BRUCELLA MELITENSIS]
MAHHHHHHMPKSMHATRNDLPSNTKTTMIALLNENLAATIDLALITKQAHWNLKGPQFI
AVHEMLDGFRAELDDHVDITIAERAVQIGGTAYGTTQVVVKESRLKPYPTDIYAVHDHLVA
LIERYGDVANLVRKSIKDADDAGDDDTADIFTAASRLDKALWFLEAHVQESN
>1U3EM 174 XRAY 2.92 0.220 0.247 no HNH homing endonuclease <UNP YG31_BPSP1>
[BACILLUS PHAGE SP01]
MEWKDIKGYEGHYQVSNTGEVYSIKSGKTLKHQIPKDGYHRIGLFKGGKGTQVHRLVA
IHFCEGYEGLVVDHKDGNKNNLSTNLRWVTQKINVENQMSRGTNLVSKAQQIAKIKNQ
KPIIVISPDGIEKEYPSTKCACEELGLTRGKVDVLKGHRHHKGYTFRYKLNG
>2CYIA 151 XRAY 1.80 0.220 0.245 no Putative HTH-type transcriptional regulator
PHI519
<UNP REG6_PYRHO> [PYROCOCUS HORIKOSHII]
MRVPLDEIDKIIKILQNDGKAPLREISKITGLAESTIHERIRKLRESGVIKKFTAIIDP
EALGYSMLAFILVKVKAGYSEVASNLAKYPEIVEVYETTGDYDMVKIRTKNSEELNNF
LDLIGSIPGVEGTHTMIVLKTHKETTELPIK
>3FPNA 119 XRAY 1.80 0.231 0.248 no Geobacillus stearothermophilus UvrA
interaction domain <PDB 3FPN> [GEOBACILLUS STEAROTHERMOPHILUS]
GSHMTIEQMVDRLLSYPERTKMQLAPIVSGKKGTHAKTLEDIRKQGYVRVRIDREMREL
TGDIELEKNKKHSIDVVDRIIKDGIAARLADSLETALKLADGKVVDVIGEGELLFS
>1XVPA 236 XRAY 2.60 0.180 0.234 no Retinoic acid receptor RXR-alpha <UNP
RXRA_HUMAN> [HOMO SAPIENS]
NEDMPVERILEAEALAVEPKTETYVEANMGLNPSSPNDPVTNICQAADKQLFTLVEWAKRI
PHFSELPLDDQVILLRAGWNELLIASFSHRSIAVKDGILLATGLHVHRNSAHSAGVGAIF
DRVLTELVS KM RDMQMDKTELGLRAIVLFNPDSKGLSNPAEVEALREKVYASLEAYCKH
KYPEQPGRFAKLLLRPALRSIGLKCLEHLFFFKLIGDTPIDTFLMEMLEAPHQMT
>1KZYC 259 XRAY 2.50 0.216 0.256 no TUMOR SUPPRESSOR P53-BINDING PROTEIN 1 <UNP
TP53B_HUMAN> [HOMO SAPIENS]
ALEEQRGPLPLNKTFLGYAFLLTMATTSKLSRSKLPDGPTGSSEEEEFLEIPPFNK
QYTESQLRAGAGYILEDNEAQNTAYQCLLIADQHCRTKRYFLCLASGIPCVSHVWVHD
SCHANQLQNYRNYLLPAGYSLEEQRILDWQPRENPFQNLKVLVSDQQQNLELWSEILM
TGGAASVKQHSSAHNKDIALGVFDVVVTDPSCPASVLKCAEALQLPVVSQEWVIQCLIV
GERIGFKQHPKYKH DYVSH
>1YJMA 110 XRAY 2.20 0.213 0.243 no Polynucleotide 5'-hydroxyl-kinase <UNP
PNKP_MOUSE> [MUS MUSCULUS]
MSQLGSRGRLWLQSPTGGPPPIFLPSDQALVLGRGPLTQVTDKCSRNQVELIADPESR
TVAVKQLGVNPSTVGVHELKPGLSGSLGDLVLYLVNGLYPLTLRWEELS
>2NTIB 246 XRAY 2.50 0.211 0.251 no DNA polymerase sliding clamp C <UNP PCNA3_SULSO>
[SULFOLOBUS SOLFATARICUS]
MMKAKVIDAVSFSYILRTVGDFLSEANFIVTKEGIRVSGIDPSRVVFLDIFLPSSYFEGF
EVSQEKEIIGFKLEDVNDILKRVLKDDTLILSSNESKLTTFDGEFTRSFELPLIQVEST
QPPSVNLEFPFKAQLLTITFADIIDELSDLGEVLNIHSKENKLYFEVIGDLSTAKVELST
DNGTLLEASGADVSSSYGMEYVANTTKMRRASDSMELYFGSQIPLKLRFKLPQEGYGDFY
IAPRAD
>4JW3C 139 XRAY 2.60 0.226 0.264 no Alpha-helical artificial proteins <PDB 4JW3>
[SYNTHETIC CONSTRUCT]

MRGSHHHHHHTDPEKVEYIKNLQDDSYFVRRAAAAALGKIGDERAVEPLIKALKDEDRF
VRSSAAYALGEIGDERAVEPLIKALKDEDFVRRAAVALGEIGGERVRAAMEKLAETGT
GFARKVAVNYLETHKSLIS
>3JTZA 88 XRAY 1.30 0.214 0.239 no Integrase <UNP Q9Z3B4_YERPE> [YERSINIA PESTIS]
MSLTDAKIRTLKPSDKPFKVSDSHGLYLLVKPGGSRHWYLYRISGKESRIALGAYPAIS
LSDARQQREGIRKMLALNINLEHHHHHH
>1IYMA 55 NMR NA NA NA no EL5 <UNP EL5_ORYSA> [ORYZA SATIVA]
AMDDGVECAVCLAELEDGEEARFLPRCGHGFHAECVDMWLGSHTCPLCRLTVVV
>3ASLA 70 XRAY 1.41 0.161 0.196 no E3 ubiquitin-protein ligase UHRF1 <UNP
UHRF1_HUMAN> [HOMO SAPIENS]
SGPSCCHKDDVNRCLRCVACACHLCGGRQDPDKQLMCDECDMAFHICYCLDPPLSSVPSSEDE
WYCPECRNDA
>3M9QA 101 XRAY 1.29 0.171 0.192 no Protein male-specific lethal-3 <UNP MSL3_DROME>
[DROSOPHILA MELANOGASTER]
MKKHHHHHHMTLREDTPLFKGEIVLCYEPDKSKARVLYTSKVLNVFERRNEHGLRFYE
YKIHFGQWRPSYDRAVRATVLLKDTEENRQLQRELAEEAAKL
>1U2WA 122 XRAY 1.90 0.236 0.261 no Cadmium efflux system accessory protein <UNP
CADC_STAAU> [STAPHYLOCOCCUS AUREUS]
MKKKDTCEIFGYDEEKVNRIQGDLTVDISGVSQILKAIADENRAKITYALCQDEELCVC
DIANILGVTIANASHHLRLTYKQGVNFRKEGKLALYSLGDEHIRQIMMIALAHKKEVKV
NV
>3U61A 199 XRAY 3.20 0.244 0.305 no DNA polymerase accessory protein 62 <UNP
DPA62_BPT4> [ENTEROBACTERIA PHAGE T4]
SLFKDDIQLNEHQVAWYSKDWTAQSAADSFKEKAENEFEEIIGAINNKTCSIAQKDYS
KFMVENALSQFPECMPAVYAMNLIGSLSDAEHFNYLMAAVPRGKRYGKWAKLVEDSTEV
LI IKLLAKRYQVNTNDAINYKSILTKNGKLPLVLKELKGLVTDDFLKEVTKNVKEQKQLK
KLALWGLEHHHHHHHHHHHH
>4LG8A 354 XRAY 1.89 0.158 0.197 no Pre-mRNA-processing factor 19 <UNP PRP19_HUMAN>
[HOMO SAPIENS]
MHHHHHSSGRENLYFQGTPEIIQKLQDKATVLTTERKERGKTVPPELVKPEELSKYRQV
ASHVGLHSASIPGILALDLCPSTNKLITGGADKNVVFDSSEQILATLKGHTKKVTSV
VFHPSQDLVFSASPDATIRIWSVPNASCVQVVRHAESAVTGLSLHATGDYLLSSDDQYW
AFSDIQTGRVLTKVTDSETSGCSLTCAQFHPDGLIFGTGTMDSQIKIIDLKERTNVANFPG
HSGPITSIAFSENGYYLATAADSSVKLWDLRKLKNFKTLQLDNNFEVKSLIFDQSGTYL
ALGGTDVQIYICKQWTEILHFTEHSGLTGVAFGHHAKFIASGMDRSLKFYSL
>2ZDSA 340 XRAY 2.30 0.167 0.210 no Putative DNA-binding protein <UNP 069946_STRCO>
[STREPTOMYCES COELICOLOR]
MPRNFTLFTGQWADLPLEEVCRLARDFGYDGLACWGDHFEVDKALADPSYVDSRHQLL
DKYGLKCWAISNHLVGQAVCDAIIDERHEAILPARIWGDGDAEGVRQAAAAEIKDTARAA
ARLGVDTVIGFTGSAIHWLVAMFPPAPESMIERGYQDFADRWNPILDVDAEGVRFAHEV
HPSEIAYDYWTTHRALEAVGHRPAFGLNFDPSHFVWQDLDPVGFLWDFRDRIYHVDCKEA
RKRLDGRNGRLGSHLPWGDPRRGWDFVSAGHGDPWEDVFRMLRSIDYQGPVSEWEDAG
MDRLQGAPEALTRLKAFDFEPPSASFDAAFNSLEHHHHHH
>20D5A 116 XRAY 1.79 0.190 0.213 no hypothetical protein <PDB 20D5> [UNCULTURED
MARINE ORGANISM]
GMTGAVETESMKTVRIREKIKKFLGDRPRNTAEILEHINSTMRHGTTSSQQLGNVLSKDKD

IVKVGYIKRSGILSGGYDICEWATRNVVAEHCPWTEGQPIILNEEGDFTLGPLPE
>4IRGA 109 XRAY 1.70 0.190 0.228 no Transcriptional regulator ERG <UNP ERG_HUMAN> [HOMO SAPIENS]
GAMGSGIQRPGSGGIQLWQFLLELLSDSSNSSCITWEGTNGEFKMTDPDEVARRWGERKS
KPNMNYDKLSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQHPPE
>1YIOA 208 XRAY 2.20 0.205 0.275 no response regulatory protein <UNP 030989_PSEFL> [PSEUDOMONAS FLUORESCENS]
MTAKPTVFVDDMSVREGLRNLLRSAGFEVETFDCASTFLEHRRPEQHGCLVDMRMPG
MSGIELQEQLTAISDGIPIVFITAHDIPMTVRAMKAGAEFLPKPFEEQALLDAIEQGL
QLNAERRQARETQDQLEQLFSSLTGREQQLTLTIRGLMNKQIAGELGIAEVTVKVHRHN
IMQKLNVRSLANLVHLEKEYESFERGVS
>2ICTA 94 XRAY 1.63 0.198 0.201 no antitoxin higa <UNP YDDM_ECOLI> [ESCHERICHIA COLI]
MKMANHPRPGDIQESLDELNVSLREFARAMEIAPSTASRLLTGKAALTPEMAIKLSVVI
GSSPQMWNLNQNAWSLAEAKTVDSRLRLVTQ
>2QUQA 562 XRAY 2.80 0.228 0.285 no Centromere DNA-binding protein complex CBF3 subunit B <UNP CBF3B_YEAST> [SACCHAROMYCES CEREVISIAE]
KLITASSKEYLPDLLLFWQNYEYWTNIGLYTKQRDLTRTPANLTDTEECMFWMNYL
QKDQSFQLMNFAMENLGALYFGSIGDISELYLRVEQYWDRRADKNHSDGKYWDALIWSV
FTMCIYYMPVEKLAEIFSVPYPLHEYLGSKNRLNWEDGMQLVMCQNFARCSLFQLKQCDFM
AHPDIRLVQAYLILATTFPYDEPLLANSLLTQCIHTFKNFHVDDFRPLLNDPVESIAK
VTLGRIFYRLCGCDYLQSGPRKPIALHTEVSSLLQHAAYLQDLPNVDVYREENSTEVLW
KIISLDRDLQYLNKSSKPLKTLDAIRRELDIFQYKVDSEEDFRSNNRQKFIALFQ
ISTVSWKLFKMYLIYYDTADSLLKVIHYSKVIISLIVNNFHAKSEFFNRHPMVMQITITRV
VSFISFYQIFVESAAVKQLLDVLTETANLPTIFGSKLDKLVYLTERRLSKLKLLWDKVQL
LDSDGSFYHPVKILQNDIKIIELEKNDMFSLIKGLGSLVPLNKLQESLLEEDENNTE
PSDFRTIVEEFQSEYNISDILS
>2K6GA 109 NMR NA NA NA no Replication factor C subunit 1 <UNP RFC1_HUMAN> [HOMO SAPIENS]

KRTNYQAYRSYLNREGPKALGSKEIPKGAENCLEGLIFVITGVLESIERDEAKSLIERYG
GKVTGNVSKTNYLVMGRDSGQSKSDKAAALGTKIIDEDGLNLNLRNLE
>1X6FA 88 NMR NA NA NA no Zinc finger protein 462 <UNP ZN462_HUMAN> [HOMO SAPIENS]
GSSGSSGLKRDFIILGNPRLQNSTYQCKHCDSKLQSTAELTSHLNIHNEEFQKRAKRQE
RRKQLLSKQKYADGAFADFKQESGPSSG
>3AAFA 134 XRAY 1.90 0.213 0.244 no Werner syndrome ATP-dependent helicase <UNP WRN_HUMAN> [HOMO SAPIENS]
GIRMDSEDTSWDFGPAFKLLSAVDILGEKFGIGLPILFLRGSNSQRLADQYRRHSLFG
TGKDQTESWWKAQSRQLITEGFLVEVSRYNKFMKICALTKKGRNWLHKANTESQSLILQA
NEELCPKKFLLPSS
>4HIKA 143 XRAY 1.64 0.195 0.216 no Protection of telomeres protein 1 <UNP POT1_SCHPO> [SCHIZOSACCHAROMYCES POMBE]
MSDSFSLLSQITPHQRCSFYAQVIKTWYSDKNFTLYVTDYTENELFFPMSPYTSSSRWRG
PFGFRSIRCILWDEHDFYCRNYIKEGDYVVMKNVTRKIDHLGYLECILHGDSAKRYNMSI
EKVDSEEPENEIKSRKRLYVQN
>3NCTA 144 XRAY 2.20 0.186 0.210 no Protein psiB <UNP PSIB1_ECOLI> [ESCHERICHIA COLI]
MKTELTLNVLQTMNAQEYEDIRAAGSDERRELTAVMRELDAPDNWTMNGEYGSEFGGFF
PVQVRFTPAHERFHLALCSPGDVSQVWVLVLNAGGEPFAVVQVQRRFASEAVSHSLALA

ASLDTQGYSVNDIIHILMAEGGQV

>3KXTA 56 XRAY 1.60 0.178 0.217 no Chromatin protein Cren7 <UNP CREN7_SULSO>
[SULFOLOBUS SOLFATARICUS]
MKPVKVKTPAGKEAELVPEKVVWALAPKGRKGVKIGLFKDPETGKYFRHKLPPDDYPI

>2AIFA 135 XRAY 1.90 0.203 0.270 no ribosomal protein L7A <UNP Q7YYQ3_CRYPV>
[CRYPTOSPORIDIUM PARVUM]
GSSQNEASEDTGFNPKAFPLASPDNNKIINLVQQACNYKQLRKGANEATKALNRGIAEI
VLLAADAEPLEILLHLPLVCEKNTYPVVFVRSKVALGRACGVS RPVIAAAITSKDGSSLS
SQITELKDQIEQILV

>4ACOA 956 XRAY 1.89 0.194 0.232 no CENTROMERE DNA-BINDING PROTEIN COMPLEX CBF3
SUBUNIT A <UNP CBF3A_YEAST> [SACCHAROMYCES CEREVISIAE]
MRSSILFLLKLMKIMDVQQQQEAMSEDRFQELVDSLKPRTAHQYKTYTYKYIQCQLNQ
IIPTEPNSVNSVPYKDLPI SAELIHWFLDLITDDKPGEKRETEDELDDEEENSFKIA
TLKKIIGSLNFLSKLCKVHENPNANIDTKYLESVTKLHWHIDSQKAITTNETNNTNTQV
LCPLLKVSLLNWNPETNHLSEKFFKTCSEKLRFLVDFQLRSYLNLSFEERSKIRFGSLK
LGKRRDAIIYHKVTHSAEKKDTPGHHQLLALLPQDCPFICPQTTLAAYLYLRFYGI PSV
SKGDGFPNLNADENGSLQDIPILRGKSLTTPREETFSNYYTTVFRYCHLPYKRREYFN
KCNLVYPTWDEDTFRFTFNEENHGNWLEQPEAFAPDKIPDFKKIMNFKSPYTSYSTNA
KKDPFPPPKDLLVQIFPEIDEYKRHDYEGLSQNSRDFDLMEVLRERFLSNLPWIYKFFP
NHDIFQDPIFGNSDFQSYFNDKTIHSGKSPILSFDILPGFNKIYKNKTNFYSLIERPSQ
LTFASSHPDTHPTQKQESGEPQMSQLDTTQLNELLKQSQFEYVQFQTL SNFQILLSVF
NKIFEKLEMKSSRGYILHQLNLFKITLDERIKKSKIDDADKFIRDNQPIKKEENIVNED
GPNTSRRTKRPKQIRLLSIADSSDESSTEDSNVFKKGESIEDGAYGENEDENDSEMEEQ
LKSMINELINSKISTFLRDQMDQFELKINALLDKILEEKVTRII EQKLSHTGKFSTLKR
PQLYMTEEHNVGFDMEVPKKLRTSGKYAETVKDNDHQAMSTTASPSPEQDQEAQSYTDE
QEFMLDKSIDSI EGIILEWFTPNAKYANQCVHSMNKSNGKSWRANCEALYKERKSIVEFY
IYLVNHESLD RYKAVIDICEKL RDQNEGSFSLAKFLRKWRHDHQNSFDGLLVYLSN

>1PL5A 142 XRAY 2.50 0.261 0.288 no Regulatory protein SIR4 <UNP SIR4_YEAST>
[SACCHAROMYCES CEREVISIAE]

SNTTEILTSVDVLGTHSQGTGTQQS NMYTSTQKTELEIDNKDSVTECSKDMKEDGLSFVDI
VLSKAASALDEKEKQLAVANEIIRSL SDEV MRNEIRITSLQGDLTFTKKCL ENARSQISE
KDAKINKLMEKDFQVNKEIKPY

>1CI4A 89 XRAY 1.90 0.210 0.262 no BARRIER-TO-AUTOINTEGRATION FACTOR (BAF) <UNP
BAF_HUMAN> [HOMO SAPIENS]
MTTSQKHRDFVAEPMGEKPVGSLAGI GEVLGKKLEERGFDKAYVVLGQFLVLKKDEDLFR
EWLKDTCGANAKQSRDCFGCLREWCDAFL

>1OY3B 136 XRAY 2.05 0.219 0.247 no Transcription factor p65 <UNP TF65_MOUSE>
[MUS MUSCULUS]
TAEIKICRVNRNSGSLGGDEIFLLCDKVQKEDIEVYFTGPGWEARGSFQADVHRQVAI
VFRTPPYADPSLQAPVRVSMQLRRPSDRELSEPMEFQYLPDTHDRHRIEEKRKRTYETFK SIMKKSPFNGPTEPRP

>1PGZA 195 XRAY 2.60 0.237 0.269 no Heterogeneous nuclear ribonucleoprotein A1
<UNP ROA1_HUMAN> [HOMO SAPIENS]
SKSESPKEPEQLRKLFIGGLSFETDESLSRSHFEQWGTLTDCVVMRDPNTKRSRGFGFVT
YATVEEVDAAMNARPHKVDGRVVEPKRAVSREDSQRPGAHLTVKKIFVGGIKEDTEEHL
RDYFEQYQKIEVIEIMTDRGSGKKRGFAFVTFDDHDSVDKIVIQKYHTVNGHNCEVRKAL
SKQEMASASSSQRGR

>3UX8A 670 XRAY 2.10 0.212 0.245 no Excinuclease ABC, A subunit <UNP E8SW61_GEOS2>
[GEOBACILLUS]

MGSSHHHHHSSGLVPRGSHMDKIIVKGARAHNLKNIDVEIPRGKLVLTGLSGSGKSSL
AFDTIYAEGQRRYVESLSAYARQFLGQMEKPDVDAIEGLSPAISIDQKTTSRNPRSTVGT
VTEIYDYLRLLFARIGRLVGKKHIGEV TAMS VTEALAFDGLTEKEAQIARLILREIR
DRLGFLQNVGLDYLTLSRSAGTSGGEAQIRLATQIGSRLTGVLYVLDEPSIGLHQRDN
DRLIATLKS MRDLGNTLIVVEHDEDTMLAADYLIDIGPGAGIHGGEVVAAGTPEEVMNDP
NSLTGQYLSGKKFIPIPAERRRPDGRWLEVVGAREHNLKNVSVKIPLGTFVAVTGVSGSG
KSTLVNEVLKALAQKLHRAKAKPGEHDIRGLEHLDKVIDIDQSPIGRTPRSNPATYTG
VFDDIRDVFASTNEAKVRGYKKGRFSFNVKGGRC EACHGDGI IKIEMHFLPDVYVPCVC
HGKRYNRETLEV TYKGKNIAEVLDMTVEDALDFFASIPKIKRKLETLYDVGLGYMKLGQP
ATTLSGGEAQRVKLAELHRRSNGRTLYILDEPTTGLHVDDIARLLDVLHRLVDNGDTV
VIEHNLVDIKTADYIIDLGPEGGRGGQIVAVGTPEEVAEVKESHTGRYLKPILERDRAR
MQARYEAAKA

>1L8YA 91 NMR NA NA NA no upstream binding factor 1 <UNP UBF1_HUMAN> [HOMO SAPIENS]
MGKLPESPKRAEEIWQQSVIGDYLARFKNDRVKALKAMEMTWNMEKKEKLMWIKKAAED
QKRYERELSEMRAPPAATNSSKLEHHHHHH

>4ER8A 165 XRAY 2.60 0.228 0.281 no TnpArep for protein <UNP YAFM_ECOLI>
[ESCHERICHIA COLI]

MSEYRRYYIKGGTWFFTVNLRNRRS QLLTTQYQMLRHAI IKVKRDRPFEINAWVVLPEHM
HCIWTLPEGDDDFSSRWREIKKQFTHACGLKNIWQPRFWEHAIRNTKDYRHHVDYIYNP
VKHGWVKQVSDWPFFSTFHRDVARGLYPIDWAGDVTDFSAGERIIS

>10V9A 50 XRAY 2.30 0.258 0.269 no VicH protein <UNP Q9KSX6_VIBCH> [VIBRIO
CHOLERAEE] SEITKTLNIRSLRAYARELTIEQLEEALDKLTTVVQERKEAEAEIEAAR

>3QMDA 79 XRAY 1.90 0.225 0.241 no CpG-binding protein <UNP CXXC1_HUMAN> [HOMO
SAPIENS] MHHHHHSSRENLYFQGGIKRSARMCGECEACRRTEDCGHCDFCRDMKKFGGPNKIRQKC
RLRQCQLRARESYKYFPSS

>1IRZA 64 NMR NA NA NA no ARR10-B <UNP ARR10_ARATH> [ARABIDOPSIS THALIANA]
TAQKKPRVLWTHELHNKFLAAVDHLGVERAVPKKILDLMNVDKLTRENVASHLQKFRVAL

KKVS

>3FYMA 130 XRAY 1.00 0.110 0.140 no Putative uncharacterized protein <UNP
Q99UJO_STAAM> [STAPHYLOCOCCUS AUREUS SUBSP. AUREUS MU50]

MKTVGEALKGRERLGMTLTELEQRTGIKREMLVHIENNEFDQLPNKNYSEGFIRKYASV
VNIEPNQLIAHQDEIPSNQAEWDEVITVFNNKDL DYKSKSKEPIQLLVIMGITVLITL
LLWIMLVLIF

>10QJA 97 XRAY 1.55 0.234 0.210 no Glucocorticoid Modulatory Element Binding
protein-1

<UNP GMEB1_HUMAN> [HOMO SAPIENS]

GAMEDMEIAYPITCGESKAILLWKKFVCPGINVKCVKFNDQLISPKHFVHLAGKSTLKD
WKRAIRLGGIMLRKMDSGQIDFYQHDKVCSNTRSTK

>4GS3A 107 XRAY 1.09 0.154 NA no Single-stranded DNA-binding protein <UNP
Q8RBI8_THETN> [THERMOANAEROBACTER TENGCONGENSIS]

SNAMAGNFLENNTVTLVGKVFTPLEFSHELYGEKFFNFILEVPRLSETKDYLPTISNRL
FEGMNLVGVTRVKIEGQLRSYNRKSPEEGKNKLITV FARDISVVPE

>3V9RB 88 XRAY 2.40 0.242 0.290 no Uncharacterized protein YDL160C-A <UNP
YDL160_YEAST> [SACCHAROMYCES CEREVISIAE]

MLSKEALIKILSQNEGGNDMKIADEVPMIQKYLDIFIDEAVLRSLQSHKDINGERGDKS
 PLELSHQDLERIVGLLLMDMLEHHHHHH
 >2DT5A 211 XRAY 2.16 0.195 0.238 no AT-rich DNA-binding protein <UNP Q5SHS3_THET8>
 [THERMUS THERMOPHILUS]
 MKVPEAAISRLITYLRILEELEAQGVHRTSSEQLGGLAQVTAQVRKDLSYFGSYGTRGV
 GYTVPVLKREL RHILGLNRKWGLCIVGMRLGSALADYPGFGESFELRGFFDVPDPEKVG
 PVRGGVIEHVDLLPQRVPGRIEIALLTVPREAAQKAADLLVAAGIKGILNFAPVVLEVPK
 EVAVENVDLAGLTRLFAILNPKWREEMMG
 >1Y6UA 70 NMR NA NA NA no Excisionase from transposon Tn916 <UNP Q79DA1_ENTFA>
 [ENTEROCOCCUS FAECALIS]
 AGHMKQTDIPIWERYTLTIEEASKYFRIGENKLRRLAENKNANWLIMNGNRIQIKRKQF
 EKIIDLDAI
 >3FRQA 195 XRAY 1.76 0.183 0.221 no Repressor protein MphR(A) <UNP Q9EVJ6_ECOLX>
 [ESCHERICHIA COLI]
 GMPRPKLKSDDEVLEAATVVLKRCGPTEFTLSGVAKEVGLSRAALIQRTNRDILLVRMM
 ERGVEQVRHYLNAIPIGAGPQGLWEFLQVLVRSMNTRNDFSVNYLISWYELQVPELRTLA
 IQNRNAVVEGIRKRLPPGAPAAAELLHLSVIAGATMQWAVDPDGELADHVLAQIAAILCL MFPEHDDFQLQAHA
 >1USTA 93 NMR NA NA NA no HISTONE H1 <UNP H1_YEAST> [SACCHAROMYCES CEREVISIAE]
 KKEEASSKSYRELIIEGLTALKERKGS SRPALKKFIKENYPIVGSASNFDLYFNNAIKKG
 VEAGDFEQPKGPAGAVKLAKKKSPEVKKEKEVS
 >3S4WB 1323 XRAY 3.41 0.241 0.272 no Fanconi anemia group D2 protein homolog <UNP
 FACD2_MOUSE> [MUS MUSCULUS]
 SHNSHEVEENGSVFVKLLKASGLTLKTGENQNQLGVDQVIFQRKLFQALRKHPAYPKVIE
 EFNGLSESYTEDSESLRNCLLSCERLQDEEASMGTFYSKSLIKLLLGIDILQPAIIKMLF
 EKVPPQLFESEN RDGINMARLIINQLKWLDRIVDGKDLTAQMMQLISVAPVNLQHDFITS
 LPEILGDSQHANGKELGELLVQNTSLTVPILDVFSRLDPNFLSKIRQLVMGKLSSVR
 LEDFPVIVKFLHLSVTDTSLEVIAELRENLVQQFILPSRIQASQSKLKSKGLASSGN
 QENS DKDCIVLVFDVIKSAIRYEKTISEAWFKAIERIESAAEHKSLDVMLLI IYSTSTQ
 TKKGVEKLLRNKIQSDCIQEQLLDSAFSTHYLVKIDICPSILLLAQTLFHSQDQRIILFG
 SLLYKYAFKFDDTYCQQEVVGALVTHVCSGTEAEVDTALDVLELIVLNASAMRLNAAFV

 KGILDYLENMSPQQIRKIFCILSTLAFSQQPGTSNHIQDDMHLVIRKQLSSTVFKYKLIG
 IIGAVTMAGIMAEDRSVPSNSSQRSANVSSEQRTQVTSLLQLVHSCTEHSPWASSLYYDE
 FANLIQERKLAPKTLEWVGQTIFNDFQDAFVVDFAAPEGDFPFPVKALYGLEEYSTQDG
 IVINLLPLFYQECADASRATSQESSQRSMSSLCLASHFRLLRLCVARQHDGNLDEIDGL
 LDCPLFLPDLEPGEKLESMSAKDRSLMCSLTFLT FNWFREVVN AFCQQTSP EMKGKVL SR
 LKDLVELQGILEKYLAIPDYVPPFASVDLDTLDMMPRKTFVSLQNYRAFFRELDIEVFS
 ILHSLGVTKFI LDTEMHTEATEVVQLGPAELLFLEDLSQKLENMLTAPFAKRICCFKNK
 GRQNI GFSHLHQRSVQDIVHCVVQLLTPMCNHNLENHNFQCLGAEHL SADDKARATAQE
 QHTMACCYQKLLQVLHALFAWKGFTHQSKHRLHLSALEVLSNRLKQMEQDQPLEELVSQS
 FSYLQNFHHSVPSFQCGLYLLRLLMALLEKSAVPNQKKEKLASLAKQLLCRAWPHGEKEK
 NPTFNDHLHDVLYIYLEHTDNVLKAIEEITGVGPVLSAPKDAASSTFPTLTRHTFVIF
 FRVMAELEKTVKGLQAGTAADSQQVHEEKLLYWNMAVRDFSILLNLMKVFD SYPVLHVC
 LKYGRRFVEAFKQCMPLLD FSFRKHREDVLSLLQTLQLNTRLLHHL CGH SKIRQDTRLT
 KHVPLLKKSLELLVCRVKAMLVLNNCREAFWLGTLKNRDLQGEIISQDPSSSESNAEDS
 EDG
 >2FXQA 264 XRAY 1.85 0.192 0.247 no Single-strand binding protein <UNP SSB_THEAQ>

[THERMUS AQUATICUS]
MARGLNQVFLIGTLTARPDTRYTPGGAILDLNLAGQDAFTDESGQEREVPWYHRVRLG
RQAEMWGDLEKQGLIFVEGRLEYRQWEKDGEKKSEVQVRAEFIDPLEGRGRETLEDARG
QPRLRRALNQVILMGNLTRDPDLRYTPQGTAVVRLGLAVNERRRGQEEERTHFLEVQAWR
ELAEWASELRKGDGLLVIGRLVNDSWTSSSGERRFQTRVEALRLRPTRGPAQAGGSRPP
TVQTGGVDIDEGLEDFPPEEDLPF
>1ZIOA 307 XRAY 2.60 0.227 0.266 no DNA gyrase subunit A <UNP GYRA_ECOLI>
[ESCHERICHIA COLI]
TQEDVVVTLSHQGYVKYQPLSEYEAQRRGGKGSAARIKEEDFIDRLLVANTHDHILCFS
SRGRVYSMKVYQLPEATRGARGRPVNNLLPLEQDERITAILPVTEFEEGVKVFMATANGT
VKKTVLTEFNRLRTAGKVAIKLVDGDELIGVDLTSGEDEVMLFSAEGKVVRFKESSVRAM
GCNTTGVRGIRLGEGDKVVSILVPRGDGAILTATQNGYGKRTAVA EYPTKSRATKGVISI
KVTERNGLVVGAVQVDDCDQIMMITDAGTLVRTRVSEISIVGRNTQGVLIRTAEDENVV
GLQRVAE
>1KKXA 123 NMR NA NA NA no Transcription regulatory protein ADR6 <UNP SWI1_YEAST>
[SACCHAROMYCES CEREVISIAE]
MRGSGSHHHHHHGSNNKQYELFMKSLIENCKKRNMLQSIPEIGNRKINLFYLYMLVQKF
GGADQVTRTQQWSMVAQRLQISDYQQLESIYFRILLPYERHMISQEGIKETQAKRILQPS
LIS
>2K75A 106 NMR NA NA NA no uncharacterized protein Ta0387 <UNP Q9HL44_THEAC>
[THERMOPLASMA ACIDOPHILUM]
SDLVKIRDVSLSTPYVSVIGKITGIHKKEYESDGTTSVYQGYIEDDTARIRISSFGKQL
QSDSVVRIDNARVAQFNGYLSLSVGDSRIESVNVNIPLEHHHHHH
>3V60A 84 XRAY 2.60 0.212 0.249 no Ubiquitin-like protein SMT3 <UNP SMT3_YEAST>
[SACCHAROMYCES CEREVISIAE]
GSHMRPETHINLKVSDGSSEIFFKIKKTTPLRRLMEAFKRQKEMDSLRFLYDGIRIQA
DQTPEDLDMEDNDIIEAHREQIGG
>2HX0A 154 XRAY 1.55 0.197 0.209 no Putative DNA-binding protein <UNP Q57K43_SALCH>
[SALMONELLA CHOLERAESUIS]
MAGDPNSMTVSHHNASTARFYALRLLPGQEVFSQLHAFVQQNQLRAAWIAGCTGSLTDVA
LRYAGQEATTSLTGTFEVISLNGTLELTGEHLHLAVSDPYGVMLGGHMPGCTVRTTLEL
VIGELPALTFSRQPCAISSGYDELHISSRLEHHHH
>1TOFA 276 XRAY 1.85 0.211 0.235 no Transposon Tn7 transposition protein tnsA
<UNP TNSA_ECOLI> [ESCHERICHIA COLI]
GSAMAKANSSFSEVQIARRIKEGRGQGHGKDYIPWLTVQVEPSSGRSHRIYSHKTGRVHH
LLSDLELAVFLSLEWESSVLDIRQFPLLPDTRQIAIDSGIKHPVIRGVDQVMSTDFLV
DCKDGPFEQFAIQVKPAAALQDERTLEKLELERRYWQQKQIPWFIFTDKEINPVVKENIE
WLYSVKTEEVSAELLAQLSPLAHILQEKGDENIINVCKQVDIAYDLELGKTLSEIRALTA
NGFIKFNIYKSFRANKCADLCISQVVNMEELRYVAN
>203CA 282 XRAY 2.30 0.199 0.236 no APEX nuclease 1 <UNP Q7SXL6_BRARE> [DANIO
RERIO] GSHMEAPILYEDPPEKLTSKDGRAANMKITSWNVDGLRAWVKKNGLDWVRKEDPDILCLQ
ETKCAEKALPADITAMPEYPHYWAGSEDKGYSGVAMLCKTEPLNVTYIGIGKEEHDKEG
RVITAEPDFFLVTAYVPNASRGLVRLDYRKTDVDFRAYLCGLDARKPLVLCGDLNVAH
QEIDLKNPKGNRKNAFTPEEREGFTQLLEAGFTDSFRELYPDQAYAYTFWTYMMNARSK
NVGWRLDYFVLSSALLPGLCDSKIRNTAMGSDHCPITLFLAV
>3SQIA 534 XRAY 2.82 0.196 0.251 no KLLAOE03807p <UNP Q6CPM4_KLULA>

[KLUYVEROMYCES LACTIS]

MSKLSLLKELPTRTAHLYSIWHKYTEWLKTMPLDTGADLKLFLSQKYIVKYIASHDDI
AKDPLPTCDAMIWFSRALDIENNDVLVLQQRLYGLVKLLEFDYSNVIAILQKISINLWNP
STDLSLQSKHFKTCQDKLKLDDFQWKFNNTVSFEDRTTVSLKDLQCILDDENGKCGLAHS
SKPNFVLVPNFQSPFTCPIFTMAVYYLRFHGVKKYYKGDGYILSQLEHIPIIRGKSLD
QYPRELTLGNWYPTIFKYCQLPYTKKHWFQVNEQWPFQPDFSDSENTSTLAESDSENTI
GIPDFYIEKMNRKTLQPCQVHVHLFPTDLPPDIQAVFDLLNSVLVTSPLLYRVFPTH
IFLDPSLKTQNI AFLTGTLPDIESQEHLAQLIDKTGTSELVNPVKIDQNEHTLTP
IGTSLSQTDIPMLDQLKTELKLIQLQTSTGFSQLITVLLEIFQRLDFKKSNNKFVIDLL
QSCRKDMRNKLMPCSLSTNFADELSDDENEKGNKTGAIDPETDNGNEESVSD

>1TZYA 129 XRAY 1.90 0.190 0.222 no Histone H2A-IV <UNP H2A4_CHICK> [GALLUS GALLUS]

MSGRGKQGGKARAKAKSRSSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYLA AVLEYLT
AEILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKLKGVTIAQGGVLPNIQAVLLPKK
TDSHKAKAK

>2ZVVA 276 XRAY 2.00 0.232 0.245 no Proliferating cellular nuclear antigen 1 <UNP PCNA1_ARATH> [ARABIDOPSIS THALIANA]

MGSSHHHHHSSGLVPRGSHMLELRLVQGSLLKKVLESIKDLVNDANFDCSSTGFSLQAM
DSSHVALVSLLLRSEGFEHYRCNRNLSMGMNLGNMSKMLKAGNDDIITIKADDGGDTVT
FMFESPTQDKIADFEMKLMIDSEHLGIPDAEYHSIVRMPSPNEFSRICKDLSSIGDVTVI
SVTKEGVKFSTAGDIGTANIVLRQNTTVDKPEDAIVIEKPVSLSFALRYMNSFTKATP
LSDTVTISLSSELPVVVEYKVAEMGYIRYYLAPKIE

>2XQCA 140 XRAY 1.90 0.176 0.209 no TRANSPOSASE <UNP 083028_DEIRA> [DEINOCOCCUS RADIOURANS]

MTYVILPLEMKKGRGYVYQLEYHLIWCVKYRHQVLVGEVADGLKDILRDIAAQNGLLEVIT
MEVMPDHVHLLLSATPQQAIPDFVKALKGASARRMFVAYPQLKEKLWGGNLWNPSYCILT
VSENTRAQIQKYIESQHDKE

>2P5MA 83 XRAY 1.95 0.187 0.224 no Arginine repressor <UNP ARGR_BACSU> [BACILLUS SUBTILIS]

MQRFNPLSKLKRALMDAFVKIDSASHMIVLKTMPGNAQAIGALMDNLDWDEMMGTICGDD
TILICRTPEDTEGVKNRLELL

>30KGA 412 XRAY 1.95 0.199 0.240 no Restriction endonuclease S subunits <UNP Q8R9Q6_THETN> [THERMOANAEROBACTER TENGCONGENSIS]

MSHHHHHSMIDIEFMTEGPYKLPPGWRWVRLGEVCLPTERRDPTKNPSTYFVYVDISAID
STVGKIVSPKEILGQHAPSARKVIRSGDVIFATTPYLNIALVPPDLGQICSTGFCV
IRANREFAEPEFLFHLCRSDFITNQLTASKMRGTSYPAVTDNDVYNTLIPLPPLQRRRI
VAKVEALMERVREVRLRAEAQKDTTELLMQTALA EVFPHPGADLPPGWRWVRLGEVCDII
MGQSPPSSTYNFEGNLPFFQKADFGDLHPTPRIWCSAPQKVARPGDVLISVRAPVGS
NVANLACCIGRLAALRPDSLRFWLLYYLHYLEPELSKMGAGSTFNAITKKDLQNVFI
PLPPLQRRIVAYLDQIQQVAALKRAQAETEAELEKRLQAILDKAFRGDL

>4HDOA 339 XRAY 2.30 0.225 0.277 no DNA double-strand break repair protein Mre11 <UNP MRE11_PYRFU> [PYROCOCUS FURIOSUS]

HHHHHMKFAHLADIHLGYEQFHKPQREEEFAEAFKNALEIAVQENVDFILIAGDLFHSS
RPSPGTLKKAIALQLIPKEHSIPVFAIEGNHRTQRGPSVLNLEDFGLVYVIGMRKEKV
ENEYLTSERLNGEYLKGVYKDEIHGMKYMSSAWFEANKEILKRLFRPTDNAILMLHQ
GVREVSEARGEDYFEIGLGDLP EGYLYYARGHIHKRYETSYSGSPVVYPGSLERWDFGDY

EVRYEWDGIKFKERYGVNKGFIYIVEDFKPRFVEIKVRPFIDVKIKGSEEEIRKAIKRLIP
 LIPKNAYVRLNIGWRKPFDLTEIKELLNVEYLKIDTWRI
 >2KHQA 110 NMR NA NA NA no Integrase <UNP Q49VW8_STAS1> [STAPHYLOCOCCUS
 SAPROPHYTICUS SUBSP. SAPROPHYTICUS ATCC 15305]
 MITFADYFYQWYEVNKLPHVSESTKRHYESAYKHIKDHFRHKLLKDIKRTEYQKFLNEYG
 LTHSYETIRKLNSYIRNAFDDAIHEGYVIKNPTYKAELHASVLEHHHHHH
 >1RW2A 152 NMR NA NA NA no ATP-dependent DNA helicase II, 80 kDa subunit <UNP
 KU86_HUMAN> [HOMO SAPIENS]
 MHHHHHHKLKTEQGGAHFSVSSLAEGSVTSVGSVNPANFRVLVKQKKASFEEASNQLIN
 HIEQFLDTNETPYFMKSIDCIRAFREEAIKFSEEQRFNFLKALQEKVEIKQLNHFWEIV
 VQDGITLITKEEASGSSVTAEEAKKFLAPKDK
 >3PGGA 121 XRAY 2.14 0.216 0.258 no U6 snRNA-associated Sm-like protein LSm5.
 SM domain
 <UNP Q5CXX3_CRYPV> [CRYPTOSPORIDIUM PARVUM]
 SYKVNYSMSETPANKSQGGSNQKGGNIILPLALIDKCIGNRIYVVMKGDKEFSGVLRGFDE
 YVMVLDDVQEYGFKADEEDISGGNKKLRVMVNRLETILLSGNNVAMLVPGGDPDSFNF
 S
 >2OKFA 140 XRAY 1.60 0.143 0.155 no FdxN element excision controlling factor
 protein
 <UNP Q3M7W6_ANAVT> [ANABAENA VARIABILIS]
 GMSARDVFHEVVKTALKKDGWQITDDPLTISVGGVNLSDLAQKLI AERQGGQKIAVEV
 KSFLKQSSAISEFHTALGQFINYRGALRKVEPDRVLYLAVPLTTYKTFFQLDFPKEIIIE
 NQVKMLVYDVEQEVIQWIN
 >3HI2B 101 XRAY 2.00 0.207 0.248 no Motility quorum-sensing regulator mqsR <UNP
 MQSR_ECOLI> [ESCHERICHIA COLI K-12]
 GSHMEKRTPHTRLSQVKKLVNAGQVTRTTRSALLNADELGLDFDGMCNVIIGLSESDFYKS
 MTTYSDHTIWQDVYRPLVTGQVYLKITVIHDVLIVSFKEK
 >1X51A 155 NMR NA NA NA no A/G-specific adenine DNA glycosylase <UNP MUTYH_HUMAN>
 [HOMO SAPIENS]
 GSSGSSGPRKASRKPPREESATCVLEQPGALGAQILLVQRPNSGLLAGLWEFPSVTWEP
 SEQLQRKALLQELQRWAGPLPATHRLHGEVVHTFSHIKLTQVYGLALEGQTPVTTVPP
 GARWLTQEEFHTAAVSTAMKKVFRVYQGGSGPSSG
 >3MUJA 138 XRAY 1.92 0.171 0.193 no Transcription factor COE3 <UNP COE3_HUMAN>
 [HOMO SAPIENS]
 SMEATPCIKAIISPSEGWTGGATVIIIGDNFFDGLQVVFGTMLVWSELITPHAIRVQTPP
 RHIPGVVEVTL SYKSKQFCKGAPGRFVYTALNEPTIDYGFQRLQKVIPRHPGDPERLPKE
 VLLKRAADLVEALYGMPH
 >2KKPA 117 NMR NA NA NA no Phage integrase <UNP Q2RHJ2_MOOTA> [MOORELLA
 THERMOACETICA ATCC 39073]
 MIEPSKITVEQWLNRLWLDYAKPHLRQSTWESYETVLRHLHVIPTLGSIPLKKLQPADIQR
 LYASKLESGLSPTRVRYIHVVLHEAMSQARESGLLLQNPTAAKPPRHPLEHHHHHHH
 >4HTOA 240 XRAY 2.81 0.210 0.259 no DNA ligase 4 <UNP DNLI4_HUMAN> [HOMO SAPIENS]
 MAASQTSQTVASHVPFADLCSTLERIQKSKGRAEKIRHFREFLD SWRKFDALHKNHKDV
 TDSFYFAMRLILPQLERERMAYGIKETMLAKLYIELNLPRDGKDALKLLNYRTPGTGTHG
 DAGDFAMIAYFVLKPRCLQKGS LTQQVNDLLDSIASNNSAKRKDLIKKSLLQLITQSSA
 LEQKWLIRMI IKDLKLGVSQQTIFSVFHNDAAELHNVTTDLEKVCRLHDPSVGLSDISI
 >1HLVA 131 XRAY 2.50 0.222 0.260 no MAJOR CENTROMERE AUTOANTIGEN B <UNP

CENPB_HUMAN> [HOMO SAPIENS]
 MGPKRRLTFREKSRIIQEVEENPDLRKGEIARRFNIPPSTLSTILKNKRAILASERKYG
 VASTCRKTNKLSPYDKLEGLLIAWFQQIRAAGLPVKGIILKEKALRIAEELGMDDFTASN GWLDRFRRRRS
 >1P92A 226 XRAY 2.10 0.243 0.280 no Diphtheria toxin repressor <UNP DTXR_CORDI>
 [CORYNEBACTERIUM DIPHTHERIAE]
 MKDLVDTTEMYLRTIYELEEEGVTPLRARIAERLEQSGPTVSQTVARMERDGLVVASDR
 SLQMTPTGRTLATAVMRKARLAERLLTDIIGLDINKVHDEACRWEHVMSDEVERRLVKVL
 KDVSRSFPGNPIGLDELGVGNSDAAAPGTRVIDAATSMRKVRIVQINEIFQVETDQFT
 QLLDADIRVGSEVEIVDRDGHITLSHNGKDVLLDDLAHTIRIEEL
 >3QU3A 137 XRAY 1.30 0.169 0.200 no Interferon regulatory factor 7 <UNP IRF7_MOUSE>
 [MUS MUSCULUS]
 GSHMAEVRGVQRVLFQDWLLGEVSSGQYEGWLNEARTVFRVPWKHFGRDLDEEDAQI
 FKAWAVARGRWPPSGVNLPPPEAAEAERRRRGWKTNFRCALHSTGRFILRQDNSGDPVD
 PHKVYELSRELGSTVGP
 >2DA7A 71 NMR NA NA NA no Zinc finger homeobox protein 1b <UNP SIP1_HUMAN> [HOMO
 SAPIENS]
 GSSGSSGSPINPYKDHMSVLKAYYAMNMEPNSEDELLKISIAVGLPQEFVKWEFEQRKVYQ YNSRSRGPSSG
 >2F7TA 227 XRAY 2.25 0.193 0.277 no Mos1 transposase <UNP 061446_DROSE>
 [DROSOPHILA MAURITIANA]
 WVPHELNERQMERRKNTCEILLSRYKRKSFHLRIVTGDEKWIFFVNPKRKKSYPDPGQPA
 TSTARPNRFGKKTMLCVWWDQSGVIYYELLKPGETVNAARYQQQLINLNRALQRKRPEYQ
 KRQHRVIFLHDNAPSHSTARAVRDTLETNLNWEVLPHAAYSPLAPSDYHLFASMGHALAEQ
 RFDSYESVKWLDEWFAAKDDEFYWRGIHKLPERWEKCVASDGKYFE
 >2ZQEA 83 XRAY 1.70 0.191 0.227 no MutS2 protein <UNP Q5SHT5_THET8> [THERMUS
 THERMOPHILUS]
 MREVKEVDLRGLTVAEALLEVDQALEEARALGLSTLRLHKGKTGALRQAIREALRRDKR
 VESFADAPPGEKGHGVTVVALRP
 >3S51A 1308 XRAY 3.30 0.259 0.278 no Fanconi anemia group I protein homolog <UNP
 FANCI_MOUSE> [MUS MUSCULUS]
 MDLKILSLATDKTTDKLQEFQLTKDDDLASLLQNQAVKGRAVGTLRAVLKGGSPCSEED
 GALRRYKIYSCCIQLVESGDLQQDVASEIIGLLMLEVHHFPGPLLVDLASDFVGAVREDR
 LVNGKSLELLPIILTALATKKEVLACGKGDNGEYKRQLIDTLCVSRWPQRYMIQLTSV
 FKDVCLTPEEMNLVAVKLTMFSLNLQEIPPLVYQLLVSSKGSRRSVLDGIIAFFREL
 DKQHREEQSSDELSELITAPADELYHVEGTIVLHIVFAIKLDCELGRELLKHLKAGQQGD

 PSKCLCPFSLALLSLTRIQRFEQVFDLLKTSVVKSFKDLQLLQGSKFQLTLPQRTCV
 STMILEVVRNSVHSDHVTQGLIEFGFILMDSYGPKKILDGKAVEIGTSLSKMTNQHACK
 LGANILLETFKIHEMIRQEILEQVLNRVVRTSSPINHFLDLFSDIIMYAPLILQNCSKV
 TETFDYLTFLPLQTVQGLLKAVQPLLKISMSMRDSLILVLRKAMFASQLDARKSAVAGFL
 LLLKNFKVLGSLPSSQCTQSIGVTQVRVDVHSRYSAVANETFCLEIIDSLKRSLGQQADI
 RLMLYDGYDVLRRNSQLASSIMQTLFSQLKQFYEPEDLLPPLKLGACVLTQGSQIFLQ
 EPLDHLLSCIQHCLAWYKSRVPLQQGDEGEEEEELYSELDDMLESITVRMIKSELEDF
 ELDKSADFQNTNNGIKNNIACLIMGVCEVLMYFNFSISNFSKSKFEEILSLFTCYKKF
 SDILSEKAGKGAKMTSKVSDSLLSLKFVSDLLTALFRDSIQSHEESLSVLRSSGEFMHY
 AVNVTLQKIQLIRTGHVSGPDGQNPDKIFQNLCDITRVLLWRYTSIPTSVESGKKEKG
 KSISLLCLEGLQKTFSVVLQFYQPKVQQFLQALDVMGTEEEEAGVTVTQRASFQIRQFQR
 SLLNLSSEEDDFNSKEALLLIAVLSTLSRLLEPTSPQFVQMLSWTSKICKEYSQEDASF

CKSLMNLFFSLHVLKSPVTLLRDLSQDIHGQLGDIDQDVEIEKTDHFAVNLRTAAPT
 CLLVLSQAEKVL EEVDWLI AKIKGSANQETLS DKVTPEDASSQAVPPTLLIEKAIVMLG
 TLVTFFHELVTALPSGSCVDTLKGLSKIYSTLTAFVKYYLQVCQSSRGIPNTVEKLVK
 LSGSHLTPVCYSFISYVQNKSSDAPKCEKEKAAVSTTMKVLR ETKPIPNLVFAIEQYE
 KFLIQLSKSKSVNLMQHMKLSTSRDFKIKGSVLDMLREDEEH HHHHHH
 >2WPOC 112 XRAY 2.67 0.228 0.266 no CHROMOSOMAL REPLICATION INITIATOR PROTEIN
 DNAA <UNP DNAA_HELPY> [HELICOBACTER PYLORI]
 MDTNNNIEKEILALVKQNPVSLIEYENYFSQLKYNPNASKSDIAFFYAPNQVLCTTITA
 KYGALLKEILSQNKVGMHLAHSVDVRIEAPKIQINAQSNINYKAIKTSVKD
 >2DQRA 122 XRAY 3.01 0.205 0.276 no Replication termination protein <UNP RTP_BACSU>
 [BACILLUS SUBTILIS]
 MKEEKRSTGFLVKQRAFLKLYMITMTEQERLYGLKLLKVLQSEFKEIGFKPNHTEVYRS
 LHELLDDGILKQIKVKEGAKLQEVVLYQFKDYEAALKYKKQLKVELDRCKKLEKALSD
 NF

Negative samples:

>20KMA 147 XRAY 1.65 0.198 0.216 no Collagen adhesin <UNP Q9EU70_ENTFA> [ENTEROCOCCUS FAECALIS]
 ERDYPFFYKVGDLGASNQVRWFLNVNLKSDVTE DISIADRQSGGQLNKESFTFDIVN
 DKETKYISLAEFEQQGYGKIDFVTDNDFNLFYRDKARFTSFIVRYTSTITEAGQH QATF ENSYDINYQLNNQDATNEKNTSQVKNV
 >1M48A 133 XRAY 1.95 0.200 0.269 no interleukin-2 <UNP IL2_HUMAN> [HOMO SAPIENS]
 APTSSSTKKTQLQLEHLLLDLQMLNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE
 EELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNR
 WITFCQSIISTLT
 >1F5NA 592 XRAY 1.70 0.224 0.255 no INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 <UNP GBP1_HUMAN>
 [HOMO SAPIENS]
 MASEIHMTGPMCLIENTNGRLMANPEALKILSAITQPMVVVAIVGLYRTGKSYLMNKL
 AGKKKGFSLGSTVQSHTKGIWMCVPHPKPGHILVLLDTEGLGDVEKGDNDQND SWIFALAV
 LLSSTFVYNSIGTINQQAMDQLYYVTELTHRIRSKSSPDENENEVEDSADFSFFPDFVW
 TLRDFSLEADGQPLTPDEYLTYSCLKKKGTSQKDETFNLPRLCIRKFFPKKKCFVDR
 PVHRRKLAQLEKLQDEELDPEFVQQVADFCSYIFSNSKTKTLGGIQVNGPRLESVLTY
 VNAISSGDLPCMENAVLALAQIENSAAVQKATAHYEQQMKGKVLPTESLQELLDLHRDS
 EREAIEVFIRSSFQKDVHFLQKELAAQLEKKRDDFCQKQNEASSDRCSGLLQVIFSPLEE
 EVKAGIYSKPGGYRLFVQKLQDLKKKYYEPRKGIQAEIILQTYLKSKE SMTDAILQTDQ
 TLTEKEKEIEVERVKAESAQASAKMLHEMQRKNEQMMEQKERSYQEHLKQLTEKMENDRV
 QLLKEQERTLALKLQEQEQLLKEGFQKESRIMKNEIQDLQTKMRRRKACTIS
 >2D42A 249 XRAY 2.07 0.230 0.265 no non-toxic crystal protein <PDB 2D42> [BACILLUS THURINGIENSIS]
 AIINLLRELEIYGMQYANSHQYTYGSSYSDDTNPIRIAGLDARIPDPIVTD PVNHIVLDR
 RIITNTTSNSLEGVFSFSNAYTSRTSSQTRDGVTAGTNITGKYFANLFFEQVGLSGRIAF
 EGAVTNENKYTL DATQDFRDSQTI RVPFHRATGVYTLEQGA FEKMTVLECVVSGNGIIR
 YYRTL PDNSYTEIVQRVNIIDVLQANGTPGFTISKEQNRAYFTGEGTISGQIGLQTFIDV
 VIEPLPGHA
 >1JUVA 193 XRAY 1.70 0.248 0.269 no DIHYDROFOLATE REDUCTASE <UNP DYP_BPT4> [ENTEROBACTERIA PHAGE
 T4]
 MIKLVFRYSPTKTVDGFNELAFLGDGLPWGRVKDLQNFKARTEGTIMIMGAKTFQSLP
 TLLPGRSHIVCDLARDYPVTKDGLAHFYITWEQYITYISGGEIQVSSPNAPFETMLDQ

NSKSVIGGPALLYAALPYADEVVSRIVKRHRVNSTVQLDASFLDDISKREMVETHWYK
IDEVTTLTESVYK

>1PU6A 218 XRAY 1.64 0.153 0.185 no 3-METHYLADENINE DNA GLYCOSYLASE <UNP 025323_HELPY>
[HELICOBACTER PYLORI]
VLDSFEILKALKSLDLLKNAPAWWWPNALKFEALLGAVLTQNTKFEAVLKSLENLKNAFI
LENDDEINLKKIAYIEFSKLAECVRPSGFYNQKAKRLIDLSGNILKDFQSFENFKQEVTR
EWLLDQKGIGKESADAILCYACAKEVMVVDKYSYFLKKLKGLIEIEDYDELQHFFFEKGVQE
NLNSALALYENTISLAQLYARFHGKIVEFSKQKLELKL

>2QKLA 127 XRAY 2.33 0.229 0.259 no SPBC3B9.21 protein <UNP Q9P805_SCHPO>
[SCHIZOSACCHAROMYCES POMBE]
MEDENILRNAVNLQVLKFHYPEIESIIDIASHVAVYQFDVGSQKWLKTSIEGTFFLVKDQ
RARVGYVILNRNSPENLYLFINHPSNVHLVDRIYLIHRTENQHVVLWMFDPNDMSRIFNI VKESLLR

>3I96A 119 XRAY 1.65 0.163 0.185 no Ethanolamine utilization protein eutS <UNP EUTS_ECOLI>
[ESCHERICHIA COLI]
MDKERIIQEFVPGKQVTLAHLIAHPGEELAKKIGVPDAGAIGIMTLTPGETAMIAGDLAL
KAADVHIGFLDRFSGALVIYGSVGAVEEALSQTVSGLGRLLNYTLCEMTKSLEHHHHHH
>1LLFA 534 XRAY 1.40 0.142 0.169 no Lipase 3 <UNP LIP3_CANRU> [CANDIDA CYLINDRACEA]
APTAKLANGDTITGLNAIINEAFLGIPFAEPPVGNLRFKDPVPYSGSLNGQKFTSYGPSC
MQQNPEGTFEENLGKTALDLVMQSKVFQAVLPQSEDCLTINVVRPPGKAGANLPVMLWI
FGGGFEIGSPTIFPPAQMVTKSVLMGKPIIHVAVNYRVASWGFLAGDDIKAEGSGNAGLK
DQRLGMQWVADNIAGFGGDPKVTIFGESAGSMSVLCHLIWNDGDNTYKGKPLFRAGIMQ
SGAMVPSDPVDGTYGNEIYDLFVSSAGCGSASDKLACLRSASSDTLLDATNNTPGFLAYS
SLRLSYLPRPDGKNITDDMYKLVRDGYASVPVIGDQNDGTFGLSSLNVTNAQARA
YFKQSFIHASDAEIDTLMAAYPDITQGSPPDTGIFNAITPQFKRISAVLGDIAFIHARR
YFLNHFQGGTKYSFLSKQLSGLPIMGTFHANDIVWQDYLLGSGSVIYNNAFIAFATDLP
NTAGLLVNWPKYTSSSSQSGNNLMINALGLYTGKDNFRTAGYDALMTNPSSFFV

>2C11A 276 XRAY 1.08 0.112 0.141 no NG, NG-DIMETHYLARGININE DIMETHYLAMINOHYDROLASE 1 <UNP
DDAH1_BOVIN> [BOS TAURUS]
ATFGRATHVVVRALPESLAQQALRRTKGDEVDFARAERQHQLYGVVLGSKLGLQVVQLPA
DESLPDCVFVEDVAVCEETALITRPGAPSRKKEADMMKEALEKLQLNIVEMKDENATLD
GGDVLFTGREFFVGLSKRTNQRGAIEILADTFKDYAVSTVPVVDALHLKSFCSMAGPNLIA
IGSSESAQKALKIMQQMSDHRVDKLTVPDDTAANCIYLNIPSKGHVLLHRTPEEYPESAK
VYEKLKDHMLIPVSNSELEKVDGLLTXSSVLINKK

>1L3LA 234 XRAY 1.66 0.246 0.266 no Transcriptional activator protein traR <UNP TRAR_9RHIZ>
[AGROBACTERIUM TUMEFACIENS]
MQHWLDKLTDLAAIEGDECILKTGLADIADHFGFTGYAYLHIQHRHITAVTNYHRQWQST
YFDKKFEALDPVVKRARSRKHIFTWSGEHERPTLSKDERAFYDHASDFGIRSGITIPIKT
ANGFMSMFTMASDKPVIDLDREIDAVAAAATIGQIHARISFLRTPTAEDAALDPKEAT
YLRWIAVGKTMEEIADVEGVKYNYSVRVKLREAMKRFDVRSKAHLTALAIRRKLI

>2FFYA 358 XRAY 1.07 0.133 0.164 no Beta-lactamase <UNP AMPC_ECOLI> [ESCHERICHIA COLI]
APQQINDIVHRTITPLIEQQKIPGMAVAVIYQGKPYFTWGYADIACKQPVTTQTLFELG
SVSKTFTGVLGGDAIARGEIKLSDPTTKYWPELTAKQWNGITLLHLATYTAGGLPLQVPD
EVKSSDLLRFYQNWQPAWAPGTQRLYANSSIGLFGALAVKPSGLSFEQAMQTRVFQPLK
LNHTWINVPPAEKNYAWGYREGKAVHVSPGALDAEAYGVKSTIEDMARWVQSNLKLPLDI
NEKTLQQGIQLAQSRWQTGDMYQGLGWEMLDWPVNPDSIINGSDAKIALAARPVKAITP
PTPAVRASWVHKTGATGGFGSYVAFIPEKELGIVMLANKNYPNPARVDAAWQILNALQ

>3QX1A 84 XRAY 1.60 0.206 0.218 no FAS-associated factor 1 <UNP FAF1_HUMAN> [HOMO SAPIENS]

GSHMEPVSKLRIRTPSGEFLERRFLASNKLQIVFDFVASKGFPWDEYKLLSTFPRRDVTQ
 LDPNKSLLLEVKLFPQETLFLEAKE
 >3C1QA 123 XRAY 1.70 0.158 0.208 no General secretion pathway protein F <UNP GSPF_VIBCH> [VIBRIO CHOLERAEE]
 MGFAPKRGISTPDLALITRQLATLVQSGMPLEECLRAVAEQSEKPRIRTMLVAVRAKVTE
 GYTLSDSLGDYPHFVDELFRSMVAAGEKSGHLDSVLERLADYAENRQKMRSKLQQASENL
 YFQ
 >3HYNA 189 XRAY 1.20 0.118 0.139 no Putative signal transduction protein <PDB 3HYN> [EUBACTERIUM RECTALE ATCC 33656]
 GMSYQNANYSAPYVSEPFSESNLGANSTHDFVYYNMLRMWKGEDNSFPFND AHDKTYNVR
 DGSDWEKTLKPRHLTRLDNSKNIIILFLSSITANSRALREEMNYGIGTKGLPVIVIPDYD
 KKSDIVDSNGNFKKQIKDLWDKLPAPFRDNMSSVATLHIPCTKSVIISALNNEFMVNTMA
 DAEKYYYYKP
 >3FOKA 307 XRAY 2.50 0.225 0.254 no uncharacterized protein Cgl10159 <UNP Q8NTZ2_CORGL> [CORYNEBACTERIUM GLUTAMICUM]
 MTPPIISPESEALRRMRAAEPMTVAERFKQRRKRELLGEDGKLFIVAADHPARGALAVG
 DNETAMANRYELLERMAIALSRPGVDGVLGTPDIIDDLAALGLLDDKIVVGSNMNRGGLRG
 ASFEMDDRYTGYNVSSMVDGRGVFAKTLVRINLS DAGTAPTLEATAHAVNEAAAAQLPIM
 LEPFMSNVVNGKVNDLSTDAVIQSVAIAAGLGNDSSYTWMKLPVVEEMERVMESTTMPT
 LLLGGEGGNDPDATFASWEHALTLPGVRGLTVGRTLLYPQDGDVAAAVDTAARLVHTDIQ
 QFTSQSI
 >1LR5A 163 XRAY 1.90 0.200 0.241 no Auxin binding protein 1 <UNP ABP1_MAIZE> [ZEA MAYS]
 SCVRDNLVRDISQMPQSSYIEGLSHITVAGALNHGMKEVEVWLQTISPGQRTPIHRHS
 CEEVFTVLKGGKTLMLGSSSLKYPGQPQEIPIFFQNTTFSIPVNDPHQVWNSDEHEDLQVL
 VIISRPPAKIFLYDDWSMPHTAAVLKFPFVWDEDCFEAAKEQL
 >1KOE1 172 XRAY 1.50 0.190 0.224 no ENDOSTATIN <UNP COIA1_MOUSE> [MUS MUSCULUS]
 QPVLHLVALNTPLSGGMRGIRGADFQCFQARAVGLSGTFRAFLSSRLQDLYSIVRRADR
 GSVPIVNLKDEVLSPSWDSLFSGSGQLQPGARIFSFDGRDVLRHPAWPQKSVWHGSDPS
 GRRLMESYCETWRTETTGTATGQASSLLSGRLLEQKAASCHNSYIVLCIENSF
 >3EAGA 326 XRAY 2.55 0.186 0.243 no UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase <UNP Q9JRY9_NEIMB> [NEISSERIA MENINGITIDIS MC58]
 SNAMKHIHIIGIGGTFMGGLAAIAKEAGFEVSGCDAKMYPPMSTQLEALGIDVYEGFDA
 QLDEFKADVYVIGNVAKRGMDVVEAILNLGLPYISGPQWLSENVLHHHWVLGVAGTHGKT
 TTASMLAWVLEYAGLAPGFLIGVPENFGVSARLPQTPRQDPNSQSPFFVIEADEYDTAF
 FDKRSKFVHYRPTAVLNNLEFDHADIFADLGAIQTQFHYLVRTVPSEGLIVCNGRQQSL
 QDTLDKGCWTPVEKFGTEHGWQAGEANADGSFVLLDGKTAGRVKWDLMGRHNRMNALAV
 IAAARHVGVDIQTACEALGAFKNVCR
 >1T3YA 141 XRAY 1.15 0.119 0.159 no Coactosin-like protein <UNP COTL1_HUMAN> [HOMO SAPIENS]
 ATKIDKEACRAAYNLVRDDGSAVIWVTFKYDGSTIVPGEQGAEQHFIIQQCTDDVRLFAF
 VRFTTGDA MSKRSKFALITWIGENVSGLQRAKTGTDKTLVKEVQNFQAEFVISDRKELE
 EDFIKSELKKAGGANYDAQTE
 >3L9VA 189 XRAY 2.15 0.215 0.262 no Putative thiol-disulfide isomerase or thioredoxin <PDB 3L9V> [SALMONELLA ENTERICA SUBSP. ENTERICA SEROVAR TYPHIMURIUM]
 SNAEWESITPPVVDAPAVVEFFSFYCPCYAFSQTMGVDQAI RHVLPQGSRMVKYHVSL
 GPLGHELTRAWALAMVKETDVIEKAFFTAGMVEKRLHSPDDVRRVFM SATGISRGEYDR
 SIKSPAVNDMVALQERLFKEYGVRGTPSVYVRGRYHINNAAFGAFSVENFRSRYAAVVRK
 LLAGNPDA
 >1SW6A 327 XRAY 2.10 0.222 0.251 no REGULATORY PROTEIN SWI6 <UNP SWI6_YEAST> [SACCHAROMYCES

CEREVISIAE]

NDDINKGPSGDNNNGTDDNDRTAGPIITFTHDLTSDFLSSPLKIMKALPSPVVDNEQK
MKLEAFLQRLLFPEIQEMPTSLNNDSSNRNSEGGSSNQQQHVSFDSLLQEVNDAFPNTQ
LNLNIPVDEHGNTPLHWLTSIANLELVKHLVKHGSNRLYGDNMGESCLVKAVKSVNNYDS
GTFEALLDYLPCLILED SMNR TILHHIIITSGMTGCSAAAKYYLDILMGWIVKKQNRPI
QSGTNEKESKPNDKNGERKDSILENLDLKI IANMLNAQDSNGDTCLNIAARLGNISIVD
ALLDYGADPFIANKSGLRPVDFGAGLE

>3CKCA 527 XRAY 1.50 0.192 0.210 no SusD <UNP Q8A1G2_BACTN> [BACTEROIDES THETA IOTAOMICRON]

GINDLDISPDPQTGGSFDDQGVFVKGYAMLGVTGQKGIDGSPDLDGQDEGESGFYRTTF
NCNELPTDECLWAWQKNQDIPQLTSISWSPSSQRTEWVYVRLGYDITQYNFFLDQTEGMT
DAETLRQRAEIRFLRALHYWYFLDLFGKAPFKEHFSNDLPVEKKGTETYTYIQNELNEIE
ADMYEPRQAPFGRADKAANWLLRLRLYNAGVYTGGTDYAKAEYASKVIGSAYKLCCTNY
SELFMADNDENENAMQEIIILPIRQDGVKTRNYGGSTYLVCGRVAGMPRMGTNGWSCIF
ARAAMVQKFFSNLEDVPMPLPADVEIPTKGLDTEQIDAFDAEHGIRTEDMIKAAGDDRAL
LYSGVGGGRRKIQTDAISGFTDGLSIVKWQNYRSDGKPVSHATYPDTDIPLFRLAEAYLT
RAEAI FRQGGDATGDINELRKRANCTRKVQTVTEQELIDEWAREFYLEGRRRSDLVRFGM
FTTNKYLDWDWKGAMNGTSVASYYNKYPIPVSDINNRRNMSQNEGYK

>4IVKA 434 XRAY 1.80 0.162 0.182 no Carboxylesterases <UNP K4HQE7_9BACT> [UNCULTURED BACTERIUM]

MKTSAKFLSFAVSFVLLIIASTSFAEGPVTATKPKEAGFTSEGLARIDAYLKNEIQAKTM
PGAVMMIKRNGETAYFSSFGRLRDPDTKEPMTAETIFRIYSMSKPIITVAAMMLVEEGKLQ
LDEPVSKYIPSFANVKVGVEKGENGMALETGPVKRAITIQDLMRHTSGITYGFVGDGLV
KKAYIASNLFDGDFDNAEFAERIAKLPLVYQPGTTWDYGHSTDILGRVVEVVSQKSLYQF
EKERLLDPLGMDTGFFVYTDPAKSLVAEAMPNDRKIGGSEMFDPVQKKEPQGGQGMVS
TIGDYARFTQMVLNGGTLDGKRYLSPKTIAYMGSNHIPQASGIVPGAYYLPGPVGFGGLG
FAVRTEAGVTPVEGSGVGLSWGGAGGTVFWDPKENLTVVFMAPMVSPRARVWRTLNRIV
YGAFDRLEHHHHHHH

>3F4AA 169 XRAY 1.80 0.168 0.211 no Uncharacterized protein YGR203W <UNP YG4E_YEAST>

[SACCHAROMYCES CEREVISIAE]

MGSSHHHHHHSSGRENLYFQGMDSYSITNVKYLDPTELHRWMQEGHTTTLREPFQVVDVR
GSDYMGGHKIDGWHYAYSRLKQDPEYLRLEKHLRLEKQADGRGALNVIFHCMLSQQRGPS
AAMLLRLSDTAELSRCRLWVLRGGFSRWQSVYGDDESVTAGYLPDLWR

>2PJUA 225 XRAY 2.10 0.204 0.252 no Propionate catabolism operon regulatory protein

<UNP PRPR_ECOLI> [ESCHERICHIA COLI]

MSLAHPRLNDDKPVIWTVSVTRLFELFRDISLEFDHLANITPIQLGFEKAVTYIRKKLA
NERCDIIAAGSNGAYLKSRLSVPVILIKPSGYDVLQFLAKAGKLTSSIGVVITYQETIPA
LVAFAQTFNLRLDQRSYITEEDARGQINELKANGTEAVVGAGLITDLAEAGMTGIFIYS
AATVRQAFSDALDMTRMSLRHNTHDATRNALRTRYVLEGHHHHHHH

>4BOUA 160 XRAY 1.55 0.177 0.229 no OTU DOMAIN-CONTAINING PROTEIN 3 <UNP OTUD3_HUMAN> [HOMO SAPIENS]

GPEFVSFANQLQALGLKLREVPGDGNCLFRALGDQLEGHSRNHLKHRQETVDYMIKQRED
FEPFVEDDIPFEKHVASLAKPGTFAGNDAIVAFARNHQLNVVIHQLNAPLWQIRGTEKSS
VRELHIAARYGEHYDSVRRINDNSEAPAHQLTDFQMLHQD

>3PE6A 303 XRAY 1.35 0.115 0.147 no Monoglyceride lipase <UNP Q6IBG9_HUMAN> [HOMO SAPIENS]

MPEESSPRRTPQSIPIYQDLPHLVNADGQYLFRCRYWAPTGTPKALIFVSHGAGEHSGRYEE
LARMLMGLDLLVFAHDHVGHGQSEGERMVVSDFHVFVRDVLQHVD SMQKDYPLPVFLLG
HSMGGAIAILTAAERPGHFAGMVLISPLVLNAPESATTFKVLAAKVLNSVLPNLSSGPID
SSVLSRNKTEVDIYNSDPLICRAGLKVCFGIQLLNAVSRVERALPKLTVPFLLLQGSADR
LCDSKGAYLLMELAKSQDKTLKIYEGAYHVLHKELPEVTNSVFHEINMWVSQRTATAGTA

SPP

>3NKZA 123 XRAY 2.11 0.158 0.192 no Flagellar protein fliT <UNP FLIT_YERE8> [YERSINIA ENTEROCOLITICA SUBSP. ENTEROCOLITICA] SNAMERHQHLLSEYQQILTSEQMLVLATEGNWDALVDLEMTYLKAVESTANITISSCSS LMLQDLLREKLRAILDNEIEIKRLLQLRLDRLSDLVGQSTKQQAVNNTYGGFPDHALLG ETQ

>3M62A 968 XRAY 2.40 0.203 0.257 no Ubiquitin conjugation factor E4 <UNP UFD2_YEAST>

[SACCHAROMYCES CEREVISIAE]

GSPEFRSMTAIEDILQITTPSDTRGYSLLKSEEVPGGSTLGVDFTLLLYQLTENEKL DKPFEYLNDCFRRNQQQKRITKNKPNAESLHSTFQEIDRLVIGYGVVALQIENFCMNGAF INYITGIVSNVNSYTDFLSQIIQRAILEGTALDLLNAVFP TLLEYCNKHVSHFDL NESVI YNNVLTIFELFVTFKPIAEIFTKIDGFFADYSCKPQDFERKTILGPILSLSPIEAAVAIR NYGDNLLRSKQQTAMIHESLQAEHKVV IDRLFFIVDKLVRGSLNSRTDMISYFAHIANKN HLRRADHPPFKELSSNGFMSNITLLLVRFSQPFLDISYKKIDKIDANYFNPNPSLFIDLSG ETRLNSDFKEADAFYDKNRKTADSKPNFISDCFFLTLYLHYGLGGTLSFEEKMGSEIKA LKEEIEKVKKIAANHVDVFARFITAQLSKMEKALKTTESLRFALQGFFAHRSLQLEVDFDI CGASTFLIRVVDPEHEFPFKQIKLPLIPDQIGVENVDNADFLRAHAPVPFKYYPEFVVEG PVNYSLYISKYQTSPIFRNPRLG SFVEFTTMVLRCP ELVSNPHLKGKLVQLLSVGAMPLT DNSPGFMMDIFEHDELVNKNLLYALLDFYVIVEKTGSSSQFYDKFNSRYSISIILEELY KIPSYKNQLIWQSQNNADFFVRV FARMNLDTFLLEGLSNLAEVHNIQNELDNRARGAP PTREEEDKELQTRLASASRQAKSSCGLADKSMKLFEIYSKDIPAAFVTPEIVYRLASMLN YNLESLVGPKCGELKVKDPQSYSFNPKDLLKALT TVYINLSEQSEFISAVAKDERSFN RN LFVRAVDILGRKTGLASPEFIEKLLNFANKAEEQRKADEEEDLEYGDVPDEFDPLMYTI MKDPVILPASKMNIDRSTIKAHLLSDSTDPFNRMPKL EDVTPNEELRQKILCFKKQKKE EAKHKASE

>1WDJA 187 XRAY 2.00 0.189 0.241 no hypothetical protein TT1808 <UNP Q5SI60_THET8> [THERMUS

THERMOPHILUS] MPLVLDLARPVSEELRRLSELNPGYQWERSPEGR LWSP TGGESGRSLQLAYQLARWN

EERGLGVVDSSTGKFPGDGSILSPDAAFVERGAWEALSEAEREGFPPLAPKAVFEVRS A

SQDPEELRAKMG IYLRNGVLLGLVDPYARAVEVFRPGKPPLRLEGVERVSLDPELPGFA

LSLPPLW

>2ZUVA 759 XRAY 1.85 0.151 0.192 no Lacto-N-biose phosphorylase <UNP Q5NU17_BIFLO> [BIFIDOBACTERIUM LONGUM]

MTSTGRFTLPSEENFAEKTKE LAELWGADAI RNSDGHLD EAVLALGKKIYNAYFPTRAH NEWITLHMDETPQVYLLTDRILAESDTVDIPLMESFFAEQLKPNRDADPHKYWEVVDRTT GEVVDSANWTLDADEDTVHVSGVAWHEYTVSFLAYIIWDPVEMYNHLTNDWGDKEHEIP FDIYHPATRK FVFDTFEQWLKDSPQTDVVRFTTFFYQFTLLFDEKRREKVVDWFGCACTV SPRALDDFEAKYGYRLRPEDFVDGGAYNSAWRVPRKAQRDWIDFLSGFVRENVKQLADMS HAAGKEAMMFLGDQWIGTEPYKDGFDLGLDAVVG SIGDGTTRMIADIPGVKYTEGRFL PYFFPDTFYEGNDPSIEGLDNWRKARRAILRSPISRMGYGGYLSLAAKFPKFVDTVTHIA NEFRDIHRTGGVAAEGELNVA ILNSWGMRSWMAFTVAHALPNKQTSYSGILESLSGM RVNVRFISFDDVLAHGIDSDIDVIINGGPVDTAFTGGDVWTPNPKLVETVRAWVRGGGAFV GVGEPSSAPRFQTGRFFQLADVIGVDEERYQTLSDVKYFPPVVPDHFITADVVPDPAARE AWEQAGYRIPLSGCGGQS I KPLGGIDFGEPVLNTYPVNENVTLRADGGQVQLATNDYG KGRGVYISGLPYSAANARLLERLVFYASHNEDKYAAWSSSNPECEVAHFPEQGLYCVINN TDQPQKTTVTLADGTTEDFDLPDSGIAWREALEHHHHHH

>3SKQA 249 XRAY 2.10 0.196 0.227 no Mitochondrial distribution and morphology protein 38 <UNP

MDM38_YEAST> [SACCHAROMYCES CEREVISIAE]

KLFPNLLPSTYESGDKQAKRNKLI EIRKKTSEFLHETLEESNLITYNTIENAEKKQKFL

NFRKLYSAKEGKIMTFQHDEISAIAQMFKNDSVLDNLSRPQLAAMSKFMSLRPFGNDNM

LRYQIRSKLDIMNDDKTIDYEGVESLSQEELYQACVSRGMKAYGVSKEDLVDNLKVVLE
 LRLRQKIPSVLMVLSSTFTFGGLPKENYSKAFSPLAEKKETKSKYDDLDDLYDGILQVL
 SSIPDPVYN
 >3C37A 253 XRAY 1.70 0.221 0.254 no Peptidase, M48 family <UNP Q74D82_GEOSL> [GEOBACTER
 SULFURREUCENS PCA] MATSMTDIKGFNMISIEQEKELGKFAVEIEKQQQPVNDPEVQRYVDKVGKRLLSGARAV
 EFDYVFKVVKDDSVNAFAIPGGRVYVHTGLLKAADNETELAGVLAHEINHAVARHGTRQM
 TQEYGYSLVLSVLGDNPNMLAQLAGQLFGKAGMMSYSREYENQADFLGVETMYKAGYNP
 NGLTSFFQKLNAMDGGTQSNVARFFSTHPLTSEIRVQAEIAKLPPQRYLTDETEFKKI
 KGRLKLEHHHHHH
 >4GORA 735 XRAY 2.70 0.216 0.217 no Capsid protein VP1 <UNP CAPSD_PAVHH> [H-1 PARVOVIRUS]
 MAPPAKRAKRGWVPPGYKYLPGNSLDQGEPTNPSDAAAKEHDEAYDQYIKSGKNPYLYF
 SPADQRFIDQTKDAKDWGGKVGHYFFRTKRAFAPKLSTDSEPGTSGVSRPGKRTKPPAHI
 FVNQARAKKKRASLAAQQRITLMSDGTETNPDTGIANARVERSADGGGSSGGGSGGGG
 IGVSTGTYNQTTYKFLGDGWVEITAHASRLHLGMPPSENYCRVTVHNNQTTGHGTVK
 GNMAYDDTHQQIWTWPWSLVDANAWGVWFQPSDWQFIQNSMESLNLDLSQELFNVVVKTV
 TEQQGAGQDAIKVYNNDLTACMMVALDSNNILPYTPAAQTSETLGFYPWKPTAPAPYRY
 FFMPRQLSVTSSNSAEGTQITDTIGEPQALNSQFFTIENTLPITLLRTGDEFTTGTIYN
 TDPLKLTHTWQTNRHLMPPRITDLPTSDTATASLTANGDRFGSTQTQNVNYVTEALRTR
 PAQIGFMQPHDNFEANRGGPFKVPVPLDITAGEDHDANGAIRFNYGKHGEDWAKQGAA
 PERYTWDAIDSAAGRDTARCFVQSAPISIPPNNQILQREDAIAGRTNMHYTNVFNISYGP
 LSAPHPDPPIYPNGQIWDKELDLEHKPRLHVTAPFVCKNNPPGQLFVRLGPNLTDQFDPN
 STTVSRIVTYSTFYWKGLKFKAKLRPNLTWNPVYQATTSVANSYMNKKWLPSATGNM
 HSDPLICRPVPHMTY
 >3S8IA 148 XRAY 1.70 0.177 0.199 no Protein DDI1 homolog 1 <UNP DDI1_HUMAN> [HOMO SAPIENS]
 MGSSHHHHHHSSGLVPRGSGQVTMLYINCKVNGHPLKAFVDSGAQMTIMSQACAERCNIM
 RLVDRRWAGVAKGVGTQRIIGRVHLAQIQIEGDFLQCSFSILEDQPMMLLGLDMLRRHQ CSIDLKKNVLVIGTTGTQTYFLPEGELP
 >3FSAA 125 XRAY 0.98 0.121 0.135 no Azurin <UNP AZUR_PSEAE> [PSEUDOMONAS AERUGINOSA]
 AECSVDIQGNDQMFTNAITVDKCKQFTVNLSPGNLPKNVMGHNVWLSTAADMQGVV
 TDGMASGLDKDYLPDDSRVIAHTKLIGSGEKDSVTFDVSKLKEGEQYMFCAHAAMKG
 TLTLK
 >1DGWA 178 XRAY 1.70 0.196 0.252 no CANAVALIN <UNP CANA_CANEN> [CANAVALIA ENSIFORMIS]
 NNPYLFRSNKFLTLFKNQHGLSRLLQRFNEDTEKLENLRDYRVLEYCSKPNTLLPHHSD
 SDLLVLVLEGQAILVLVNPDRDITYKLDQGDIAIKIAGTPFYLINPDNNQNLRLKFAIT
 FRRPGTVEDFFLSSTKRLPSYLSAFSKNFLEASYDSPYDEIEQTLLQEEQEGVIVKMP
 >4DCMA 375 XRAY 2.30 0.203 0.252 no Ribosomal RNA large subunit methyltransferase G <UNP
 RLMG_ECOLI> [ESCHERICHIA COLI]
 HMRSITLQRFPATDDVNPLQAWAADEYLLQQLLDDEIRGPVLILNDAFGALSCALAEHK
 PYSIGDSYISELATRENRLNGIDESSVKFLDSTADYPQQPGVLIKVPKTLALLEQQLR
 ALRKVVTSDTRIIAGAKARDIHTSTLELFEKVLGPTTTTLAWKKARLINCTFNEPQLADA
 PQTVSWKLEGTDWTIHNVANVFSRTGLDIGARFFMQHLPENLEGEIVDLGCGNGVIGLTL
 LDKNPQAKVVFVDESPMAVASSRLNVETNMPEALDRCEFMNNALSGVEPFRFNAVLCNP
 PFHQQHALTDNVAWEMFHHARRCLKINGELYIVANRHLDYFHKLKKIFGNCTTIATNNKF
 VVLKAVKLEHHHHHH
 >2Q4KA 251 XRAY 2.50 0.166 0.236 no Uncharacterized protein C11orf68 <UNP CK068_HUMAN> [HOMO
 SAPIENS]
 MEPGEELEEEGSPGGREDGFTAHLAAEAMAADMPWLVDARTTPATELDAWLAKYPPS
 QVTRYGDPGSPNSEPVGWIAVYGGQGYSPNSGDVQGLQAAWEALQTSGRPITPGTLRQLAI

THHVLSGKWLMLHAPGFKLDHAWAGIARAVVEGRLQVAKVSPRAKEGGRQVICVYTDDFT
 DRLGVLEADSIRAAGIKLLTYKPDVYTYLGIYRANRWHLCPTLYESRFQLGGSARGSR
 VLDRANNVELT
 >3JZLA 409 XRAY 1.91 0.211 0.241 no Putative cystathionine beta-lyase involved in aluminum resistance
 <UNP_Q720C5_LISMF> [LISTERIA MONOCYTOGENES STR. 4B]
 GMNNIQAIRKKVETQIDDLQNKTDIEAFNQAKVLDAFQENKVSDFHHPSTGYGYDDEG
 RDTLERVYATVFKTEAALVRPQIISGTHAISTVLFGILRPDDELLYITGQPYDTLEEIVG
 IRKQGGGSLKDFHIGYSSVPLENGDVDFPRIAKMTPKTKMIGIQRSGYADRPSTFIE
 KIKEMIVFVKINPEVIVFDNCGYGEFVEYQEPPEVGADIIAGSLIKNPGGGLAKTGGYI
 AGKEALVDLCGYRLTPPGIGREAGASLYSLEMYQGFFLAPHVTAQAIKGARFTAAMLAE
 FGVEADPVWDAPRTDLIQSVSFHNKEKMFVAFQAIIQAASPVNAHVLPIGAYMPGYEDDVI
 MAAGTFIQGASLELTADGPPIREPYQLYVQGGGLTYEHIKIAVTRAIQKIV
 >1QWRA 319 XRAY 1.80 0.199 0.232 no Mannose-6-phosphate isomerase <UNP_MANA_BACSU> [BACILLUS
 SUBTILIS] SNAMTQSPIFLTPVFKEKIWGGTALDRFGYSIPSESTGECWAISHPKGPSTVANGPYK
 GKTIELWEHREVFGGVEGDRFPLLTCLLDVKEDTSIKVHPDDYYAGENEELGKTEC
 WYIIDCKENAEIYGHRTARSKTELVTMINSGDWEGLLRRIKIKPGDFYYVPSGTLHALCK
 GALVLETQQNSDATYRVYDYDRLDSNGSPRELHFAKAVNAATVPHVDGYIDESTESRKG
 TIKTFVQGEYFSVYKWDINGEAEMAQDESFLICSVIEGSGLLKYEDKTCPLKKGDHFIPL
 AQMPDFTIKGTCTLIIVSHI
 >1GPOA 143 XRAY 1.40 0.209 0.237 no CATION-INDEPENDENT MANNOSE-6-PHOSPHATE RECEPTOR <UNP
 MPRI_HUMAN> [HOMO SAPIENS]
 MKSNEHDDCQVTNPSTGHLFDLSSLSGRAGFTAAYSEKGLVYMSICGENENCPPGVGACF
 GQTRISVGKANKRLRYVDQVLQLVYKDGSPCPSKSGLSYKSVISFVCRPEAGPTNRPLI
 SLDKQTCTLFFSWHTPLACEQAT
 >1QD6C 240 XRAY 2.10 0.226 0.283 no OUTER MEMBRANE PHOSPHOLIPASE (OMPLA) <UNP_PA1_ECOLI>
 [ESCHERICHIA COLI]
 FTLYPYDTNYLIYTQTSDLNKEAIASYDWAENARKDEVKFQLSLAFPLWRGILGPNSVLG
 ASYTQKSWWQLSNSEESSPFRETNYPQLFLGFATDYRFAGWTLRDVEMGYNHDSNGRSD
 PTSRSWNRLYTRLMAENGNWLVEVKPWYVVGNTDDNPDIKYMGYYQLKIGYHLGDAVLS
 AKGQYNWNTGYGGAELGLSYPIHKHRLYTQVYSGYGESLIDYNFNQTRVGVGVMNLDF
 >2QNAB 66 XRAY 2.84 0.235 0.282 no Snurportin-1 <UNP_SPN1_HUMAN> [HOMO SAPIENS]
 MEELSQUALASSFSVSDLNSTAAPHPRLSQYKSKYSSLEQSERRRRLELQKSKRLDYVN
 HARRLA
 >1GQEA 365 XRAY 1.81 0.222 0.247 no RELEASE FACTOR 2 <UNP_RF2_ECOLI> [ESCHERICHIA
 COLI] MFEINPVNRIQDLTERSVDLRGYLDYDAKKERLEEVNAELEQPDVWNEPERAQAALGKER
 SSLEAVDITLDQMKQGLDVSGLLELAVEADDEETFNEAVAELDALEEKLAQLEFRRMFS
 GEYDSADCYLDIQAGSGGTEAQDWASMLERMYLRWAESRGFKTEIIIESEGEVAGIKSVT
 IKISGDYAYGWLRTETGVHRLVRKSPFDGSGRRHTSFSSAFVYPEVDDDDIEINPADLR
 IDVYRASGAGGQHVNRTESAVRITHIPTGIVTQCQNDRSQHKNKDQAMQMKAKLYEVEM
 QKKNAEKQAMEDNKSIDIGWSQIRSYVLDDSRIDKDLRTGVETRNTQAVLDGSLDQFIEAS
 LKAGL
 >4G4S0 276 XRAY 2.49 0.184 0.232 no Proteasome chaperone 1 <UNP_POC1_YEAST> [SACCHAROMYCES
 CEREVISIAE]
 MLFKQWNDLPEPKHLLDLPEISKNLQSLEVCVPKVEFPQDLDPQYSTAVITTKIMNPL
 FPKNLLQLTSIGEIKTTLTVKSPSLPQSSGKHSWNYDENFPNEVDPDQKNDTADETVYGF
 SFPIYSFGKTLFLSMEENFISISPIFGNMISRSIISQLAQFSPDIIIVIGTSDKIASMKVM
 TENECTLPQPEFITGFIGSVLTQLIVGPSKGLKFKCLVAPSEGPNGFELSLSDMGSLVD
 LCGQWLGFEPSRYSEECYRLWRCDAAIGAQSGLYI

>2VGNA 386 XRAY 2.50 0.210 0.251 no DOM34 <UNP DOM34_YEAST> [SACCHAROMYCES CEREVISIAE]
 MKVISLKKDSFNKGGAVITLLPEDKEDLFTVYQIVDKDELIFKKKFTSKLDEAGKKKST
 DLVKLKIKVISEDMDKDEYLKYKGVTVTDESGASNDIPVGKYSFTLDYVYPFTI IKQ
 NFNKFMQKLLNEACNIEYKSDTAAVVLQEGIAHVCLVTSSSTILKQKIEYSMPKKKRTD
 VLKFDEKTEKFYKAIYSAMKKDLNFDKLTII LCSPGFYAKILMDKIFQYAEHHNKKIL
 DNKGMFFIAHCSTGYLQGINEVLKNPLYASKLQDTKYSKEIMVMDEFLHLNKDDDKAWY
 GEKEVVKAAEYGAISYLLLTDKVLHSDNIAQREEYLKLMDSVESNGGKALVLSTLHSLGE
 ELDQLTGIACILKYPLPDLEDDGEE

>1WFA 179 XRAY 2.05 0.213 0.258 no Peroxisome biogenesis factor 1 <UNP PEX1_MOUSE> [MUS
 MUSCULUS]
 SSDRLAGAGSGGAVVTVAFTNARDCFHLPRRLVAQLHLLQNQAIEVASDHQPTYLSWVE
 GRHFNDQSENVAEINRQVGQKLGLSSGDQVFLRPCSHVVSQQVEVEPLSADDWEILELH
 AISLEQHLLDQIRIVFPKAVPIWVDQQTIFYIFIQIVTLMPAAPYGRLETNTKLLIQPKT

>2YEXA 276 XRAY 1.30 0.135 0.164 no SERINE/THREONINE-PROTEIN KINASE CHK1 <UNP CHK1_HUMAN>
 [HOMO SAPIENS] MAVPFVEDWDLVQTLGEGAYGEVQLAVNRVTEEAVAVKIVDMKRAVDCPENIKKEICINK
 MLNHENVVKFYGHRREGNIQYLFLEYCSGGELFDRIEPDIGMPEPDAQRFHQLMAGVVY
 LHGIGITHRDIKPENLLLDERDNLKISDFGLATVFRYNNRERLLNKMCGTLPYVAPELLK
 RREFHAEPVDVWSCGIVLTAMLAGELPWDQPSDSCQEYSDWKEKKTYLNPWKKIDSAPLA
 LLHKILVENPSARITIPDIKKDRWYNKPLKKGAKRP

>3GKUA 225 XRAY 2.95 0.223 0.287 no Probable RNA-binding protein <PDB 3GKU> [CLOSTRIDIUM
 SYMBIOSUM ATCC 14940]
 SNAMDMVTVAKTVEEAVTKALIELQTTSKLTYEIVEKGSAGFLGIGSKPAIIRAKRKE
 TLQDKAIEFLEQVFDAMNMAVDISVEYNETEKEMNVNLKGDDMGILIGKRGQTLDLSLQYL
 VSLVVNKSSSDYIRVKLDTENYRERRKETLETLAKNIAVKVKTGRSVSLEPMNPYERRI
 IHAALQNDKYVVTRSDGEEPFRHVIISLKRENRRDRNDRSDRNEK

>2FJRA 189 XRAY 1.95 0.219 0.247 no Repressor protein CI <UNP RPC1_BP186> [ENTEROBACTERIA PHAGE 186]
 DSLGWSNVDVLDRIEAYGFSQKIQLANHFDAISSLSNRYTRGAISYDFAAHCALETGA
 NLQWLLTGEGEAFVNNRESSDAKRIEGFTLSEEILKSDKQLSVDAQFFTKPLTDGMAIRS
 EGKIYFVDKQASLSDGLWLVDIKGAISIRELTKLPGRKLHVAGGKVPFECGIDDIKTLGR
 VVGYYSEVN

>3T3PA 457 XRAY 2.20 0.189 0.220 no Integrin alpha-IIb <UNP ITA2B_HUMAN> [HOMO SAPIENS]
 LNLDPVQLTFYAGPNGSQFGFSLDFHKDSHGRVAIVVGAPRTLGPSEQEETGGVFLCPWRA
 EGGQCPSSLFLDRDETNRVGSQTLQTFKARQGLGASVVSWSDVIVACAPWQHWNVLEKTE
 EAEKTPVSGCFLAQPESGRRAEYSPCRGNTLSRIYVENDFSWDKRYCEAGFSSVVTQAGE
 LVLGAPGGYYFLGLLAQAPVADIFSSYRPGILLWHVSSQSLSFSSNPEYFDGYWGYSVA
 VGEFDGDLNTTEYVVGAPTWSWTLGAVEILDSYYQRLHRLRGEQMASYFGHSAVTDVNG
 DGRHDLVLGAPLYMESRADRKLAEVGRVYFLQPRGPHALGAPSLLLTGTQLYGRFGSAI
 APLGDLDRDGYNDIAVAAPYGGPSGRGQVLVFLGQSEGLRSRPSQVLDSFPFTGSAFGFS
 LRGAVIDDNGYPDLIVGAYGANQVAVYRAQPVVKAS

>3EC3A 250 XRAY 1.92 0.190 0.236 no Protein disulfide-isomerase A4 <UNP PDIA4_RAT> [RATTUS
 NORVEGICUS]
 GPLGSPPSKEILTLKQVQEFLKDGDDVVILGVFQGVGDPGYLQYQDAANTLREDYKFHHT
 FSTEIAKFLKVS LGKLVLMQPEKFQSKYEPRMHVMDVQGSTEASAIKDYVVKHALPLVGH
 RKTSNDAKRYSKRPLVVVYYSVDFSFYRTATQFWRNKVLEAKDFPEYTFIAIDEEDYA
 TEVKDLGLSESGDVNAAILDESGKKFAMEPEEFDSDALREFVMAFKKGKLPVKSQPV
 PKNNKGAAAS

>3NNRA 228 XRAY 2.49 0.232 0.260 no Transcriptional regulator, TetR family <UNP A1U6M1_MARAV>

[MARINOBACTER AQUAEOLEI] GMTMKTRDKILLSLELFNDKGERNITTNHIAAHLAISPGNLYYHFRNKSDIIYEIFQEY
EKLVDYYLDIPEDRPITLEDMTFYLESVFDGLWSYRFFHRDLEYLLDSDPRLRQDYREFT
NRCLAAINRIFAKLADAGIIQPQPEDLRSAmslnvwlvitnwmaflktahaaeepasls
TELKQGIYQVLTLEVPLYTPEYRERVLALEKYRPTLPEAQGISGVEA
>4NHEA 328 XRAY 1.95 0.177 0.207 no Oxidoreductase, Gfo/Idh/MocA family <UNP Q97PV8_STRPN>
[STREPTOCOCCUS PNEUMONIAE] SNAMLKLGVIPTGAISHHFIEAAHTSGEYQLVAIYSRKLETAATFASRYQNIQLFDQLEV
FFKSSFDLVYIASPNSLHFAQAKAALSAGKHVILEKPAVSQPQEWFDLIQTAEKNNCFIF
EAARNYHEKAFTTIKNFLADKQVLGADFNAYKYSSKMPDLLAGQTPNVFSDRFAGGALMD
LGIYPLYAAVRLFGKANDATYHAQQLDNSIDLNGDILFYPDYQVHIKAGKNITSNLPC
IYTTDGTLLNTIEHIRSAIFTDHQGNQVQLPIQQAPHTMTEEVAFAHMIQQPDLNLYQ
TWLYDAGSVHELLYTMRQTAGIRFEAEK
>2AVTA 378 XRAY 2.00 0.245 0.284 no DNA polymerase III beta subunit <GB AAF98349> [STREPTOCOCCUS
PYOGENES]
MIQFSINRTLFIAHLNTTKRAISTKNAIPILSSIKIEVTSTGVTLTGSNGQISIENTIPV
SNENAGLLITSPGAILLEASFFINISSLPDISINVKEIEQHQQVLTSGKSEITLKGKDV
DQYPRLQEVSTENPLILKTKLLKSIIAETAFAASLQESRPILTGVHIVLSNHKDFKAVAT
DSHRMSQRLITLNTSADFMVVLPSKSLREFSAVFTDDIETVEVFFSPSQILFRSEHISF
YTRLLEGNYPDTRLLMTEFETEVVFNTQSLRHAMERAFLISNATQNGTVKLEITQNHIS
AHVNSPEVGKVNEDLDIVSQSGDLTISFNPTYLIESLKAIKSETVKIHFLSPVRPFTLT
PGDEEESFIQLITPVRTN
>3D37A 381 XRAY 2.10 0.222 0.273 no Tail protein, 43 kDa <UNP Q9JZC8_NEIMB> [NEISSERIA
MENINGITIDIS MC58]
MQNNSYGYAVSVRVGGKEHRHWERYDIDSDFLIPADSFDFVIGRLGPEAAIPDLSGESCE
VVIDGQIVMTGIIGSQRHGKSKGSRELSLGRDLAGFLVDCSAPQLNVKGMTVLDAKKL
AAPWPQIKAVVLKAENPALGKIDIEPGETVWQALTHIANSVGLHPWLEPDGTLVVGGAD
YSSPPVATLCWSRTDSRCNIERMDIEWDTDNRFSEVTFLAQSHGRSGDSAKHDLKWVYKD
PTMTLHRPKTVVVSADNLAALQKQAKKQLADWRLEGFTLTITVGGHKTRDGVWLPGLR
VHVIDDEHGIDAVFFLMGRRFMLSMDGTQTELRLKEDGIWTPDAYPKKAEAAARKRKGR KGVSHKGGKGGKKQETAVFE
>1NNHA 294 XRAY 1.65 0.172 0.191 no asparaginyl-tRNA synthetase-related peptide <UNP Q8TZN6_PYRFU>
[PYROCOCCUS FURIOSUS]
MNAVEIISREISPTLDIQTKILEYMTDFFVKEGFKWLLPVIISPITDPLWPDPAGEGMEP
AEVEIYGVMRLTHSMILHKQLAIAMGLKKIFVLSPNIRLESQKDDGRHAYEFTQLDFE
VERAKMEDIMRLIERLVYGLFRKAEWGTGREFPKTRFEVFEYSEVLEEFSGDEKASQEM
EPPFWIINIPREFYDREVDGFWRNYDLILPYGYGEVASGGEREWEYKIVAKIRKAGLNE
DSFRPYLEIAKAGKLKPSAGAGIGVERLVRVIVGAKHIAEVQPPFPRIPGIPAVI
>3MFIA 520 XRAY 1.76 0.165 0.187 no DNA polymerase eta <UNP POLH_YEAST> [SACCHAROMYCES
CEREVISIAE] GPGGDPHMSKFTWKELIQLGSPSKAYESSLACIAHIDMNAFFAQVEQMRCGLSKEDPVVC
VQWNSIIAVSYAARKYGISRMDTIQEALKKCSNLIPIHTAVFKKGEDFWQYHDGCGSWVQ
DPAKQISVEDHKVSLEPYRRESRKALAIKFWACDLVERASIDEVFLDLGRICFNMLMFDN
EYELTGDLKLDALSNIREFIGGNYDINSHLPLIPEKIKSLKFEQDVFNPEGRDLITDW
DDVILALGSQVCKGIRDSIKDILGYTTSCGLSSTKNVCKLASNYKKPDAQTIVKNDCLLD
FLDCGKFEITSFWTLGGVLGKELIDVLDLPHENSIKHIRETWPDNAGQLKEFLDAKVKQS
DYDRSTSNIDPLKTADLAELFKLSRGRYGLPLSSRPVVKSMMSNKNLRGKSCNSIVDCI
SWLEVFCaelTSRIQDLEQYENKIVIPRTVSI SLKTKSYEVYRKSGPVAYKGINFQSHL
LKVGIKFVTDLDIKGNKSYPLTKLSMTITNFDIIDLQK
>3U2GA 286 XRAY 2.30 0.180 0.221 no S-layer protein MA0829 <UNP Q8TSG7_METAC> [METHANOSARCINA
ACETIVORANS]

MGYEIRGQVASGFGDQSWDASSFAGFYDIDNVSTETLTVSDLDGNVIPEGGLVYTTT
 IADVDFEYNPDAWDQYPVMGFFAEYIPINPKADKIAKLVLSDDKYTIRTGEMLDL
 GEGYAIEAKQVDVDGEKVLFTKDGFEVDDEIISVSTADDEANTWDVELDDIEDEDDVV
 VLKVHVNVQVFQGAVDIAQIEGLWLIDYANAMTIESDDEFGNLDVDSIDGDTLKISNEDT
 FTLTRDSEEEIGEGMYFMIADTSSSDLRYYPYVEKTIGLEHHHHHHH
 >1VROA 247 XRAY 2.49 0.192 0.229 no Probable 2-phosphosulfolactate phosphatase <UNP COMB_CLOAB>
 [CLOSTRIDIUM ACETOBUTYLICUM]
 MGSDKIHSHHHHMKIDLIISADDIKEEKVNKTAVVIDMLRATSVITTALNNGCKRVVPV
 LTVEEALKKVKEYGKDAILGGERKGLKIEGFDFSNPMEYTEDVVKGKTLIMTTTNGTRA
 IKGSETARDILIGSVLNGEAVAELVELNNDVIVNAGTYGEFSIDDFICSGYIINCVM
 RMKKLELTDAATTAQYVYKTNEDIKGFVKYAKHYKRIMELGLKKDFEYCKKDIVKLVPQ
 YTNGEIL
 >106DA 163 XRAY 1.66 0.229 0.261 no Hypothetical UPF0247 protein TM0844 <UNP Y844_THEMEA>
 [THERMOTOGA MARITIMA] MSLRVRIAVIGKLDGFIKEGKHYEKFLLRFCKPEVLEIKRVHRGSIEEIVRKETEDLTN
 RILPGSFVMVMDKRGEESSEEFADFLKDLEMKGKDITILIGGPYGLNEEIFAKAHRVFS
 LSKMTFTHGTVLIVLEQIFRAFKIIHGENYHYEGGSHHHHHH
 >2DB7A 64 XRAY 1.90 0.192 0.220 no Hairy/enhancer-of-split related with YRPW motif 1 <UNP
 HEY1_HUMAN> [HOMO SAPIENS]
 GSSGSSGGYFDAHALAMDYRSLGFRECLAEVARYLSIIEGLDASDPLRVRLVSHLNYYAS
 QREA
 >1AISB 200 XRAY 2.10 0.212 0.268 no TRANSCRIPTION INITIATION FACTOR IIB <UNP TF2B_PYRWO>
 [PYROCOCCUS WOESSEI]
 VSDAAERNLAFALSELDRTAQLKLPRHVEEEAARLYREAVRKGLIRGRSIESVMAACVY
 AACRLKVPRTLDEIADIARVDKKEIGRSYRFIARNLNLTPKKLFVKPTDYVNKFADDEL
 LSEKVRRAIEILDEAYKRGLTSGKSPAGLVAAALYIASLLEGEKRTQREVAEVARVTEV
 TVRNRYKELVEKLKIKVPIA
 >2FD6U 276 XRAY 1.90 0.239 0.276 no Urokinase plasminogen activator surface receptor <UNP
 UPAR_HUMAN> [HOMO SAPIENS]
 SLRCMQCKTNGDCRVEECALGQDLCRTTIVRLWEEGEELELVEKSCETHSEKTNRTLSYRT
 GLKITSLETVVCGLDLCNQGNSGRAVITYSRSYLECI SCGSSDMSCERGRHQSLQCRSPE
 EQCLDVVTHWIIQEGEGRPKDDRHLRGCGYLPGPCGSGNFHNNDTFHFLKCCNTTKCNEG
 PILELENLPQNGRQCYCKGNSTHGCSEETFLIDCRGPMNQCLVATGTHEPKNQSYMVR
 GCATASMCQHAHLGDAFSMNHIDVSCCTKSGCNHPD
 >2PJZA 263 XRAY 1.90 0.198 0.242 no Hypothetical protein ST1066 <UNP
 Q972R9_SULTO> [SULFOLOBUS TOKODAI]
 MIQLKNVGITLSGKGYERFSLENINLEVNGEKVIIILGPNGSGKTTLLRAISGLLPYSGNI
 FINGMEVRKIRNYIRYSTNLPEAYEIGVTVNDIVLYEELKGLDRDLFLEMLKALKLGE
 ILRRKLYKLSAGQSVLVRTSLALASQPEIVGLDEPFENVDAARRHVISRYIKEYGKEGIL
 VTHELDMLNLYKEYKAYFLVGNRLQGPISVSELLESSIVEGERNDALLVLDIMDKKVSIV
 KGDLMGKFGALGSLNRIYGIIGA
 >3LUIA 115 XRAY 1.80 0.203 0.245 no Sorting nexin-17 <UNP SNX17_HUMAN> [HOMO SAPIENS]
 SNAMHFSIPETESRSGSGSAYVAYNIHVNGVLHCRVRSQLLGLHEQLRKEYGANVLP
 AFPPKKLFSLTPAEVEQRREQLEKYMQAVRQDPLLGSSETFNSFLRRAQETQQV
 >3OLOA 118 XRAY 2.09 0.180 0.227 no Two-component sensor histidine kinase <UNP Q8YZM9_ANASP>
 [NOSTOC SP.] SNAMNIQSELEFKFAHYL INNAVEASFCLGDNWQFLYVNDATCRMTEYSREQLLSMNLQD
 IDVDFALHDWEEIRKNNYTFKTRYRSQSGRIFLVEMSLTFLEDQERRFSCVVFVREKS
 >4DNHA 396 XRAY 2.50 0.177 0.240 no Uncharacterized protein <UNP Q92T60_RHIME> [SINORHIZOBIUM
 MELILOTI]

SLVSDLPIDIEGLRLARYDLTGRPVFPNSRDAKAFSRVAFAAHVADPLADNDPWLAPAI
WERTLAFRHRLWDLGLGVAESMDTAQRGMGLGWPEARELIRSLAEARGRPDALIACGAG
TDHLAPGPDVSIDDILAAYESQIEAIEAEGGRIILMASRALAAAAKGPEDYIRVYDRVLS
QVKEPVI IHWLGEMFDPALEGYWGNADHMAAMKTCLDVLEAHAAKVDG IKISLLSKEKEI
VMRRQLPKGVRMYTGDDFNYAELIAGDEEGHSDALLGIFDAIAPVASAALEALGSGRNGE
FFELLEPTVPLSRHIFKAPTRFYKTGVVFLAYLNLQDHFVMIGGQQSARSLVHLAELFR
LADKAGALADPELATARMRRVLAMHGVEEGHHHHH

>1LJ8A 493 XRAY 1.70 0.171 0.197 no mannitol dehydrogenase <UNP 008355_PSEFL> [PSEUDOMONAS
FLUORESCENS] MKLNKQNLTLAPEVKLPAYTLADTRQGIAHIGVGGFHHRAHQAYYTDALMNTGEGLDWSI

CGVGLRSEDRKARDDLACQDYLFTLYELGDTDDTEVRVIGSISDMLLAEDSAQALIDKLA
SPEIRIVSLTITEGGYCIDDSNGEFMAHLPQIQHDLAHPSSPKTVFGFICAALTQRRAG
IPAFTVMSCDNLPHNGAVTRKALLAFAALHNAELHDWIKAHVSFPNAMVDRIPTMTSTAH
RLQLHDEHGIDDAWPVCEPFVQWVLEDKFVNGRPAWEKVGQFTDDVTPYEEMKIGLLN
GSHLALTYLGFLLKGYRFVHETMNDPLFVAYMRAYMDLDVTPNLAPVPGIDLTDYKQTLVD
RFSNQAIADQLERVCSGSSKFPKFTVPTINRLIADGRETERAALVVAWALYLGVDEN
GVSYTIPDPRAEFCQGLVSDDALISQRLLAVEEIFGTAIPNSPEFVAAFERCYGSRLDNG VTTTLKHLKKPV

>4HVT A 711 XRAY 1.70 0.172 0.209 no Post-proline cleaving enzyme <UNP Q68XJ3_RICTY> [RICKETTSIA
TYPHI]

MAHHHHHHMAMEDNNKQIFNPKETKFLAEAEGVEALEWAKERTSKTEKALQAMQEYKQIK
KEIETIFYDQRKTPYGVIRKGYVNFWMDDKNPQGLWRRTLVDNYSKDKPNWEVLIDFDK
LSKKIGKKVAYRGVSNCFQNPNNRYLISMSFGGKDEMFREWDLEKKDFVKNGFEPITNSG
KLEGGKFTYPTWINKDTIIFNLVLHKNEITSSLYPNSLYIWKRGESIEKAKKLFEPKEY
IYVSAGKLLSDTISSSLIFISANKDFYNYDNYILDTKYKNLKLQKINMPSDATLQGSFKE
YVFWLLRSDWKFKSHNIKAGSLVALHFTDLLKTESDKTSLKILFTPTANEVNFISTTKD
RVFLATYDNNVAKVVTFTLENEQWTKPVVLKLPYQNAIFGMSSYYYYEEALITIENSIVP
PTIYLWVKTHELKIIRKALYSFDSENVYLEQKEATSFDGVKIPYFLVYKKGKIFDGKNPT
LLEAYGGFQVINAPYFSRIKNEVWVNAGVSVLANIRGGGEFGPEWHKSAQGIKRQTAFN
DFFAVSEELIKQNTSPEYLGKGGSSNGLLVSVAMTQRPELFGAVACEVPILDMIRYKE
FGAGHSWVTEYGDPEIPNDLLHIKKYAPLENLSLTQKYPTVLITDSVLDQRVHPWHGRIF
EYVLAQNPNTKTYFLESKDSGHGSGSDLKESANYFINLYTFFANALKLIN

>3KVHA 214 XRAY 1.70 0.185 0.217 no Protein syndesmos <UNP SDOS_HUMAN> [HOMO SAPIENS]

MVPELKQISRVEAMRLPGWWSHCHAMLYAANPGQLFGRIPMRFSVLMQMRFDGLLGFP
GFVDRRFWSLEDGLNRVLGLGLCLRLTEADYLSHLETEGPHRVVAHLYARQLTLEQLHA
VEISAVHSRDHGLEVLGLRVPLYTQKDRVGGFPNFLSNAFVSTAKCQLLFALKVLNMM
PEKLVEALAAATEKQKKALEKLLPASSAHHHHH

>4IIYA 371 XRAY 1.20 0.164 0.175 no MccF <UNP Q2KKH9_ECOLX> [ESCHERICHIA COLI]

MGHHHHHHHHHHSSGHIDDDDKHMLEMIQSHPLLAAPLAVGDTIGFFSSAPATVTAK
NRFFRGVEFLQRKGFKLVSGKLTGKTDIFYRSGTIKERAQEFNELVYNPDITCIMSTIGGD
NSNSLLPFLDYDAIIANPKIIIGYADTTALLAGIYAKTGLITFYGPALIPSFGEHPPLVD
ITYESFIKILTRKQSGIYTYTLPEKWSDESINWENKILRPKKLYKNNCAFYSGKVEGR
VIGGNLNTLTGIWGSEWMEIRNGDILFIEDSRKSIATVERLFSMLKLNRFVDKVSAIL
GKHELFDCAKSKRRPYEVLTEVLDGKQIPVLDGFDCSHTHMLTLPLGVKLAIDFDNKN
SITEQYLSTEK

>IS9RA 410 XRAY 1.60 0.168 0.202 no Arginine deiminase <UNP ARCA_MYCAR> [MYCOPLASMA ARGININI]

MSVFDKFKGIHVYSEIGELESVLVHEPGREIDYITPARLDELLFSAILESHDARKEHKQ
FVAELKANDINVVELIDLVAETYDLASQEAKDKLIEEFLEDSEPVLSSEHKVVVRNFLKA
KKTRELVEIMMAGITKYDLGIEADHELIVDPMPNLYFTRDPFASVGNVGTIHYMRYKVR

QRETLSRFVFSNHPKLINTPWYYDPSLKLSIEGGDVFIYNNDTLVVGVSERTDLQTVTL
 LAKNIVANKECEFKRIVAINVPKWTNLMHLDTWLTMLDKDKFLYSPIANDVFKFWDYDLV
 NGGAEPQPVENGLPLEGLLQSIINKKPVLPIIAGEGASQMEIERETHFDGTNYLAIRPGV
 VIGYSRNEKTNAALEAAGIKVLPFHGNQLSLGMGNARCMSMPLSRKDVKW
 >2Y1EA 398 XRAY 1.65 0.187 0.213 no 1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE <UNP
 A2VLK3_MYCTU> [MYCOBACTERIUM TUBERCULOSIS]
 TMAHHHHHVTNSTDGRADGRRLRVVLGSGSIGTQALQVIADNPDRFEVVGLAAGGAHL
 DTLRQRAQTGVTNIAVADEHAAQRVGDIPYHGSDAATRLVEQTEADVVLNALVGALGLR
 PTLAALKTGARLALANKESLVAGGSLVLAARPGQIVPVDSEHSALAQCLRGGTPDEVAK
 LVLASGGPFRGWSAADLHVTPAQAGAHPTWSMGPMNTLSASLVNKGLEVIETHLLFG
 IPYDRIDVVHPQSI IHSMTFIDGSTIAQASPPDMKLPISLALGWPRRVSGAAAACDFH
 TASSWEFEPLDLDVFPVELARQAGVAGGCMTAVYNAANEEAAAAFLAGRIGFPAIVGII
 ADVLHAADQWAVEPATVDDVLDARWARERAQRAVSGM
 >2FK5A 200 XRAY 1.90 0.190 0.233 no fucose-1-phosphate aldolase <UNP Q5SHB9_THET8> [THERMUS
 THERMOPHILUS]
 MRARLYAAFRQVGEDLFAQGLISATAGNFSVRTKGGFLITKSGVQKARLTPEDLLEVPLE
 GPIPEGASVESVVHREYVRTGARALVHAHPRVAVALSFHLSRLRPLDLEGQHYLKEVPV
 LAPKTVSATEEAALSVAEALREHRACLLRGHGAFVGLKEAPEEALLEAYGLMTTLEESA
 QILLYHRLWQGAGPALGGGE
 >1MQVA 125 XRAY 1.78 0.220 0.265 no CYTOCHROME C <UNP CYCP_RHOPA> [RHODOPSEUDOMONAS
 PALUSTRIS] ATDVIAQRKAILKQMGEATKPIAAMLKGEAKWDQAVVQKSLAAIADDSKKLPALFPADSK
 TGGDTAALPKIFEDKAKFDDLFAKLAAAATAAQGTIKDEASLKANIGGVLGNCKSCHDDF
 RAKKS
 >3LAAA 200 XRAY 1.35 0.115 0.128 no Haemagglutinin family protein <UNP Q3JLD6_BURP1>
 [BURKHOLDERIA PSEUDOMALLEI]
 MAHHHHHHMTLEAQTQGPMSGSLSTSISITNTNTNLGNSTAAALGGGATYDPATGAI
 SAPSYTTYNANGTTATNTSVGAADINANGIKYFHANSTDPDSVATGTNSVAIGPNAVA
 NVDYSVAIGSGATTSAAPVVASASVGGTLFGGFAGSAPIGVFSVGAPGAERQITNVAAGR
 ISAASTDAVNGS QLYATNSN
 >4NMA 259 XRAY 1.50 0.143 0.179 no Pimelyl-[acyl-carrier protein] methyl ester esterase <UNP
 BIOH_SALTY> [SALMONELLA ENTERICA SUBSP. ENTERICA SEROVAR TYPHIMURIUM]
 SNAMNDIWWQTYGEGNCHLVLLHGWGLNAEVWHCIREELGSHFTLHLVDLPGYGRSSGFG
 AMTLEEMTAQVAKNAPDQAIWLWGLVSLGGLVASQMALHPERVQALVTVASSPCFSAREGW
 PGIKPEILGGFQQQLSDDFQRTVERFLALQTLGTETARQDARTLKS VVLAQPMPDVEVLN
 GGLEILKTVDLREALKNVNMPFLRLYGYLDGLVPRKIVPLDLTWPHSTSQIMAKAAHAP
 FISHPA AFCQALMTLKSSL
 >4JDNA 152 XRAY 2.00 0.157 0.191 no Virulence plasmid protein pGP3-D <UNP D7DHH5_CHLTL>
 [CHLAMYDIA TRACHOMATIS]
 SLGLLKAFNNFPITNKIQCNGLFTPSNIETLLGGTEIGKFTVTPKSSGSMFLVSADIIAS
 RMEGGVVLALVREGDSKPCAISYGYSSGVPNLCSLRTSITNTGLTPTTYSRLRVGGLESGV
 VVWNALSNGNDILGITNTSNVSFLEVIPQTNA
 >2QDJA 304 XRAY 2.00 0.231 0.276 no Retinoblastoma-associated protein <UNP RB_HUMAN> [HOMO
 SAPIENS] TEEPDF TALCQKLIKPDHVRERAWLTWEKVSSVDGVLGGYIQKKELWGICIFIAVDLD
 EMSFTFTELQKNIEISVHKFFNLLKEIDTSTKVDNAMSRLKKYDVL FALFSKLERTCEL
 IYLTQPSSSISTEINSALVLKVS WITFLAKGEVLQMEDDLVISFQMLCVLDYFIKLS P
 PMLLKEPYKTAVIPINGSRPTPRRGQNRSARIAKQLENDTRIIEVLCKEHECNIDEVKNV
 YFKNFIPFMNSLGLVTSNGLPEVENLSKRYEEIYLKNKDL DARLFLDHDKTLQTDSIDSF

ETQR

>1Y8QB 640 XRAY 2.25 0.208 0.248 no Ubiquitin-like 2 activating enzyme E1B <UNP ULE1B_HUMAN>
[HOMO SAPIENS]

MALSRGLPRELAEAVAGGRVLVVGAGGIGCELLKNLVLTFGSHIDLIDLDITDVSNLNRQ
FLFQKKHVGRSKAQVAKESVLQFYPKANIVAYHDSIMNPDYNVEFFRQFILVMNALDNRA
ARNHVNRMCLAADVPLIESGTAGYLGQVTTIKKGVTECYECHKPKTQRTFPGATIRNTPS
EPIHCIVWAKYLFNQLFGEEDADQEVSPDRADPEAAWEPTAEARARASNEDGDIKRIST
KEWAKSTGYDPVKLFTKLFKDDIRYLLTMDKLWRKRKPPVPLDWAQVQSQGEETNASDQQ
NEPQLGLKDQQVLDVKSARLFSSKIETLRVHLAEKGDGAELIWDKDDPSAMDFVTSAN
LRMHIFSMNMKSRFDIKSMAGNIIPAIAATTNAVIAGLIVLEGLKILSGKIDQCRTIFLNK
QPNPRKLLVPCALDPPNPNCYVASKPEVTVRLNVHKVTVLTLQDKIVKEKFAMVAPDV
QIEDGKGTILISSEEGTEANNHKKLSEFGIRNGSRLQADDFLQDYTLINILHSEDLGK
DVEFEVVGDAPEKVGPKQAEDAASITNGSDDGAQPSTSTAQEQDDVLIVDSDEEDSSNN
ADVSEEERSRKRKLEKENLSAKRSRIEQKEELDDVIALD

>2NSOA 85 XRAY 2.00 0.190 0.216 no Hypothetical protein <UNP Q0S2K3_RHOSR> [RHODOCOCCLUS SP.]
MTVSDRELEECIRALLDARADSASICPSDVARAVAPDDWRPLMEPVREAAGRLADAGEVE
VTQKGAVDPRSARGPIRIRWTRTD

>4JOSA 250 XRAY 1.45 0.152 0.175 no Adenosylhomocysteine nucleosidase <UNP BOTZL4_FRAP2>
[FRANCISELLA PHILOMIRAGIA SUBSP. PHILOMIRAGIA]
MHHHHHSSGVDLTENLYFQSMKKIAILGAMEIEIQPILQKLEKYETVEYANNKYVYV
YNGIELVVAYSKIGKVFSSLTATIMIEHFGVDALLFTGVAGGLQDLQVGDMAATATVQH
DVDITAFGYPGKIPISEVEIATSARILEQAKVIAKELNLTHTGVIATGDQFVHSAERK
DFVVKFEFDAKAIEMEGASVNLICNEMNIPSFILRSISDTADGDAPDNFDEFKMAANRSA
DFVMKLVDR

>3R6DA 221 XRAY 1.25 0.150 0.179 no NAD-dependent epimerase/dehydratase <UNP D1BQI7_VEIPT>
[VEILLONELLA PARVULA DSM 2008] SNAMYKYITILGAAGQIAQKLATLLTYTDMHITLYGRQLKTRIPPEIIDHERVTVIEGS
FQNPQKLEQAVTNAEEVVFVGAMESGSDMASIVKALSARNIRRVIGVSMAGLSGEFPVALE
KWTFDNLPISYVQGERQARNVLRSLNLTILRLTWLYNDPEKTDYELIPEGAQFNDAQV
SREAVVKAIFDILHAADETPFHRTSIGVGEPTGTHYDKPSFH

>3CZ7A 364 XRAY 2.00 0.158 0.189 no Regulator of Tyl transposition protein 109 <UNP RT109_YEAST>
[SACCHAROMYCES CEREVISIAE]
MSLNDFLSSVLPVSEQFEYLSLSIPLETHAVVTPNKDDKRVPKSTIKTQHFFSLFHQK
VFFSLEVYVYVTLWDEADAERLIFVSKADTNGYCNTRVSVRDITKIILEFILSIDPNYYL
QKVKAIGGSGFQQDLYSFTCPREILTKICLFTRPASQYLPDSSKNSKKHILNGEELM
KWWGFILDRLLIECFQNDTQAKLRIPGEDPARVRSYLRGMKYPLWQVGDIFTSKENSLAV
YNIPLFPDDPXARFIHQLAEDRLLKVSLSFWIELQERQEFKLSVTSSVMGISGYSLAT
PSLFPSSADVIVPKSRKQFRAIKKYITGEEYDTEGAIEAFTNIRDFLLRMATNLQSLT
GKRE

>2NYKA 285 XRAY 2.10 0.215 0.240 no M157 <UNP Q6XK79_9BETA> [MURID HERPESVIRUS 1]
IFNPDPDDTYIVNMDDFQFTFTMEFEVTVTRGGVHKRTISVDNGRPVVVDVGDRLDPKIC
KICPDVSSDIEYVFLDIQKMLNLLTQSLWDTQRICVRYACFLGFDVICDVYHTTDT
VRVAYTGQTGKINIQSGKFSTSDAKEIGTYMIKSNVREIKNRWRSTVQKLKQLAYMNAT
EVEFWYNTTGLTTCVVTSSRSNVPFTVELSLNTNCSAIVTDESTVDCQILTVKAPGSHAQR
CYVTSSLGKGVVTPPSQYRTKRVPVNISSSKWTGIVNWKGNVNR

>1RV9A 259 XRAY 1.53 0.197 0.209 no conserved hypothetical protein NMB0706 <GB NP_273748>
[NEISSERIA MENINGITIDIS] MKTITETLNLAPKGNFLTADWPAPANVKTLITTRNGGVSQGAYQSLNLGTHVGDNPEAV
RRNREIVQQVGLPVAYLNLQIHSTVVVNAEALGGTPDADASVDDTGKVACAVMTADCLP

VLFCDRAGTAVAAAAGWRGLAGGVLQNTIAAMKVPPVEMMAYLGPASADAFEVGQDVF
 DAFCTPMPEAATAFEGIGSGKFLADLYALARLILKREGVGGVGGTHCTVLERDTFFSYR
 RDGATGRMASLIWLDGNAV
 >2BPA1 426 XRAY 3.00 0.209 NA no SUBUNIT OF BACTERIOPHAGE PHIX174 <UNP VGF_BPPHX>
 [ENTEROBACTERIA PHAGE PHIX174]
 SNIQTGAERMPHDLSHLGLAGQIGRLITISTTPVIAGDSFEMDAVGALRLSPLRRGLAI
 DSTVDIFTFYVPHRHVYGEQWIKFMKDGVNATPLPTVNTTGYIDHAAFLGTINPDTNKIP
 KHLFQGYLNIYNNYFKAPWMPDRTEANPNELNQDDARYGFRCHLKNIWTAPLPPETELS
 RQMTTSTTSIDIMGLQAAYANLHTDQERDYFMQRYRDVSSFGGKTSYDADNRPLLVMRS
 NLWASGYDVGDTQTSLGQFSGRVQQTYKHSVPRFFVPEHGTMTLALVRFPTATKEIQ
 YLNAKGALTYTDIAGDPVLYGNLPPREISMKDVFRSGDSSKKFKIAEGQWYRYAPSYVSP
 AYHLEGFPPFIQEPSPGDLQERVLIRHHDYDQCFQSVQLLQWNSQVKFNVTVYRNLPTTR
 DSIMTS
 >3EGLA 277 XRAY 2.41 0.181 0.218 no DegV family protein <UNP Y2349_CORGL> [CORYNEBACTERIUM
 GLUTAMICUM]
 SNAMPVRVIVDSSACLPTHVAEDLDITVINLHVMNNGEERSTSGLSSLELAASYARQLER
 GGDGVLALHISKELSSWSAAVTAFAVDDSVRVDTSSLGMAVGAAAMAAARMKDG
 ASLQECYDIAVDTLKRSETWIYLRIDEIWKSGRISTATAMVSTALATRPIMRFNGGRME
 IAAKTRTQSKAFKLVELAQIRADGEPVFIAIGQNEAREAAKQLEELLRNALPEGSSFMS
 VDIDPTLAVHSGPGAVSVSAVFANQAPELSTGKAGAK
 >2EVVA 207 XRAY 2.59 0.224 0.262 no hypothetical protein HP0218 <UNP 025006_HELPY> [HELICOBACTER
 PYLORI]
 MGSSHHHHHHSSGRENLVYFQGHMKTFEVMIQTDSKGYLDAKFGGNAPKAFLNSNGLPTYS
 PKISWQKVEGAQSYALELIDHDAQKVCMPFVHWVGNIAHNVLEENASMMDKRIVQGVN
 SLTQGFIRSPLENESEKQRSNLNNSVYIGMPMPNGDHHYLIQVYALDIPKLALKAPFFLGD
 LHDKMRNHIIAIGRKEFLYKQFVRKGS
 >2R8BA 251 XRAY 2.56 0.197 0.253 no Uncharacterized protein Atu2452 <UNP Q8UCN1_AGR5>
 [AGROBACTERIUM TUMEFACIENS STR.]
 GHMPRPSLRGEETSGARSLHEIAPPAEKAVRKPLNLLPFRKDTPTKDSYFHKSRAGVA
 GAPLFVLLHGTGGDENQFFDFGARLLPQATILSPVGDVSEHGAAFFRRTGEGVYDMVDL
 ERATGKMADFIKANREHYQAGPVIGLGSNGANILANVLEIEQPELFDAAVLMHPLIPFEP
 KISPAKPTRRVLITAGERDPICPVQLTKALEESLKAQGGTVETVWHPGGHEIRSGEIDAV
 RGFLAAYGGGS
 >4C7AA 193 XRAY 2.30 0.238 0.284 no SMOOTHENED <UNP Q90X26_DANRE> [DANIO RERIO]
 MAVILHPNETIFNDFCKKSTTCEVLKYNTCLGSPLPYHTSLILAEDSETQEEAFEKLAM
 WSLRNAPRCWAVIQPLLCAVYMPKCENGKVELPSQHLCAATRNPCSIIVERERGWPNFLK
 CENKEQFPKGCQNEVQKLKFNSTSGQCEAPLVKTDIQASWYKDVCGGIQCDNPLFTEDEH
 SDMHKLEHHHHHH
 >2NWAA 88 XRAY 2.70 0.271 0.285 no Hypothetical protein ytmB <UNP YTM_BACSU> [BACILLUS SUBTILIS]
 MGMPVEFNTLIVTKGKEVRIDENIFTLEKDGVRYPMEIPMDVRKTKFGEKSGTAEVQKL
 QWEEGRTIITYKLTSLHSVNLEHHHHHH
 >4LBOA 348 XRAY 1.70 0.159 0.192 no Uncharacterized protein <UNP B9JQV3_AGRVS> [AGROBACTERIUM
 VITIS]
 SMRWKRMQLLDVHCEGEIGKVAIGGVPKIPGDTVADQLHWLNTDPKGRELHRHFLVLEPR
 GAPIGSVNLLPAKDSRAAFAIILQPDQAHASSGSNSICVTTALLESGLMIEMQEPETVV
 MLETAAGLVKAVAQCRDGHCDSVTLTMVPSFVHELDAQIATESWGEIRFDLAYGGVFYAL
 VDVRQLGLTIEPGNARRLVEAGMLLKGEINQRIQVVHPDIPAISGVAYVMFRDEDPDGAV

RTCTTMWPGRVDRSPCGTGNSANLATLHARGRVKPGDSFLSRSIIGSQFTVGLQGLTTVA
 GRSVAIPTITGRGFTYGIHQVALDAFDPLGGGFVLTVDWGAAETIKI
 >3NHVA 144 XRAY 2.50 0.204 0.247 no BH2092 protein <UNP Q9KB42_BACHD> [BACILLUS HALODURANS]
 ANPNEAYRHYMKKLSYETDIADLSIDIKGYEGIIIVDVRDAEAYKECHIPTAISIPGNK
 INEDTTKRLSKEKVIITYCWGPACNGATKAAAKFAQLGFRVKELIGGIEYWRKENGVEG
 TLGAKADLFWNMKKESLEHHHHHH
 >1SZ7A 200 XRAY 1.55 0.207 0.245 no Trafficking protein particle complex subunit 3 <UNP TPPC3_HUMAN>
 [HOMO SAPIENS]
 MSHHHHHHGSSRQANRGTESKKMSSEFTLTLYGALVTQLCKDYENDEVDNKLQDKMGFNI
 GVR LIEDFLARSNVGRCHDFRETADVIAKVAFKMYLGITPSITNWSAGDEFSLILENNP
 LVDFVELPDNHSSLIYNNLLCGVLRGALEMVQMAVEAKFVQDTLKG DGVTEIRMR FIRRI
 EDNLPAGEEAAAWSHPPQFEK
 >3C8DA 403 XRAY 1.80 0.150 0.194 no Enterochelin esterase <UNP Q83SB9_SHIFL> [SHIGELLA FLEXNERI 2A
 STR. 2457T]
 SNAMTALKVGSSEWWQSKHGPEWQRLNDEMFEVTFWWRDPQGSEEYSTIKRVVYITGVT
 DHHQNSQPQSMQRIAGTDVWQWTTQLNANWRGSCYCFIPTERDDIFSAPSPDRLELREGWR
 KLLPQAIADPLNPQSWKGGLGHAVSALEMPQAPLQPGWDCPQAPEIPAKEIWKSERLKN
 SRRVWIFTTGDVTAERPLAVLLDGEFWAQSMVPVPLTSLTHRQQLPPAVYVLIDAIT
 THRAHELPCNADFWLAVQQELLPLVKVIAPFSDRADRTVVAGQSFGGLSALYAGLHWPER
 FGCVLSQSGSYWWPHRGGQQEGVLLEKLKAGEVSAEGLRIVLEAGIREPMIMRANQALYA
 QLHP IKESIFWRQVDGGHDALCWRGGLMQGLIDLWQPLFHDRS
 >2I2XB 258 XRAY 2.50 0.184 0.231 no Methyltransferase 1 <UNP P94920_METBA> [METHANOSARCINA
 BARKERI]
 MLDFTEASLKKVLTRYNVALEKALTPEEAAEELYPKDELIYPIAKAIFEGEEDDVVEGLQ
 AAIEAGKDPIDLIDDALVMGMGVVIRLYDEGVIFLPNMMADAMLEGIEYCKENSGATP
 KTKGTVVCHVAEGDVHDIGKNIVTALLRANGYNVVDLGRDVPAAEVLA AVQKEKPIMLTG
 TALMTTMYAFKEVNDMLLENGIKIPFACGGGAVNQDFVSQFALGVYGEAAADAPKIADA
 I IAGTTDVTTELREKFHKK
 >3DMLA 116 XRAY 1.90 0.157 0.201 no Putative uncharacterized protein <UNP Q8KM22_PARDE> [PARACOCUS
 DENITRIFICANS]
 MRGSHHHHHHGSDDDKAELRLLMFEQPGCLYCARWDAEIA PQYPLTDEGRAAPVQRLQM
 RDPLPPGLELARPVTFTPTFVLMAGDVESGRLEGYPGEDFFWPLARLIGQAEPGQ
 >1GQIA 708 XRAY 1.48 0.133 0.168 no ALPHA-GLUCURONIDASE <PDB 1GQI> [PSEUDOMONAS CELLULOSA]
 EDGYDMWLRYQPIADQTLTKTYQKQIRHLHVAGDSPTINAAAAELQRGLSGLLNKPIVAR
 DEKLKDYSLVIGTPDNSPLIASLNLGERLQALGAEGYLLEQTRINKRHVVIVAANS DVG
 LYGSFHLRLIQTQHAEKLSLSSAPRLQHRVNVHWDNLNRVVERGYAGLSLWDWGLPN
 YLAPRYTDYARINASLNGT VINNVNADPRVLS DQFLQKIAALADAFRYPYIKMYLSIN
 FNSPRAFGD VDTADPLDPRVQQWWKTRAQKIYSYIPDFGGFLVKADSEGQPGPQGYGRDH
 AEGANMLAAALKPFGGVVFWRAFVYHPDIEDRFRGAYDEFMPLDGKFADNVILQIKNGPI
 DFQPREPFSALFAGMSRTNMMMEFQITQEYFGFATHLAYQG PLFEESLKTETHARGEEST
 IGNILEGKVFKTRHTGMAGVINPGTDRNWTGHPFVQSSWYAFGRMAWDHQISAATAADEW
 LRMTFSNQPAFIEPVKQMLVSREAGVNYRSPLGLTHLYSQGDHYGPAPWTD DLPRADWT
 AVYYHRASKTGIGFNRTKTGSNALAQYPEPIAKAWGDLNSVPEDLILWFHHSWDHRMQS
 GRNLWQELVHKYYQGVQVRAMQRTWDQQEAYVDAARFAQVKALLQVQEREAVRWRNSCV
 LYFQSVAGRP IPANYEQPEHDLEYKMLARTTYVPEPWHPASSRVLK
 >4HYLA 117 XRAY 1.75 0.209 0.229 no Stage II sporulation protein <UNP DOLNN2_HAL01> [HALIANGIUM
 OCHRACEUM]

SNATDTQIRTEQGIDIITLHGLDTRSSPAVQAAVLPRVTAKGKMILDLREVSYMSSAGL
RVLLSLYRHTSNQGGALVLGVGSEEIRDTEITGFWNFFTACASMDEALRILGSESA
>3W08A 352 XRAY 1.80 0.158 0.189 no Aldoxime dehydratase <UNP Q7WSJ4_9PSED> [PSEUDOMONAS
CHLORORAPHIS]
MESAIDTHLKCPRTLSRRVPEEYQPPFPMWVARADEQLQQVVMGYLGVQYRGEAQREAAL
QAMRHIVSSFSPLDGPQTHDLTHHTDSSGFDNLMVVGWYKDPAAHCRWLSAEVNDWWTS
QDRLGEGLYFREISAPRAEQFETLYAFQDNLPVGAVMDSTSGEIEEHGYWGSMRDRFP
ISQTDWMKPTNELQVVAGDPAKGRVVMIGHDNIALIRSGQDWADAEAEERSLYLDEILP
TLQDGMDFLRDNGQPLGCYSNRFVRNIDLDGNFLDVSYNIGHWRSLEKLERWAESHPTHL
RIFVTFFRVAAGLKKRLRYHEVSVSDAKSQVFEYINCHPHTGMLRDVAVAPT
>2GIYA 191 XRAY 1.78 0.198 0.220 no Glycoprotein E <UNP VGLE_HHV11> [HUMAN HERPESVIRUS 1]
GAPEVSHVRGVTVRMETPEAILFSPGETFSTNVSIIAHDDQTYSDVWLRFDVPTSC
AEMRIYESCLYHPQLPECLSPADAPCAASTWTSRLAVRSYAGCSRTNPPRCSAEAHMEP
VPLAWQAASVNLEFRDASPQHSGLYLCVYVNDHIIHAWGHITISTAAQYRNAVVEQPLD
IEGRGHHHHHH
>2XN6A 350 XRAY 1.29 0.209 0.235 no THYROXINE-BINDING GLOBULIN <UNP THBG_HUMAN> [HOMO SAPIENS]
SSQP NATLYKMSSINADFAFNLYRRFTVETPDKNIFFSPVSISAALVMSFGACCSTQTE
IVETLGFNLTDTPMVEIQHGFQHLICSLNFPKKELELQIGNALFIGKHLKPLAKFLNDVK
TLYETEVFSTDFSNISAAKQEINSHVEMQTKGKVGLIQDLKPNTIMVLVNYIHFKAQWA
NPFDP SKTEDSSSFLIDKTTTVQVPMHQMDQYYHLVDMELNCTVLQMDYSKNALALFVL
PKEGQMESVEAAMSSKTLKWNRLQKGWVDFVFPKFSISATYDLGATLLKMGIQHAYSE
NADFSGLTEDNGLKLSNAAHKAVLHIGEGKTEAAGAMFLEAIPRSIPNTF
>2WMYA 150 XRAY 2.21 0.209 0.261 no PUTATIVE ACID PHOSPHATASE WZB <UNP Q9X4B8_ECOLX> [ESCHERICHIA
COLI]
GAMAKLMFDSILVICTGNICRSPIGERLLRRLPSKKINSAGVGALVDHTADESAIRVAE
KNGLCLKGHRGTFKTSALARQYDLLLVMEYSHLEQISRIAPARGKTMLFGHWLDSKEIP DPYRMSDEAFDSVYQLEQASKRWA EKLGE
>4J5RA 146 XRAY 1.25 0.120 0.153 no 0-acetyl-ADP-ribose deacetylase 1 <UNP OARD1_HUMAN> [HOMO SAPIENS]
GSHMGSRITYVKGDLFACPKTDSLACISEDCRMGAGIAVLFKKKFGGVQELLNQKKSG
EVAVLKRDGRYIYYLITKKRASHKPTYENLQKSLEAMKSHCLKNGVTDLSMPRIGCGLDR
LQWENVSAMIEEVFEATDIKITVYTL
>1RRMA 386 XRAY 1.60 0.193 0.211 no Lactaldehyde reductase <UNP FUCO_ECOLI> [ESCHERICHIA COLI]
MMANRMILNETAWFGRGAVGALTDEVKRRGYQKALIVTDKTLVQCGVAKVTDKMDAAGL
AWAIYDGVVPNTITIVVKEGLGVFQNSGADYLIAIGGGSPQDTCKAIGIISNNPEFADVR
SLEGLSPTNKPSVPILAIPTTAGTAAEVTINYVITDEEKRRKFVCVDPHDIPQVAFIDAD
MMDGMPPALKAATGVDA LTHAIEGYITRGAWALTDALHIKAIEIIAGALRGSVAGDKDAG
EEMALGQYVAGMGFSNVGLGLVHGMAHPLGAFYNTPHGVANAILLPHVMRYNADFTGEKY
RDIARVMGVKVEGMSLEEARNAEAVFALNRDVGIPHLRDVGVRKEDIPALAAALDD
VCTGGNPREATLEDIVELYHTAWEGG
>3HVZA 78 XRAY 2.20 0.226 0.254 no Uncharacterized protein <UNP A7VWX7_9CLOT> [CLOSTRIDIUM LEPTUM]
MDLAPEEVFVFTPKGDVISLPIGSTVIDFAYAIHSAVGNRMIGAKVDGRIVPIDYKVKTG
EIIDVLTTKLEHHHHHH
>1CFBA 205 XRAY 2.00 0.202 NA no DROSOPHILA NEUROGLIAN <UNP NRG_DROME> [DROSOPHILA
MELANOGASTER]
IVQDVPNAPKLTGITCQADKAEIHWEQQGDNRSPIHYTIQFNTSFTPASWDAAAYEKVPN
TDSSFVVQMSPWANYTFRVIAFNKIGASPPSAHSDSCTTQPDVPFKNPDNVVGQGTEPN
LVISWTPMPEIEHNAPNFHYYSWKRDIPAAAWENNNIFDWRQNNIVADQPTFVKYLK
VVAINDRGESNVAAEEVVGYSGEDR

>2V8TA 302 XRAY 0.98 0.101 0.117 no MANGANESE-CONTAINING PSEUDOCATALASE <UNP Q84DB4_THETH> [THERMUS THERMOPHILUS]
MFLRIDRLQIELPMPKEQDPNAAAQVALLGGRFGEMSTLMNMYQSFNFRGKKALKPYY
DLIANIATEELGHIELVAATINSLAKNPGKDLEEGVDPASTPLGFAKDVRNAAHFIAGG
ANSLVMGAMGEHWNGEYVFTSGNLILDLLHNFFLEVAARTHKLRYEMTDNPVAREMIGY
LLVRGGVHAAAYGKALESITGVEMTKMLPIPKIDNSKIPEAKKYMDLGFHRNLYRFSPED
YRDLGLIWKGASPEDGTEVVVVDGPPTGGPVFDAGHDAAEFAPEFHPGELYEIAKKLYEK
AK

>2BWFA 77 XRAY 1.15 0.185 0.195 no UBIQUITIN-LIKE PROTEIN DSK2 <UNP DSK2_YEAST>
[SACCHAROMYCES CEREVISIAE]
LDMSLNIIHKSGQDKWEVNVAPESTVLQFKEAINKANGIPVANQRLIYSGKILKDDQTV
SYHIQDGHSHLVKSSQP

>3RNLA 311 XRAY 1.75 0.157 0.181 no Sulfotransferase <UNP C8WTE4_ALIAD> [ALICYCLOBACILLUS
ACIDOCALDARIUS SUBSP. ACIDOCALDARIUS]
SNAMGVARPNFFIVGAAKCGTSSLDRLSQHPDIYIPPKKEAHFFSIPDFPERFTGPGDE
GMNLYTIRDEDAYMRLFDGVRGERAVGEASVFYLFYPGTAQRMYPDAYPAKILIMLRNPV
DRAFSAYMHLVRDERETLSFRESLAKEEERIRQHYEPLWYYRAVGLYAAQVKRYLDVFG
EQVKVILFEEFARDPVQVVRDCCAFGLGVSTDFVPDTSIRHNESGVPKSRSLYFIAPNA
LKEIVKPFIPA AVRERLGNRAKSMVLGRMEMEPLREELTAFFAPDVARLEALIHRLSA
WRRPARAAGSQ

>4I00A 497 XRAY 1.90 0.182 0.214 no Protein ELYS <UNP ELYS_MOUSE> [MUS MUSCULUS]
PGSMQDLTAQVTSDDLHFPEVTIEALGEDEITLESVLRGKFAAGKNGLACLACGPQLEVV
NSLTGERLSAYRFGSVNEQPPVVLAVKEFSWHKRTGLLIGLEADGSVLCCLYDLGISRVV
KAVVLPGRVTAIEPIINHGGASASTQHLHPSLRWLFVAAVVDVGQILLIDLCLDDLSC
SQNEVEASDLEVITGIPAEVPHIRERVMREGRHLCFQLVSPLGVAISTLSYINRTNQLAV
GFS DGYLALWNMKS MKREYTTQLEGGRPVHAVAQEPENDPRNCCYLWAVQSTQDSEGD
VLSLHLLQLAFGDRKCLASGQILYEGLEYCEERYTDLAGGTFPLRGQTSNTKLLGCQSI
ERFPPSHGDREESMREALSPDTSVSVFTWQVNIYQGKPSVYLG LFDINRWYHAQMPDSLR
SGESLHNCSYFALWSDSVSRTSPHHILDILVHERSLNRGVPPSYPPPEQFFNPSTFNF
DATCLLD SGVIHVT CAG

>3T8JA 311 XRAY 1.60 0.157 0.170 no Purine nucleosidase, (IunH-1) <UNP Q97ZS5_SULSO> [SULFOLOBUS
SOLFATARICUS]
MRHFIIDCDTAEDDVL SLYLLLKNNDVVAVTIVEGNISYEQEVKNALWALEQVNREIPV
YPGANKPLLKNYITVEKVHGKGGIGDVTVEPKRLKAQEKHAALAIIDLANEYAGELEFLA
ISPLTNLALAYLLDNSIVKKIKKVWMGGAVFGIGNITPVAEFNIWDPDAKIVFNAGF
DITMIPWDV IINYPVTDEEWNVIKMKTRMSELYVSMYLHYRQYSSTVQKINGHPHPDAI
TTAIAIDGSIATRREKRFVVIDNTDNITRGM TLVDRFDADTSWSDKPN AEIVYEINKKSF
MEKIYDLLNWF

>2H1EA 177 XRAY 2.20 0.192 0.246 no Chromo domain protein 1 <UNP CHD1_YEAST> [SACCHAROMYCES
CEREVISIAE]
MKKHHHHHHEDFHGIDIVINHRLKTSLEEGKVLEKTVPD LNNCKENYEFLIKWTDESH LH
NTWETYESIGQVRGLKRLDNYCKQFIIEDQQVRLDPYVTAEDIEIMDERERRLDEFEEF

HVPRIIDSQRASLEDGTSQLQYLVKWRRLNYDEATWENATDIVKLAPEQVKHFQKK
 >4E2VA 386 XRAY 1.18 0.139 0.153 no Queuine tRNA-ribosyltransferase <UNP TGT_ZYMMO>
 [ZYMOMONAS MOBILIS]
 MVEATAQETDRPRFSFSIAAREGKARTGTIEMKRGVIRTPAFMPVGTAAATVKALKPETVR
 ATGADIILGNTYHMLRPGAERIAKLGGLHSFMGWRPILTDSGGFQVMSLSSLTKQSEE
 GVTFKSHLDGSRHMLSPERSIEIQHLLGSDIVMAFDEVTPYPATPSRAASSMERSMRWAK
 RSRDAFDSRKEQAENAALFGIQQGSVFENLRQQSADALAEIGFDGYAVGGLAVGEGQDEM
 FRVLDFSVPMLPDDKPHYLMGVGKPDIVGAVERGIDMFDCVLPTRSGRNGQAFTWDGPI
 NIRNARFSEDLKPLDSECHCAVCQKWSRAYIHHLIRAGEILGAMLMTENIAFYQQLMQK
 IRDSISEGRFSQFAQDFRARYFARN
 >10TGA 125 XRAY 2.10 0.179 NA no 5-CARBOXYMETHYL-2-HYDROXYMUCONATE ISOMERASE <UNP
 HPCD_ECOLI> [ESCHERICHIA COLI]
 PHFIVECSDNIREADLPGLFAKVNPTLAATGIFPLAGIRSRVHWVDTWQADGQHDIYAF
 VHMTLKIGAGRSLESRRQAGEMLFELIKTHFAALMESRLALSFEIEELHPTLNFKQNNV
 HALFK
 >3G89A 249 XRAY 1.50 0.184 0.210 no Ribosomal RNA small subunit methyltransferase G <UNP
 RSMG_THET8> [THERMUS THERMOPHILUS]
 MFHGKHPGGLSERGRALLLEGKALGLDKPHLEAFSRLYALLQEASGKVNLTALRGEE
 VVVKHFLDSLTLRLPLWQGPLRVLDLGTGAGFPGLPLKIVRPELELVLDATRKKVAFV
 ERAIEVLGLKGARALWGAEVLAREAGHREAYARAVARAVAPLCVSELPLPFLEVGGAA
 VAMKGRVVEELAPLPALERLGGRLGEVLALQLPLSGEARHLVVLEKTAPTPPAYPRRP
 GVERHPLC
 >3IB7A 330 XRAY 1.60 0.218 0.177 no Icc protein <UNP 006629_MYCTU> [MYCOBACTERIUM
 TUBERCULOSIS]
 GAMGIRNSKAYVEHRLRAAEHPRPDYVLLHISDTHLIGDDRRLYGAVDADDRLGELLEQL
 NQSGLRPDAIVFTGDLADKGEPAAAYRKLRLGLVEPFAAQLGAELVWVMGNHDDRAELRKFL
 LDEAPSMAPLDRVCMIDGLRIIVLDTSPGHHGEIRASQLGWLAEELATPAPDGTILAL
 HHPPIPSVLDMAVTVELRDQAALGRVLRGTDVRAILAGHLHYSTNATFVGIPVSVASATC
 YTQDLTVAAGGTRGRDGAQGCNLVHVYPDVTVVHSVIPLGGGETVGTFTVSPGQARRKIAES
 GIFIEPSRRDSLFKHPPMVLTSAPRSPVD
 >4I5VA 333 XRAY 2.70 0.185 0.261 no 5',5''-P-1,P-4-tetraphosphate phosphorylase 2 <UNP
 APA2_YEAST> [SACCHAROMYCES CEREVISIAE]
 MGHHHHHHMIENLKQKIHDKFVAAKNGHLKVTHAESKCLKDPQTTTQYWVTFAPSLAL
 KPDANKNSDSKAEDPFANPDEELVVTEDLNGDGEYKLLLNKFPVPEHSLVTSEFKDQR
 SALTPSDLMTAYNVLCSLQGDKDDVTCEYLVFYNGPHSGSSQDHKALQIMQMPEKFI
 PFQDVLNCGKDHFLPTFNAEPLQDDKVSFAHFVLPPESSDQVDELLAMCYVSLMQRAL
 TFFQDWTNESPELTSYNVLLTKKWICVVRSHAKSGPPLMLNINSTGYCGMILVKDREK
 LENLTEDPHLVDSLLQCGFPNTAGQKPTEYHY
 >4J5TA 811 XRAY 2.04 0.226 0.235 no Mannosyl-oligosaccharide glucosidase <UNP CWH41_YEAST>
 [SACCHAROMYCES CEREVISIAE]
 AEFMEYQKFTNESLLWAPYRSNCYFGMRPRYVHESPLIMGMWFNSLSQDGLHSLRHFA
 TPQDKLQKYGWEVYDPRIGGKEVFIDEKNLNLTVYFVSKNGENWSVRVQGEPLDPKRP
 STASVLYFSQNGGEIDGKSSLAMIGHDGPNDMKFFGYSKELGEYHLTVKDNFGHYFKNP
 EYETMEVAPGSDCSKTSLSLQIPDKEVWKARDVFQSLVSDSIRDILEKEETKQRPADLI
 PSVLTIRNLNFNPGNFHYIQKTFDLTKKDGQFDITYNKLGTTSISTREQVTELITWS
 LNEINARFDKQFSFGEGPDSIESVEVKRRFALETLSNLLGGIGYFYGNQLIDRETEFDES
 QFTEIKLLNAKEEGPFELFTSVPSRGFFPRGFYWDEGFHLLQIMEYDFDLAFEILASWFE
 MIEDDSGWIAREIILGNEARSKVPQEFQVQNPNIANPPTLLAFSEMLSRAIENIGDFNS

DSYHQVMFNSRTAKFMTNNLEANPGLLTEYAKKIYPKLLKHYNWFRKSQTGLIDEYEEIL
EDEGIWDKIHKNEVYRWVGRFTTHCLPSGMDYPRAQPPDVAELNVDALAWVGMTRSMK
QIAHVLKLTQDEQRYAQIEQEVVENDLLHWSSENDNCYCDISIDPEDDEIREFVCHGYV
SVLPFALKLIPKNSPKLEKVVMSDPEKIFSDYGLLSLSRQDDYFGKDENVYWRGPIWMN
INYLCLDAMRYYYPEVILDVAGEASNAKKLYQSLKINLSNNIYKVWEEQGYCYENYSPID
GHGTGAEHFTGWTALVVNILGRFRSHHHHHH

>2VJWA 149 XRAY 2.00 0.210 0.249 no GAF FAMILY PROTEIN <UNP AOR2U9_MYCS2> [MYCOBACTERIUM
SMEGMATIS]

DPATVFRLVAAEALTLTGADGTLVAVPADPDASAAEELVIVEVAGAVPAEVEASAIPVQD
NAIGQAFRDRAPRRDLVDLGPGLGGPALVPLRATDTVAGVLAVQSGGARPFTAEQLEM
MTGFADQAAVAWQLASSQRRMSELDILAD

>2BM1A 691 XRAY 2.60 0.220 0.297 no ELONGATION FACTOR G <UNP EFG_THETH> [THERMUS
THERMOPHILUS]

MAVKVEYDLKRLRNIVIAAHIDAGKTTTTTERILYYTGRIHKIGEVHEGAATMDFMEQERE
RGITITAAVTTCTFKDHRINIIDTPGHVDFTIEVERSMRVLDAIVVFDSSQGVEPQSET
VWRQAEKYKVPRIAFANKMDKTGADLWLVRTMQERLGARPVVMQLPIGREDTFSGIIDV
LRMKAYTYGNDLGTDIRIPIPEEYLDQAREYHEKLVEVAADFENIMLKYLEGEEPTTE
ELVAAIRKGTIDLKITPVFLGSALKNGVQLLLDAVVDYLPSPLDIPPIKGTTPGEVVE
IHPDPNGPLAALAFKIMADPYVGRITFIRVYSGTLTSGSYVYNTTKGRKERVALLRMHA
NHREEVEELKAGDLGAVVGLKETITGDTLVGEDAPRVIIESIEVPEPVIDVAIEPKTKAD
QEKLSQALARLAEDPTFRVSTHPETGQTIISGMGELHLEIIVDRLKREFKVDANVGKPQ
VAYRETIITKPVDEGKFIRQTGGRGQYGHVKIKVEPLPRGSGFEFVNAIVGGVIPKEYIP
AVQKGIEEAMQSGPLIGFPVVDIKVTLYDGSYHEVDSSEMAFKIAGSMAIKEAVQKGPV
ILEPIMRVEVTTPEEYMGDVIGDLNARRGQILGMEPRGNAQVIRAFVPLAEMFGYATDLR
SKTQGRGSFVMFFDHYQEVPKQVQEKLIKQ

>3RPJA 134 XRAY 1.90 0.184 0.211 no Curlin genes transcriptional regulator <UNP B4EUU9_PROMH>
[PROTEUS MIRABILIS]

SNAMTSSLHPTRGKLLKRFQIGPYIREQQCESQFFFDCLAVCVNKKVTPEKREFWGW
MELERNGEQLIYYYQVGLFDKNGDWNQVISKDVIESIHETLIRFHDFLQAAVSELEMT
LVPDEKMSNFPLPL

>1PL8A 356 XRAY 1.90 0.195 0.222 no human sorbitol dehydrogenase <UNP DHSO_HUMAN> [HOMO
SAPIENS]

AAAAKPNNSLVVHGPGDLRLNYPPIPEPGPNEVLLRMHSGICGSDVHYWEYGRIGNFI
VKKPMVLGHEASGTVEKVGSSVKHLKPGDRVAIEPGAPRENDEFCKMGRYNLSPSIFCA
TPDDGNLCRFYKHNAFCYKLPDNTFEEGALIEPLSVGIHACRRGGVTLGHKVLVCGA
GPIGMVTLVLVAKAMGAAQVVVTDLSATRLSKAKEIGADLVLQISKESPQEIARKVEGQLG
CKPEVTIECTGAEASIQAGIYATRSGGTLVLVGLGSEMTTVPLLHAAIREVDIKGVFRYC
NTWPVAISMLASKSVNVKPLVTHRFPLEKALEAFETFKKGLGLKIMLKCDPSDQNP

>3T94A 270 XRAY 1.45 0.170 0.185 no 5'-methylthioadenosine phosphorylase (MtaP) <UNP
Q97W94_SULSO> [SULFOLOBUS SOLFATARICUS]

MIEQNEKASIGIIGSGLYDPGIFSESKEIKVYTPYGQPSDFITIGKIGNKSVAFLEPRHG
RGHRIPPHKINYRANIWALKELGVRWVISVAVGSLRMDYKLGDFVIPDQFIDMTKNREY
SFFDGPVVAHVSMADPFCNSLRKLAIAETAKELNIKTHESGTYICIEGPRFSTRAESRTWR
EVYKADIIGMTLVPEVNLACEAQMCYATIAMVTDYDVFAEIPVTAEVTRVMAENTEKAK
KLLYALIQKLEKPEEGSCSCCNLSLTALV

>3N0AA 361 XRAY 2.20 0.173 0.200 no Tyrosine-protein phosphatase auxilin <UNP AUXI_BOVIN>
[BOS TAURUS]

DTLKDTSRVIQSVTSYTKGDLDFTYVTSRIIVMSFPLDSVDIGFRNQVDDIRSFLDSRH
LDHYTVYNLSPKSYRTAKFHSRVSECSWPIRQAPSLHNLFAVCRNMYNWLQNPKNVCVV

HCLDGRAASSILVGAMFIFCNLYSTPGPAVRLLYAKRPGIGLSPSHRRYLGYMCDLLADK
 PYRPHFKPLTIKSITVSPVPFFNKQRNGCRPYCDVLIGETKIYTTCADFERMKEYRVQDG
 KIFIPLSITVQGDVVVSMYHLRSTIGSRLQAKVTNTQIFQLQFHTGFIPLDTTVLKFTKP
 ELDACDVPEKYPQLFQVTLDELQPHDKVMELTPPWEHYCTKDVNPSILFSSHQEHQDTL
 V
 >2AHRA 259 XRAY 2.15 0.175 0.210 no putative pyrroline carboxylate reductase <UNP
 Q9A1S9_STRP1>
 [STREPTOCOCCUS PYOGENES]
 SNAMKIGIIGVGKMASAIKGLKQTPHELIISGSSSLERSKEIAEQALALPYAMSHQDLIDQ
 VDLVILGIKPLFETVLKPLHFKQPIISMAAGISLQRLATFVGQDLPLLRIMPNMNAQIL
 QSSTALTGNALVSQELQARVRDLTDSFGSTFDISEKDFDTFTALAGSSPAYIYLFIEALA
 KAGVKNIGIPKAKALEIVTQTVLASASNLKTSSQSPHDFIDAICSPGGTTIAGLMELERLG
 LTATVSSAIDKTIDKAKSL
 >3S2RA 83 XRAY 1.14 0.187 0.199 no AT5g51720/MIO24_14 <UNP Q9FLI7_ARATH> [ARABIDOPSIS
 THALIANA]
 GSHMRKQQRMVVVRAEGGGGINPEIRKNEDKVVDSSVVVTELSKNITPYCRCWRSCTFPLC
 DGSCVKHNKANGDNVGPLLLKKQ
 >3UP3A 243 XRAY 1.25 0.167 0.180 no aceDAF-12 <PDB 3UP3> [ANCYLOSTOMA CEYLANICUM]
 GSYQLNAAELQALDLIQEAFKGMNDPMEQGRQATSFLKNEKSPADIMNIMDVTMRRFVKM
 AKRLPAFNDLSQDGKFALLKGGMIEMLTVRGVRRFDSSSGSWTPTLGESSEVSINMFDQ
 LNADVRSEQKMRFLQFFKIFHEDIRSNDLVISMIMLIVLFSRDSITDPEDRRIIARHHE
 QFSALLNRYLESLYGDDAHQLNEQLPTALRMLREISASSGMLFLGTVNTSEAEPLPREFF
 KVE
 >2QJWA 176 XRAY 1.35 0.184 0.216 no Uncharacterized protein XCC1541 <UNP Q8PAE4_XANCP>
 [XANTHOMONAS CAMPESTRIS PV. CAMPESTRIS]
 GMSRGHCILAHGFESGPDALKVTALAEEVAERLGTWHERPDFTDLDARRDLGQLGDVRGRL
 QRLLEIARAATEKGPVVLAGSSLGSYIAAQVSLQVPTRALFLMVPPTKMGPLPALDAAAV
 PISIVHAWHDELIPAADVIAWAQARSARLLLVDGHRGHAHVQAASRAFAELLQSL
 >3EATX 293 XRAY 2.50 0.189 0.225 no Pyoverdine biosynthesis protein PvcB <UNP Q9I1L4_PSEAE>
 [PSEUDOMONAS AERUGINOSA]
 GHMNAIYSDQPVRLSPLRDEQGNQPRFGLLLEPGRPGMHVGEPAQWLKGLARSHHLLLL
 RGFAAFADAESLTRYCHDFGEVMLWPFQAVLELVEQEGAEDHIFANNYVPLHWDGMYLET
 VPEFQVFHCVDAPGDSGGRITFSSTPAALQLADSSELELWRRASGRYQSAAHYSSRSA
 APIVERHPRREFPILRFCEPPVEGDASFINPSEFHYDGAPEQRGELLASLRCLYHPQA
 HYAHRWRSDDLVIADNLTLLHGREAFAHRAPRHLRRVHIHAEPALRNPHLQRD
 >1ZUPA 315 XRAY 2.20 0.230 0.266 no hypothetical protein TM1739 <UNP Q9X261_THEMA>
 [THERMOTOGA MARITIMA]
 MGSDKIHIIHHHMHMQVRIERAERIESELEEHVGDQTFVEESRFLEEDQREGEILDQIIFV
 DGKRRSFVRITTDGEGITGIFAELCVGAVIWDREGGKTFLSPDKPPVKERVLGFSQSFQE
 EGYEEVGGILFKVKEGKDAMQSIDLYMRSLEIEEVRKHMDKNILIVKDGPAAARELPFEE
 NVGPIGLVKNIGVTELSKEDFKKLRLKKGKRSKMFVSSRETPLKKVGAYVKLIDGEGIR
 GLVRLETYVKDDNQIPYIRKVFDDLAKTLPHLTADLPIRLPENILPIQFLEENLSYYLT
 DKNYMNTRLFAYIGR
 >3JYBA 145 XRAY 2.04 0.201 0.235 no Sensor protein <UNP Q9HUV7_PSEAE> [PSEUDOMONAS
 AERUGINOSA]
 ATTPSANQNWRLLRDESAQLRIADVLQRKEQFRPLAKRSFIFPASPQAVWLQVQLPAQKV
 PSWLWIFAPRVQYLDYVLVDGQLVRDQHTGESRPFQERPLPSRSLFSLPVDGKPMPLY
 VRMTSNHPLMAWFDQIDEAGLVGLE
 >2XEPA 458 XRAY 1.50 0.201 0.217 no ORF12 <UNP Q83Z62_STRCL> [STREPTOMYCES CLAVULIGERUS]

MMKKADSVPTPAEALAAQTALAADDSPMGDAARWAMGLLTSSGLPRPEDVAARFIPTFA
AAGNFAETVREWRSGPFTVRAYHPVAHKGWVLSAPAGVRYILSLTDSSGLIRILTLK
PETVIPDMVTWNDVEETLHTPGVQHSVYAVRLTPDGHEVLHASAPERPMPTGSAYKLYLM
RALVAEIEKGTVGWDEILTLTPELRSPLTGDMDQLPDGTRVTVRETAHKMIALSDNTGAD
LVADRLGREVVERSLAAAGHHDPSLMRPFLTSHEVFELGWGDPERRAEWVRQDEAGRREL
LEKMAGVMTVRGSDLGATVHQLGIDWHMDAFDVVRVLEGLLQDSGRDTS GTVEEILTAYP
GLLIDEERWRRVYFKAGSSPGVMFCWLLQDHAGISYVLVLRQSADEQRLIGDGLFLRGI
GAKIIEAEAKLLSSGERRGAGTAAAGDDRASAGEAARR

>1VH5A 148 XRAY 1.34 0.188 0.228 no Hypothetical protein ydiI <UNP YDII_ECOLI> [ESCHERICHIA COLI]

MSLIWKRKITLEALNAMGEGNMVGFLDIRFEHIGDDTLEATMPVDSRTKQPFGLLHGGAS
VVLAESIGSVAGYLCTEGEQKVVGLEINANHVRSAAREGRVRGVCKPLHLGSRHQVWQIEI
FDEKGRGCCSSRLTTAILEGGSHHHHHH

>2QXFA 482 XRAY 1.50 0.200 0.224 no Exodeoxyribonuclease I <UNP EX1_ECOLI> [ESCHERICHIA COLI]

MMNDGKQQTFLFDYETFGTHPALDRPAQFAAIRTDSEFNVIGEPEVFYCKPADDYLPQ
PGAVLITGITPQEARAKGENEAFAARIHSLFTVPKTCILGYNNVRFDDDEVTRNIFYRNF
YDPYAWSQHDNSRWDLDMRACYALRPEGINWPENDDGLSPFRLEHLTKANGIEHSNA
HDAMADVYATIAMAKLVKTRQPRLFDFYLFTHRNKHKLMALIDVPQMPLVHVS GMFGAWR
GNTSWVAPLAWHPENRNAVIMVDLAGDISPLLELSDTLRERLYTAKTDLGDNAAVPVKL
VHINKCPVLAQANTLRPEDADRLGINRQHCLDNLKILRENQVREKVVAIFAEAEPTPS
DNVDAQLYNGFFSDADRAAMKIVLETEPRNLPALDITFVDKRIEKLNFYRARNFPGLTD
YAEQQRWLEHRRQVFTPEFLQGYADELQMLVQQYADDKEKVALLKALWQYADEIVEHHHH
HH

>2IP2A 334 XRAY 1.80 0.196 0.247 no Probable phenazine-specific methyltransferase <UNP Q9HWH2_PSEAE> [PSEUDOMONAS AERUGINOSA]

MNNSNLAAARNLIQVVTGEWKSRCVYVATRLGLADLIESGIDSDETAAAVGSDAERIHR
LMRLLVAFEIFQGDTRDGYANTPTSHLLRDVEGSFRDMVLFYGEEFHAAWTPACEALLSG
TPGFELAFGEDFYSLKRCPDAGRFRLLAMKASNLA FHEIPRLDFRGRSFVDVGGSGE
LTKAILQAEPSARGVMLDREGSLGVARDNLSLLAGERVSLVGGDMLQEVPSNGDIYLLS
RIIGDLDEAASRLLLGNCREAMAGDGRVVVIERTISASEPSPMSVLWDVHFLMACAGRHR
TTEEVDLLGRGGFAVERIVDLPMETRMIVAARA

>2HQ9A 149 XRAY 1.95 0.183 0.243 no M11668 protein <UNP Q988L5_RHILO> [MESORHIZOBIUM LOTI]

GMLVRTLSALECTKVLTA NRVGRLACAKDGQPYVVPLYAYSDAHLAYAFSMPGKKIEWMR
ANPRVSVQVDEHGQGRGWSVVVDGRYEELPDLIGHKLQRDHAWSVLSKHTDWWEPGALK
PVTPTADSAPHVFFRILIEQVSGREASE

>2HAZA 105 XRAY 1.70 0.219 0.286 no Neural cell adhesion molecule 1 <UNP NCA12_HUMAN> [HOMO SAPIENS]

GSHMDTPSSPSIDQVEPYSSTAQVQFDEPEATGGVPILKYAEWRAVGEEVWHSKYDAK
EASMEGIVTIVGLKPETTYAVRLAALNGKGLGEISAASEFKTQPV

>2VSOE 284 XRAY 2.60 0.215 0.260 no EUKARYOTIC INITIATION FACTOR 4F SUBUNIT P150 <UNP IF4F1_YEAST> [SACCHAROMYCES CEREVISIAE]

MLVPSANRWVPKFKSKKTEKKLAPDGKTELLDKDEVERKMKSLNKL TLEMFD AISSEIL
AIANISVWETNGETLKAVIEQIFLKACDEPHWSSMYAQLCGKVVKELNPDITDETNEGKT
GPKLVHLVARCHAEFDKGWTDKLP TNE DGTPEPEMMSEYYAAASAKRRGLGLVRFI
GFLYRLNLLTGMMFECFRRLMKDLTDSPEETLESVVELLNTVGEQFETDSFRTGQATL
EGSQLDLSLFGILDNIIQTAKISSRIKFKLIDIKELRHDKNWS

>1H12A 405 XRAY 1.20 0.108 0.130 no ENDO-1, 4-BETA-XYLANASE <UNP Q8RJN8> [PSEUDOALTEROMONAS HALOPLANKTIS]

AFNNNPSSVGAYSSGTYRNLAQEMGKTNIQQKVNSTFDNMFYNNNTQQLYPYPTENG VYK

AHYIKAINPDEGDDIRTEGQSWGMTAAVMLNKQEEFDNLWRFKAYQKNPDNHPDAKKQG
VYAWKLKLNQNGFVYKVDEGPAPDGEEYFALLNASARWGNSGEFNYYNDAITMLNTIK
NKLMEQIIRFSPYIDNLTDPYHIFAFYDYFANNVTNQADKNYWRQVATKSRTLLKNHF
TKVSGSPHWNLPTFLSRLDQSPVIGYIFNGQANPGQWYEFDAWRVIMNVGLDAHLMGAQA
WHKSAVNKALGFLSYAKTNNKNCYEQVYSYGAQNRGCAGEGQKAANAVALLASTNAGQ
ANEFNEFWLSQPTGDYRYNGSLYMLAMLVSGNFKFYNNTFN

>1VLYA 338 XRAY 1.30 0.136 0.168 no Unknown protein from 2D-page <UNP UP14_ECOLI> [ESCHERICHIA COLI]

MGSDKIHSHHHMAFTPFPPRQPTASARLPLTMTLDDWALATITGADSEKYMGGQVTAD
VSQMAEDQHLLAAHCDAGKGMWSNLRLFRDGDGFAWIERRSVREPQLTELKKYAVFSKVT
IAPDDERVLLGVAGFQARAALANLSELPSEKQVVEGATTLLWFEHPAERFLIVTDEA
TANMLTDKLRGEAELNNSQQWLALNIEAGFPVIDAANSQGQFIPQATNLQALGGISFKKGC
YTQGMVARAKFRGANKRALWLAGSASRLPEAGEDLELKMGENWRRRTGTVLA AVKLEDG
QVVVQVVMNDMEPDSIFRVRDDANTLHIEPLPYSLEE

>2X1QA 127 XRAY 1.06 0.214 0.229 no GELSOLIN NANOBODY <PDB 2X1Q> [LAMA GLAMA]

QVQLQESGGGLVQPGGSLRLSCAASGRFSTNYRMGWFRQAPGKEREFVATISQSGAATAY
ADSVKGRFTFSRDNAKNNLYLEMLSLPEDTAVYYCAASSRVFYTEVLQTTTGIDYWGQG
TQVTVSS

>3GYBA 280 XRAY 1.60 0.219 0.231 no Transcriptional regulators (LACI-FAMILY TRANSCRIPTIONAL REGULATORY PROTEIN) <UNP Q8NTY1_CORGL> [CORYNEBACTERIUM GLUTAMICUM]

MSLRTQLIAVLIDDYSNPWFIDLIQSLSDVLT PKGYRLSVIDSLTSQAGTDPITSALSMR
PDGIIIAQDIPDFTPDLSPPFVIAGTRITQASTHDSVANDDFRGAEIATKHLIDLGHTH
IAHLRVGSGAGLRREFSEATMRAHGLEPLSNDYLGPAVEHAGYTETLALLKEHPEVTAI
FSSNDITAIGALGAARELGLRVPEDLSIIGYDNTPLAQTRLINLTIDDNSIGVGYNAAL
LLLSMLDPEAPHPEIMHTLQPSLIERGTCAPREGHHHHH

>3BA3A 145 XRAY 1.55 0.171 0.196 no Pyridoxamine 5'-phosphate oxidase-like protein <UNP Q890D6_LACPL> [LACTOBACILLUS PLANTARUM WCFS1]

GMDISLLKQVQSTNKIALSTAVNNEADV KIVNFVWEAQPDITLYFSSVKTSPALKVYDQ
NPDI AFITIPNDGTAGNPYLRQHVKLQRSTKTMTDLLPQYLETVPNYQQVWDAIGSTLV
VFELKLTDLFVDAGVGGEKQTLTFN

>3H6QA 169 XRAY 1.64 0.162 0.193 no Macrocypin 1a <UNP B9V973_9AGAR> [MACROLEPIOTA PROCERA]

MGFEDGFYTIHLAEGQHPNSKIPGGMYASSKDGKDVPTAEPLGPQSKIRWWIARDPQA
GDDMYTITEFRIDNSIPGQWSRSPVETEVVYLYDRIKAEETGYTCAWRIQPADHGADGV
YHIVGNVRIGSTDWADLREEYGEPQVYMKPVPVIPNVYIPRWFILGYEE

>3L7IA 729 XRAY 2.70 0.213 0.260 no Teichoic acid biosynthesis protein F <UNP Q5HLM5_STAEQ> [STAPHYLOCOCCUS EPIDERMIDIS]

MNKLTIIVTYNAEEYITGCLESIKQRTQDFNLIIVNDGSTQSKKLMDEAIKDYDKNI
RFIDLDENSGHAHARNIALEEETPYFMFLDADDELASYAITFYLEKFNNTDGLIAPIHS
FTTQRPQFVDLDRVRVEYFNAKENINSFLRKQSACNIIIFRTAIVRAHHIRFNENLNTYVD
WSFVLEYMKYVNVKVRIFNFPFYFRGEVYDPFETLTLSEQNFDILFKDYVNSFYDAIKRA
TNPKVREFIVTKMGNKIANEFEPTRYDINERYQTHKDTLVELSKFLHVHLVKNQKLINKI
ETILLMNETDKAFKVNQFRKTLRHVKNIIVLRKNKERSLYDLTDKEDNVKPKTIVFESF
GGKNYSDSPKYIYEYMQYYPNYRYIWSFKNPDKNVVPGSAEKVKRNSAEYYQAYSEASH
WVSNARTPLYLNKKENQTYIIQTHGTPKRLANDMKVVRMPGTTTPKYKRNFNRET SRWD
YLISPNRYSTEIFRSFWMDEERILEIGYPRNDVLNRRANDQEYLDEIRTHLNLPSDKKV
IMYAPTWRDDEFVSKGYLFELKIDLDNLYKELGDDYVILLRMHYLISNALDLSGYENFA
IDVSNYNDVSELFLISDCLITDYSSVMFDYGILKRPQFFAYDIDKYDKGLRGFYMNME
DLP GPIYTEPYGLAKELKNLDKVQQYQEKIDAFYDRFCSDNGKASQYIGDLIHKDIKE
QLEHHHHHH

>1HI9A 274 XRAY 2.40 0.232 0.268 no DIPEPTIDE TRANSPORT PROTEIN DPPA <UNP DPPA_BACSU> [BACILLUS SUBTILIS]
 MKLYMSVDMEGISGLPDDTFVDSGKRNRYERGLIMTEEANYCIAEAFNSGCTEVLVND SH
 SKMNNLMVEKLHPEADLISGDVVKPFMSVEGLDDTFRGALFLGYHARASTPGVMSHSMIFG
 VRHFYINDRPVGELGLNAYVAGYYDVPVLMVAGDDRAAKEAEELIPNVTTAAVKQTISRS
 AVKCLSPAKRGRLTEKTAFALQNKDKVKPLTPPDRPVLSIEFANYGQAEWANLMPGTEI
 KTGTTTVQFQAKDMLEAYQAMLVMTLAMRTSF

>4E0JB 258 XRAY 1.65 0.197 0.215 no Cyclin-A2 <UNP CCNA2_HUMAN> [HOMO SAPIENS]
 VPDYHEDIHTYLREMEVKCKPKVGYMKKQPDITNSMRAILVDWLVEVGEEYKLQNETLHL
 AVNYIDRFLSSMSVLRGKQLVGTAAMLLASKFEEIYPPEVAEFVYITDDTYTKKQVLRM
 EHLVLKVLTFDLAAPTQNFQTLQYFLHQQPANCKVESLAMFLGELSLIDADPYLKYLPSV
 IAGAAFHLLALYTVTGQSWPESLIRKTGYTLESCLKPCLMDLHQTYLKAPQHAQQSIREKYK
 NSKYHGVSLNPPETLNL

>1J5PA 253 XRAY 1.90 0.224 0.260 no ASPARTATE DEHYDROGENASE <UNP Q9X1X6_THEMA> [THERMOTOGA MARITIMA]
 MGSDKIHSHHHHMTVLIIGMGNIGKKLVELGNFEKIYAYDRISKDIPGVVRLDEFQVPSD
 VSTVVECASPEAVKEYSLQILKNPVNYIIISTSAFADEVFRERFFSELKNSPARVFFPSG
 AIGGLDVLSSIKDFVKNVRIETIKPPKSLGLDLKGKTVVFEQSVEEASKLFPRNINAVST
 IGLIVGFEKVKVITIVADPAMDHNIHIVRISSAIGNYEFKIENIPSPENPKTSMLTVYSIL
 RTRLNLESKIIIFG

>3CU5A 141 XRAY 2.60 0.189 0.300 no Two component transcriptional regulator, AraC family
 <UNP A9KIW7_CLOPH> [CLOSTRIDIUM PHYTOFERMENTANS ISDG]
 MSLRILIVDDEKLTRDGLIANINWKALSFDQIDQADDGINAIQIALKHPPNVLLTDVRMP
 RMDGIELVDNLIKLYPDCSVIFMSGYSDKEYLKAAIKFRAIRYVEKPIDPSEIMDALKQS
 IQTVLQHQAQQDSEGHSHHHHH

>1QWOA 442 XRAY 1.50 0.162 0.186 no phytase <UNP PHYA_ASPFU> [ASPERGILLUS FUMIGATUS]
 SAGSKSCDVTDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGA
 RYPTSSKSKYKLVTAIQANATDFKGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFY
 QRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQAKLADPGATNRAAPAISVIIPESET
 FNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIRARAETHLPVTLTDEDVVSMDMCS
 FDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLGKYGYGAGNPLGPAQGIGFTNELIA
 RLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFSHDMSMVSIFALGLYNGTEPLSRTS
 VESAKELDGYSASVVPFGARAYFETMQCKSEKEPLVRALINDRVVPLHGCVDVCLKGRCK
 LNDFVKGLSWARSGGNWGECS

>5CSMA 256 XRAY 2.00 0.186 0.236 no CHORISMATE MUTASE <UNP CHMU_YEAST> [SACCHAROMYCES CEREVISIAE]
 MDFTKPETVLNLQNIREDLVRMEDSIIKFIERSHFATCPSVYEANHPGLEIPNFKGSFL
 DWALSNLIEAHSRIIRRFESPDETPFFPDKIQKSFLPSINYPQILAPYAPEVNYNDKIKKV
 YIEKIIPLISKRDGDDKNNFGSVATRDIECLQSLSRRIHFGKFVAEAKFQSDIPLYTKLI
 KSKDVEGIMKNITNSAVEEIKLERLTKKAEVYGVDPTEIRRIERRISPEYLVKIYKEIVIP
 ITKEVEVEYLLRLEE

>3U12A 141 XRAY 2.08 0.210 0.232 no USP37 protein <UNP Q86W68_HUMAN> [HOMO SAPIENS]
 MGSSHHHHHSSGLVPRGSLKIHGPIRIRSMQTGITKWEKSFEIVEKENKVSLSLVVHYNT
 GGIPRIFQLSHNIKNVLRPSGAKQSRMLTLQDNSFLSIDKVPSKDAEEMRLFLDAVHQ
 NRLPAAMKPSQSGSFGAILG

>3ABHA 312 XRAY 2.00 0.234 0.271 no Protein kinase C and casein kinase substrate in neurons protein 2
 <UNP PACN2_HUMAN> [HOMO SAPIENS]
 GSSGSSGMSVTYDDSVGVEVSSDSFWEVGNKYKRTVKRIDDGHRLCSDLMNCLHERARIEK

AYAQQLEWARRWRQLVEKGPQYGTVEKAWMAFMSEAERVSELHLEVKASLMNDDFEKIK
 NWQKEAFHKQMMGGFKETKEAEDGFRKAQKPWAKKLKEVEAAKKAHHAACKEEKLAISRE
 ANSKADPSLNPEQLKKLQDKIEKCKQDVLKTKEKYEKSLKELDQGTPQYMENMEQVFEQC
 QQFEEKRLRFFREVILLEVQKHLDSLNVAGYKAIYHDLEQSIRAADAVEDLRWFRANHGPG
 MAMNWPQFEWS
 >3C0FB 91 XRAY 1.80 0.207 0.226 no Uncharacterized protein AF_1514 <UNP Y1514_ARCFU>
 [ARCHAEoglobus fulgidus DSM 4304]
 MEIMDEIKVNLQKEVSLEEAERYAKNIASKYGDGILLSVHDSKTYRAPEVYCCGEKPWE
 VYACNRGANLKISVNQFEFYFRIEVEGQAKY
 >1Z6RA 406 XRAY 2.70 0.206 0.263 no Mlc protein <UNP MLC_ECOLI> [ESCHERICHIA
 COLI] MVAENQPGHIDQIKQTNAGAVYRLIDQLGPVSRIDLSRLAQLAPASITKIVHEMLEAHLV
 QELEIKEAGNRGPAVGLVETEAWHYLSLRISRGEIFLALRDLSSKLVEESQELALKD
 DLPLLDRIISHIDQFFIRHQKKLERLTSIAITLPGIIDTENGIVHRMPFYEDVKEMPLGE
 ALEQHTGVPVYIQHDISAWTMAEALFGASRGARDVIQVVIDHNVGAGVITDGHLLHAGSS
 SLVEIGHTQVDPYQKRCYCGNHGCTETIASVDSILELAQLRLNQSMSSMLHGQPLTVDSL
 CQAALRGDLLAKDIITGVGAHVGRILAIMVNLFPQKILIGSPLSKAADILFPVISDSIR
 QQALPAYSQHISVESTQFSNQGTMAGAALVKDAMNGSLLIRLLQG
 >3P1UA 529 XRAY 2.05 0.244 0.265 no SusD homolog <UNP A6L9L2_PARD8> [PARABACTEROIDES
 DISTASONIS ATCC 8503]
 GNENPDKPTDDVNYNMNEPRLASTLRGGLIEGNVEQRLKPLQIDFYSQMTVDGGGWTGK
 NYIQDDEWNNLVWEEYLKQIASINIVIRSLTEKDKDAYANTIAFARIWRVYVHTLAADKF
 GPMFPAYEIVEANPPYKSLKDIYDEYFRELDAANGFNDSAQPIFSDAGIDLIYKNDVS
 KWKRFLANSLRLRLAVRLTEVDQEKICAEANAAISSPAGLISDKADNAYMPPKADGSWGQD
 YNYTMFQITWSPICMSKSVEKLVNIGGVAWPQGVVNTSGVAVSSVHPEKVDPRAPKI
 FQPGIENGDWKGLVYGPAKEEANTGIYQSKQCAELGFIKDGYPYKSRPYDLFLSEEVHF
 LKAELYARGFIAGDAKSEYEAGVRASFATWGVTSVDDYLTSTEKNEAGTSARYDDQQA
 GNTALEKIIITQKYIAGIPDLAQEGWNDKRRLLNPLRDVAVYRDQAVYNNNDKDILKSANF
 IKRMRYPTKESLINATEYEKGKSMGLGKGDIVSTPLWWDKNSNYCTSSK
 >2OZVA 260 XRAY 1.70 0.180 0.214 no Hypothetical protein Atu0636 <UNP Q8UHP4_AGR5>
 [AGROBACTERIUM TUMEFACIENS STR.]
 MGSSHHHHHSSGRENLYFQGHMDAMLLASLVADDRACRIADLGAGAGAAGMAVAARLEK
 AEVTLYERSQEMAEFARRSLELPDAAFSARIEVLEADVTLRAKARVEAGLPDEHFHHVI
 MNPPYNDAGDRTPDALKAEAHAMTEGLFEDWIRTASAIMVSGGQLSLISRPQSVAEIIA
 ACGSRFGGLEITLIHPRPGEDAVRMLVTAIKGSRARLTFRAPLIMHETGSHAFTPFVDDL
 NNGRAAYARNVRAIRTASGS
 >1DJ8A 89 XRAY 2.00 0.209 0.261 no PROTEIN HNS-DEPENDENT EXPRESSION A <UNP HDEA_ECOLI>
 [ESCHERICHIA COLI]
 ADAQKAADNKKPVNSWTCEDFLAVDESFPQPTAVGFAEALNNKDKPEDAVLDVQGIATVTP
 AIVQACTQDKQANFKDKVKGEDKIKKDM
 >2ZE7A 253 XRAY 2.10 0.195 0.254 no Isopentenyl transferase <UNP IPTZ_AGR5> [AGROBACTERIUM
 TUMEFACIENS]
 MLLHLIYGPTCSGKTDMAIQIAQETGWPVVALDRVQCCPQIATGSGRPLESELQSTRRIY
 LDSRPLTEGILDAESAHRRLIFEVDWRKSEGLILEGGSISLLNCMAKSPFWRSGFQWHV
 KRLRLGDSDAFLTRAKQRAEMFAIREDRPSLLEELAEWNPAAARPILEDIDGYCAIR
 FARKHDLAISQLPNIDAGRHVELIEAIANEYLEHALSQERDFPQWPEDGAGQVPCPVTLT
 RIRGSRSHHHHHH
 >2W3GA 153 XRAY 1.40 0.193 0.217 no TWO COMPONENT SENSOR HISTIDINE KINASE DEVS (GAF FAMILY
 PROTEIN) <UNP P95194_MYCTU> [MYCOBACTERIUM TUBERCULOSIS]

GAMDPDLEATLRAIVHSATSLVDARYGAMEVHDRQHRVLHFVYEGIDEETVRRIGHLPKG
 LGVIGLLIEDPKPLRLDDVSAHPASIGFPPYHPPMRTFLGVPVRVRDESFGTLYLTDKTN
 GQPFSDDEVLVQALAAAAGIAVANARLYQQAK
 >1000A 147 XRAY 1.85 0.215 0.262 no Mago nashi protein <UNP MGN_DROME> [DROSOPHILA
 MELANOGASTER]
 MSTEDFYLRYYVGHKGFGEHFEFEPDGLRYANNSNYKNDTMIRKEAFVHQSVME
 LKRIIIDSEIMQEDDLPPPPDRVGRQELEIVIGDEHISFTTSKTGSLVDVNRSKDPEGL
 RCFYYLVQDLKCLVFSLIGLHFKIKPI
 >1BS0A 384 XRAY 1.65 0.178 0.212 no 8-AMINO-7-OXONANOATE SYNTHASE <UNP BIOF_ECOLI>
 [ESCHERICHIA COLI]
 MSWQEKINAALDARRAADALRRYPVAQAGRWLVADDRQYLNFSNDYLGLSHHPQIIR
 AWQQAEQFGIGSGSGHVSYSVHHQALEEELAEWLGYSRALLFISGFAANQAVIAAMM
 AKEDRIAADRLSHASLLEAASLSPSQLRRFAHNDVTHLARLLASPCPGQMVVTEGVFSM
 DGDSAPLAEIQVVTQQHNGWLMVDDAHGTGVIGEQQRGSCWLQKVKPELLVVTFGKFGV
 SGAAVLCSTVADYLLQFARHLIYSTSMPPAQAQALRASLAVIRSDEGDARREKLALIT
 RFRAGVQDLPTLADSCSAIQPLIVGDNSTRALQLAEKLRRQGCWVTAIRPPTVPAGTARL
 RLTLTAAHEMQDIDRLLEVLHGNG
 >1VQOT 120 XRAY 2.20 0.215 0.246 no 50S ribosomal protein L24P <UNP RL24_HALMA> [HALOARCU
 LAMARISMORTUI]
 MSKQPKQKRSQRRAPLHERHKQVRATLSADLREEYQQRNVRNAGDTVEVLRGDFAGEE
 GEVINVDLDKAVIHVEDVTLEKTDGEEVPRPLDTSNVRVTDLDLEDEKREARLESEDDSA
 >1VR7A 142 XRAY 1.20 0.120 0.150 no S-adenosylmethionine decarboxylase proenzyme <UNP
 SPEH_THEMA> [THERMOTOGA MARITIMA]
 MGSDKIHSHHHHMKSLGRHLVAEFYECREVDNVQLIEQEMKQAAYESGATIVTSTFHR
 FLPYGVSGVVVISESHITIHTWPEYGYAIDLFTCGEDVDPWKAFEHLKKALKAKRVHVV
 EHERGRYDEIGIPEDSPHKAAY
 >2ID6A 202 XRAY 1.75 0.211 0.251 no TRANSCRIPTIONAL REGULATOR, TetR FAMILY <UNP Q9XOCO_THEMA>
 [THERMOTOGA MARITIMA]
 GHMLSKRDAILKAAVEVFGKKGYDRATTEIAEKAGVAKGLIFHYFKNKEELYQAYMSV
 TEKLQKEFENFLMKNRNRDIFDFMERWIEKKLEYSASHPEEADFLITLVSVDGLRKRIL
 LDLEKSQRVFFDFVREKLKDLDAEDVTEEIALKFLMWFFSGFEEVYLRITYQGKPELLKR
 DMNTLVEEVKVMLRILKKGMTK
 >1GNYA 153 XRAY 1.63 0.152 0.177 no XYLANASE 10C <UNP Q59675> [PSEUDOMONAS CELLULOSA]
 GNVVIEVDMANGWRGNASGSTSHSGITYSADGVTFALGDGVGAVFDIARPTTLEDAVIA
 MVNVNSAEFKASEANLQIFAQLKEDWSKGEWDCLAGSSELTADTDLTLCTIDEDDDKFN
 QTARDVQVGIQAKGTPAGTITIKSVTITLAQEA
 >4FMRA 265 XRAY 2.25 0.171 0.213 no uncharacterized hypothetical protein <UNP
 A6L2B2_BACV8> [BACTEROIDES VULGATUS]
 GAKNVLKAWLVNDVTDDTKIFQLETTSIDKEIILDRMVAKNPGVRRETALGIEL
 MEEVVAEALMNGESVNTGLFRGVAQFRGVAKQNAWDAATNSIYVSLTQKALREAIKDTR
 VDLGERPTKFYIGSGQDATTRATDFSATAGRNFTLFGKNLTVAGTDPSVGVTLASAATG
 TVTKIDNDMIVLNPSRLIILLPASLEDGEYMLTVTTQYRGGGALLKTPRSTSHTIYIG
 GAPETGGSTGPPGSDGDLNENPLG
 >1CC5A 83 XRAY 2.50 0.290 NA no CYTOCHROME C5 <UNP CYC5_AZOVI> [AZOTOBACTER VINELANDII]
 GGGARSGDDVVAKYCNACHGTGLLNAPKVGDSAAWKTRADAKGGLDGLLAQSLSGLNAMP
 PKGTCADCSDDELKAAIGKMSGL
 >2GJ4A 824 XRAY 1.60 0.189 0.226 no Glycogen phosphorylase, muscle form <UNP PYGM_RABIT>
 [ORYZOLAGUS CUNICULUS]
 QISVRGLAGVENVTELKKNFNRHLHFTLVKDRNVATPRDYFALAHTVRDHLVGRWIRTQ

QHYYEKDPKRIYYLSLEFYMGRTLQNTMVNLALENACDEATYQLGLDMEELIEEDAGL
 GNGGLGRLAACFLDSMATLGLAAYGYGIRYEFQIFNQKICGGWQMEEADDWLRYPNWEK
 ARPEFTLPVHFYGRVEHTSQGAKWVDQVVLAMPYDTPVPGYRNNVNTMRLWSAKAPND
 FNLKDFNVGGYIQAVLDRNLAENISRVLYPNDNFFEGKELRLKQYFVVAATLQDIIRRF
 KSSKFGCRDPVRTNFDAPDKVAIQLNDTHPSLAIPELMRVLVDLERLDWDKAWETVKT
 CAYTNHTVLPEALERWPVHLETLPRHLQIIEINQRFLNRVAAAFPGDVDRLRMSLV
 EEGAVKRINMAHLCIAGSHAVNGVARIHSEILKKTIFKDFYELEPHKFQNKNGITPRRW
 LVLCPGLAEIIAERIGEEYISDLDQLRKLLSYVDDEAFIRDVAKVKQENKLFAYLER
 EYKVHINPNSLFDVQVKRIHEYKRQLNCLHVITLYNRIKKEPNKFVVPRTVMIGGKAAP
 GYHMAKMI IKLITAIGDVVNHDPPVVGDRLRVIFLENYRVSLAEKVIPAADLSEQISTAGT
 EASGTGNMKFMLNGALTIGTMDGANVEMAEAGEENFFIFGMRVEDVDRLDQRGYNAQEY
 YDRIPELRQIEQLSSGFFSPKQPDLFKDIVNMLMHHDRFKVFADYEEYVKCQERVSALY
 KNPREWTRMIRNIATSGKFSSDRTIAQYAREIWGVEPSRQRLP

>2RBFA 54 XRAY 2.25 0.208 0.246 no Bifunctional protein putA <UNP PUTA_ECOLI> [ESCHERICHIA
 COLI] GHMGTTTGMVKLDDATREIKSAATRDRTPHWLIKQAIIFSYLEQLENSDTLPE

>2F4IA 197 XRAY 2.25 0.193 0.248 no hypothetical protein TM0957 <UNP Q9X052_THEME> [THERMOTOGA
 MARITIMA]

MGSDKIHSHHHHEEMKGFDPKRYARELWFKLQDMNEGLGYDAVEVLNTLDENPELAHQ
 KFAKVVGVSNRYRYIIQGVGEIVEIKDDGILVKVRENKVPDLFLSNHIFGNGIVNATGI
 AKMEDFDRIIDFNLATLENKIVKEEVNSFLKQLSKGAGSVGSLVRFIAVFTLLKDEEI
 KYPIEAIPLYLEIQGGF

>1R7AA 504 XRAY 1.77 0.164 0.195 no sucrose phosphorylase <UNP Q84HQ2_BIFAD>
 [BIFIDOBACTERIUM ADOLESCENTIS]

MKNKVQLITYADRLGDGTIKSMTDILRTRFDGVYDGVHILPFFTPFDGADAGFDPIDHTK
 VDERLGSWDDVAELSKTHNIMVDAIVNHMSWESKQFQDVLAKGEESEYPMFLTMSSVFP
 NGATEEDLAGIYRPRPGLPFTHYKFAGKTRLVWVSFTPQQVDIDTSDKGWEYLMSIFDQ
 MAASHVSYIRLDAVGYGAKEAGTSCFMTPKTFKLISRLREEGVKRGLEILIEVHSYKKQ
 VEIASKVDRVYDFALPPLLLHALSTGHVEPVAHWTDIRPNNAVTVLTDHIGIGVIDIGSD
 QLDRSLKGLVPDEVDNLVNTIHANTHGESQAATGAAASNLDLYQVNSTYYSALGCNDQH
 YIAARAVQFFLPGPVQVYVYGALAGKNDMELLRKTNNGRDINRHYYSTAEIDENLKRPPV
 KALNALAKFRNELDAFDGTFSTYTTDDDSISFTWRGETSQATLTFEPRKGLGVDNTTPVA
 MLEWEDSAGDHRSDDLIANPPVVA

>1NRIA 306 XRAY 1.90 0.216 0.246 no Hypothetical protein HI0754 <UNP Y754_HAEIN> [HAEMOPHILUS
 INFLUENZAE]

SNAMNDIILKSLSTLITEQRNPNSVDIDRQSTLEIVRLMNEEDKLVPLAIESCLPQISLA
 VEQIVQAFQGGRLIYIGAGTSGRLGVLDASECPPTFGVSTEMVKGIIAGGECAIRHPVE
 GAEDNTKAVLNDLQSIHFSKNDVLVGIAASGRTPYVIAGLQYAKSLGALTISIASNPKSE
 MAEIADIAIETIVGPEILTGSRLKSGTAQKMVLNMLTTASMILLGKCYENLMVDVQASN
 EKLKARAVRIVMQATDCNKTAEQTLLEADQNAKLAIMMILSTLSKSEAKVLLERHQGKL
 RNALSK

>3IWFA 107 XRAY 1.40 0.179 0.205 no Transcription regulator RpiR family <UNP Q8CNB1_STAES>
 [STAPHYLOCOCCUS EPIDERMIDIS]

MPNILYKIDNQYPYFTKNEKKIAQFILNYPHKVVNMTSQEIANQLETSSTSIIRLSKKVT
 PGGFNELKTRLSKFLPKEVTQYNVELVDNESTISLKNKLHSRKAAL

>2YZQA 282 XRAY 1.63 0.225 0.243 no Putative uncharacterized protein PH1780 <UNP
 059416_PYRHO> [PYROCOCCUS HORIKOSHII]

MRVKTIMTQNPVTITLPAATRYALELFKKYKVSFPVNNKEGKLVGIIISVKRILVNPDEE
 QLAMLVKRDVPVVKENDTLKKAACLMLDYRRVVVDSKGPVGIITVGDIIIRRYFAKS

EKYKGVEIEPPYQRYVSIVWEGTPLKAALKALLSNSMALPVVDSEGNLVGIVDETDLR
DSEIVRIMKSTELAASSEEWEILESHPTLLFEKFELQLPNKPVAEIMTRDVIVATPHMTV
HEVALKMAKYSIEQLPVIRGEDLIGLIRDFDLKVLVKSKA
>20IXA 186 XRAY 1.80 0.212 0.259 no Xanthomonas outer protein D <UNP Q3BYJ5_XANC5>
[XANTHOMONAS EUVESICATORIA]
ATSWLLDGHLRAYTDDLARRLRGEPNAHLLHFADSQVVTMLSSADPDQQAQRLLAGDD
IPPIVFLPINQPNAHWSLLVDDRKNDAVAAYHYDSMAQKDPQQRYLADMAAYHLGLDYQ
QTHEMPIAIQSDGYSAGDHVLTGIEVLAHVRVLDGTFDYAGGRDLTDIEPDRGLIRDRLAQ
AEQAPA
>4IUJA 464 XRAY 1.90 0.175 0.201 no Polymerase acidic protein <UNP PA_I33A0> [INFLUENZA A
VIRUS] GNARIEPFLKSTPRPLRLPDGPPCSQRSKFLMDALKLSIEDPSHEGEGIPLYDAIKCMR
TFFGWKEPNVVKPHEKGINPNYLLSWKQVLAELQDIENEEKIPRTKNMKKTSQLKWALGE
NMAPEKVDFFDCKDVGDLKQYDSDEPELRSLASWIQNEFNKACELTDSSWIELDEIGEDA
APIEHIASMRNYFTAESHCRATEYIMKGVYINTALLNASCAAMDDFQLIPMISKCRTK
EGRKTNLYGFI IKGRSHLRNDTDVNVFVSMEFSLTDPRLPHKWEKYCVLEVGDMLLRS
AIGHVSRPMFLYVRTNGTSKIKMKWGMEMRRCLLQSLQQIESMIEAESSVKEKDMTKEFF
ENKSETWPVGESPKGVEEGSIGKVCRTLLAKSVFNSLYASPLQLEGFSAESRKLLLIVQAL
RDNLEPGTFDLGGLYEAIEECLINDPWVLLNASWFNSFLTHALR
>2XMEA 232 XRAY 1.89 0.208 0.237 no CTP-INOSITOL-1-PHOSPHATE CYTIDYLYLTRANSFERASE <UNP
029976_ARCFU> [ARCHAEOGLOBUS FULGIDUS]
MINVDGEYLIKIFAGRIKLMKAVILAAGLTRLGGVPKPLVRVGGCEIILRTMKLLSPHVS
EFIIVASRYADDIDAFLKDKGFNYKIVRHRPEKNGYSLLVAKNHVEDRFILTMGDHVV
SQQFIEKAVRGEVGIADREPRFVDIGEATKIRVEDGRVAKIGKDLREFDCVDTGFFVLDD
SIFEHAEKLRDREEIPLSEIVKLARLPVTVYVDGELWMDVDTKEDVRRANRAL
>2XTSA 390 XRAY 1.33 0.107 0.111 no SULFITE DEHYDROGENASE <UNP P72178_PARDE> [PARACOCUS
PANTOTROPHUS]
AGTPDLITEIQPWASEFGEAVDAHPYGLPIHFESHVKRQYVEWLTESPVSSINFTPIHA
LEGTITPQGCAFERHHSGAIELSKQDYRLMINGLVEKPLVFTFEDLLRFPRTTTTAFCEC
AANGMEWGGAQLEGCQYTQGMIHNM EYVGVPLSVLLAEAGVKPEGKWLVAEGADASSNG
RSFPMKVMDDVMLAFFANGEALRKEHGYPARLVVPGWEGNMVWKVRRLLGIYDKAVESR
EETSKYTDLMPDGRARKWTWVMDAKSVITSPSPQVPIRHGKGPLVISGLAWSNGRITRV
DVSLDGKNWTTARITGQALPKALTRFHLDDWDGSEMLLQSRVDETGYVQPTKDALRA
IRGRNNVYHNGIQTWVWKADGEVENVEIA
>3FS3A 359 XRAY 2.30 0.218 0.285 no Nucleosome assembly protein 1, putative <UNP
Q8I608_PLAF7> [PLASMODIUM FALCIPARUM]
MAANEGNQPIPEEEKEISSLLESIKIGKTSKYRCFYLYDDKMTDLTEEQKETLKKLKL
YQKEYDYESKFEYELFLLRQKYHDLYGPIYDKRREALVGNGEAKIGTPNLPEFWLRALR
NNNTVSHVIEDHDEEILVYLNDRCDYIKKNKEKKEGFILSFYFATNPFFSNSVLTKTYH
MKCVDCDNEPVLLHTEATVIDWYDNKNILKKNVKKQHKNKSREVKTQQTVNRDSFFHF
FTSHKVPNSNVIKQLSKHEVAQLEMIIEGDYEVALTIKERIIPYAVDYLYGIIIESESNS
IVSDVDSSYSSSENNSYNSYESNNSAYNDENSNDTNEYDDNEEEEGAKSNEDPLTS
>1EKQA 272 XRAY 1.50 0.216 0.251 no HYDROXYETHYLTHIAZOLE KINASE <UNP THIM_BACSU> [BACILLUS
SUBTILIS]
MDAQSAKCLTAVRRHSPLVHSITNNVTNFTANGLLALGASPMAYAKEEVADMAKIAG
ALVLNIGTSLKESVEAMIIAGKSANEHGVPIILDPVGAGATPFRTESARDIIREVRLAAI
RGNAEIAHTVGVDWLIGVDAGEGGGDIIRLAQQAQKLNVTIAITGEVDVIADTSHV
YTLHNGHKLLTKVTGAGCLLTSVVGAFCAVEENPLFAAIAAIISSYGVAQAQQAQTADKG
PGSFQIELLNKLSVTTEQDVQEWATIERVTVS
>4KM6A 208 XRAY 1.55 0.171 0.200 no Folate receptor alpha <UNP FOLR1_HUMAN> [HOMO SAPIENS]

GSSRTELLNVMNAKHHKEKPGPEDKLHEQCRPWKNACCSTNTSQEAHKDVSYLRYFNW
NHCGEMAPACKRHF IQDTCLYECSPNLGPWIIQQVDQSWRKERVNLVPLCKEDCEQWWEDC
RTSYTCKSNWHKGWNWTSGFNKCAVGAACQPFHFYFPTPTVLCNEIWTHSYKVSNSYRGS
GRCIQMWFDPAQGNPNEEVARFYAAAMS

>2ASTB 336 XRAY 2.30 0.203 0.221 no S-phase kinase-associated protein 2 <UNP SKP2_HUMAN> [HOMO SAPIENS]

RENFPGVSWDSLPELLLGIFSCCLPELLKVSQVCKRWYRLASDESLWQTLDTGKNLH
PDVTGRLLSQGVIAFRCPFSFMDQPLAEHFSPPRVQHMDLSNSVIEVSTLHGILSQCSKL
QNLGLEGLRLSDPIVNTLAKNSNLVRLNLSGCSGFSEFALQTLSSCSRLDELNLSWCFD
FTEKHVQVAHAVHSETITQLNLSGYRKNLQKSDLSTLVRRCPNLVHLDLSDSVMLKNDKF
QEFFFQLNYLQHLSSRCYDIIPETLLELGEIPTLKTQVFGIVPDGTLQLLKEALPHLQI
NCSHFTTIARPTIGNKKNQEIWGIKCRLTQKPSCL

>3JU2A 284 XRAY 1.80 0.201 0.246 no uncharacterized protein Smc04130 <UNP Q92T58_RHIME> [SINORHIZOBIUM MELILOTI]

MSLQVEGLSINLATIREQCGFAEAVDICKHGITAIPWRDQVAAIGLGEAGRIVRANGL
KLTGLCRGGFFPAPDASGREKAIDNNRAVDEAAELGADCLVLVAGGLPGGSKNIDAARR
MVVEGIAAVLPHARAAGVPLAIEPLHPMYAADRACVNTLGQALDICETLPGVGVAIDVY
HVWWDPLANQIARAGKMKAILAHHICDWLVPTKMDLTDRGMMGDGVIDLKGIRRRIEAA
GFHGAQEVEIFSADNWWKRPADVIATCVERYRNCCEGHHHHHH

>3AXGA 355 XRAY 2.00 0.211 0.240 no Endotype 6-aminohexanoate-oligomer hydrolase <UNP Q1EPR5_9MICO> [AGROMYCES]

MNTTPVHALTDIDGGIAVDAPRLAGPPVFGGPGNDAFDLAPVRSTGREMLRFDFFPGVSI
GAAHYEEGPTGATVIHIPAGARTAVDARGGAVGLSGGYDFNHAICLAGGASYGLEAGAGV
SGALLERLEYRTGFAEALVSSAVIYDFSARSTAVYPDKALGRAALEFAVPGFEFPQGRAG
AGMSASAGKVDWDRTEITGQGAFFRRLGDVRILAVVVPNPVGVIMDRAGTVVRGNDAQT
GVRRHVPFDYQEAFAEQVPPVTEAGNTTISAIVTNVRMSPVELNQFAKQVHSSMHRGIQP
FHTDMDGDTLFAVTTDEIDLPTPGSSRGRLSVNATALGAIASEVMWDAVLEAGK

>2I6TA 303 XRAY 2.10 0.183 0.230 no UBIQUITIN-CONJUGATING ENZYME E2-LIKE ISOFORM A <UNP Q6P2F0_HUMAN> [HOMO SAPIENS]

GSSKSWANHENTVNKITVVGGLGIACTLAISAKGIADRLVLLDLSEGTKGATMDLEI
FNLNPVEISKDLSASAHSKVIFTVNSLGSSQSYLDVVQSNVDMFRALVPALGHYSQHSV
LLVASQPVEIMTYVTWKLSTFPANRVIGICNLDSQRLQYIITNVLKAQTSKGKEVWIGE
QGEDKVLTWSGQEEVVSHTSQVQLSNRAMELLRVKGQRSWSVGLSVADMVDSIVNNKKKV
HSVSALAKGYDINSEVFLSLPCILGTNGVSEVIKTTLKEDTVTEKLQSSASSIHSLLQQQ
LKL

>4LHPA 136 XRAY 2.02 0.196 0.241 no FG41 Malonate Semialdehyde Decarboxylase <UNP F2Z288_9CORY>

[CORYNEFORM BACTERIUM]

PLIRIDLTSDRSREQRRAIADAVHDALVEVLAIPARDRFQILTAHDPDSIIAEDAGLGFQ
RSPSVVIIHVFTQAGRTIETKQRVFAAITESLAPIGVAGSDVFIAITENAPHDWSFGFGS
AQYVTGELAIPATGAA

>3Q40A 196 XRAY 1.34 0.189 0.228 no Uncharacterized protein MJ0754 <UNP Y754_METJA> [METHANOCALDOCOCUS JANNASCHII]

MGSSHHHHHSSGLVPRGSHMQPISEEEKEGLIEMREEKLARDVYLTLYNKWKLQIFKN
IAESEQTHMDAVKYLLEKYNIPDPVKNDISGVFSNPKFEELYKKLVEKGDKSEVDALKVG
ATIEDLDIADLEKWINKTDNEDIKFVYENLMKGSRNHMAFVRMLNNYGSNYTPQYISKE
EYEEIISSTERGMNR

>3CNVA 162 XRAY 2.00 0.167 0.217 no Putative GntR-family transcriptional regulator <UNP Q7WD95_BORBR> [BORDETELLA BRONCHISEPTICA RB50]

VRYRFLRLAPDEEGEGGRAESRILECRRLRAPAEIARALELRAGETVVTIRRQLSMNHMP
TVIDDLWLPGTHFRGLTLELLTASKAPLYGLFESEFGVSMVRADEKLRAVAASPEIAPLL
GVEPGRPLLQVDRISYTYGDRPMEVRRGLYLT DHYHYRNSLN

>4M5DA 1237 XRAY 1.97 0.210 0.238 no U3 small nucleolar RNA-associated protein 22 <UNP
UTP22_YEAST>

[SACCHAROMYCES CEREVISIAE]

MATSVKRKASETSDQNIIVKVQKKHSTQDSTTDNGSKENDHSSQAINERTVPEQENDES
SPESNEVATNTAATRHNGKVTATESYDIHIARETAE LFKSNIFKLQIDELLEQVKLKQKH
VLKVEKFLHKLIDILQEIPDWEESLAEVDSFFKNKIVSVPFVDPKPIQNTNYKFNYKK
PDISLIGSFALKAGIYQPNGSSIDTLLTMPKELFEKKDFLNFRCLHKRSVYLAYLTHLL
ILLKKDKLDSFLQLEYSYFDNDPLLPILRISCSKPTGDSLSDYNFYKTRFSINLLIGFPY
KVFEPPKLLPNRNCIRIAQESKEQSLPATPLYNFVLSSTHENYLYKYTKKQTESFV
EATVLGRLWLQQRGFSSNMHSGSLGGFGTFEFTILMAALLNGGGINSNKILLHGFSSYQ
LFGKVIKYLATMDLCHDGHQLQFHSNPENSSSPASKYIDEGFQTPTLFDKSTKVNILTKM
TVSSYQILKEYAGETLRMLNNVVQDQFSNIFLTNISRFNLYDLCYDVQLPLGKYNNLE
TSLAATFGSMERVKFITLENFLAHKITNVARYALGDRIKYIQIEMVGGKSDFPITKRKVY
SNTGGNHFNDFVRVKLIVNPSECDKLVTGPAHSETMSTAAVFNFWGKSSLRRFKD
GSITHCCVWSTSSSEPIISSIVNFALQKHVSCKAQISNETIKKFHNFLPLPNLPSSAKTS
VLNLSFFNLKKSFDLYKII FQMKLPLSVKSILPVGSAFRYTS LCQVPVFAYS DPDFQ
DVILEFETSPKWPDEITSLEKAKTAFLLKIQEELSANSSTYRSFFSRDESIPYNLEIVTL
NLTPEGYGFKFRVLTERDEILYLRAIANARNELKPELEATFLKFTAKYLASVRHRTLE
NISHSYQFYSPVRLFKRWLDTHLLGHITDELAELIAIKPFVDPAPYFIPGSENGFLK
VLKFISQWNWKDDPLILDVLPEDDIRDTFETSIGAGSELD SKTMKLSERLTLAQYKGI
QMNFTNLNSDPNGTHLQFFVASKNDPSGILYSSGIPLPIATRLTALAKVAVNLLQTHGL
NQQTINLLFTPGLKDYDFVVDLRTPIGLKSSCGILSATEFKNITNDQAPSNFPENLNDLS
EKMDPTYQLVKYLNLYKYNLSILSSRYIGVNGGEKGDKNVITGLIKPLFKGAHKFRVNL
DCNVKPVDDENVILNKEAIFHEIAAFGNDMVINFETD

>3KGWA 393 XRAY 1.65 0.171 0.198 no Alanine-glyoxylate aminotransferase <UNP Q8R128_MOUSE>

[MUS MUSCULUS]

GMGSYQLLVPPPEALSKPLSVPTRLLLGPGPSNLAPRVLAAGSLRMIGHMQKEMLQIMEE
IKQGIQYVFQTRNPLTLVSGSGHCAMETALFNLEPGDSFLTGTNGIWMRAAEIADRI
GARVHQMIKKPGEHYTLQEEVEGLAQHKPVLLFLVHGESSGTVVQPLDGFGECHRYQCL
LLVDSVASLGGVPIYMDQQGIDIMYSSSQKVLNAPPGISLISFNDKAKYKVYSRKTTPVS
FYTDITYLAKLWGCEGETRVIHHTTPVTSLYCLRESLALIAEQGLENCWRRHREATAHLH
KHLQEMGLKFFVKDPEIRLPTITTTVTPAGYNWRDIVSYVLDHFSIEISGGLGPTTEERVL
RIGLLGYNATTENVDRVAEALREALQHCPKNKL

>1MNA 340 XRAY 1.40 0.195 0.206 no NDT80 protein <UNP NDT80_YEAST> [SACCHAROMYCES
CEREVISIAE]

MNEMENTVPVLQDDLVSKEYERELSTEQEEDTPVILTQLNEDGTTSNYFDKRKLKIAPRST
LQFKVGPPFELVRDYCPVVESHTGRTLDLRIIPRIDRGFDHIDEWVGKRYFTLVSTF
ETANCDLDTFLKSSFLLVEDSSVEGRLRVQYFAIKIKAKNDDDDTEINLVQHTAKRDKG
PQFCPSVCPLVPSPLPKHQTIREASNVNRNITKMKKYDSTFYLRHDHVNYEYGVDSLLFS
YPEDSIQKVARYERVQFASSISVKKPSQQNKHFSLVHILGAVVDPDTFHGENPGIPYDEL
ALKNGSKGMFVYLQEMKTPPLIIRGRSPSNYASSQRITVR

>3JQOA 227 XRAY 2.60 0.229 0.259 no TraF protein <UNP Q46705_ECOLX> [ESCHERICHIA COLI]

SNSPGAQPDNETSEGSSALAKNLTPARLKASRAGVMANPSLTPVPGKMIPCGTGTELDT
TVPGQVSCRVSQDVYSADGLVRLIDKGSWVDGQITGGIKDGQARVFLWERIRNDQDGTI
VNIDSAGTNSLGSAGIPGQVDAHMERLRGAIMISLFSDTLTALVNQTQSNNIQYNSTEN

SGGQLASEALRSYMSIPPTLYDQQGDAVSIFVARDLDFSGVYTLADN

>2YX0A 342 XRAY 2.21 0.194 0.242 no radical sam enzyme <UNP 059412_PYRHO> [PYROCOCCUS HORIKOSHII]

MMEMITIKPGKITVQANPNMPKEVAELFRKQHYEIVGRHSGVKLCHWLKSLTEGRFCYK
QKFYGIHSHRCLQMTPLVLAWCTHNCIFCWRPMENFLGTLPQPWDDPAFIVEESIKAQRK
LLIGYKGNPKVDKKKFEEAWNPTAAISLSGEPMLYPYMGDLVEEFHKRGFTTFIVTNGT
IPERLEEMIKEDKLPTQLYVSITAPDIETYNVSNIPMIPDGWERILRFLELMRDLPTRTV
VRLTLVKGENMHSPEKYAKLILKARPMFVEAKAYMFVGYSRNLRTINNMPSHQDIREFAE
ALVKHLPGYHIEDEYEPSRVVLI MRDDVDPQGTGVEGRFIKH

>2WXFA 940 XRAY 1.90 0.211 0.240 no PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE 3-KINASE CATALYTIC SUBUNIT DELTA ISOFORM <UNP Q3UDT3_MOUSE> [MUS MUSCULUS]

GGDRVKKLINSQISLLIGKGLHEFDSL RDPEVNDFR TKMRQFCEEAAHRQQLGWVWEWLQ
YSFPLQLEPSARGWRAGLLRVSNRALLVNVKFEGSEESFTFQVSTKDMPLALMACALRKK
ATVFRQPLVEQPEEYALQVNGRHEYLYGNYPLCHFQYICSLHSGLTPHLMVHSSSILA
MRDEQSNPAPQVQKPRAKPPP IPAKKPSSVSLWSLEQPF SIELIEGRKVNADERMKLVVQ
AGLFHGNEMLCKTVSSSEVNVCEPVWKQRLEFDISVCDLPRMARLCFALYAVVEKAKKA
RSTKKKSKKADCP IAWANLMLFDYKDLKTGERCLYMWPSVPDEK GELLNPA GTVRGNPN
TESAAALVIYLPEVAPHPVYFPALEKILELGRHGERGRITEEQQLQREILERRGSGELY
EHEKDLVWKM RHEVQEHFPEALARLLLVTKNKHEDVAQMLYLLCSWPPELPVLSALELLD
FSFPDCYVGSFAIKSLRKLTDDEL FQYLLQLVQVLKYESYLDCELTKFLLGRALANRKIG
HFLFWHLRSEMHVPSVALRFG LIMEAYCRGSTHHMKVLMKQGEALSKLKALNDFVKVSSQ
KTTKPQTKE MMHMC MRQETYMEALSHLQSPLDPSTLLEEVCVEQCTFMDSKMKPLWIMYS
SEEAGSAGNVGII FKN GDDL RQDMLTLQMIQLMDVLWKQEGDLRMT PYGCLPTGDRTGL
IEVVLHSDTIANIQLNKS NMAATAAFNKDALLNLWLSKNPGEALDRAIEEFTLSCAGYCV
ATYVLGIGDRHSDNIMIRESGQLFHIDFGHFLGNFKTKFGINRERVPFILTYDFVHVIQQ
GKTNNSEKFERFRGYCERAYTILRRHGLLFLHLFALMRAAGLPELSCSKDIQYLKDSLAL
GKTEEEALKHFRVKFNEALRESWKT KVNWLAHNVSKDNRQ

>2A2MA 258 XRAY 1.88 0.143 0.165 no hypothetical protein BT3146 <UNP Q8A309_BACTN> [BACTEROIDES THETA IOTAOMICRON]

MGSDKIH HHHHHMND FKNQWLKRRTFAIPASRLTGRLTTLKSDVPAADSLFWKLWNGSLD
TAVQVLQTDYFKGIAAGTLDPNAYGSLMVQDGY YCFRGRDDYATAATCAQDET LREFFKA
KAKSYDEYNETYHQTWHLREASGLIPGTDIKDYADYEAYVAGSLASPYMCVVM LPCEYLW
PWIANFLDGYTPTNSLYRFWIEWNGGTPNGAYQMGNMLEQYRDKIDEDKAVEIFNTAMNY
ELKVFTSSTILTTIENGK

>3IAXB 115 XRAY 2.60 0.193 0.257 no Colicin-A <UNP CEA_CITFR> [CITROBACTER FREUNDII]

MPGFNYGGKGDGTWSSERGS GPEPGGGSHGNSGGHDRGDSSNVGNESVTVMKPGDSYNT
PWGKVIINAAGQPTMNGTVM TADNSSMVPYGRGFTRVLNSLVNPNVSL EHHHHHHH

>3N7CA 130 XRAY 2.26 0.236 0.293 no ABR034Wp <UNP Q75DJ0_ASHGO> [ASHBYA GOSSYP II]

MSLTNGEENEEVL FCEKAKLLIFDS TKGYTSRGV GELKLLRKKDDKGKVRVLCRSEGMG
HVLLNTSVVKSFKYQPIDADNENLIKWPIITDGKLETFI IKVKQKADGRRLVGAVADAQQ
AMEGHHHHHH

>1D2TA 231 XRAY 1.90 0.219 0.257 no ACID PHOSPHATASE <UNP Q9S1A6_ESCBL> [ESCHERICHIA BLATTAE]

LALVATGNDTTTKPDLYY LKNS EAINSLALLPPPPAVGSIAFLNDQAMYEQGRLLRNTER
GKLAEDANLSSGGVANAFSGAFGSPITEKDAPALHKLLTNMIEDAGDLATRS AKDHMYR
IRPFAFYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATALVLA EINPQRQNEILKRGYELG
QSRVICGYHWQSDVDAARVVGSAVVATLHTNPAFQQQLQKAKAEFAQHQQK

>3VHXB 120 XRAY 2.81 0.262 0.232 no Kinesin-like protein KIF23 <UNP KIF23_HUMAN> [HOMO

SAPIENS]
 GSLLFQPDQNPPIRLRHRRSRASGDRWVDHKPASNMQTETVMQPHVPHAITVSVANEKA
 LAKCEKYM LTHQELASDGEIETKLIKGDYKTRGGGQSVQFTDIETLKQESPNGSRKRRS
 >1FITA 147 XRAY 1.85 0.202 0.225 no FRAGILE HISTIDINE PROTEIN <UNP FHIT_HUMAN> [HOMO SAPIENS]
 MSFRFGQH LKPSVFLKTELSFALVNRKPVVPGHVLVCLRPVERFHDLRPDEVADLFQ
 TTQRVGTVVEKH FHGTS LTFSMQDGPEAGQTVKHVHVHLPRKAGDFHRNDSIYEELQKH
 DKEDFPASWRSEEEMAAEAAALRVYFQ
 >3DXLA 303 XRAY 1.30 0.189 0.214 no Allergen Aed a 2 <UNP D7_AEDAE> [AEDES AEGYPTI]
 MGPFDPPEMLFIFTRCMEDNLEDGANRLPMLAKWKEWINEPVDSPATQCFGKCVLVRTGL
 YDPVAQKFDASVIEQFQKAYPSLGEKSKVEAYANAVKQLPSTNNDCAAVFKAYDPVHKAH
 KDTSKNFLFHGNKELTKGLYEKLGKDIRQKKQSYFEFCENKYYPAGSDKRQQLCQIRQYTV
 LDDALFKEHTDCVMKGI RYITKDNQLDVEEVKRD FKL VNKDTKALEEVLNDCKSKEPSNA
 KEKSWHYKCLVESSVKDDFKEAFDYREVRSQIYAFNLPKNQAYS KPAVQSQVMEIDGKQ
 CPQ
 >1F1MA 164 XRAY 1.80 0.201 0.235 no OUTER SURFACE PROTEIN C <UNP Q9AGB1_BORBU> [BORRELIA
 BURG DORFERI]
 KGNL TEISKKITESNAVLAVKEVETLLTSIDELAKAIGKKIKSDVSLDNEADHNGSLM
 SGAYLISTLITKKISAIDSGELKAEIEKAKKCSEEF TAKLGEHTDLGKEGVTDDNAKK
 AILKTNDKTKGADELEKLFESVKNLSKAAKEMLTNSVKELTSP
 >2P6VA 114 XRAY 2.00 0.214 0.248 no Transcription initiation factor TFIID subunit 4 <UNP
 TAF4_HUMAN> [HOMO SAPIENS]
 TVPGATTSSAATETMENVKKCKNFLSTLIK LASSGKQSTETAANVKELVQNLLDGKIEA
 EDFTSRLYRELNSSPQPYLVPFLKRSLPALRQLTPD SAAFIQQSQQQPPPTSQ
 >2F6MA 65 XRAY 2.10 0.242 0.261 no Suppressor protein STP22 of temperature-sensitive
 alpha-factor receptor and arginine permease <UNP STP22_YEAST> [SACCHAROMYCES CEREVISIAE]
 MTDGLNQLYNLVAQDYALTD TIEALSRLHRGTIPLDTFVKQGRELARQQFLVRWHIQRI
 TSPLS
 >4EI7A 389 XRAY 1.90 0.185 0.237 no Plasmid replication protein RepX <UNP REPX_BACC1>
 [BACILLUS
 CEREUS]
 MAGNFSEIESQGNISLKFGLGLGMGGCAIAAECANKETQIKNNKYPYRAILVNTNSQDF
 NKIEIKNTGNVRKIQLEGYEQGAARNPQVGEEAFVKHETKIFEAVKQEFEDRDFIWITCG
 LGGGTGTGALLKAIEMLYEH DYNFGLLLTLPRDAEALKVLENATSRIRSIAMNQEAFGSI
 VLIDNAKLYRKFEENPSALANEYTSYSNKYIADALHEINLVTSSFTPFSDTHFDASEFA
 QVINTPGVLSLAKLELKS NQLDTENPLGYLTQLGNALEKGVLYDTEREELESAKKSALSI
 VTSPLRAGRLYNFSFLNQMENFLKERTPYVDERPIAPYVNKHTTKKEEDIVKFYSVVAGL
 PLPKRVSDIIDEITRIKEEREQANSKKSN
 >3T30A 562 XRAY 2.50 0.230 0.285 no Metal dependent hydrolase <UNP Q72JJ7_THET2> [THERMUS
 THERMOPHILUS HB27]
 MSHHHHHSSQGGPQDHVEIIP LGGMGEIGKNITVFRFRDEIFVLDGGLAFPEEGMPGVD
 LLIPRV DYLIEHRHKIAWVLTHGAEDHIGGLPFLLP MIFGKESVPYIYGARLTGLLRG
 KLEEFGLRPGAFNLKEISPDDR IQVGRYFTLDLFRMTHSIPDNSGVVIRTPIGTIVHTGD
 FKLDPTPIDGKVSHLAKVAQAGAEVLLLIADATNAERPGYTPSEMEIAKELDRVIGRAP
 GRVFVTTFASHIHR IQSVIWA AEKYGRKVAMEGRSMLKFSRIALELGYLKVKDRLY TLEE
 VKDLPDHQV LILATGSQGQPM SVLHRLAFEGHAKMAIKPGD TVILSSSIPGN EEA VNRV
 INRLYALGAYVLYPPTYKVHASGHASQEELKLILNLTPRFFLPWHGEVRHQMNFKWLAE
 SMSRPPEKTLIGENGAVYRLTRET FEKVGEVPHGVLYVDGLGVGDITEEILADRRHMAEE
 GLVVITALAGEDPVVEVVS RGFVKAGERLLGEVRRMALEALKNGVREKKPLERIRDDIYY

PVKKFLKKATGRDPMILPVVIE

>2HBJA 410 XRAY 2.10 0.239 0.292 no Exosome complex exonuclease RRP6 <UNP RRP6_YEAST>
[SACCHAROMYCES CEREVISIAE] GMVEKPQLKFKSPIDNSESHPFIPLLKEKPNALKPLSESLRLVDDDENNP SHYPHPYEYE
IDHQEYSPEILQIREEIIPSKSWDDSVPIWVDSTELESMLEDLKNTKEIAVDLEHHDYRS
YYGIVCLMQISTRERDYLVDTLKLRENHILNEVFTNPSIVKVFHGAFMDIIWLQRDLGL
YVVGFLFDYHASKAIGLPRHSLAYLLENFANFKTSKKYQLADWRIRPLSKPMTAAARADT
HFLLNIVDQLRNKLIESNKLAGVLYESRNVAKRRFEYSKYRPLTPSSEVYSPIEKESPWK
ILMYQYNIPPEREVLVRELYQWRDLIARRDDESPRFVMPNQLLAALVAYTPTDVIGVVSL
TNGVTEHVRQNAKLLANLIRDALRNKNTNEEATPIPSSETKADGILLET

>1PBJA 125 XRAY 1.40 0.192 0.202 no hypothetical protein <UNP 027659_METTH>
[METHANOTHERMOBACTER THERMAUTOTROPHICUS STR. DELTA H]
MRVEDVMVTDVDTIDITASLEDVLRNYVENAKGSSVVVKEGVRVGIVTTWDVLEAIAEGD
DLAEVKVWEVMERDLVTISPRATIKEAAEKMVKNVWRLLEEDDEIIGVISATDILRAK
MAKRY

>2ERVA 150 XRAY 2.00 0.200 0.233 no hypothetical protein Paer03002360 <UNP Q9HVD1_PSEAE>
[PSEUDOMONAS AERUGINOSA]
ADVSAAVGATGQSGMTYRLGLSWDWDKSWWQTSTGRLTGYWDAGYTYWEGGDEGAGKHS
SFAPVFVYEFAGDSIKPFI EAGIGVAAFSGTRVGDQNLGSSLNFEDRIGAGLK FANGQSV
GVRAIHYSNAGLKQPN DGIESYSLFYKIPI

>1GZSB 165 XRAY 2.30 0.226 0.255 no SOPE <PDB 1GZS> [SALMONELLA TYPHIMURIUM]
GSLTNKVVKDFMLQTLNDIDIRGSASKDPAYASQTREAILS AVYSKNKDQCCNLLISKGI
NIAPFLQEIGEA AKNAGLP GTTKNDVFTSPGAGANPFITPLISSANSKYPRMF INQHQQA
SFKIYAEKIIMTEVAPLFNECAMP TPQQFQLILENIANKYIQNTP

>1LMIA 131 XRAY 1.50 0.198 0.252 no Immunogenic protein MPT63/MPB63 <UNP MP63_MYCTU>
[MYCOBACTERIUM TUBERCULOSIS]
SAYPITGKLGSELTMTDTVGQVVLGWKVS DLKSSTAVIPGYPVAGQVWEATATVN AIRGS
VTPAVSQFNARTADGINYRVLWQAAGPDTISGATIPQGEQSTGKIYFDVTGPSPTIVAMN
NGMEDLLIWEP

>1C8UA 285 XRAY 1.90 0.230 0.248 no ACYL-COA THIOESTERASE II <UNP TESB_ECOLI> [ESCHERICHIA
COLI] SQALKNLLTLLNLEKIEEGLFRGQSEDLGLRQVFGGQVVGQALYAAKETVPEERLVHSFH
SYFLRPGDSKKPIIYDVETLRDGN SFSARRVAAIQNGKPIFYMTASFQAPEAGFEHQKTM
PSAPAPDGLPSETQIAQSLAHL LPPVLKDKFICDRPLEVRPVEFHNPLKGHVAEPHRQVW
IRANGSV PDDL RVHQYLLGYASDLNFLPVALQPHGIGFLEPGIQIATIDHSMW FHRPFNL
NEWLLYSVESTSASSARGFVRGEFYTQDGV LVASTVQEGVMRNHN

>3VS8A 410 XRAY 1.76 0.185 0.230 no Type III polyketide synthase <PDB 3VS8> [AZOTOBACTER
VINELANDII] HMNDMAHPNSAVLADFI PVQLAKPVPQRITL ELTAYGFARAHCLSNGITDEEGFVQVYKT
VKEKFDKYAVSPAQIKRQLVYFPKLTDIRFGDGNFDIADPEPDQAHLRLFDIKKDP RGA
DLKTRHESYAKVVGKGLEQMFEGTLEAPDDL IHVTCGYLAPSPAERMVADRGWFETT VT
HSYNGMCGYGAFFPAIKMAHGMLASAQWGATPPKTRVDIAHTELM SAHN NIAESRVDNIISA
TLFSDGLIKYSVPEDELRRQGLRGLRILAMSEHLLPDSADTMTGVPGSHQFVMTLSPLV
PAIIKRHVRAFAVDLLRRAGMDFERDKDALSFAIHPGGPKIVDHVQEELGLAEDQVAISK
SVFLENGNMSSSTIPHILKAYLEEATVGTRIA CLGFGPGLTAAAGLVLEKI

>1ZOWA 207 XRAY 1.20 0.137 0.181 no Putative protease La homolog type <UNP
LONH_ARCFU> [ARCHAEoglobus FULGIDUS]
DYKLFITEGYEVRVNGLAVIGESAGIVLP IIAEVTPSMSKSEGRVIATGRLQE IAREAV
MNVSAIIKKYTGRDISNMDVHIQFVGTYEGVEGDSASIS IATAVISAIEGIPVDQSVAMT
GSLSVKGEVLPVGGVTQKIEAAIQAGLKKV IIPKDNIDDVLLDAEHEGKIEVIPVSRINE
VLEHVLEDGKKKNRLMSKFKELELA AV

>3VODA 339 XRAY 1.10 0.141 0.161 no Voltage-sensor containing phosphatase <UNP Q4W8A1_CIOIN> [CIONA INTESTINALIS]
 GHMKASSRRTISQNKRRYRKDGFDLDTYVTDHVIAMSFSSGRQSLFRNPIGEVSRRFFK
 TKHPDKFRIYNLCSERGYDETKFDNHVYRVMIDHDNVPTLVDLLKFIDDAKVWMTSDPDH
 VIAIHSKGGKGRGTGLVSSWLLDGKFDTAKEALEYFGSRRTDFEVDGVFQGVETASQIR
 YVGYFEKIKKNYGGQLPPMKLKVTVGTITAIQGVGRNGSDLSMQIVSERQEVLLCKFA
 EGYNCALQYDATDDCVTCEVKNCPLAGDIKVRFMSTSKSLPRGYDNCPPYFWNTSLVE
 GDHVTLKREEIDNPHKKKTWKIYRDNFTVKLTFSDAEDI

>2E3HA 90 XRAY 1.45 0.193 0.215 no Restin <UNP REST_HUMAN> [HOMO SAPIENS]
 ELKIGDRVLVGKTKAGVVRFLGETDFAKGEWCGVELDEPLGKNDGAVAGTRYFQCQPKYG
 LFAPVHKVTKIGFPSTTPAKAKANAVRRVM

>2EWCA 126 XRAY 2.15 0.164 0.204 no conserved hypothetical protein <UNP Q99XS4_STRP1> [STREPTOCOCCUS PYOGENES]
 MKTIRRYDVNEDRGHTGLVEAGDFYYLNYCVGNVGGQDIESQINGAFDEMERRLALVGLTL
 DAVVQMDCLFRDVWNIPVMEKMIKERFNGRYPARKSIQTEFAHHGGPQGLLFQVDGVAYS
 KHISMT

>3OCJA 305 XRAY 1.39 0.189 0.211 no Putative exported protein <UNP Q7WBE0_BORPA> [BORDETELLA PARAPERTUSSIS]
 SNAMSPSPLISHRAASADLAGMVRQARQRILLQGNVPGFDVARQIELLHGLAESELGRFL
 LLYRGLNAEWTHRLVTHQPGSGALAPLERVFYERLPAVLATRERHGHFRRALQRHLRPGC
 VVASVPCGWMSELLALDYSACPGVQLVGIDYDPEALDGATRLAAGHALAGQITLHRQDAW
 KLDTRREGYDLLTSNGLNIYEPDDARVTELYRRFWQALKPGGALVTSFLTTPPALSPDSPW
 DMQAIDPHDLQLQLVFTRLIQPRWNALRTHAQTRAQLEEAGFTDLRFEDDRARLFPTVI
 ARKPA

>3FXDB 73 XRAY 2.10 0.210 0.250 no Protein IcmR <UNP Q5ZYC9_LEGPH> [LEGIONELLA PNEUMOPHILA SUBSP. PNEUMOPHILA STR. PHILADELPHIA 1]
 EIGEPDVTATLGSVYSEIISPVKDCILTVAKAVSFNPGGKDNTDAVEVLTELNTKVERA
 ALNQPIILTTKTER

>3DXRA 89 XRAY 2.50 0.247 0.275 no Mitochondrial import inner membrane translocase subunit TIM9 <UNP TIM9_YEAST> [SACCHAROMYCES CEREVISIAE]
 GSMDALNSKEQQEFQKVVEQKQMKDFMRLYSNLVERCFTDCVNDFTTSKLTNKEQTCIMK
 CSEKFLKHSERVGQRFQEQAALGQGLGR

>2HHCA 330 XRAY 1.54 0.183 0.197 no Nodulation fucosyltransferase NodZ <UNP Q9AQ17_BRASW> [BRADYRHIZOBIUM SP.]
 MTKERFVISRRRTGFGDCLWSLASAWSYAQRTGRTLVIDWRGSCYVEQPFSNAFFAFFEP
 VEDIAGVPVICDDRNVQLSFGPPFFPRWWNRPSIDCINRPDEQIFRERDELTELFQARED
 SEANTIVCDACLMWRCSEEAERLIFRNILRSEIRARIDALYEEHFSGHSIIGVHVRHGN
 GEDIMEHAPYWADSELALHQVCMAIRKAKALSYKPKVKVFLCTDSAQVLDQVSGLFPDVF
 AVPKRFQADRAGPLHSAEMGIEGGASALIDMYLLARCATVIRFPPTSFAFTRYARLLVPRI
 IEFDLNPNGLTMDNPNYEHFAASHHHHHH

>3V46A 170 XRAY 1.55 0.174 0.210 no Cell division control protein 73 <UNP CDC73_YEAST> [SACCHAROMYCES CEREVISIAE]
 GIDPFTSSGGPRKDPIILIPSAASSILTVANIKQFLLESKYVNPRLPSVPNGLVNIEKN
 FERISRPIRFIIVDNTRMFTKPEYWDRVVAIFTTGHTWQFNQYQWNSPQELFQRCCKGYFF
 HFAGDSVPQHVQQWNEKVELDKNKRFDVEVVRYFWHSLEKELISRGYR

>3K69A 162 XRAY 1.95 0.174 0.218 no Putative transcription regulator <UNP Q88ZG1_LACPL> [LACTOBACILLUS PLANTARUM]
 GMGGSNMKLDVSVAVHSILYLDHRDSKVASRELAQSLHLNPVMIRNLSVLHKHGYLTG

TVGKNGGYQLDLALADMNLGDLYDLTIPPTISYARFITGPSKTDEQADQSPIAANISETL
TDLFTVADRQYRAYYHQFTMADLQADLNHHGTFLQHEQDSES
>1SG4A 260 XRAY 1.30 0.157 0.202 no 3,2-trans-enoyl-CoA isomerase, mitochondrial <UNP D3D2_HUMAN>
[HOMO SAPIENS]
GSQRVLVEPDAGAGVAVMKFNPPVNSLSLEFLTELVISLEKLENDKSFRGVILTSRPG
VFSAGLDLTEMCGRSPAHYAGYWKAVQELWLRLYQSNLVLVSAINGACPAGGCLVALTCD
YRILADNPRYCIGLNETQLGIIAPFWLKDLENTIGHRAAERALQLGLFPFAEALQVGI
VDQVVPVEEQVQSTALSAIAQWMAIPDHARQLTKAMMRKATASRLVTQRDADVQNFVSFIS
KDSIQKSLQMYLERLKEEG
>4IKNA 261 XRAY 1.85 0.194 0.237 no AP-3 complex subunit mu-1 <UNP AP3M1_RAT>
[RATTUS NORVEGICUS]
GAMDPEFIPWRRAGVKYTNNEAYFDVVEEIDAIIDKSGSTVFAEIQGVIDACIKLSGMPD
LSLSFMNPRLLDDVSFHPICIRFKRWESERVLSPFPDGNFRLISYRVSSQNLVAIPVYVK
HNISFKENSSCGRFDITIGPKQNMGTIEGITVTVMHPKVVLNMNLTPQTGQSYTFDPVTK
VLAWDVGKITPQKPLSLKGLVNLQSGAPKPEENPNLNIQFKIQQLAISGLKVNRLDMYGE
KYKPFKGVKIITKAGKFQVRT
>2OH1A 179 XRAY 1.46 0.170 0.193 no Acetyltransferase, GNAT family <UNP Q722P7_LISMF>
[LISTERIA MONOCYTOGENES STR. 4B]
GMNQNKITAGGLEFLVRFAAPTDRKINDLMIDTARWLKESGSTQWSDILHGFVDVHNIEQ
RIELGEVALFETEAGALAGAMIIRKTPSDWDTDLWEDLAIDKAYYLHRIMVSRAFSGISL
SKQMIYFAEKLGIEMSVPFIRLDCIESNETLNQMYVRYGFQFSGKKNGFYLYQKELSQQ
>4F43A 320 XRAY 2.35 0.239 0.290 no Protelomerase <UNP Q7CWV1_AGRT5> [AGROBACTERIUM
TUMEFACIENS]
DYPKTGVATSIVEKIERAEFNTAGRKPTVLLRIADFIAMNGMDAKQDMQALWDAEIAIM
NGRAQTIIISYITKYRNAIREAFGDDHMLKIATGDAAMYDEARRVKMEKIANKHGALIT
FENYRQVLKICEDCLKSSDPLMIGIGLIGMTGRAPYEVFTQAEFSPAPYKGVSKWSILF
NGQAKTKQEGTKFGITYEIPVLRSETVLAAYKRLRESGQGLWHGMSIDDFSSETRLL
LRDVTVFNLFEDVWPKEELPKPYGLRHLYAEVAYHNFAPPHVTKNYSYFAAILGHNNNDLET
SLSYMTYTLPEDRDNALRL
>1UYNX 308 XRAY 2.60 0.231 0.285 no NALP <UNP Q8GKS5> [NEISSERIA MENINGITIDIS]
DGVRIFNLSLAATVYADSTAAHADMQGRRRLKAVSDGLDHNGTGLRVIAQTQQDGGTWEQGG
VEGKMRGSTQTVGIAAKTGENTTAAATLGMGRSTWSENSANAKTDSISLFAIRHDAGDI
GYLKGLFSYGRYKNSISRSTGADEHAEGSVNGTLMQLGALGGVNPFAATGDLTVEGGLR
YDLLKQDAFAEKGSALGWSGNSLTEGTLVGLAGLKSQPLSDKAVLFATAGVERDLNGRD
YTVTGGFTGATAATGKTGARNMPHTRLVAGLGADVEFGNGWGLARYSYAGSKQYGNHSG
RVGVGYRF
>3MKCA 394 XRAY 1.77 0.237 0.241 no racemase <UNP B6R2Z6_9RHOB> [PSEUDOVIBRIO SP. JE062]
MSLALNPAVAPIKSIEFIPVNYQASNWSQNTVVVKVTDENGYYGLGEADGSPDAILAYAN
IETEHKWLNTITEKAIGRLPIEINAIWDAMYDATQWQGMRLGMFALSGIDMALYDLAGK
QLGVPAYQLLGGTNKDKVHPYLTLYPAIPVDASLDVAIKGYAPLLEKAKAHNIRAVKVCV
PIKADWSTKEVAYYLRELRLGHDTHMMVDYLYRFTDWYEVARLLNSIEDLELYFAEAT
LQHDDLSGHAKLVENTRSRICGAEMSTTRFEAEWITKGVHLLQSDYNRCGGLTELRI
TEMATANNVQVMPHNWKTGITSAAAIHYQFAVGNAPYFEYVHPEFCDGELRKYLVTPEAE
LVDGGFAKPTAPGLGIDLNQEFSLASLEGHHHHHH
>1GNLA 544 XRAY 1.25 0.130 0.145 no HYBRID CLUSTER PROTEIN <UNP PRIS_DESDE> [DESULFOVIBRIO
DESULFURICANS]
SNAMFCYQCQETVGNGCTQVGVCGKKPETAALQDALIYVTKGLGQIATRLRAEGKAVDH
RIDRLVTGNLFATITNANFDDDLAERVMTCAAKKELAASLTDKSGLSDAALWEASEKS

AMLAKAGTVGVMATDDDDVRSRLWLITFGLKGMAAYAKHADVLGKHENSLDAFMQEALAK
 TLDDSLSVADLVALTLETGKFGVSAMALLDAANTGTYGHPEITKVNIGVGSNPGLISGH
 DLRDLEMLLKQTEGTGVDVYTHSEMLPAHYYPAFKKYAHFKGNYNWWKQKEEFESFNG
 PVLLTTNCLVPPKDSYKDRVYTTGIVGFTGCKHIPGEIGEHKDFSIIAHAKTCPAPTEI
 ESGEIIGGFAHNQVLALADKVIDAVKSGAIKKFVVMAGCDGRAKRSRYTDFAEGLPKDT
 VILTAGCAKYRYNKLNLGDIGGIPRVLDAQCNDSSYLAVIALKLKEVFGLEDVNDLPIV
 YNIAWYEQKAVIVLLALLSLGVKNIHLGPTLPAFLSPNAKVLVEQFNIGGITSPQDDLK
 AFFG

>3QTMA 346 XRAY 2.15 0.180 0.213 no Uncharacterized protein C4B3.07 <UNP
 YJ27_SCHPO> [SCHIZOSACCHAROMYCES POMBE]

MEHHHHHTMLVYTEEDNISQLWGLYEMSREKLENDIDASVSLVFGTIHEADRILRNTE
 DISTLPKDFHAAYSSALLAVSELFEIAQKRLKETNTEESYIDAAIERAQLGLDAPGNESR
 LFLALARAYLEKVRVLVWRHDNEESLANIPVTQLVNPYIEKAIQYLRPLAQDSTEYFDAL
 TPDSLRPLYILSSYLFQFGDQFSEAFLLDVCSIIITLWLSVVDPNTPAYYKLIQAEAVL
 NNYTTFAEYYMDLLDNSESNDL INKASSWLNNSVDTWNVITYLTKSPERLLKLADIKM
 DLAQIVQDEASQDNYLKEACNAIKEAQSGVELSPDYVEFVEAYSA

>2IT2A 200 XRAY 1.50 0.250 0.265 no UPF0130 protein PH1069 <UNP Y1069_PYRHO> [PYROCOCUS
 HORIKOSHII]

MLLYMRFTENFERAKKEALMSLEIALRKGEVDEDIIPLLKINSIENYFTTSSCSGRISV
 MEMPHFGDKVNAKWLKGWHREVSLEYVLEAIKKHRSGQLWFLVRSPILHVGAKTLEDAVK
 LVNLAVSCGFKYSNIKSISNKKLIVEIRSTERMDVLLGENGEIFVGEYLNKIVEIANDQ
 MRRFKEKLKRLSKINALNR

>3F3BA 126 XRAY 2.50 0.230 0.263 no Phage-like element PBSX protein xkdH <UNP XKDH_BACSU>
 [BACILLUS SUBTILIS]

MSYRQMLIHRCDIYHEAAQPSAGRFGIPADRLQPVISYPTDPEQDVPCYFTEKTQQLI
 QEEPDTQVYHSFLVHFPLSADIRVNDKIIWENHKYILKLPKRIRHHHWEVVAVRDESLE
 HHHHHH

>3DEFA 262 XRAY 1.96 0.173 0.213 no T7I23.11 protein <UNP 023680_ARATH> [ARABIDOPSIS THALIANA]

MGLSVREWVGFPQAATQEKLIEFFGKLKQKDMNSMTVLVLGKGGVGKSSTVNSLIGEQ
 VVRVSPFQAELRPVMVSRTMGFTINI IDTPGLVEAGYVNHQALELIKGLVNRTIDVL
 LYVDRLDVYAVDELKQVIAITQTFGKEIWCKTLLVLTHAQFSPPELSYETFSSKRSD
 SLLKTI RAGSKMRKQEFEDSAIAVVYAENSGRCSKNDKDEKALPNGEAWIPNLVKAITDV
 ATNQRKAIHVDAALAEHHHHHH

>3GM8A 801 XRAY 2.40 0.229 0.287 no Glycoside hydrolase family 2, candidate beta-glycosidase
 <UNP

A6KXE5_BACV8> [BACTEROIDES VULGATUS]

SLAGETINFCKGWKFHLGDAGKGASSSYNDSQWRILNIPHDWSIEGTYKQFENGTDWQS
 GFLPAGISWYRKTFITPSKWKNKVQILFEGVYLNSEVWINGHWLGKRPNGYISFVYDLT
 PYLQEGKNQIAVKVDHASKALTGRWYTGSGIYRPVYLLVSNPHTIPYSGIHFRSKLQNKQS
 ATYTLSIEIETQEKPIKVKTYLQAPNGSIADTSEKIFVSSADSLCFLSGSIRKPLLWSP
 DSPNVYTLICQLTRDNKILDECRLPVGFRQLEFNPVSGFLLNGKSLKIKGVCDDHHTVGAV
 GAAVPDDLHLYRLKLLKDMGCNAIRTSNPFSPAFYNLCDTMGIMVLNEGLDGWNQPKAA
 DDYGNFYDEWWQKMDTDFIKRDRNHPSIMWSIGNEVTGATPEIQHNLVSLFHQLDPDRP
 VTQGGTDPTRGMTDYQKKFNYLDIIGFNGNGEEIGELEHFHKNYPTLCAIATEVPHTYQ
 TRGVYRSQTQWRRRDFPAPWEKGNNWEQFKHRVFPIDLTEKECFPEESDYPYQSSYD
 NASVRISARKSWQRTCSFPWLMGEFRWGSFDYLGEAEWPQRCGNFGIIDIAAIPKDAYFL
 YQSLWTDKPMVHLLPHWTHPGKEGKTIPVVIYTNCDAVELFINNVLGSKPYTGEQLIWL
 VPYSPGKIEARGIKKGKIVATDCYQSAEAPHSVALASNKYSVKAGSDEVIRIEIDITDKN

GIPCPYASNELSFHVSGLRLLGVDNGNPTDMFPYQQPHCRFCRGRKCVLLQSDEEKGG
TLTVQGTLVEKKLIEVIEG

>10FDA 1520 XRAY 2.00 0.194 0.231 no FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE 2 <UNP
GLTS_SYNY3> [SYNECHOCYSTIS SP.]

CGVGFIANLRGKPDHTLVEQALKALGCMHRGGCSADNDSGDGAGVMTAIPRELLAQWFN
TRNLPMPDGDRLGVGMVFLPQEPSAREVARAYVEEVVRLEKLTVLGWREVPVNSDVLGIQ
AKNNQPHIEQILVTCPEGCAGDELDRRLYIARSIIGKKLAEDFYVCSFSCRTIVYKGMVR
SIIILGEFYLDLKNPGYTSNFAVYHRRFSTNTMPKWPLAQPMRLLGHNGEINTLLGNINWM
AAREKELEVSGWTKAELEALTPIVNQANSDSYNLDSALELLVRTGRSPLEAAMILVPEAY
KNQPALKDYPEISDFHDYISGLQEPWDGPALLVFSKGKIVGAGLDRNGLRPARYCITKDD
YIVLGSEAGVVDLPEVDIVEKGR LAPGQMIAVDLAEQKILKNYQIKQQAQKYPYGEWIK
IQRQTVASDSFAEKTFLNDAQTVLQQQAAGFYTAEDVEMVVVPMASQGKEPTFCMGDDTP
LAVLSHKPRLLYDYFKQRFQVNTNPPIDPLRENLMVSLAMFLGKRGNNLEPKAESARTIK
LRSPLVNEVELQAIKTGQLQVAEVSTLYDLGVSLEDAITNLVKTAIATVQAGAEILVL
TDRPNGAILTENQSFIPLLAVGAVHHHLIRAGRLKASLIVDTAQCWSTHHFACLVGYG
ASAICPYLALESVRQWWLDEKTKQLMENGRDRIDLPALKNYRQSVEAGLFKILSKMGI
SLLASYHGAQIFEAIGLGAELVEYAFAGTTSRVGGTIADVAGEVMVFHGMAFPMAKKL
ENFGFVNYRPGGEYHNMSPMSKSLHKAVAAYKVGNGNGEAYDHYELYRQYLKDRPVT
ALRDLDFNADQPAISLEEVESVESIVKRFCTGGMSLGALSREAHETLAIAMNRLGAKSN
SGEGGEDVVRYLTLDVDSEGNSTPLPHLHGLQNGDTANSAIKQIASGRFGVTPEYLMMSG
KQLEIKMAQGAKEGGQLPGKKVSEYIAMLRRSKPGVTLSPPPHDIYSIEDLAQLIY
DLHQINPEAQVSVKLVAEIGITIAAGVAKANADI IQISGHDGGTGASPLSSIKHAGSPW
ELGVTEVHRVLMENQLRDRVLLRADGGLKTGWVMAALMGAEYGFSGSIAMIAEGCIMA
RVCHTNCPVGVATQQRERLRQRFKGVPGQVVNFFYFIAEEVRSLLAHLGYRSLDDIIGRT
DLLKVRSDVQLSKTQNLTLDCLLNLPDTKQNRQWLNHEPVHNGPVLDDDILADPDIEA
INHQTATKTYRLVNTDRVTGTRLGSAIAKKYGNGFEGNITLNFQGAAGQSFGAFNLG
MTLHLQGEANDYVVGKMGNGEIVIVPHPQASFAPEDNVIIGNTCLYGATGGNLYANGRAG
ERFAVRNSVGKAVIEGAGDHCCEYMTGGVIVVLGPVGRNVGAGMTGGLAYFLDEVGDLPE
KINPEIITLQRITASKGEEQLKSLITAHVEHTGSPKGAAILANWSDYLGKFWQAVPPSEK
DSPEANDVSLTGEKTLTSV

>1KEAA 221 XRAY 2.00 0.212 0.248 no Possible G-T mismatches repair enzyme <UNP GTMR_METTF>
[METHANOTHERMOBACTER THERMAUTOTROPHICUS]

MDDATNKKRKVFVSTILTFWNTDRRDFPWRHTRDPYVILITEILLRRTTAGHVKKIYDKF
FVKYKCFEDILKTPKSEIAKDIKEIGLSNQRAEQLKELARVVINDYGGVRPNRKAIDL
PGVGKYTCAAVMCLAFGKKAAMVDANFVRVINRYFGGSYENLNYNHKALWELATLVPGG
KCRDFNLGLMDFSAIICAPRKPKCEKCGMSKLCSEYKST

>3CU2A 237 XRAY 1.91 0.168 0.205 no Ribulose-5-phosphate 3-epimerase <UNP Q0I165_HAES1>
[HAEMOPHILUS SOMNUS]

GMSKLSLIQQLKQKLSVGILSANWLQLNEEVTTLENQINVLHFDIADGQFSSLTVGA
IGIKYFPTHCFKDVHLMVRNQLEVAKAVVANGANLVTLEQYHDFALTIEWLAKQKTTY
ANQVYPVLIGACLPETPISELEPYLDQIDVILQLLTDPRNGTKYPSELILDRVIQVEKR
LGNRRVEKLINIDGSMTELEAKYFKQGT HQIDWLVSQSALFSGELKTNLKVWKSSIM

>2YBXA 394 XRAY 2.56 0.191 0.238 no PHOSPHATIDYLINOSITOL-5-PHOSPHATE 4-KINASE TYPE-2 ALPHA
<UNP PI42A_HUMAN> [HOMO SAPIENS]

MHHHHHSSGVDLGTENLYFQSMPLLSVLMWGVNHSINELSHVQIPVMLMPDDFKAYSK
IKVDNHLFNKENMPSHFKFEYCPMVFRLRERFGIDQDFQNSLTRSAPLPNDSQARSG
ARFHTSYDKRYIIKTITSEDVAEMHNILKKYHQYIVECHGITLLPQFLGMYRLNVDGVEI
YVIVTRNVFSHRLSVYRKYDLKGSTVAREASDKEKAKELPTLKDNDFINEGQKIYIDNN

KKVFLEKLKDVFLAQLKMDYSLVGIHDVERAEQEEVECEENDGEEGESDGTHPVG
 TPPDSPGNTLNSSPPLAPGEFDPNIDVYGIKCHENSPPRKEVYFMAIIDILTHYDAKKAA
 HAAKTVKHGAGAEISTVNPEQYSKRFLDFIGHIL

>1Y66A 52 XRAY 1.65 0.190 0.228 no engrailed homeodomain <PDB 1Y66> [ESCHERICHIA COLI]
 MKQWSEEVERKLKEFVRRHQEITQETLHEYAQLGLNQQAIQFFREFEQRK

>1TUWA 109 XRAY 1.90 0.199 0.245 no Tetracenomycin polyketide synthesis protein
 tcmI <UNP TCM1_STRGA> [STREPTOMYCES GLAUDESCENS]
 MAYRALMVLRLMDPADAHVAAFAEHDTELPLEIGVRRRVLFRFHDLYMHLIEADDDIM
 ERLYQARSHPLFQEVNERVGQYLTPYAQDWEELKDSKAEVFYSWTAPDS

>1HQZ1 141 XRAY 2.10 0.215 0.259 no ACTIN-BINDING PROTEIN <UNP ABP1_YEAST> [SACCHAROMYCES
 CEREVISIAE]
 MALEPIDYTTSHREIDAAYLKIVRGSDPDTTWLIISPNAKKEYEPESTGSSFHDFLQLFD
 ETKVQYGLARVSPPGSDVEKIIIGWCPDSAPLKTRASFAANFAAVANNLFKGYHVQVTA
 RDEDDLLENELLMKISNAAGA

>3BQPA 80 XRAY 1.30 0.177 0.234 no Proactivator polypeptide <UNP SAP_HUMAN> [HOMO SAPIENS]
 DGGFCEVCKKLVGYLDRNLEKNSTKQEILAALEKGCFLPDYPYQKQCDQFVAEYEPVLIE
 ILVEVMDPSFVCLKIGACPS

>1IXMA 192 XRAY 2.60 0.217 0.314 no SPORULATION RESPONSE REGULATORY PROTEIN <UNP SPOB_BACSU>
 [BACILLUS SUBTILIS]
 MKDVSKNQEENISDTALTNELIHLGHSHRHDWMNKLQLIKGNLSLQKYDRVFEMIEEMVI
 DAKHESKLSNLKTPHLAFDFLTFNWKTHYMTLEYEVLGEIKDLSAYDQKLAKLMRKLPHL
 FDQAVSRESENHLTVSLQTDHPDRQLILYLDHFHGAFAFPSAFDDIRQNGYEDVDIMRFEI
 TSHECLIEIGLD

>1M15A 357 XRAY 1.20 0.125 0.140 no arginine kinase <UNP KARG_LIMPO> [LIMULUS POLYPHEMUS]
 MVDQATLDKLEAGFKKLQEASDCKSLLKKHLTKDVFDSEIKNKTGMGATLLDVIQSGVEN
 LDGSGVIYAPDAESYRTFGPLFDPIIDDYHGGFKLTDKHPKQWGDINTLVGLDPAGQFI
 ISTRVRCGRSLQGYFPNCLTAEQYKEMEEKVSSTLSSMEDELKGTYYPLTGMSKATQQQ
 LIDDHFLFKEGDRFLQTANACRYWPTGRGIFHNDAKTFLVWVNEEDHLRIISMQKGGDLK
 TVYKRLVTAVDNIESKLFPSSHDRFGFLTFCPTNLGTTMRASVHIQLPKLAKDRKVLEDI
 ASKFNLQVRGTRGEHTESEGQVYDISNKRRLGLTEYQAVREMQDGILEMIKMEKAAA

>1RT8A 513 XRAY 2.00 0.237 0.270 no fimbrin <UNP FIMB_SCHPO> [SCHIZOSACCHAROMYCES POMBE]
 GSPEFMHTINEERREFIKHINSVLGADPDVGSVRVPINTETFEFFDQCKDGLILSKLIND
 SVPDTIDERVNLKQRNNKPLDNFKCIENNNVVINSAMGGISITNIGAGDILEGREHLI
 LGLVWQIIRRGLLGKIDITLHPELYRLLEDETLDQFLRLPPEKILLRWFNYHLKAANWP
 RTVSNFSKDVSDGENYTVLLNLAPELCSRAPLQTTDVLQRAEQVLQNAEKLCDRKYLTP
 TAMVAGNPKNLAFVAHLFNTHPGLEPLNEEEKPEIEPFDAGEGAREARVFTLWLSLDVT
 PSIHDFNLRDGLILLQAYDKITPNTVNWKKVNKAPASGDEMFRFKAVENTNYAVDLGK
 NQGFSLVGIQGADITDGSRTLTLALVWQMMRMNITKTLHSLSRGGKTLSDSDMVAWANS
 AAKGGKGSQIRSFDRPSISTGVFVLDVLHGKSEYVDYNLVTDGSTEELAIQNARLAISI
 ARKLGAIVIFILPEDIVAVRPRLVLHFIGSLMAV

>3LFRA 136 XRAY 1.53 0.177 0.212 no putative Metal ion transporter <UNP Q87VX8_PSESM>
 [PSEUDOMONAS SYRINGAE]
 ADLQVRDIMVPRSQMISIKATQTPREFLPAVIDAAHSRYPVIGESHDDVLGVLLAKDLLP
 LILKADGSDDDVKLLRPATFVPESKRLNVLLREFRANHNMIAIVIDEYGGVAGLVTIED
 VLEQIVGDIEDEHDVE

>3D59A 383 XRAY 1.50 0.142 0.191 no Platelet-activating factor acetylhydrolase <UNP
 PAFA_HUMAN> [HOMO SAPIENS]
 AAASFGQTKIPRGNGPYSGCTDLMFDHTNKGTFRLRYPSQDNDRLDTLWIPNKEYFWG

LSKFLGTHWLMGNILRLFLGSMTPANWNSPLRPGEKYPLVVFHSHGLGAFRTLISAIGID
LASHGFIIVAAVEHRDRSASATYYFKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRA
KECSQALSLILDIDHGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSFSGGATVIQTLSED
QRFRCGIALDAWMFPLGDEVYSRIPQPLFFINSEYFQYPANIKMKKCYSPDKERKMITI
RGSVHQNFADFTFATGKIIGHMLKLKGDIDSNVAIDLSENKASLAFLQKHLGLHKDFDQWD
CLIEGDDENLIPGTNINTTNQHI

>1R0RI 51 XRAY 1.10 0.159 0.184 no Ovomucoid <UNP IOVO_MELGA> [MELEAGRIS GALLOPAVO]
VDCSEYKPACTLEYRPLCGSDNKTYGNKCNFCNAVVESNGTLTSLHFGKC
>3D5NA 197 XRAY 2.80 0.231 0.266 no Q97W15_SULSO <UNP Q97W15_SULSO> [SULFOLOBUS
SOLFATARICUS]

MNIGVIIAAGEGKRFGDKLLAKIDNTPIIMRTIRIYGDLEKIIIVGKYVNEMLPLLMD
QIVIYNPFWNEGISTSLKLGLRFFKDYDAVLVALGDMFPVTKEDVNKIINTFKPNCKAVI
PTHKGERGNPVLISKSLFNEIEKLRGDVGARVILNKIKIEELCFIECSEGLIDIDKKED
LMRLRDFHPLEHHHHHH

>1XRKA 124 XRAY 1.50 0.175 0.194 no Bleomycin resistance protein <UNP BLE_STRHI>
[STREPTOALLOTEICHUS HINDUSTANUS]
MAKLTSAPVLTARDVAEAVEFWTDRLGFSRVFVEDDFAGVVRDDVTLFISAVQDQVVPD
NTQAWVWVRGLDELYAEWSEVVSTNFRDASGPAMTEIVEQPWGREFALRDPAGNCVHFVA
EEQD

>3KG7A 293 XRAY 2.77 0.208 0.269 no CurH <UNP Q6DNE5_9CYAN> [LYNGBYA MAJUSCULA]
SNASGQQVHRLGNKLELASTGQTIYHQDINLNNHPWIGDHRVYDTPVIPGVSYIAMTLA
AVGVPAAVEDINFQQPLFLAESNTTRETQLMLHTADNVGKQFVEVFSRDGAKQEEWQQHA
SMSVSENPPPPPTLSVDIPALCEQLRPLDIDLTEIYASISLVYGPMLQAVRQAWIGEET
SLLIEVPKALAFQLAGEPIHPVLIDACTRLTPDLDFSSDSGVFWAPWRVKEMTSLHPT
PSRFYAYVEEPSRVNEQLQTRSIDIQLLDETGAQFRINGFTVKRAPSQFLK

>3LXZA 229 XRAY 1.76 0.197 0.229 no Glutathione S-transferase family protein <UNP
Q88RE7_PSEPK> [PSEUDOMONAS PUTIDA]
MSLKLYGFSVSNYYNMVKLALLEKGLTFEEVTFYGGQAPQALEVSPRGKVPVLETEHGFL
SETSVILDYIEQTQGGKALLPADPFGQAKVRELLKEIELYIELPARTCYAESFFGMSVEP
LIKEKARADLLAGFATLKRNGRFAPYVAGEQLTLADLMFCFSVDLANAVGKKVLNIDFLA
DFPQAKALLQLMGENPHMPRILADKEASMPAFMEMIRSGKREGHHHHHH

>3EBEA 200 XRAY 2.30 0.205 0.247 no Protein MCM10 homolog <UNP MCM10_XENLA> [XENOPUS LAEVIS]
GPSVPGQQYHVEKFSGLRIRKPRVSSSEMERKMNGRKLIRLAQLQNKIATEKLEEDWVT
FGVIVKKITPQSSNNGKTFSIWRLNDLKDLDKYISLFLFGDVHKEHWKTDQGTVIGLLNA
NPMKPKEGTDEVCLSDNPQKVLMDGDAVDLGTCKARKKNGDPCTQMVNLNDCEYCYHV
QAQYKKVSSKRADLQSSYSG

>2BJQA 345 XRAY 1.75 0.191 0.230 no MFP2A <UNP Q7YXK2_ASCSU> [ASCARIS SUUM]
MTTKEFEDTWAYNTIGSPFPDNPVRVKGQQNMYVALWYKFGKPIHGRAWNGNVECSFP
YNKVELTGARDLGGQIQILTATEQDPTEQFKKTGFWEWRPYKDRVNDQLQLVRCGST
PVIMKTKDGKDLLGYIDMSTEVAAVGVSGKSEQVAGGPIQDMLVLFRNVKAPPKGIKIYD
DTWLDLKYRDPFAARNPIAAGGRKVKSDDGTEMFYVALWYEHGQPVFGRAYPDSADKT
LANFGWGGQENAGAEIGSFQMLVVPDPDILGFEYKWIPYKEAKAGGPFKPLHVGECTPCL
LKDANGTERLGNLHMGMEKATAGLAGKDSAVSGPAVGDFLVLCRN

>4GAKA 250 XRAY 1.90 0.187 0.224 no Acyl-ACP thioesterase <UNP D2QU30_SPILD> [SPIROSOMA
LINGUALE]
SNAMAFIQTDFTLRGYECDAFGRMSIPALMNLQESANRNAIDYGIGIADLAQKGVGWM
LMRFCLRIHQYPRYGTIQLMTYPTTVDKYFIHRDFRVLATDGTLLADARSTWLVFSMEK
RSMVPLPDFIRQLSPPANVDPLPALPLKPDFQTASFATAASKSVQVGWLNIDQNQHVN
AYVQWLLEGVDSEIVQTREIAEIDLVRTESHWHDWLSVQSVTETDNSVLHRISQTESGK

DVLLARSRWR

>4K7RA 446 XRAY 2.09 0.216 0.250 no Cation efflux system protein CusC <UNP CUSC_ECOLI>
[ESCHERICHIA COLI]
CSLAPDYQRPAMPVPQQFSLSQNLVNAADNYQNAGWRTFFVDNQVKTLLISEALVNNRDL
RMTATLVQEARAQYRLTDADRYPLNGEGSGSWGNLKGNTATTREFSTGLNASFDLDF
GRLKNMSEARQNYLATEEAQRAVHILLVSNVAQSYFNQQLAYALQIAEETLRNYQQSY
AFVEKQLLTGSSNVLAEQARGVIESTRSDIAKRQGELAQANNALQLLGSYGKLPQAQT
VNSDSLQSVKLPAGLSSQILLQRPDIMEAEHALMAANANIGAARAAFFPSISLTSGISTA
SSDLSSLFNASSGMWNFIPIKIEIPFNAGRQANLDIAEIRQQQSVVNYEQKIQNAFKEV
ADALALRQSLNDQISAQQRYLASLQITLQARALYQHGAVSYLEVLDAERSLFATRQTLL
DLNYARQVNEISLYTALGGGHHHHHH

>3AABA 123 XRAY 1.85 0.228 0.238 no Putative uncharacterized protein ST1653 <UNP Q970D9_SULTO> [SULFOLOBUS TOKODAI]
MYYLKQELQKRSEELSRGFYELVYPPVDMYEEGGYLVVVADLAGFNKEKIKARVSGQNEL
IIEAEREITEPGVKYLTQRPKYVRKVIRLPYNVAKDAEISGKYENGVLTIIRIPIAGTSVF
KFE

>3GVZA 299 XRAY 2.80 0.259 0.290 no Uncharacterized protein CV2077 <UNP Q7NWB3_CHRVO>
[CHROMOBACTERIUM VIOLACEUM ATCC 12472]
MNVMRHSLAVAGIAGLLAFPPVDACTLWGAAGTASMEGSLAKNRDWPDAQSLRLLH
PEHGAYLGLYADNGSEPGIKAGVNQKGLAVVAEASSLPALRADSRHGVLTLLRDY
GSLDEVASAADKLFQAQRPVFLLLADAGGLMQVEIGQHGRYRLIRQQSGTLAHTNHYADT
SLLDGAQTIGPSSQARLERIRFLDQHPAHTLSEFERLSRDRHDGPDNSLWRSGREHTLA
GWRIALPAGAPPRLQLTLANPGRERDGDYALDSAFWAQPARTLLPKLAAALEHHHHHH

>1DJUA 388 XRAY 2.10 0.185 0.254 no AROMATIC AMINOTRANSFERASE <UNP 059096_PYRHO>
[PYROCOCUS HORIKOSHII]
ALSDRLELVSASEIRKLFDAAGMKDVISLGIGEPDFDTPQHIKEYAKEALDKGLTHYGP
NIGLLELREAIAEKLKKQNGIEADPKTEIMVLLGANQAFLMGLSAFLKDGEVLIPTPAF
VSYAPAVILAGGKPEVEPTYEEDEFRLNVDELKKYVTDKTRALIINSPCNPTGAVLTKD
LEEIADFVVEHDLIVISDEVYEHFIYDDARHYSIASLDGMFERTITVNGFSKTFAMTGWR
LGFVAAPSWIIERMVKFQMYNATCPVTFIQYAAAKALKDERSWKAVEEMRKEYDRRRLV
WKRLNEMGLPTVKPKGAFYIFPRIKDTGLTSKKFSELMLEKEARVAVVPGSAFGKAGEGYV
RISYATAYEKLLEAMERMERVLKERLV

>3DR2A 305 XRAY 1.67 0.211 0.239 no Exported gluconolactonase <PDB 3DR2>
[XANTHOMONAS CAMPESTRIS PV. CAMPESTRIS]
MDSHCRVRPAGPAVPADCDPPRITHAALARLGDARLLTYDQATWSEGAWEAQRTL
WSDLVGRRLVWREDGTVDVLLDATAFTNGNAVDAQQLVHCEHGRRITRSDADGGAHL
LVGRYAGKRLNSPNDLIVARDGAIWFTDPPFGLRKPSQGCADPELAHHSVYRLPPDGSP
LQRMADLDHPNGLAFSPDEQTLVVSQTPEQGHGSVEITAFWRDGAHDDRHFASVPDGL
PDGFCVDRGGWLWSSSGTGVCVFDSDGQLLGHIPPTGASNCTFDQAQQLFITGGPCLW
MLPLP

>2062A 270 XRAY 1.75 0.168 0.208 no hypothetical protein <PDB 2062> [NOSTOC PUNCTIFORME]
GMKSQWECFLQNLGVWEGSFSNFSPEGTLNLTSSRLCLEGLNNQTVRLTLRSKGDDV
IREFRSVGGGLFFENGSEGLIQLGPFSEFGGELAFVHENRRLRLVQLFDRNGHLNGL
TLIREHLAGTPVAERPLLQINDLLGEWRGQAVTIYRDLRPPDIYSTTLKIQLDDAGRLMQ
STSFGERTITSTATIKGSIVLFDQDPEKQVQVLLLPDGASATSPLKVQLRQPLFLEAGWL
IQSDLRQRMIRSNDKGEWVSLTLVTEERV

>2B2AA 199 XRAY 2.22 0.238 0.258 no Telomerase reverse transcriptase <UNP TERT_TETTH>

[TETRAHYMENA THERMOPHILA]

MKKHHHHHHQKINNINNNKQMLTRKEDLLTVLKQISALKYVSNLYEFLLATEKIVQTSEL
DTQFQEFLLTTTIIASEQNLVENYKQKYNQPNFSQMTIKQVIDDSIILLGNKQNYVQQIGT
TTIGFYVEYENINLSRQTLYSSNFRNLLNIFGEEDFKYFLIDFLVFTKVEQNGYLQVAGV
CLNQYFSVQVKQKKWKYNN

>1GKPA 458 XRAY 1.29 0.154 0.184 no HYDANTOINASE <PDB 1GKP> [THERMUS SP.]

PLLIKNGEIIITADSRKADIYAEGETITRIGQNLEAPPGTEVIDATGKYVFPGFIDPHVH
IYLPFMATFAKDTHTGSKAALMGGTTTYIEMCCPSRNDDALEGYQLWKSKAEGNSYCDY
TFHMAVSKFDEKTEGQLREIVADGISSFKIFLSYKNFFGVDDGEMYQTLRLAKELGVIVT
AHCENAELVGRLLQKLLSEGKTGPEWHEPSRPEAVEAEGTARFATFLETTGATGYVVHLS
CKPALDAAMAARKGVPIYIESVIPHFLDKTYAERGGVEAMKYIMSPPLRDKRNQKVLW
DALAQGFIDTVGTDHCPFDTEQKLLGKEAFTAIPNGIPAIEDRVNLLTYGVSRGRLDIH
RFVDAASTKAAKLFGLFPRKGTIAVGSDADLVVYDPQYRGTISVKTQHVNNDYNGFEGFE
IDGRPSVVTVRGKVAVRDGGQFVGEKGWGLLRREPMYF

>1N71A 180 XRAY 1.80 0.208 0.245 no aac(6')-Ii <UNP Q47764_ENTFC> [ENTEROCOCCUS FAECIUM]

MIISEFDRNNPVLKQDLSDLLRLTWPEEYGDSSAEEVEEMNPERIAVAANDQDELVGFI
GAIPQYGITGWELHPLVVESSRRKNQIGTRLVNYLEKEVASRGGITIYLGTDLDHGTTL
SQTDLYEHTFDKVASIQNLREHPYEFYEKLGKIVGVLPNANGWDKPDIMAKTIIPRPD

>2XMJA 64 XRAY 1.08 0.117 0.149 no SSR2857 PROTEIN <UNP P73213_SYNY3> [SYNECHOCYSTIS SP. PCC 6803]

MTIQLTVPTIACEACAEAVTKAVQNEDAQATVQVDLTSSKKVTITSALGEEQLRTAIASAG
HEVE

>3CZ1A 119 XRAY 1.50 0.153 0.198 no Pheromone-binding protein ASP1 <UNP Q9U9J6_APIME> [APIS MELLIFERA]

APDWVPPEVFDLVAEDKARCMEHGTTQAQIDDDVDKGNLVNEPSITCYMYCLLEAFSLVD
DEANVDEDIMLGLLPDQLQERAQSVMGKCLPTSGSDNCNKIYNLAKCVQESAPDVWFVI

>3EBWA 163 XRAY 2.80 0.231 0.276 no Per a 4 allergen <UNP Q1MOY5_PERAM> [PERIPLANETA AMERICANA]

DDSCQIGTSFTGLDMTKYVGTWYELFRTPNSDEEDFTNCEYDKYTLDENGVIQVTSVAYT
NSIRGFITSTGTVPSTWEDTFDIAYGDDTWSSTYFMVGTDTYQYSIVAGCLDNDYSRHL
YWIASHETSFDATKAKVNEVLAPYNLSLDDMEPVDQSYCVQY

>3LLKA 261 XRAY 2.00 0.237 0.272 no Sulphydryl oxidase 1 <UNP QSOX1_HUMAN> [HOMO SAPIENS]

IAPTVMKLADRSKIYMALESALHYILRIEVGRFPVLEGQRLVALKKFVAVLAKYFPGRP
LVQNFLHSVNEWLKRQKRNKIPYSFFKTALDDRKEGAVLAKKVNWIGCQGSEPHFRGFPC
SLWVLFHFLTVQAARQNVDSQAAKAKEVLPAIRGYVHYFFGCRDCASHFEQMAAASMH
RVGSPNAAVLWLWSSHNVRNARLAGAPSEDPQFPKVQWPPRELCSACHNERLDVPVWDVE
ATLNLKAHFSPSNIILDFPA

>3K4IA 244 XRAY 1.69 0.180 0.214 no uncharacterized protein <UNP Q880F6_PSESM> [PSEUDOMONAS SYRINGAE PV. TOMATO]

MSLSVPFEYTPIAQSVLDECEHLDTASLSDALDSLIGDGLPGIASQVPGTRCVGIAFTV
QYQPVDASEGFRGAANYIDQVPSGSVIVSSNSGRHDCTVWGDIMTHFALANGIKGTVIDG
VARDIDTVINCNYPLFSRGRFMQSAKNRTQLKAVQVPLVIDGITIQPGDLMVCDGSGCVV
VPQQLAAEVVLRARAVEQTERRITIEAIISSGSTLEQARMTYRYDQPWLSEAEHGGTQEGHH
HHHH

>20SXA 481 XRAY 1.10 0.122 0.139 no Endoglycoceramidase II <UNP O33853_RHOSO> [RHODOCOCBUS SP.]

MGSSHHHHHSSGLVPRGSHMSGSGSGGTALTPSYLKDDDGRSLILRGFNTASSAKSAP
DGMPQFTEADLAREYADMGTNFVRFLISWRSVEPAPGVYDQQYLDREVDRVGYAERGYK
VMLDMHQDVYSGAITPEGNSGNGAGAIENGAPAWATYMDGLPVEPQPRWELYYIQPGVMR

AFDNFWNTTGKHPELVEHYAKAWRAVADRFADNDVAVAYDLMNEPFGGSLQGPAFEAGPL
AAMYQRTTDAIRQVDQDTWVCVAPQAIGVNQGLPSGLTKIDDPRAQQRIAYCPHLYPLP
LDIGDGHEGLARTLTDVTIDAWRANTAHTARVLGDVPIILGSFGLDTTLPGARDYIERVY
GTAREMGAGVSYWSSDPGPWGPYLPDGTQTLLVDTLNKPYPRAVAGTPTIEWSSTSRLQL
TIEPDAAITAPTEIYLPEAGFPDGVHVEGADVVGWDRQSRLLTVRTPADSGNVTVTPA
A

>3GUYA 230 XRAY 1.90 0.202 0.249 no Short-chain dehydrogenase/reductase SDR <UNP
A6B7Q2_VIBPA>
[VIBRIO PARAHAEMOLYTICUS]
MSLIVITGASSGLGAELAKLYDAEGKATYLTGRSESKLSTVTNCLSNVGYRARDLASHQ
EVEQLFEQLDSIPSTVVHSAGSGYFGLLQEQDPEQIQTLIENNLSSAINVLRELVKRYKD
QPVNVVMIMSTAAQQPKAQUESTYCAVKWAVKGLIESVRLELKGKPMKIIAVYPGGMATEF
WETSGKSLDTSSFMSAEDAALMIHGALANIGNGYVSDITVNRGHHHHHH

>3R62A 129 XRAY 1.52 0.179 0.208 no Complement factor H <UNP CFAH_HUMAN> [HOMO SAPIENS]
EAEFGKCGPPPIDNGDITSFPLSVYAPASSVEYQCQNLQLEGNKRITCRNGQWSEPPK
CLHPCVISREIMENYNIALRWRAKQKLYSRTGESVEFVCKRGYRLSSRSHTLRITTCWDGK
LEYPTCAKR

>3DK9A 478 XRAY 0.95 0.123 0.152 no Glutathione reductase <UNP GSHR_HUMAN> [HOMO SAPIENS]
ACRQEPQPGPPAAGAVASYDYLVIIGGSGGLASARRAAELGARAAVVESHKLGGTCVN
VGCVPKKVMWNTAVHSEFMHDHADYGFPSCEGKFNWRVIEKRDAYVSRLNAIYQNNLTK
SHIEIIRGHAAFTSDPKPTIEVSGKKYTAPHILIATGGMPSTPHESQIPGASLGITSDGF
FQLEELPGRSVIVGAGYIAVEMAGILSALGSKTSLMIRHDKVLRSDSMISTNCTELEN
AGVEVLKFSQVKEVKKTLSGLEVSMVTAVPGRLPVMTMIPDVCLLWAIGRVPNTKDLSL
NKLGIQTDDKGHIIVDEFQNTNVKGIYAVGDVCGKALLTPVAIAAGRKLHRLFEYKEDS
KLDYNNIPTVVFSPPIGTVGLTEDEAIHKYGIENVKTYSTSFTPMYHAVTKRKTCKVMK
MVCANKEEKVVGIIHQGLGCDEMLQGFVAVKMGATKADFNTVAIHPTSSEELVTLR

>2QVKA 192 XRAY 1.45 0.163 0.192 no Sodium/calcium exchanger 1 <UNP NAC1_CANFA> [CANIS LUPUS
FAMILIARIS]
GPGHAGIFTFEEPVTHVSESIGIMEVKVLRRTSGARGNVIVPYKTIEGTARGGGEDFEDTC
GELEFQNDIVKTSISKVIDDEEYKNTFFLEIGEPRLVEMSEKKALLNELGGFTITG
KYLGGQPVFRKVHAREHIPSTVITIAEEYDDKQPLTSKEEEEERRIAEMGRPILGEHTKL
EVIIEESYEFKS

>3TEEA 219 XRAY 1.95 0.201 0.218 no Flagella basal body P-ring formation protein flgA <UNP
FLGA_SALTY> [SALMONELLA TYPHIMURIUM]
QDINAQLTWFSQLAGFSDEVVTLRSPNLLPSCEQPAFSMTGSAKLWGNVNVVARCA
NEKRYLQVNVQATGNVAVAAPIARGGKLTANVTLKRGRDLQPPRTVLDIRQIQDAVS
LRDLAPGQPVQLTMIRQAWRVKAGQRVQVIANGEGFSVNAEGQAMNNAVAQNARVRMTS
GQIVSGTVDSGNILINLDPNSSSVDKLAAALEHHHHHH

>3HRZA 627 XRAY 2.20 0.181 0.226 no Cobra venom factor <UNP CO3_NAJKA> [NAJA
KAOUTHIA] ALYTLITPAVLRTDTEEQILVEAHGDSTPKQLDIFVHDFPRKQKTLFQTRVDMNPAGGML
VTPTIEIPAKEVSTDSRQNYVVVQVTGPQVRLEKVLLSYQSSFLFIQTDKGIYTPGSP
VLYRVFSMDHNTSKMNKTIVIEFQTPEGILVSSNSVDLNFVWPYNLPDLVSLGTWRIVAK
YEHSPENYTAIFDVRKYVLPSEFVRLQPEKFFYIDGNENFHVSIARYLYGEEVEGVAF
VLFVGKIDDAKKSIPDSLTRIPIIDGDGKATLKRDTFRSRFPNLNLVGHNTLYASVTVMT
ESGSDMVVTEQSGIHIVASPYQIHFTKTPKYFKPGMPYELTVYVTNPDGSPAHPVSE
AFHSMGTTLSDGTAKLILNIPLNAQSLPITVRTNHGDLPRERQATKSMTAIAYQTQGGSG
NYLHVAITSTEIKPGDNLVFNFNKGNANSLKQIKYFTYLILNKGKIFKVGRQPRRDGQN
LVTMNLHITPDLIPSFRFVAYYQVGNNEIVADSVWVDVKDTCMGTLVVKGDNLIQMPGAA

MKIKLEGDPGARVGLVAVDKAVYVLNDKYKISQAKIWDTIIEKSDFGCTAGSGQNNLGVFE
 DAGLALTTSTNLNTKQRSAAKCPQAN
 >2HW2A 143 XRAY 1.45 0.137 0.185 no Rifampin ADP-ribosyl transferase <UNP 067972_MYCSM>
 [MYCOBACTERIUM SMEGMATIS]
 MVANPPKPFVHESGAYLHGTKAELKVGDRLVPGRESNFEAGRIMNHIYITQTLDAAVWG
 AELAAGEGRGRIFIVEPEGAIEDDPNVTDKKLPGNPTRS YRTREP VVWIVGELTDWVGHP
 EQLAAMRQGLEELRRKGLAVIYD
 >1GG3A 279 XRAY 2.80 0.226 0.276 no ERYTHROID MEMBRANE PROTEIN 4.1R <UNP 41_HUMAN> [HOMO
 SAPIENS]
 MHCKVSLDDTVYECVVEKHAKGQDLLKRVCEHLNLEEDYFGLAIWDNATSKTWLDSAK
 EIKKQVRGVPWNFTFNVKFYPPDPAQLTEDITRYYLCLQLRQDIVAGRLPCSFATLALLG
 SYTIQSELGDYDPELHGVYVSDFKLAPNQKELEEKVMELHKSYSRMTPAQADLEFLEN
 AKKLSMYGVDLHKAKDLEGVDIILGVCSSGLLVYKDKLRINRFPWPVKLKISYKRSSFFI
 KIRPGEQEYESTIGFKLPSYRAAKKLWKVCVEHHTFFR
 >3HIMA 211 XRAY 2.20 0.200 0.248 no Probable transcriptional regulator <UNP Q0SD48_RHOSR>
 [RHODOCOCCLUS JOSTII]
 MDASLTGAVAE LGTSKAAARIRAAAIEVFAAKGYGATTTREIAASLDMSPGAVYPHYKTK
 ELLYAISLEGHHSVLAAITAADFPDIAAPDRLMSTVTAYVTWHADNRASARVGQYELRS
 LSPEHFAIIADIRRTTKVFTRII EAGATAGDFHPFDIEAALAITSLGIDVSRWFPSHT
 YSDPRIIAARYVELALRMVGCADRQPLDKPS
 >2V89A 82 XRAY 1.10 0.123 0.155 no VDJ RECOMBINATION-ACTIVATING PROTEIN 2 <UNP RAG2_MOUSE>
 [MUS MUSCULUS]
 GPLGSPEFGYWITCCPTCDVDINTWVPFYSTELNKPAMIYCSHGDGHVHAQCMDLEERT
 LIHLEGSNKYYCNEHVQIARA
 >4FWGA 732 XRAY 1.99 0.231 0.259 no TTC1975 peptidase <UNP C9DRU9_9DEIN> [MEIOTHERMUS
 TAIWANENSIS]
 MRLSYEALEWRTPIENSTEPVSLPPPPFFGQERAREALELAIRGGFHAYLVGPPSLGKH
 EALLAYLSTQSVETPPDLLYVPLSERKVAVMTLPSGQEIHLAEAVEGLLLEVNRLDELFR
 QGSFLREKTQLEARFKEAREQQLEALRREAQAGFALSTNGERLELTGPGVPVPAELSARL
 EEVTLGSMASAELEVALRRLRRDWALHYLNNRFEPLFQRFPPQARAYLEALRARLARYAE
 TGEPLDPAQWRPNLLTSSSSGTPPIVYEPYATAPRLFGRDYLVDRGVWSTNVSLIRPG
 AVHRAQGGYLILDALSLKREGTWEAFKRALRNGQVEPVTEPQAPAGLEVEFPFIQMVM
 VGTPEAFEGLEEDPAFSELFRIAEFSPTMPASPENCTALGGWLLAQGFQLTQGGLTRLY
 DEARRMAEQDRMDARLVEIRALAEAAVLGGGLTAESVEQAIAAREHRSFLSEEEFLR
 AVQEGVIRLRTTGRAVGEVNSLVVVEAAPYWGRPARLTARAAPGRDHLISIDREAGLGGQ
 IFHKAVLTLAGYLRSMIEHGSLPVTISLAFEQNYVSIEGDSAGLAELVAALSAIGNLPL
 RQDLAVTGAVDQTGKVLAVGAINAKVEGFVRVCKALGLSGTQGVILPEANLANLTLRAEV
 LEAVRAGQFHIYAVETAEQALEILAGARMEGFRGLQEKIRAGLEAFARLEEGLHDKEDREK
 LAAALEHHHHH
 >107DE 126 XRAY 2.70 0.257 0.289 no LYSOSOMAL ALPHA-MANNOSIDASE <UNP M2B1_BOVIN> [BOS
 TAURUS]
 PRTQFSGLRRELPPSVRLTLARWGPETLLLRLEHQFAVGEDSGRNLSSPVTLDLTNLS
 AFTITNLRETTLANQLLAYASRLQWTTDTGTPHPSRPSRVSATITLQPMIERTFLASV
 QWEEDG
 >4JYKA 212 XRAY 1.70 0.122 0.170 no HTH-type transcriptional regulator RutR <UNP RUTR_ECOLI>
 [ESCHERICHIA COLI]
 MTQGA VKTTGKRSRAVS AKKKAILSAALDTFSQFGFHGTRLEQIAELAGVSKTNLLYYFP

SKEALYIAVLRQILDIWLAPLKAFREDFAPLAAIKEYIRLKLEVSRDYPQASRLFCMEML
AGAPLLMDEL TGD LKAL IDEKSALIAGWVKSGKLAPIDPQH LIFMIWASTQHYADFAPQV
EAVTGATLRDEVFFNQTVENVQRIIEGIRPR

>3C5PA 197 XRAY 2.90 0.178 0.226 no Protein BAS0735 of unknown function <UNP Q81UT7_BACAN>
[BACILLUS ANTHRACIS STR.] SNAMTNI IKIRASVFIPMSWTEAKMDMETGQVIQFEGDSREFTPHAVNTMRSRVEQEVVV
DFYKQEVFSYANTGITTEKVISPDGSVNKRTGKASTENIVCTDIVWNSGGVQFKMSASAS
NPLNVYAPPVDYVLNVCVKKDGSIDVQGEHDGFFCFEFYKQVDFGPFEKIYTHDFRETGD
TAAALGGNMDYSFTKRL

>3B9WA 407 XRAY 1.30 0.151 0.171 no Ammonium transporter family <UNP Q82X47_NITEU> [NITROSOMONAS
EUROPAEA] SAVAPAEINEARLVAQYNYSINILAMLLVGFGFLMVFRYGFSSATGTYL VVATGLPLY
ILLRANGIFGHALTPHSVDAVIYAEFAVATGLIAMGAVLGRLRVFQYALLALFIVPVYLL
NEWLVLDNASGLTEGFQDSAGSIAIHAFGAYFGLGV SIALTTAAQRAQPIESDATSDRFS
MLGSMVLWLFWPSFATAIVPFEQMPQTIVNTLLALCGATLATYFLSALFHKGKASIVDMA
NAALAGGVAIGSVCNIVGPFVGAFIGLLGGAISVVG FVFIQPMLESKAKTIDTCGVHNLH
GLPGLGGFSAILIVPGIAVAQLTGIGITLALALIGGVIAGALIKLTGTTKQAYEDSHEF
IHLAGPEDEHKAERLVLEAKTEIQGLKNRIDA AVL SAKSEGHHHHHH

>4B4DA 262 XRAY 1.50 0.209 0.230 no FERREDOXIN-NADP REDUCTASE <UNP Q8PMHO_XANAC>
[XANTHOMONAS AXONOPODIS PV. CITRI STR. 306]
GSHMSSAFGAETVLEVRHWTDAYFSFTTTRDAGFRFENGQFVMIGLETETRPLLRAYSIA
SANWEEHLEFFSIKVPDGLTSLRLQHIQPGDKVLVGKKPTGTLLISDLHPGRNLYLLGTG
TGLAPWLSIIKDPETYERFDKVLITQGVRFVQDLAYRDYFERELPQHEFLGDLLREKLLY
YPAVTRETFANQGRLTELMADGRMQTLGLPTLDPANDRFMICGSPQMLADLRSLDSRG FQTSPRIGTPGHYVFERAFVEK

>3H7AA 252 XRAY 1.87 0.207 0.241 no short chain dehydrogenase <UNP Q6NDT3_RHOPA>
[RHODOPSEUDOMONAS PALUSTRIS]

MSLTPRNATVAVIGAGDYIGAEIAKKFAAEGFTVFAGRRNGEKLAPLVAEIEAAGGRIVA
RSLDARNEDEVTAFLNAADAHAPLEV TIFNVGANVNFPILETTDRVFRK VWEMACWAGFV
SGRESARLMLAHGQGIFFTGATASLRGGSGFAAFASAKFGLRAVAQSMARELMPKNIHV
AHLIIDSGVDTAWVRERREQMFGKDALANPDLLMPPAVAGAYWQLYQQPKSAWTFEME I
RPYGE GHHHHHH

>3M8JA 111 XRAY 1.40 0.197 0.222 no FocB protein <UNP Q93K76_ECOLX> [ESCHERICHIA COLI]
GAMAQHEVITRGGDAFL LKLRESALSSGSMSEEQFLLIGISSIHSR VILAMKDYLVSG
HSRKDVCEKYQMNGYFSTTLGRLTRLNLVVARLAPYYTDSVSAIAEASL

>2RHWA 283 XRAY 1.57 0.173 0.200 no 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase
<UNP BPHD_BURL> [BURKHOLDERIA XENOVORANS]

LTESSTSKFVKINEKGFSDFNHYNEAGNETVIMLHGGGPGAGGWSNYRNVGPFVDAG
YRVILKDSPGFNKSDAVVMDEQRGLVNARAVKGLMDALDIDRAHLVGNAMGGATALNFAL
EYPDRIGKLILMGPGGLGSPMFAPMPMEG IKLLFKLYAEP SYETLKQMLQVFLYDQSLIT
EELLQGRWEAIQRQPEHLKNFLISAQKAPLSTWDVTARLGEIKAKTFITWGRDDR FVPLD
HGLKLLWNIDDARLHVFSKCGHWAQWEHADEFNRLVIDFLRHA

>2UWIA 338 XRAY 1.95 0.186 0.229 no PLASTID DELTA4 MULTIFUNCTIONAL ACYL-ACYL CARRIER PROTEIN
DESATURASE <PDB 2UW1> [HEDERA HELIX]

MQVTHSMPPQKLEIFKSLDDWARNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQVRELRE
RAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWTAEENR
HGDLLNKYLYLSGRVDMRKIEKTIQYILIGSGMDIKSENSPYLGFIYTSFQERATFISHAN
TAKLAQHYGDKKLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMMRKKITM

PAHLMYDGSDELLFKHFTAVAQRLGVYSALDYCDILEFLVDKWNVERLTGLSDEGRKAQE
YVCELGPKIRRLERAQGRAKEAPTMPFSWIFDRQVKL

>1JI1A 637 XRAY 1.60 0.182 0.206 no ALPHA-AMYLASE I <UNP NEPU1_THEVU> [THERMOACTINOMYCES
VULGARIS]

AANDNNVEWNGLFHDQGPLFDNAPEPTSTQSVTLKLRTFKGDITSANIKYWDTADNAFW
VPMVWDSNDPTGTFDYWKGTIPASPSIKYYRFQINDGTSTAWYNGNGPSSTEPNADDFYI
IPNFKTPDWLKNQVMYQIFPDRFYNGDSSNDVQTGSYTYNGTPTTEKKAWGSSVYADPGYD
NSLVFFGGDLAGIDQKLGKIKKTLGANILYLNPFIKAPTNNHKYDTQDYMAVDPAFGDNST
LQTLINDIHSTANGPKGYLILDGVFNHTGDSHPWFDKYNFSSQGAYESQSSPWYNYTTF
YTWPDSYASFLGFNSLPKLNNGSGSAVRGVIYNNSNSVAKTYLNPYSVDGWRLDAAQY
VDANGNGSDVTNHQIWSEFRNAVKGVNSNAIIIGEYWGNNANPWTAAQGNQWDAATNFDGF
TQPVSEWITGKDYQNNASISTTQFDSWLRGTRANYPTNVQQSMMNFLSNHDITRFATRS
GGDLWKTYLALIFQMTYVGTPTIYYGDEYGMQGGADPDNRRSFDWSQATPSNSAVALTQK
LITIRNQYPALRTGSFMTLITDDTNKIYSYGRFDNVNRIAVVLNDSVSHTVNVVPVWQLS
MPNGSTVTDKITGHSYTVQNGMVTVAVDGHYGAVALAQ

>3OR1B 386 XRAY 1.76 0.193 0.212 no Sulfite reductase beta <PDB 3OR1> [DESULFOVIBRIO
GIGAS]

MAFISSGYNPAKPMENRITDIGPRKFTFFPPVIAKNAGNWDYHEILEPGILVHVAKNGD
KVFTVRCGAARLMSTSHIREACEIAKKFCNGHLRFTTRNNIEFMVDNEETLKALVADLKT
RKFAAGSFKFPIGGTGASISNIVHTQGWVYCHTPATDASGPVKAVMDELFEFTSMRLPA
IVRVSLACCINMCGAVHCSDIGLVGIHRKPPMIDHENLAELCEIPLAACAACPTAAVKPIT
AEVNGQKVKSAINNDRCMYCGNCYTMCALPLSDGTGDGIAIMVGGKISNRIKVPFSFSK
VVVAFVPNEPPRWPTMAKIVKKIVEVYAEDARKYERIGDWIHRIGWETFYEKTGLEFSHH
CIDDFRDPAYYTWRQSTQFKFVSFDS

>1TU1A 148 XRAY 1.95 0.205 0.237 no hypothetical protein PA0094 <UNP Q9I738_PSEAE> [PSEUDOMONAS
AERUGINOSA]

GHMTLYRLHEADLEIPDAWQDQSIKFLPASGPAREASFVISRDASQGDAPFADYVARQ
LENAEKQLPGFKLHKRWIDINIHGHAALLDYQWQREGRDLMLRQVFIERRPAVLITLTT
TPADLPHHEPAWKQAMQTLVPRPTPSGS

>3HNXA 110 XRAY 1.37 0.170 0.210 no Cyanovirin-N-like protein <UNP Q5MK11_TUBBO> [TUBER
BORCHII, NEUROSPORA CRASSA, TUBER BORCHII]

GSHMSYADSSRNAVLNNGRTRLAECRNADGNWVTSELDLDTIIGNNDGHFQWGGQNFTE
TAEDIRFHPKEGAEEQPIILRARLRDCNGEFHDRVNLNRIQNVNGLRVFQ

>3EEBA 209 XRAY 2.10 0.202 0.243 no RTX toxin RtxA <UNP Q9KS12_VIBCH> [VIBRIO CHOLERAEE]

ADGKILHNQNVNSWGPITVPTTDGGETRFDGQIIVQMENDPVVAKAAANLAGKHAESSV
VVQLDSGDGNYRVVYGDPSKLDGKLRLVQLVGHGRDHSETNTRLSGYSADELAVKLAKFQQ
SFNQAENINNKPDISIVGCSLVSDDKQKGFQHFINAMDANGLRVDVSVRSSELAVDEA
GRKHTKDANGDWVQKAENNKVSLSWDAQG

>2E11A 266 XRAY 1.73 0.188 0.217 no Hydrolase <UNP Q8P8M3_XANCP> [XANTHOMONAS CAMPESTRIS PV.
CAMPESTRIS]

MHDLRISLVQGSTRWHPAGNRDYYGALLEPLAGQSDLVILPETFTSGFSNEAIDKAEDM
DGPTVAWIRTQAARLGAATGSGVQLRTEHGTVFNRLWATPDGALQYYDKRHLFRFGNEHL
RYAAGRERLCVEWKGWRINPVQVCYDLRFPVFCRNRFDVERPGQLDFDLQLFVANWPSARA
YAWKTLLRARAIEMLCFVAAVNRVGVGNQLHYAGDSVIDFLGQPQVEIREQEQQVTTT ISAAALAEHRARFPAMLDGDSFVLGE

>2BC4A 211 XRAY 2.27 0.261 0.268 no HLA class II histocompatibility antigen, DM alpha chain <GB
NP_006111> [HOMO SAPIENS]

VPEAPTPMWPDDLQNHTFLHTVYCQDGSPSVGLSEAYDEDQLFFDFSQNTRVPRLPEFA
DWAQEQGDAPAILFDKEFCEWMIQQIGPKLDGKIPVSRGFPPIAEVFTLPLEFGKPNLTV
CFVSNLFPPMLTVNWQHHSVPVEGFGPTFVSAVDGLSFQAFSYLNTPEPSDIFSCIVTH EIDRYTAIAYWVPRNALPSDLLEDYKDDDDK
>2CVEA 191 XRAY 1.60 0.215 0.238 no hypothetical protein TTHA1053 <UNP Q5SJF5_THET8> [THERMUS
THERMOPHILUS]

MSLTLADKVVYEEIIQKSRIAKAAPVASEEEALAFLEENREPEATHNGHAYKIGLLYRF
SDDGEPSTAGRPILHAIEAQGLDRVAVLVVRYFGGVKLGAGGLVRAYGGVAAEALRRAP
KVPLVERVGLAFLVPFAEVGRVYALLEARALKAEETYTPGVRFALLLPKPEREGFLRAL
LDATRGQVALE

>2R4GA 267 XRAY 1.71 0.202 0.239 no Telomerase reverse transcriptase <UNP TERT_TETTH>
[TETRAHYMENA THERMOPHILA] MKGFQFKVIEKQLGRQFINSKIKPDHPQTIKKTLKEYQSKNFSCQEERDLFLEFTE
KIVQNFHNINFNLLKKFCKLPENYQSLKSQVKQIVQSENKANQQSCENLFNSLYDTEIS
YKQITNFLRQIIQNCVPNQLLGKKNFKVLEKLYEFVQMKRFENQKVLDYICFMDVFDVE
WFDLKNQKFTQKRKYISDKRKILGDLIVFIINKIVIPVLRNFYITEKHKEGSQIFYR KPIWKLVSKLTIVKLEENLEKVEEKL

>3CZ8A 319 XRAY 2.20 0.198 0.258 no Putative sporulation-specific glycosylase ydhD <UNP
YDHD_BACSU> [BACILLUS SUBTILIS SUBSP. SUBTILIS STR. 168]

MSLSNYIAGTSLSFYVLRNPDLDRELINDYAPYSSSISIFEYHIAPNGDIANQLNDAAAIE
TTWQRRVTPLATITNLTSGGFSTEIVHQVLNNPTARTNLVNNIYDLVSTRGYGGVTIDFE
QVSAADDRDLFTGFLRQLRDLQAGGYVLTIAVPAKTSNIPWLRGYDYGGIGAVVNYMFI
MAYDWHHAGSEPGVPAPITEIRRTIEFTIAQVPSRKIIIGVPLYGYDWIIPYQPGTVASA
ISNQNAIERAMRYQAPIQYSAEYQSPFFRYSDQQGRTHEVWFEGVRSMSRKMQIVREYRL
QAIGAWQLTLAEGHHHHHH

>1LFBA 99 XRAY 2.80 0.212 0.364 no LIVER TRANSCRIPTION FACTOR (LFB1) <UNP HNF1A_MOUSE> [RATTUS
NORVEGICUS]

ARIDPTKKGRRNRFKWGPASQQILFQAYERQKNPSKEERETLVEECNRAECIQRGVSPSQ
AQGLGSNLVTEVRVYNWFANRRKEEAFRHKLAMDTYKLN

>1REPC 251 XRAY 2.60 0.213 0.274 no REPLICATION INITIATION PROTEIN <UNP REPE1_ECOLI>
[ESCHERICHIA COLI]

MAETAVINHKKRKNSPRIVQSNDLTEAAYSLSRDQKRMLYLFVDQIRKSDGTLQEHDGIC
EIHVAKYAEIFGLTSAEASKDIRQALKSFAGKEVVFYRPEEDAGDEKGYESFPWFIPAH
SPSRGLYSVHINPYLIPFFIGLQNRFTQFRLSETKEITNPYAMRLYESLCQYRKPDSGI
VSLKIDWIIERYQLPQSYQRMPDFRRRFLQVCVNEINSRTPMRLSYIEKKKGRQTTHIVF
SFRDITSMTTG

>2W31A 162 XRAY 1.50 0.168 0.207 no GLOBIN <UNP Q747F6_GEOSL> [GEOBACTER SULFURREDUCTENS]
MLTMQEIKAHYRFTDEDAELLGSLFPLAETNKERLADQFYDYLLGIPETAFLKEDLVQ
KLKQTHQDWFVSLFAGSYDNRYIHNLQKIGHAHVRVGLNAHYVNVAMNVVRQFTLSIIQD
NFPDPEERRQRREAVEKILDINLDIMSASYREEEMRKFVSH

>2PTRA 462 XRAY 1.85 0.183 0.216 no Adenylosuccinate lyase <UNP PUR8_ECOLI> [ESCHERICHIA COLI]
MELSSLTAVSPVDGRYDKVSALRGIFSEYGLLKFRVQVEVRWLQKLAHAHAIKEVPAFA
ADAIGYLDIVASFSEDAARIKTERTTNHDVKAVEYFLKEKVAEIPELHAVSEFIHFA
CTSEDINNLSHALMLKTARDEVILPYWRQLIDGLKD LAVQYRDIPLLSRTAGQPATPSTI
GKEMANVAYRMERQYRQLNQVEILGKINGAVGNNAHIAAYPEVDWHQFSEEFVTSGLIQ
WNPYTTQIEPHDYIAELFDCVARFNTILIDFDRDVWGYYIALNHFKQKTIAGEIGSSTMPH
KVNPIDFENSEGNLGLSNAVLQHLASKLPVSRWQRDLTDSTVLRNLGVGIGYALIAQST
LKGVSKEVNRDHLDELHDHNEVLAEPITQVMRRYGIEKPYEKLKELTRGKRVDAEGMK

QFIDGLALPEEEKARLKAMTPANYIGRAITMVDELKHHHHHH

>2WN3A 254 XRAY 1.59 0.153 0.180 no DISCOIDIN-1 SUBUNIT A <UNP DIS1A_DICDI> [DICTYOSTELIUM DISCOIDEUM]

AMSTQGLVQLLANAQCHLRTSTNYNGVHTQFNSALNYKNNGTNTIDGSEAWCSSIVDTNQ
YIVAGCEVPRTFMCVALQGRGDADQWVTSYKIRYSLDNVSWFEYRNGAAVTGVTDRNTVV
NHFFDTPIRARSIAIHPLTWNGHISLRCEFYTPVQSSVTQVGADIYTGDNALNTGSGK
REVVVPVKFQFEFATLPKVALNFDQIDCTDATNQTRIGVQPRNITTKGFDCVFYTWNENK
VYSLRADYIATALE

>1DYO A 160 XRAY 2.10 0.190 0.250 no ENDO-1, 4-BETA-XYLANASE Y <UNP XYNX_CLOTM> [CLOSTRIDIUM THERMOCELLUM]

KPEEPDAGYYHDTFEGSVGQWTARGPAEVLLSGRTAYKGSESLVRNRTAAWNGAQRAL
NPRTFVPGNTYCFSVVASFIEGASSTFCMKLQYVDGSGTQRYDTIDMKTGPNQWVHLY
NPQYRIPSDATDMYVYVETADDTINFYIDEAIGAVAGTVI

>1UA4A 455 XRAY 1.90 0.168 0.205 no ADP-dependent glucokinase <UNP GLKA_PYRFU> [PYROCOCCUS FURIOSUS]

MPTWEELYKNAIEKAIKSVPKVKGVLGYNTNIDAIKYLDSDKLEERI KAGKEEVIKYS
EELPDKINTVSQLLGSILWSIRRGKAAELFVESCVRFYMKRWGNELRMGGQAGIMANL
LGGVYGVPIVHVPQLSRLQANFLDGP IYVPTLENGEVKLIHPKEFSGDEENCIHYIYE
FPRGFRVFEFEAPRENRFISADDYNTTLFIREEFRESFSEVIKNVQLAILSGLQALTKE
NYKEPFEIVKSNLEVLNEREIPVHLEFAFTPDEKVR EEILNVLGMFYSVGLNEVELASIM
EILGEKKLAKELLAHPVDPIAVTEAMLKLAKKTGVKRIHFHTYGYLALTEYKGEHVRD
ALLFAALAAA KAMGNITSLEEIREATSVPVNEKATQVEEKLRAEYGIKEGIGEGVEGYQ
IAFIPTKIVAKPKSTVGIGDTISSAFIGFSFTL

>2QZJA 136 XRAY 2.89 0.257 0.285 no Two-component response regulator <UNP Q180B0_CLOD6> [CLOSTRIDIUM DIFFICILE]

MSLQTKILI IDGDKDNCQKLKGFLEEKGISIDLAYNCEE AIGKIFS NKYDLIFLEIILSD
GDGWTLCCKIRNVTTCP IYVMTYINEDQSILNALNSGGDDYLIKPLNLEILYAKVKAILR
RMNSYVNNEGHHHHHH

>3TU8A 210 XRAY 1.04 0.129 0.160 no Burkholderia Lethal Factor 1 (BLF1) <UNP Q63UP7_BURPS> [BURKHOLDERIA PSEUDOMALLEI]

PNSLEAQIRQAMKTGSTLTIEFDQALNQKSPGT LNVFLHPANGGVRIDLDSGNQGEPAKI
LWLPWKQ GELQTLQPGSISTVDMLFFTYYLSGCKVFAGDGGPVWHIDAPVEANQFWRMS
SDEWMEDWEVGTDRQVAYLHRAGQSDSLWNLSAYLEGAAPSTYGRDNLGQAVVGGIVTGR
QQMSLYQYATTSSGSSAWSPLTYTLQQRKQ

>3LTJA 201 XRAY 1.80 0.177 0.227 no AlphaRep-4 <PDB 3LTJ> [SYNTHETIC]

MRGSHHHHHHTDPEKVE MYIKNLQDDSYVVRRAAAYALGKIGDERAVEPLIKALKDEDAW
VRRAAADALGQIGDERAVEPLIKALKDEDGWVRQSAVALGQIGDERAVEPLIKALKDED
WVFRIAA AFALGEIGDERAVEPLIKALKDEDGWVRQSAADALGEIGGERVRAAMEKLAET
GTGFARKVAVNYLETHKSLIS

>2PONA 172 XRAY 1.41 0.170 0.203 no Hypothetical protein NMB1532 <UNP Q9JYL1_NEIMB> [NEISSERIA MENINGITIDIS]

SNAMNPFETKSVTFAEPIEMLYACHGKVRRCGQVAMLSDYIAENG CNQIVLQTIRQIAQ
YFNVAAPLHHEDEEENFFPLLLQYAPQAQESVDELLRQHIGLHDNWA AVSAEFAKLEADN
AYVPDEEAFKRFRVAGYDVHLAIEEPLFDMGNTFIPKEKLTEIGEIMAARRRK

>3LLOA 143 XRAY 1.57 0.156 0.196 no Prestin <UNP S26A5_RAT> [RATTUS NORVEGICUS]

SPSYTVLGQLPDTDVYIDIDAYEEVKEIPGIKIFQINAPIYYANSPLYSSALKRKTGVNG
SENIHTVILDFTQVNFMDSVGKTLGIVKEYGDVGIYVYLAGCSAQVNDLTSNRFFEN
PALKELLFHSIHDAVLGSQVREA

>1V6TA 255 XRAY 1.70 0.202 0.227 no Hypothetical UPF0271 protein PH0986 <UNP Y986_PYRHO>
[PYROCOCCUS HORIKOSHII]

MRVDLNSDLGESFGRYKGLDEEVMKYITSANVACGWHAGDPLVMRKTVRLAKENDVQVG
AHPGYPDLMGFGRRYMKLTPEEARNYILYQVGALYAFKAEGLELQHVKPHGALYNAMVK
EEDLARAVIEGILDFDKDLILVTLSNSRVADIAEEMGLKVAHEVFADRAYNPDGTLVPRG
RPGAVIEDKEEIAERVISMVKDGGIRAINGEWVDLKVDTCVHGDNPKAVEITSYIRKVL
EEEGVKIVPMKEFIR

>3NOWA 810 XRAY 2.99 0.202 0.235 no UNC-45 protein, SD10334p <UNP Q960B1_DROME> [DROSOPHILA
MELANOGASTER]

NAKTSTKVKQMMDLTFDLATPIDKRRAAANNLVLAKEQTGAELLYKDHCIKVASLTKV
EKDQDIYVNMVHLVAALCENSVERTKGVLTGLVGPWFMRVLDQKHENCVSTAQFCLQTIL
NALSGLKNKPDSPDKELCTRNNREIDTLLTCLVYSITDRTISGAARDGVIELITRNVHY
TALEWAERLVEIRGLCRLLDVCSELEDYKYESAMDITGSSSTIASVCLARIYENMYDEA
KARFTDQIDEYIKDKLLAPDMESKVRVTVAITALLNGPLDVGNQVVAREGILQMILAMAT
TDDELQQRVACECLIAASSKKDKAKALCEQGV DILKRLYHSKNDGIRVRALVGLCKLGSY
GGQDAAIRPFGDGAALKLAEACRRFLIKPGDKDIRRWAADGLAYLTDAECKELIEDK
ASIHALMDLARGGNQSCLYGVVTTFVNL CNAYEKQEMLEPEMIELAKFAKHIPPEEHEDD
VDFINKRITVLANEGITTALCAKTESHNSQELIARVLNAVCGKLKRGKVVQEGGVKA
LLRMALEGTEKGRHATQALARIGITINPEVSFSGQRSLDVIRPLLNLQQDCTALENFE
SLMALTNLASMNESVRQRIKEQGVSKIEYYLMEDHLYL TRAAAQCLCNLVMSEDVIKMF
EGNDRVKFLALLCEDEDEETATACAGALAIITSVSVKCEKILAIASWLDILHTLIANP
SPAQQHRGIVIIILNMINAGEEIAKKLFETDIMELLSGLGQLPDDTRAKAREVATQCLAAA
ERYRIIERSDNAEIPDVFAENSKISEIID

>2P38A 166 XRAY 1.80 0.210 0.257 no Protein involved in ribosomal biogenesis <UNP
Q9V219_PYRAB> [PYROCOCCUS ABYSSI]

MSGELRVRRASSWELDLILKEAEKYGELLHEFFCVVEGKYRDVYAVNEEVWKI IEDINMR
PYSLGTFVGTIRVDENLVEKFYPNLEFFSLIKLEKNYVILGPKASFLFTTGKDAPKEAVR
EIKWQGSKRVVVNLGDIIGIGLINPKSDRRFIKLNKDVGEFLRR

>4BWZA 394 XRAY 2.98 0.224 0.248 no NA(+)/H(+) ANTIporter <UNP Q72IM4_THET2> [THERMUS
THERMOPHILUS]

MHGAHLLLEIFYLLAAQVCAFIFKRLNQPVVIGEVLGVLVGPALLGLVHEGEILEFLA
ELGAVFLLFMVLETRLKDILAVGKEAFLVAVLGVALPFLGGYLYGLEIGFETLPALFLG
TALVATSVGITARVLQELGVLSRPYSRIILGAAVIDDVLGLIVLACVNGVAETGQVEVGA
ITRLIVLSVVFVGLAVFLSTLIARLPLERLPVGSPLGFALALGVGMAALAASIGLAPIVG
AFLGGMLLSEVREKYRLEEFIFAIESFLAPIFFAMVGVRLSALASPVVLVAGTVVTVI
AILGKVLGGFLGALTQGVRSALTGCGMAPRGEVGLIVAALGLKAGAVNEEYAIVLFMV
VFTTLFAPFALKPLIAWTERERAKEGSENLYFQ

>4HTYA 359 XRAY 2.00 0.155 0.169 no Cellulase <UNP I6PLH5_9BACT> [UNCULTURED BACTERIUM]

MGSSHHHHHSSGLVPRGSHMDNAWETTSGWWNASDIPAFDKSKITRQLPLIKVEGNRFV
DEQGKTIVFRGVNISDPDKIDKDKRFSKKHFEVIRSWGANVVRVPVHPRAWKERGKGYL
ELLDQVVAWNNELGIYTILDWHSIGNLKSEMFQNNSYHTTKGETFDFWRRVSERYNGINS
VAFYEIFNEPTVFNGRLGIATWAEWKAINEEAITIIQAHNPKAIALVAGFNWAYDLKEAA

ANPIDRQNIAYVSHYPYQKVGAPYQANWERDFGFMADKYPVFATEIGYQRATDKGAHIPV
 IDGSGYGPRTIDYFNSKGISWVAVFDPDWSPQLFTDYQTYTPTMQGEHFRKVMLQDNK
 >1FLOA 422 XRAY 2.65 0.254 0.297 no FLP RECOMBINASE <UNP_FLP_YEAST> [SACCHAROMYCES CEREVISIAE]
 PQFDILCKTPPKVLVRQFVERFERPSGEKIALCAAELTYLCWMITHNGTAIKRATFMSYN
 TIISNSLSFDIVNKSLLQFKYKTQKATILEASLKKLIPAWFTIIPYYGQKHQSDITDIVS
 SLQLQFESSEEDKGNSSHKKMLKALLSEGESIWEITEKILNSFEYTSRFTKTKTLYQFL
 FLATFINCGRFSDIKNVDPKSFKLQNKYLGVIQCLVTETKTSVSRHIYFFSARGRIDP
 LVYLDEFNRNPEVLKRVNRTGNSSSNKQEQYQLKDNLVRSYNKALKKNAPYSIFAING
 PKSHIGRHLMTSFLSMKGLTELTVVGNWSDKRASAVARTTYTHQITAIPDHYFALVSRY
 YAYDPISKEMIALKDETNPIEEWQHIEQLKGSAGSIRYPAWNGIISQEVLDYLSSYINR
 RI
 >3QRLA 140 XRAY 1.70 0.190 0.235 no Transcription initiation factor TFIID subunit 14 <UNP_TAF14_YEAST> [SACCHAROMYCES CEREVISIAE]
 GSHMVATVKRTIRIKTQQHILPEVPPVENFPVRQWSIEIVLLDDEGKEIPATIFDKVIYH
 LHPTFANPNRTFTDPPFRIEEQWGGFPLDISVFLLEKAGERKIPHDNLFLQESYEVEHV
 IQIPLNKPILLTEELAKSGST
 >4IABA 142 XRAY 1.66 0.164 0.184 no hypothetical protein <UNP_A7V626_BACUN> [BACTEROIDES
 UNIFORMIS]
 GQESAERPAELAGIWQLCHYVSEIPDVPGLKPSNTFKVLSDDGRIVNFTMIPGKDAII
 TGYGTYQQLTDNSYKESIEKNIHPLMDHKDNILEFEIGDDGVMYLYFIAKDLNGNELN
 TWFHETWKRVGMPAKFPEDLVR
 >3B79A 129 XRAY 1.37 0.158 0.182 no Toxin secretion ATP-binding protein <UNP_Q87FE3_VIBPA> [VIBRIO
 PARAHAEMOLYTICUS RIMD 2210633]
 SNAMKDPLLNSLIYVSRYGLANSPEALVNGPLSDGKLTPLLPRAAERAGLVAKENRA
 ELEKISSLILPAILVLKGGDSCVLNSINMETREAEVTTLESMPVISPILDLEQYTGR
 YFLVKKQFR
 >1LFWA 470 XRAY 1.80 0.174 NA no pepV <UNP_PEPV_LACDL> [LACTOBACILLUS DELBRUECKII]
 MDLNFKELAEAKKDAILKDLEELIAIDSSDLENATEEYYPVGKGPVDAMTKFLSFAKRDG
 FDTENFANYAGRVNFGAGDKRLGIIGHMDVVPAGEGWTRDPFKMEIDEEGRIYGRGSADD
 KGPSLTAYYGMILLKEAGFKPKKKIDFVLGTNEETNWVGIDYLYLKHEPTPDIVFSPDAEY
 PIINGEQGIFTLEFSFKNDTKGDYVLDKFKAGIATNVTPQVTRATISGPDLEAVKLAYE
 SFLADKELDGSFEINDESADIVLIGQGAHASAPQVGKNSATFLALFLDQYAFAGRDKNFL
 HFLLAEVEHEDFYGKKLGFHDDLMGDLASSPSMFDYEHAGKASLLNNVRYPGTDPDTM
 IKQVLDKFSGLDVTYNGFEPEHYVPGSDPMVQTLLKVYEKQTGKPGHEVVIGGGTYGRL
 FERGVAFGAQPENGPMVMHAANEFMMLDDLILSIAIYAEAIYELTKDEEL
 >3GWCA 258 XRAY 1.90 0.189 0.229 no Thymidylate synthase thyX <UNP_THYX_MYCTU>
 [MYCOBACTERIUM TUBERCULOSIS]
 MAETAPLRVQLIAKTDFLAPPDVPWTTDADGGPALVEFAGRACYQSWSKPNPKTATNAGY
 LRHIIDVGHFVLEHASVSFYITGISRSCTHELIRHRHFSYSQLSQRYVPEKDSRVVPP
 GMEDDADLRHILTEAADAARATYSELLAKLEAKFADQPNAILRRKQARQAARAVLPNATE
 TRIVVTGNRAWRHFIAMRASEHADVEIRRLAIECLRQLAAVAPAVFADFVTTLDGTE
 VATSPLATEALEHHHHHH
 >1AOCA 175 XRAY 2.00 0.191 0.282 no COAGULOGEN <UNP_COAG_TACTR> [TACHYPLEUS TRIDENTATUS]
 ADTNAPICLCDEPGVLGRTQIVTTEIKDKIEKAVEAVAQESGVSGRGFSIFSHHPVFREC
 GKYECRTVRPEHSRCYNFPFTHFKSECPVSTRDCEPVFGYTVAGEFRVIVQAPRAGFRQ

CVWQHKKRFGSNSCGYNGRCTQQRSVVRLVTYNLEKDGFLCESFRGCCGPCRSF

>2ZFYA 234 XRAY 1.69 0.195 0.239 no Ubiquitin thioesterase OTUB1 <UNP OTUB1_HUMAN> [HOMO SAPIENS]

GSEIAVQNPLVSRLELSVLYKEYAEDDNIYQQKIKDLHKKYSYIRKTRPDGNCFYRAFG
FSHLEALLDDSKELQRFKAVSAKSKEDLVSQGFTEFTIEDFHNTFMDLIEQVEKQTSVAD
LLASFNDQSTSDYLVVYLRLLTSGYLQRESKFFEHFIEGGRTVKEFCQQEVEPMCKESDH
IHIALAQALSVSISQVEYMDRGEGETTNPHIFPEGSEPKVYLLYRPGHYDILYK

>1VKMA 297 XRAY 1.90 0.156 0.200 no conserved hypothetical protein TM1464 <UNP Q9X1H5_THEMA> [THERMOTOGA MARITIMA]

MGSDKIHIIHHHHVIIIESRIEKGKPVVGMETTVFVHGLPRKEAIELFRRAKEISREKGFQL
AVIGILKGKIVAGMSEEELEAMMREGADKVGTR EIPVVAEGKNAATTVSATIFLSRRIG
IEVVVTGGTGGVHPGRVDVSQDLTEMSSSRVAVLVSSGIKSILDVEATFEMLETL EIPLVG
FRTNEFPLFFSRKSGRRVPRIENVEEVLKIYESMKEMELEKTLMLVNPVPEEYEIPHDEI
ERLLEKIELEVEGKEVTPFLKKLVEMTNGRTLKANLALLEENVKLAGEIAVKLKRS

>2DBSA 90 XRAY 2.10 0.256 0.271 no hypothetical protein TTHC002 <UNP Q5SGN2_THET8> [THERMUS THERMOPHILUS]

MVNP AERLAELDGVLMQYLLEADLLREL PPTYRLVLLPLDEPEVAAQALAWAMEAPNPEG
WPSVYALFLQGRPIRLLLLKGEEVAPRAA

>2OCGA 254 XRAY 1.75 0.182 0.201 no Valacyclovir hydrolase <UNP BPHL_HUMAN> [HOMO SAPIENS]

SVTSKAVAVNGVQLHYQQTGEGDHAVLLLPGLGSGETDFGPQLKNLNKKLFTVVAWDPR
GYGHSRPPDRDFPADFFERDAKDAVDLMKALKFKKVSLLGWSGGITALIAAAKYP SYIH
KMWIWGANAYVTDEDSMIYEGIRDVSKWSERTRKPLEALYGYDYFARTCEKWVDGIRQFK
HLPDGNICRHLLPRVQCPALIVHGEKDPLVPRFHADF IHKHVKGSRHLMLPEGKHNHLR
FADEFNKLAEDFLQ

>2ODVA 235 XRAY 2.05 0.212 0.256 no Plectin 1 <UNP Q6S383_HUMAN> [HOMO SAPIENS]

GSHMRANELQLRWQEYRELVL LLLQWMRHHTAAFEERRFPSSFEEIEILWSQFLKFEME
LPAKEADKNRSKGIYQSLEGAVQAGQLKVPPGYHPLDVEKEWGLHVAILEREKQLRSEF
ERLEALQRIVTKLQMEAGLAEELNQADALLQSDVRLLAAGKVPQRAGEVERDLKADSM
IRLLFNDVQTLKDGRHPQGEQMYRRVYRLHKRLVAIRTEYNLRLKAGVAAPATQV

>4HI8B 72 XRAY 1.20 0.145 0.168 no LIM and senescent cell antigen-like-containing domain protein 1 <UNP LIMS1_HUMAN> [HOMO SAPIENS]

SENL YFQGSASATCERCKGFAPA EKIVNSNGELYHEQCFVCAQCFQQFPEGLFYEFEGR
KYCEHDFQMLFA

>3MTOA 290 XRAY 1.58 0.178 0.204 no uncharacterized protein PA1789 <UNP Q9I2V3_PSEAE> [PSEUDOMONAS AERUGINOSA]

SNAMQAIR SILVIEPDQLEGLALKRAQLIAGVTQSHLHLVCEKRRDHS AALNDLAQEL
REEGYSVSTNQAWKDSLHQTIIEAQEAEGGLI IKQHFPDNP LKAILTPDDWKLLRFAP
CPVLMTKTARPTWGKILAAVDVGNNDGEHRS LHAGIISHAYDIAGLAKATLHVISAHPS
PMLSSADPTFQLSETIEARYREACRTFQA EYGFSDQLHIEEGPADVLIPRTAQKLDAVV
TVIGTVARTGLSGALIGNTA EVVLDTLES DVLVLPDDIIAHLEELASKE

>3RF3A 258 XRAY 1.61 0.184 0.195 no Vinculin <UNP VINC_HUMAN> [HOMO SAPIENS]

MPVFHTRTIESILEPVAQQISHLVIMHEEGEVDGKAIPDLTAPVA AVQA AVSNLVRVGKE
TVQTTEDQILKRMPPAFIKVENACTKL VQAAQMLQSDPYSPARDYLIDGSRGILSGTS
DLLLTFDEAEVRKIIRVCKGILEYLTVA EVVETMEDLVITYTKNLGPGMTKMAKMIDERQQ
ELTHQEHRVMLVNSMNTVKELLPVLISAMKIFVTTKNSKNQ GIEEALKNRNFTVEKMSAE

INEIIRVLQLTSWDEDAW

>3NYMA 128 XRAY 1.90 0.174 0.208 no uncharacterized protein <UNP Q9JS17_NEIMB> [NEISSERIA MENINGITIDIS SEROGROUP B]

SNAMETLNDIKKILINVGLYQGFDLTDPKVSEEVNHHETANMKWIKDYTSDGNWDNEFKED
LKNFLDYMEVCQLALNDKNFKIASNSLFMAMIYAGNLSLIFDSIKTDISTLLSAEYKKNS
FSWPSLDE

>3JU8A 490 XRAY 1.82 0.160 0.196 no Succinylglutamic semialdehyde dehydrogenase <UNP ASTD_PSEAE> [PSEUDOMONAS AERUGINOSA]

SNAMMSTHYIAGQWLAGQGETLES�DPVGQGVVWSGRGADATQVDAAVCAAREAFPAPAWR
RPLEQRIELLERFAATLKSRADLARVIGEETGKPLWESATEVTSMVNVKVAISVQAFRER
TGEKSGPLADATAVLRHKPHGVAVFGPYNFPGHLPNGHIVPALLAGNCVVFKEPSELTPK
VAELTLKAWIQAGLPAGVLNLVQGGRETGVALAAHRLDGLFFTGSSTGNLLHSQFGGQ
PQKILALEMGGNNPLVVEEVADLDAVYTI IQSAFISAGQRCCTCARRLLVPQGAWDALL
ARLVAVSATLRVGRFDEQPAFPMGAVISLSAAEHLLKAQEHLLIGKGAQPLLAMTQPIDGA
ALLTPGILDVSAVAERPDEEFFGPLLQVIRYSDFAAAIREANATQYGLAAGLLSDSRERF
EQFLVESRAGIVNWNKQLTGAASSAPFGGIGASGNHRPSAYYAADYCAYPVASLESPPSVS
LPATLTPGIS

>2HLYA 207 XRAY 1.60 0.174 0.214 no Hypothetical protein Atu2299 <UNP Q8UD29_AGRT5> [AGROBACTERIUM TUMEFACIENS STR.]

GYFEGMLIKQTDYFRIYRVINSLISQNDPASASMYFSTFGAFILQQHYKVKAVPKGGL
AAYNLGGTVLLFADHREDGYVTGAGENFHCWVEADGWIDFMAPAFSEGTDALAVPAKMF
QRPLSAMAASINDLGQSGDFFYRSEPEATARRFADWHKQAMIGDMASVAANWFRKSPKQM
AASLSVTD RDGKARTVPLTGEMLTGAW

>1KWGA 645 XRAY 1.60 0.168 0.184 no BETA-GALACTOSIDASE <UNP O69315_9DEIN> [THERMUS THERMOPHILUS]

MLGVCYYPEHWPKERWKEDARRMREAGLSHVRIGEFAWALLEPEPGRLEWGWLDEAIATL
AAEGLKVVLGTPTATPPKWLVDYPEILPVDREGRRRRFGRRHYCFSSPVYREEARRIV
TLAERYGGLEAVAGFQTDNEYGCHDTVRCYCPRCQEAFRGWLEARYGTIEALNEAWGTA
FWSQRYRSFAEVELPHLTAEPNP SHLLDYRFASDQVRAFNRQLQVEILRAHAPGKFVTH
NFMGFFTDLDAFALAQDLDFASWDSYPLGFTDLMPLPPEEKLRARTGHPDVAAFHHDLY
RGVGRGRFWVMEQQPGPVNWPAPGNPSPAPGMVRLWTWEALAHGAEVVS YFRWRQAPFAQE
QMHAGLHRPDSAPDQGF FEAKRVAEELALALPPVAQAPVALVFDYEAAWIYEVQPQGAE
WSYGLVLYLFYSALRRLGLDVDVPPGASLRGYAFVVP SLPIVREEALEAFREAE GPVL
FGPRSGSKTETFQIPKELPPGPLQALLPLKVV RVESLPPGLLEVAEGALGRFPLGLWREW
VEAPLKPLLTFQDGKGALYREGRYLYLAAPSP ELAGRLLSALAAEAGLKVLSLPEGLRL
RRRGTVWFVAFNYGPEAVEAPASEGARFLLGSRRVGPYDLAVWEEA

>2B4HA 254 XRAY 1.60 0.204 0.225 no Outer capsid protein VP4 <UNP Q91HI9_ROTTH> [RHESUS ROTAVIRUS]

MGSSHHHHHHSSGLVPRGSHMRAQANEDIVSKTSLWKEMQYNRDITIRFKFASSIVKSG
GLGYKWSEISFKPANYQYTYTRDGEEVTAHTTCSVNGMNDNFNGGSLPTDFVISRYEVI
KENSYYVVDYWDQSQAFRNMVYVRS LAANLSVICTGGDYSFALPVGQWPVMTGGAVSLH
SAGVTLSTQFTDFVSLNSLRFRFRLTVEEPSFSITRTRVSRLYGLPAANPNNGKEYYEVA
GRFSLISLVPSNDD

>4GOAA 317 XRAY 2.10 0.175 0.205 no Non-structural protein 2 <UNP NSP2_ROTTH> [SIMIAN 11 ROTAVIRUS]

MAELACFCYPHLEND SYKFI PFNNLAIKAMLTAKVDKKMDKFYDSIIYGIAPPPQFKKR

YNTNDNSRGMNFETIMFTKVAMLICEALNSLKVTQANVSNVLSRVVSIRHLENLVIRKEN
PQDILFHSKDLLLKSTLIAIGQSKEIETTITAEGGEIVFQNAAFMWKLTYLEHQLMPIL
DQNFIEYKVTLNEDKPIDSVHVVELVAELRWQYNKFAVITHGKGHYRIVKYSSVANHADR
VYATFKSNVKTGVNDFNLLDQRIIWQNWYAFTSSMKQGNTLDVCKRLLFQKMKPEKNPF
KGLSTDRKMDEVSQVGV

>2XZEA 146 XRAY 1.75 0.193 0.227 no STAM-BINDING PROTEIN <UNP STABP_HUMAN> [HOMO SAPIENS]
MSDHGDVSLPPEDRVRLSQLGSAVEVNEDIPPRRYFRSGVEIIRMASIYSEEGNIEHAF
ILYNYKITLFIIEKLPHRDYKSAVIPEKKDVTKKLKEIAFPKAEELKAELLKRYTKEYTE
YNEEKKKEAEELARNMAIQQELEKEK

>3AJIB 83 XRAY 2.05 0.171 0.229 no Proteasome (Prosome, macropain) 26S subunit, ATPase, 4 <UNP Q6ZWN9_MOUSE> [MUS MUSCULUS]
MDRRQKRLIFSTITSKMNLSEEVDLEDYVARPDKISGADINSICQESGMLAVRENRYIVL
AKDFEKAYKTVIKKDEQEHEFYK

>3L4RA 170 XRAY 1.45 0.158 0.168 no Minor allergen Can f 2 <UNP ALL2_CANFA> [CANIS FAMILIARIS]
MEGNHEEPQGGLEELSGRHSVALASNSDLIKPWGHRVFIHMSAKDGNLHGDILIPQ
DGQCEKVSLETAFTATSNKFDLEYWGHNDLYLAEVDPKSYLILYMINQYNDTSLVAHLM
VRDLRQQDFLPAFESVCEDIGLHKDQIVVLSDDDRCCQSRDLEHHHHHH

>3PIUA 436 XRAY 1.35 0.149 0.171 no 1-aminocyclopropane-1-carboxylate synthase <UNP 1A1C_MALDO> [MALUS DOMESTICA]
MRMLSRNATFNSHGQDSSYFLGWQEYKPNYHEVHNTNGIIQMGLAENQLCFDLLESWLA
KNPEAAAFKNGESIFAELALFQDYHGLPAFKKAMVDFMAEIRGNKVTDFPNHLVLTAGA
TSANETFIIFCLADPGEAVLIPTPYYPGFDRDLKWRGTVEIVPIHCTSSNGFQITETALEE
AYQEAERNLRVKGVLTNPSPNPLGTTMTRNELYLLLSFVEDKGIHLISDEIYSGTAFSS
PSFISVMEVLKDRNCENSEVWQRVHVVSLSKKDLGLPGFRVGAISNDMMVAAATKM
SSFGLVSSQTQHLLSAMLSDKKLTKNYIAENHKRLKQRQKLVSGLQKSGISCLNGNAGL
FCWVDMRHLLRSNTFEAEMELWKKIVYEVHLNISPGSSCHCTEPGWFRVCFANLPERTLD
LAMQRLKAFVGEYYNV

>20Z4A 265 XRAY 2.70 0.209 0.253 no Intercellular adhesion molecule 1 <UNP Q5NKV7_HUMAN> [HOMO SAPIENS]
VLPATPPQLVSPRVLEVDLTQGTVVCSLDGLFPVSEAQVHLALGDQRLNPTVTYGNDSFSA
KASVSVTADEGTQRLTCAVILGNQSQETLQTVTIYSFPAPNVILTKPEVSEGTEVTVKC
EAHPRAKVTNLGVPAQPLGPRAQLLLKATPEDNGRSFSCSATLEVAGQLIHKNQTRRLV
LYGPRLDERDCPGNWTWPENSQQTPMCQAWGNPLPELKCLKDGTFLPIGESVTVTRDLE
GTYLCRARSTQGEVTREVTNVLSLSP

>3MDPA 142 XRAY 1.90 0.183 0.227 no Cyclic nucleotide-binding domain (CNMP-BD) protein <UNP Q39VF8_GEOMG> [GEOBACTER METALLIREUCENS]
GMISPERLRVYRFFASLTDEQLKDIALISEEKSFTGSGVIFKENSKADNMLLLEGGVEL
FYSNGGAGSAANSTVCSVPGAIFGVSSLIKPYHYTSSARATKPVVRVDINGARLREMSE
NNQALGQVLMNNVAAVLARLH

>1B9LA 120 XRAY 2.90 0.188 0.259 no EPIMERASE <UNP FOLX_ECOLI> [ESCHERICHIA COLI]
MAQPAAIIRIKNLRLRTFIGIKEEEINNRQDIVINVTIHYPADKARTSEDINDALNYRTV
TKNIIQHVENNRFSLEKLTQDVLDIAREHHWVTYAEVEIDKLHALRYADSVMTLSWQR

>4HH3C 240 XRAY 1.75 0.171 0.198 no AppA protein <UNP Q53119_RHOSH> [RHODOBACTER SPHAEROIDES]
VEADTFALYALTEAQAGRSGRAKAVARLSDLLSTDPLGRLTEVEELLRAHAPTAADFARL
FEACAERLTRALAEDRISRMQVTLAYSALQMALRRIHHLDPQKSVGAVLVAGVPGHKPI

LEAALAAEMLRAVGWSTSVVHPESVAALAAARLKTSRTSTLVVAPSLLEGTEQEADTLRFV
SALRARTDLPLGLSILVGGRLAQLPPSKLKDSGADAGFAHLALLPAALARVASSAHHHHHH
>3I6EA 385 XRAY 1.70 0.236 0.263 no Muconate cycloisomerase I <UNP Q5LM96_SILPO> [RUEGERIA
POMEROYI]
MSLGDLEQKIIAMDLWHLALPVVSARDHGI GRVEGSCEIVLRLVAEGGAEGFGEASPA
VFTGTPEASYAALDRYLRLPLVIGRRVGDRAIMDEAARAVAHCTEAKAALDSALLDLAGR
ISNLPVWALLGGKCRDTIPLSCSIANPDFDADIALMERLRADGVGLIKLKTGFRDHAFDI
MRLELIARDFPEFRVRVDYNQGLEIDEAVPRVLDVAQFQPDFIEQPVRAHHFELMARLRG
LTDVPLLADESVYGPEDMVRAAHEGICDGVSIKIMKSGGLTRAQTVARIAAAHGLMAYGG
DMFEAGLAHLAGTHMIAATPEITLGCIFYQASYFLNEDILETPFRVEAGQVIVPDGPGLG
ARADPEKLEHYAVRRSGEGHHHHHH
>3TRTA 77 XRAY 2.30 0.234 0.298 no Vimentin <UNP VIME_HUMAN> [HOMO SAPIENS]
GGSKPDCTAAMRDVRQQYESVAAKNLQEAEEWYKSKFADLSEAANRNDALRQAKQESTE
YRRQVQSLTMEVDALKG

>1GHEA 177 XRAY 1.55 0.209 0.230 no ACETYLTRANSFERASE <UNP TTR_PSESZ> [PSEUDOMONAS SYRINGAE
PV. TABACI]
MNHAQLRRVTAESFAHYRHGLAQLLFETVHGGASVGFMA DLDMQQAYAWCDGLKADIAAG
SLLLWVVAEDDNV LASAQLSLCQKPNGLNRAEVQKLMVLPSARGRLGRQLMDEVEQVAV
KHKRGLLHLDTEAGSVAEFYSALAYTRVGELPGYCATPDGRLHPTAIYFKTLGQPT
>1QFOA 119 XRAY 1.85 0.200 0.234 no SIALOADHESIN <PIR S50065> [MUS MUSCULUS]
TWGVSSPKNVQGLSGSCLLIPCIFSYPADVPVSNGITAIWYDYSGKRQVVIHSGDPKLV
DKRFRGRAELMGNMDHKVCNLLLKDLKPEDSGTYNFRFEISDSNRWLDVKGTTVTVTTD
>3QVAA 116 XRAY 1.75 0.200 0.223 no Transthyretin-like protein <UNP A6T926_KLEP7> [KLEBSIELLA
PNEUMONIAE SUBSP. PNEUMONIAE]
ENLYFQGHMSTLSTHILDISTGTPAEGVTVSLSREGETLANLV TNAQGRIATFSAAPLPA
GRYCLTAETGAWFARAGRESVFTRAQIDFVIGEEAEDHFHLPFLIAPGGWSTYRGS
>2RAAA 204 XRAY 2.12 0.217 0.251 no Pyruvate synthase subunit porC <UNP PORC_THEMA>
[THERMOTOGA MARITIMA MSB8] MGSDKIH HHHHMPVAKKYFEIRWHGRAGQGAKSASQMLAEAALEAGKYVQAFPEYGAER
TGAPMRAFNRIGDEYIRVRS AVENPDVVVIDETLLSPAIVEGLSEDGILLVNTVKDFEF
VRKKTGFNGKICVVDATDIALQEIKRGIPNTPMLGALVRVTGIVPLEAIEKRIEKMFGKK
FPQEVIDANKRALRRGYEEVKCSE
>1WE30 100 XRAY 2.80 0.239 0.279 no cpn10(GroES) <UNP CH10_THET2> [THERMUS THERMOPHILUS]
AAEVKTVIKPLGDRVVVKRIEEEPKTKGGIVLPDTAKEKPQKGKVIAGTGRVLENGQRV
PLEVKEGDIVVFAKYGGTEIEIDGEEYVILSERDLLAVLQ
>3K3VA 100 XRAY 1.80 0.208 0.224 no Protein SMY2 <UNP SMY2_YEAST> [SACCHAROMYCES CEREVISIAE]
GSNGMSQLPAPVSVESWRYIDTQGGIHGPFTTQMMSQWYIGGYFASTLQISRLGSTPET
LGINDIFITLGELMTKLEKYDTPFTTFDKLHVQTTSSDS
>3S6MA 167 XRAY 1.65 0.148 0.183 no Peptidyl-prolyl cis-trans isomerase <UNP Q3JQT3_BURP1>
[BURKHOLDERIA PSEUDOMALLEI]
PGSGMVELHTNHGVIKLELDEAKAPKTVENFLNYVKKGHYDGTIFHRVINGFMIQGGGFE
PGLKQKPTDAPIANEANGLKNDTYTIAMARTNDPHSATAQFFINVNDNEFLNHSSPTPQ
GWGYAVFGKVVVEGQDIVDKIKAVKTGSKGFHQDVPNDVVIKAVVV
>4F8LA 145 XRAY 1.50 0.141 0.182 no pH 6 antigen <UNP PSAA_YERPE> [YERSINIA PESTIS]

MNTFHVDFAPNTGEIFAGKQPGDVTMFTLTMGDTAPHGGWRLIPTGDSKGGYMISADGDY
VGLYSYMSWVGIDNNWYINDDSPKDIKDHLYVKAGTVLKPTTYKFTGRVEEYVFDNKQS
TVINSKDVSGEVTVKQGLEHHHHHH

>3IUOA 122 XRAY 1.60 0.190 0.221 no ATP-dependent DNA helicase RecQ <UNP Q7MX11_PORGI>
[PORPHYROMONAS GINGIVALIS] ENEIERPEDMRVRTLANKSKMKVSIVQQIDRKVALDDIAVSHGLDFPELLSEVETIVYSG
TRINIDYFINEVMDHLEDIFEYFKESTTDSLEEAMQELGKDYSEEEIRLVRIKFLSEM
AN

>1YQSA 349 XRAY 1.05 0.114 0.136 no D-alanyl-D-alanine carboxypeptidase <UNP DAC_STRSR>
[STREPTOMYCES SP.]

ADLPAPDDTGLQAVLHTALSQGAPGAMVRVDDNGTIHQLSEGAD RATGRAITTTDRFRV
GSVTKSFSAVVLLQLVDEGKLDLDASVNTYLPGLLPDDRITVRQVMSHRSGLYDYTNDMF
AQTVPGFESVRNKVFSYQDLITLSLKHGVTNAPGAAYSNTNFVAGMLIEKLTGHSVA
TEYQNRIFTPLNLTDTFYVHPDVTIPGTHANGYLTPDEAGGALVDSTEQTVSWAQSAGAV
ISSTQDLDTFFSALMSGQLMSAAQLAQMQQWTTVNSTQGYGLGLRRRDLSCGISVYGHTG
TVQGYTYAFASKDGKRSVTALANTSNNVNLNTMARTLES AFCGKPTT

>1J1IA 296 XRAY 1.86 0.217 0.248 no meta cleavage compound hydrolase <UNP Q84II3_9BURK>
[JANTHINOBACTERIUM]

MLNKAEQISEKSERAYVERFVNAGGVETRYLEAGKGQPVILIHGGGAGAESEGNWRNVIP
ILARHYRVIAMDMLGFGKTAKPDIEYTQDRRIRHLHDFIKAMNFDGKVSIVGNSMGGATG
LGVSVLHSELVNALVLMGSAGLVVEIHEDLRPIINYDFTREGMVHLVKALTNDGFKIDDA
MINSRYTYATDEATRKYAVTMQWIREQGGLFYDPEFIRKVQVPTLVVQKDDKVVPVET
AYKFLDLIDDSWGYIIPHCGHWAMIEHPEDFANATLSFLSLRVDITPAAHHHHHH

>2A2FX 325 XRAY 2.50 0.243 0.276 no Exocyst complex component Sec15 <UNP SEC15_DROME>
[DROSOPHILA MELANOGASTER]

MVNILWELLHNMRDHYNEVLLQRWVHVFREILDKEQFLPMVVQNTTEYECIIERFPFHSE
QLENAPFPKFPFSRMVPEVYHQAKEFMYACMKFAEELTSPNEVAAMVRKAANLLLRS
FSGCLSVVFRQPSITLTQLIQI I IDTQYLEKAGPFLDEFVCHMTNTERSVSQTPSAMFHV
ARQDAEKQVGLRICKIDEFFELSAYDWLLVEPPGIASAFITDMISYLSKSTFDSFAFKLP
HIAQAACRRTFEHAIEKIYSIMYDEDEVKQISTGALTQINLDMQCEFFAASEPVPGLKEG
ELSKYFLNRNQLDLLILEHHHHHH

>2WEKA 341 XRAY 1.90 0.168 0.214 no ZINC-BINDING ALCOHOL DEHYDROGENASE DOMAIN- CONTAINING
PROTEIN 2 <UNP ZADH2_HUMAN> [HOMO SAPIENS]

SMMQKLVVTRLSPNFREAVTLSRDCPVPLPGDGDLLVRNRFVGVNASDINYSAGRYDPSV
KPPFDIGFEGIGEVVALGLSASARYTVGQAVAYMAPGSFAEYTVVPASIATPVPSVKPEY
LTLLVSGTTAYISLKEGLSEGKKVLVTAAGGTGQFAMQLSKKAKCHVIGTCSSDEKS
AFLKSLGCDRPINYPTEPVGTVLKQYEPGVVVYESVGGAMFDLAVDALATKGRLIVIG
FISGYQTPTGLSPVKAGTLPKALLKKSASVQGFNLHYLSKYQAAMSHLLEMCVSGDLVC
EVDLGDLSPEGRFTGLESIFRAVNYMYMGKNTGKIVVELPH

>4GMFA 372 XRAY 1.85 0.198 0.242 no Yersiniabactin biosynthetic protein YbtU <UNP
A1JTG0_YERES> [YERSINIA ENTEROCOLITICA SUBSP. ENTEROCOLITICA]

MPSASPKQRLIVGAKFGEMYLNFMQPPGLELVGLLAQGSARSRELAHAFGIPLYTSP
EQITGMPDIACIVVRSTVAGGAGTQLARHFLARGVHVHIEHPLHPDDISSLQTLAQEQGC
CYWINTFYPHTRAGRTLWRDAQQLRRCLAKTPPVVHATTSRQLLYSTLDLLLLALGVDTA
AVECDVVGVSDFHCLRLFWPEGEACLLQRYLDPDDPDMHSLIMHRLLLGWPEGHLSLE

ASYGPVIWSSSLFVADHQENAHSLYRRPEILRDPPLTRSAAPLSWRDCCETVGPEGVSW
LLHQLRSHLAGEHPPVACQNVHQIALSRLWQQILRKTGNAEIRRLTPPHDRLAGFYND
DKEALEHHHHHH

>2EDMA 161 XRAY 2.20 0.278 0.278 no 22kDa structural protein VP22 <UNP Q9ICG6_WSSV> [SHRIMP
WHITE SPOT SYNDROME VIRUS]

SVVANYDQMMRVPIQRRAKVMSIRGERSYNTPLGKVAMKNGLSDKMDKVSADLVISTVT
APRTDPAGTGAENSNMTLKILNNTGVDLLINDITVRPTVIAGNIKNTMSNTYFSSKDIK
SSSSKITLIDVCSKFEDGAAFEATMNIGFTSKNVIDIKDEI

>1H3FA 432 XRAY 2.00 0.234 0.261 no TYROSYL-TRNA SYNTHETASE <UNP SYI_THETH> [THERMUS
THERMOPHILUS]

MAGTGHTPEEALALLKRGAEIIVPEEELLAKLKEGRPLTVKLGADPTRPDLHLGHAVVLR
KMRQFQELGHKVVLIIGDFTGMIGDPSGRSKTRPPLTLEETRENAKTYVAQAGKILRQEP
HLFELRYNSEWLEGLTFKEVVRLTSLMTVAQMLEREDFKKRYEAGIPISLHELLYPFAQA
YDSVAIRADVEMGGTDQRFNLLVGREVQRAYGQSPQVCFLMPLLVLGDGREKMSKSLDNY
IGLTEPPEAMFKLMRVPDPLPSYFRLLTDLEEEEIEALLKAGPVPAPHRVLARLLTAAY
ALPQIPPRIDRAFYESLGYAWAFAFRDKEAGPEEVRRAEARYDEVAKGGIPEEIPVETIP
ASELKEGRIWVARLFTLAGLTPSNAEARRLIQNRGLRLDGEVLTDPMLQVDLSRPRILQR
GKDRFVRVRLSD

>1YBKA 52 XRAY 1.45 0.211 0.226 no tetrabrachion <UNP Q54436_STAMA> [STAPHYLOTHERMUS MARINUS]
GSIINETADDIVYRLTVIIDRYESLKNLITLRADRLEMIINDNVSTILASI

>2X4IA 114 XRAY 2.20 0.243 0.277 no UNCHARACTERIZED PROTEIN 114 <UNP Y114_SIRV1> [SULFOLOBUS
ISLANDICUS RUDIVIRUS 1 VARIANT XX]

MNKVYLANAFSINMLTKFPTKVVIDKIDRLEFCENIDNEDIINSIGHDSTIQLINSLCGT
TFQKNRVEIKLEKEDKLYVVQISQRLEEGKILTLEEILKLYESGKVQFFEIIVD

>2F5TX 233 XRAY 1.45 0.164 0.195 no archaeal transcriptional regulator TrmB <GB AAG45392>
[THERMOCOCCUS LITORALIS]

AIWRSRSFDEAIEMFRESLYSAKNEIVVTPSEFFETIREDLIKTLERGVTVSLYIDKIP
DLSEFGKGNFFVRQFYKLNHLIGMTDGKEVVTIQNATFDSIGPPSFKSTYPEIIFSQYS
LIIIEIFKESTLEKEIIGNPKDIRFFAMFHAVDFVKNHLKNRNIYAEITGNLESGRLETL
TGRVVGTYLSLREAVNNIHLETENGVVKGGMFAVEDYESTEIKFIMGGSRS

>3FNIA 159 XRAY 2.30 0.212 0.252 no Putative diflavin flavoprotein A 3 <UNP DFA3_ANASP>
[NOSTOC SP.]

TKAETSIGVFYVSEYGYSDRLAQAIINGITKTGVGVDDVLDGAAVDLQELRELVGRCGL
VIGMSPAASAASIQALSTILGSVNEKQAVGIFETGGGDDEPIDPLLSKFRNLGLTTAFP
AIRIKQTPPTENTYKLCEEAGTDLGQWVTRDRLEHHHHHH

>1WC2A 181 XRAY 1.20 0.147 0.162 no ENDOGLUCANASE <UNP GUN_MYTED> [MYTILUS EDULIS]

NQKCSGNPRRYNGKSCASTNYHDSHGACGCPASGDAQFGWNAGSFVAAASQMYFDSG
NKGWCGQHCGQCIKLTTGGYVPGGGPVREGLSKTFMITNLCPNIYPNQDWCNQGSQYG
GHNKYGYELHLDLENGRSQVTGMGWNPNPETTWEVNCDEHNHHRTPSNSMYGQCQCAH
Q

>3LOFA 162 XRAY 1.35 0.136 0.175 no C-phycocyanin alpha chain <UNP PHCA_THEEB>
[THERMOSYNECHOCOCCUS ELONGATUS]

MKTPITEAIAAADTQGRFLSNTELQAVDGRFKRAVASMEARALTNNAQSLIDGAAQAVY
QKFPYTTMQGSQYASTPEGKAKCARDIGYYLRMVTYCLVAGGTGPMDEYLIAGLSEINS

TFDLSPSWYIEALKYIKANHGLTGQAAVEANAYIDYAINALS

>4KQPA 232 XRAY 0.95 0.115 0.120 no Glutamine ABC transporter permease and substrate binding protein protein <UNP Q9CES5_LACLA> [LACTOCOCCUS LACTIS SUBSP. LACTIS]

GMATPKKDVTYIASDNSFAPFEFQNDKQFTGIDVDLLNAIAKNQGFKLKWNFIGFQAAV
DSVQSGHADGMMMSGMSITDARKQVFDYGSPPYSSNLTIATSSDDSIKSWKDLKGKTLGA
KNGTASFDYLNHAHAKEYGYTVKTFDTATMYSSLNNGSINALMDDEPVIKYAIKQGQKFA
TPIKPIPDGQYGFVAKKGSNPELIEMFNNGLANLRANGEYDKIIDKYLESDA

>2EB1A 200 XRAY 2.00 0.212 0.234 no Endoribonuclease Dicer <UNP DICER_HUMAN> [HOMO SAPIENS]

MNHLISGFENFEKKINRYRFKNKAYLLQAFTHASYHYNTITDCYQRLEFLGDAILDYLITK
HLYEDPRQHSPGVLTDRLSALVNNTIFASLAVKYDYHKYFKA VSPELFHVIDDFVQFQLE
KNEMQGMDSSELRRSEEDKEEDIEVPKAMGDIFESLAGAIYMDSGMSLETVWQVYYPM
RPLIEKFSANVPRSHHHHHH

>2JHPA 644 XRAY 2.50 0.229 0.289 no VP4 CORE PROTEIN <UNP VP4_BT10> [BLUETONGUE VIRUS 10 (ISOLATE USA)]

MPEHAVLYVTNELSHIVKDGFLPIWKLGTDESNDLWLENGKYATDVYAYGDVSKWTIR
QLRGHGFIFISTHKNVQLADIIKTVDRIPREVARSHDMKAFENEIGRRRIRMRKGFDA
LRNYAFKMAIEFHGSEAETLNDANPRLHKIYGMPEIPPLYMEYAEIGTRFDDEPTDEKLV
SMLDYIVYSAAEVHYIGCGDLRTLMQFKKRSPGRFRRVLWHVYDPIAPECSDPNVIVHNI
MVDSKKDILKHMFLKRVERLFIWDVSSDRSQMNDHEWETTRFAEDRLGEEIAYEMGGAF
SSALIKHRIPNSKDEYHCISTYLFPPQADADMYELRNFMRLRGYSHVDRHMPDASVTK
VVS RDVRKMVELYHGRDRGRFLKRLFEHLHIVRKNGLLHESDEPRADLFYLTNRCNMGL
EPSIYEVMMKSVIATAWVGRAPLYDYDDFALPRSTVMLNGSYRDIRILDGNGAILFLMWR
YPDIVKKDLTYDPAWAMNFAVSLKEIPDPVPDISLCRFIGLRVSSVLRVRNPTLHET
ADELKRMDLDSGLHYVTLMGAYVTDLFWWFKMILDWSAQNREQKLRDLKRSAAEVIEW
KEQMAERPWHVRNDLIAALREYKRKMGMREGASIDSWLELLRHL

>1WURA 220 XRAY 1.82 0.206 0.237 no GTP cyclohydrolase I <UNP Q5SH52_THET8> [THERMUS THERMOPHILUS]

MSPGPQSGGQERGSMEKRMVELEDGTGLTFATEVDLERLQALAAEWLQVIGEDPGREGLLK
TPERVAKAWAFLTRGYRQRL EEVVGAVFPAEGSEM VVVKGVEFYSMCEHLLPFFGKVH
IGYIPDGKILGLSKFARIVDMFARRLQVQERLAVQIAEAIQEVLEPQGVGVVEGVHLCM
MMRGVEKQHSRTVTSAMLGVFRENQKTREEFLSHLRDGT

>3TBIA 115 XRAY 3.00 0.253 0.295 no RNA polymerase-associated protein Gp33 <UNP VG33_BPT4> [ENTEROBACTERIA PHAGE T4]

GPHMTQFSLNDRPVDETGLSEKELSIKKEKDEIAKLLDRQENGFIIEKMVEEFGMSYLE
ATTAFLEENSIPETQFAKFIPSGIIEKIQSEAIDENLLRPSVVRCEKTNTLDLFL

>2RDMA 132 XRAY 1.76 0.189 0.220 no Response regulator receiver protein <UNP A6UIY7_9RHIZ> [SINORHIZOBIUM MEDICAE]

MSLEAVTILLADDEAILLLDFESTLTDAGFLVTAVSSGAKAIEMLKSGAAIDGVVTDIRF
CQPPDGWQVARVAREIDPNMPIVYISGHAALEWASNGVPDSIILEKPFTSAQLITAVSQL
LNAREGHHHHHH

>3M7KA 142 XRAY 1.92 0.173 0.201 no restriction endonuclease PacI <PDB 3M7K> [PSEUDOMONAS ALCALIGENES]

MTQCPRCQRNLAADDEFYAGSSKMCKGCMTWQNL SYNANKEGHANTFTKATFLAWYGLSAQ
RHCGYCGISEAGFTSLHRTNPRGYHIQCLGVDRSDSFEGYSPQNARLACFICNRIKSNIF

SASEMDVLGEAISKAWHGRGIA

>3TOWA 152 XRAY 1.34 0.166 0.193 no Multivesicular body subunit 12B <UNP F125B_HUMAN> [HOMO SAPIENS]

MDPITGVGVVASRNRAPTGYDVVAQTADGVDADLWKDGLFKSKVTRYLCFTRSFSEKNSH
LGNVLVDMKLIDIKDTLPVGFPIPIQETVDTQEVAFRKKRLCIKFIPRDSTEAAICDIRIM
GRTKQAPPQYTFIGELNSMGIWYRMGHHHHH

>3E7LA 63 XRAY 2.25 .211 0.243 no Transcriptional regulator (NtrC family) <UNP O66551_AQUAE> [AQUIFEX AEOLICUS]

RDLSYLLKIKELKEAKKEFEKIFIEEKLREYDYDLKRTAEEIGIDLSNLYRKIKSLNIRV
KSS

>2XF1A 129 XRAY 1.96 0.189 0.230 no COFILIN ACTIN-DEPOLYMERIZING FACTOR HOMOLOG 1 <UNP CADF1_PLAF7> [PLASMODIUM FALCIPARUM]

GPLGSMISGIRVNDNCVTEFNMKIRKTCGGWIIIFVIQNCCEIIHSGASTTLTELVQS
IDKNEIQCAYVVFDAVSKIHFFMYARESSNSRDRMTYASSKQAILKKIEGVNVLTSVIE
SAQDVADLK

>1T77A 414 XRAY 2.40 0.220 0.258 no Lipopolysaccharide-responsive and beige-like anchor protein <UNP LRBA_HUMAN> [HOMO SAPIENS]

GPVSLSTPAQLVAPSVVVGKTLSTSELYFEVDEEDPNFKKIDPKILAYTEGLHGKWL
TEIRSIFSRRYLLQNTALEIFMANRVAVMFNFPDPATVKKVNFPLRVGVGTSFGLPQTR
RISLASPRQLFKASNMTQRWQHREISNFEYLMFLNTIAGRSYNDLNQYPVFPWVITNYES
EELDLTLPTNFRDLSKPIGALNPKRAAFFAERYESWEDDQVPKFHYGTHYSTASFVLAWL
LRIEPFTTYFLNLQGGKFDHADRTFSSISRWRNSQRDTSDIKELIPEFYLPPEMFVNFN
NYNLGVMDDGTVVSDVELPPWAKTSEEFVHINRLALESEFVSCQLHQWIDLIFGYKQGP
EAVRALNVFYLYTYEGAVNLNSITDPVLREAVEAQIRSFGQTPSLLIEPHPPR

>1MTYG 162 XRAY 1.70 0.183 NA no METHANE MONOOXYGENASE HYDROXYLASE <UNP MEMG_METCA> [METHYLOCOCCUS CAPSULATUS STR. BATH]

LGHSNDTRDAWVNKIAHVNTLEKAAEMLKQFRMDHTTPFRNSYELDNDYLWIEAKLEEK
VAVLKARAFNEVDFRHKTAFGEDAKSVLDGTVAKMNAADKWEAEKIHIGFRQAYKPPIM
PVNYFLDGERQLGTRLMELRNLNYYDTPLEELRKQRGVRVVH

>1XAWA 140 XRAY 1.45 0.275 0.284 no Occludin <UNP OCLN_HUMAN> [HOMO SAPIENS]

AKGRAGRSKRTEQDHYETDYTTGGESCELEEDWIREYPPITSDQQRQLYKRNFDTGLQE
YKSLQSVLDEINKELSRDKELDDYREESEEYMAAADEYNRLKQVKGSAKYKSKNHCKQ
LKSLSHIKKMVG DYDRQKT

>2YFVC 63 XRAY 2.32 0.222 0.257 no SCM3 <UNP Q6CL77_KLULA> [KLUYVEROMYCES LACTIS NRRL Y-1140]
RDGVVYIMSKENRLIPKLSDEEVMERHKKADENMKRVWSQIIQKYESIDNQGDVIDLQTG
EVI

>3RQ9A 85 XRAY 1.00 0.147 0.176 no Type VI secretion immunity protein <UNP Q9IOD9_PSEAE> [PSEUDOMONAS AERUGINOSA]

MNLKPQTLMVAIQCVAARTRELDALQNDPQNAAELEQLLVGYDLAADDLKNAYEQALG
QYSGLPPYDRLIEEPASLEHHHHH

>4F67A 265 XRAY 1.79 0.170 0.201 no UPF0176 protein lpg2838 <UNP Y2838_LEGPH> [LEGIONELLA PNEUMOPHILA SUBSP. PNEUMOPHILA]

MGHHHHHSHMVKDIIASFYKFIPLNDFRSLREPILTKMHEIGIKGTIIAHEGVNGGF
AGNREQMNVFYDYLRSDSRFADLHFKETYDNKNPFDKAKVKLRKEIVTMGVQKVDPSYNA

GTYLSPEEWHQFIQDPNVILLDRNDY EYELGTFKNAINPDIENTFREFPDYVQRNLIDKK
DKKIAMFCTGGIRCEKTTAYMKELGFEHVYQLHDGILNYLESIPESLWEGKCFVFDDR
VAVDQKLD RVPQLPQDYKYEREQK

>3LHLA 287 XRAY 2.30 0.193 0.238 no Putative agmatinase <UNP Q18A84_CL0D6> [CLOSTRIDIUM
DIFFICILE]

MSLNYEESNLIVFGVFGDGTTSNRPGARFASSSMRKEFYGLETYSPFLDLLEDYNICDY
GDLEISVGSTEQVLKEIYQETYKIVRDSKVPFMIGGEHLVTLPAFKAVHEKYNDIYVIHF
DAHTDLREEYNSKNSHATVIKRIWDIVGDNKIFQFGIRSGTKEEFKFATEEKHTYMEIG
GIDTFENIVNMLNGKNIYLTIDLDVLDASVFPGTGTPEPGGVNYREFQEIFKIIKNSNIN
IVGCDIVELSPDYDTTGVSTVIACKILRELCLIIISDKIKEGHHHHHH

>2A1RA 430 XRAY 2.60 0.221 0.236 no Poly(A)-specific ribonuclease PARN <UNP PARN_HUMAN> [HOMO
SAPIENS]

MEIIRS NFKSNLHKVYQAIEEADFFAIDGEFSGISDGPSVSALTNGFDTPEERYQKLKKH
SMDFLLFQFGLCTFKYDYTDSKYITKSFNFYVFPKPFNRSSPDVKFVCQSSSIDFLASQG
FDFNKFVRNGIPYLNQEEERQLREQYDEKRSQANGAGALSYSPNTSKCPVTIPEDQKKF
IDQVVEKIEDLLQSEENKNDLEPCTGFQRKLIYQTL SWKYPKGIHVETLETEKKERYIV
ISKVDEEERKRREQQKHAKKEQELNDAVGFSRVIHA IANSGKLVIGHNMLLDVMHTVHQF
YCLPADLSEFKEMTTTCVFPRLD TKLMAS TQPFKDIINNTSLAELEKRLKETPFNPPKV
ESAEGFPSYDTASEQLHEAGYDAYITGLCFIS MANYLGSFLSPPKIHVSARSKLIEPFFN
KLFLMRVMDI

>20GYA 262 XRAY 2.30 0.188 0.234 no 5-methyltetrahydrofolate corrinoid/iron sulfur protein
methyltransferase <UNP Q46389_MOOTH> [MOORELLA THERMOACETICA]

MLII GERINGMFGDIKRAIQERDPAPVQEWARRQEEGGARALDLNVGPAVQDKVSAMEWL
VEVTQEVSNLTLCLDSTNIKAI EAGLKKCKN RAMINSTNAEREKVEKLFPLAVEHGAALI
GLTMNKTGIPKDS DTRLAFAMELVAAADEFG LPMEDLYIDPLILPANVAQDHAPEVLKTL
QQIKMLADPAPKTVLGLSAVSQNCQNRPLINRTFLAMAMACGLDAAIADACDEAL IETAA
TAEILLNQTVYCDSFVKMFKTR

>1ZHXA 438 XRAY 1.50 0.225 0.233 no KES1 protein <UNP KES1_YEAST> [SACCHAROMYCES CEREVISIAE]

GAMDPSQYASSSSWTSFLKS IASFNGDLSLSAPPFILSPISLTFESQYWA EHPFLFLEP
SFINDDNYKEHCLIDPEVESPELARM LAVTKWFISTLKSQYCSRNESLGSEKKPLNPFLG
ELFVGK WENKEHPEFGETVLLSEQVSHPPVTAFSIFNDKNVKLQGYNQIKASFTKSLM
LTVKQFGHTMLDIKDES YLTPPPLHIEGILVASPFVELEGKSYIQSSTGLLCVIEFSGR
GYFSGKNSFKARIYKDSKDSKDEKALY TISGQWSGSSKIIKANKKEESRLFYDAARIP
AEHLNVKPLEEQHPLESRKAWYDVAGAIKLGDFNLI AKTKTELEETQREL RKEEEAKGIS
WQRRWFKDFDYSVTPEEGALVPEKDDTFLKLASALNLSTKNAPSGTLVGDKEDRKEDLSS
IHWRFQRELWDEEKEIVL

>2XUAA 266 XRAY 1.90 0.185 0.241 no 3-OXOADIPATE ENOL-LACTONASE <UNP Q13KT2_BURL>
[BURKHOLDERIA XENOVORANS]

GSHMPYAAVNGTELHYRIDGERHGNAPWIVLSNSLGTDL SMWAPQVAALSKHFRVLR YDT
RGHGHSEAPKGPYTIEQLTGDVLGLMDTLKIARANFCGLSMGGLTGVALAARHADRIERV
ALCNTAARIGSPEVWVPRAVKARTEGMHALADAVLPRWFTADYMEREPVVLAMIRDV FVH
TDKEGYASNCEAIDAADLRPEAPGIKVPALVISGTHDLAATPAQGRELAQA IAGARYVEL
DASHISNIERADAFTKTVDFLTEQK

>3QWEA 279 XRAY 2.40 0.227 0.231 no GEM-interacting protein <UNP GMIP_HUMAN> [HOMO SAPIENS]
GGEELDLRLIRTKGGVDAALEYAKTWSRYAKELLAWTEKRASYELEFAKSTMKIAEAGKV

SIQQQSHMPLQYIYTLFLEHDLSLGTLAMETVAQQKRDYYQPLAAKRTIEKWRKEFKEQ
 WMKEQKRMNEAVQALRRAQLQYVQRSEDLRARSQGSPEDSAPQASPGPSKQQERRRSRE
 EAQAKAQEAALYQACVREANARQQDLIAKQRIVSHVRKLVFQGDEVLRRTLSLFLGLR
 GAQAERGPRAFALAECAPFEPGQRYQEFVRALRPEAP
 >2DXAA 166 XRAY 1.58 0.180 0.215 no Protein ybaK <UNP YBAK_ECOLI> [ESCHERICHIA COLI]
 GSSGSSGMTPAVKLEKNKISFQIHTYEHDPATNFGDEVVKKLGLNPDQVYKTLVAVN
 GDMKHLAVAVTPVAGQLDLKKVAKALGAKKVMADPMVAQRSTGYLVGGISPLGQKKRLP
 TIIDAPAQEFATIIYVSGGKRGLDIELAAGDLAKILDAKFADIARRD
 >2W6KA 145 XRAY 1.70 0.202 0.250 no COBE <UNP Q9HZQ0_PSEAE> [PSEUDOMONAS AERUGINOSA]
 GSHMPLPIPSLLIAGIGCRRGCSAEHLRALLERTLGEHGRSLAELDALASIDGKRDEPGL
 RQLATLLERPVLHFLAPVLHDYEPRLSPSAVALRETGCSSVAEAAAALALAERLGGGRAD
 LLGAKRSDDRASIALARLLTERELP
 >3EGNA 143 XRAY 2.50 0.199 0.236 no RNA-binding protein 40 <UNP RBM40_HUMAN> [HOMO SAPIENS]
 GPLGSDSEMPSECISRRELEKGRISREEMETLSVFRSYEPGEPNCRIYVKNLAKHVQEK
 DLKYIFGRYVDFSSETQRMFDIRLMKEGRMKGAFIGLPNEKAAAKALKEANGYVLF GK PMVVQFARSARPKQDPKEGKRKC
 >1ITHA 141 XRAY 2.50 0.147 NA no HEMOGLOBIN (CYANO MET) <UNP HBF1_URECA> [URECHIS CAUPO]
 GLTAAQIKAIQDHWFLNIKGLCAAADSIFFKYLTAYPGDLAFFHKFSSVPLYGLRSNPA
 YKAQTLTVINYLDKVV DALGGNAGALMKAKVPSHDAMGITPKHFGQLLKLVGGVFQEEFS
 ADPTTVAAWGDAAGVLVAAMK
 >3UJCA 266 XRAY 1.19 0.146 0.167 no Phosphoethanolamine N-methyltransferase <UNP
 Q6T755_PLAFA> [PLASMODIUM FALCIPARUM]
 MTLIENLNSDKTFLENNQYTDEGVKVYEFIFGENYISSGGLEATKKILSDIELNENSKVL
 DIGSGLGGGCMYINEKYGAHTHGIDICSNIVNMANERVSGNNKIIFEANDILTKEFPENN
 FDLIYSRDAIILALSLENKKNLFQKCYKWLKPTGTLLITDYCATEKENWDDDEFKEYVKQRK
 YTLITVEEYADILTACNFKNVVSKDLSDYWNQLLEVEHKYLHENKEEFLKLFSEKKFISL
 DDGWSRKIKDSKRKMQRWGYFKATKN
 >3PKZA 124 XRAY 1.80 0.209 0.246 no Recombinase Sin <UNP D2J612_STAAU> [STAPHYLOCOCCUS
 AUREUS]
 MIIGYARVSSLDQNLERQLENLKTFGAEKIFTEKQSGKSIENRPILQKALNFVEMGDRFI
 VESIDRLGRNYNEVIHTVNYLKDKEVQLMITS LPMNEVIGNPLLDKFMKDIIIRILAMV
 SEQE
 >3T97B 65 XRAY 2.80 0.231 0.271 no Nuclear pore complex protein Nup54 <UNP NUP54_RAT> [RATTUS
 NORVEGICUS]
 GSHMTKQHQTRLDIISEDISELQKNQTTMAKIAQYKRKLMDLSHRTLQVLIKQEIQRKS
 GYAIQ
 >1L6PA 125 XRAY 1.65 0.141 0.226 no Thiol:disulfide interchange protein dsbD <UNP DSBD_ECOLI>
 [ESCHERICHIA COLI] GLFDAPGRSQFVPADQAFADFQQNQHDNLNLTWQIKDGYLYRKQIRITPEHAKIADVQL
 PQGVWHEDEFYKGSEIYRDRLTLPVTINQASAGATLTVTYQGCADAGFCYPPETKTVPLS
 EVVAN
 >3EZQB 122 XRAY 2.73 0.236 0.278 no Protein FADD <UNP FADD_HUMAN> [HOMO SAPIENS]
 GEEDLCAAFNVICDNVGKDWRRLARQLKVS DTKIDSIEDRYPRNLTERVRESLRIWKNT
 KENATVAHLVGALRSCQMNVLADLVQE VQQARDLQNRSGAMSPMSWNSDASTSEASHHHH
 HH
 >4EDPA 351 XRAY 1.85 0.164 0.191 no ABC transporter, substrate-binding protein <UNP

Q0TR20_CLOP1> [CLOSTRIDIUM PERFRINGENS]
 SNAMKKKILATLLTGLVLGTSLVGCGKTEGAEAGKKLVVSTWGLNEDVLKETVFEFPAKE
 HGVEIVLDIGNNSERLTKMKNPNNSQIDITYLAESFAEQGVEAGIFDKLDYSKIPNASEM
 NEKAKSTVEAGYGPAYTLNSIGIVDPSAGIEINSWEDLWKPELKNKIAIPDITTTNGPA
 MVEIAAEKAGVDVKTNDGEAAFKLEALKPNVVKTYSSDLANMFSNGEIVAAVASDFA
 FGTISKAKPEVINVIPESGYLNFNTININKNSKNKDLAYEFINYALSKEVQEKTAKALN
 ESPVNKEVKLSEEETKNLTYGPPVDNAKVIDFKFVNSVMDQWVNNWNRIMN
 >3RJ2X 138 XRAY 2.20 0.201 0.275 no Putative uncharacterized protein <UNP Q5YFA7_9VIRU>
 [SINGAPORE GROUPE IRIDOVIRUS]
 MGWAIIVANCEFVNATGKKTTLVNNWAKYCWIIWYKFPEKYTLRYSVDGEMFMRHRVT
 FFNATGRYITHLNLHGLEDVLEGLAVPKDAAYARIHAAINVSILTNP GDVHMHYDETEG
 EQIRSYDAAEFARTLAAY
 >2Q66A 525 XRAY 1.80 0.191 0.225 no Poly(A) polymerase <UNP PAP_YEAST> [SACCHAROMYCES
 CEREVISIAE]
 KVFGITGPVSTVGATAENKLNDSLILQELKKEGSFETEQETANRVQVLKILQELAQRFBVY
 EVSKKKNMSDGMARDAGGKIFTYGSYRLGVHGPSIDITLVVVPKHVTREDDFTVFDSSL
 RERKELDEIAPVPDAFVPIIKIKFSGISIALICARLDQPVPLSLTSLDKNLLRNLDKDE
 LRALNGTRVTDEILELVPKPNVFRIALRAIKLWAQRRAYANIFGFPGGVAVAMLVARIC
 QLYPNACSAVILNRFIIILSEWNWPQPVILKPIEDGPLQVRVWNPKIYAQDRSHRMPVIT
 PAYPSMCATHNITESTKKVILQEFVRGVQITNDIFSNNKSWANLFEKNDFFRYKFYLEI
 TAYTRGSDEQHLKWSGLVESKVRLLVMKLEVLAKIAHPFTKPFESSYCCPTEDDYEMI
 QDKYGSHTETALNALKLVTDENKEESIKDAPKAYLSTMYIGLDFNIENKKEKVDIHIP
 CTEFVNLCRSFNEDYGDHKVFNALRFVKGVDLPDEVFDENEKRP
 >303XA 198 XRAY 1.45 0.152 0.181 no gp41-5 <PDB 303X> [ARTIFICIAL GENE]
 SGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILSGGSGGWMEWDREINNYTSLIHSL
 IEESQNNQEKNEQELLGGSGGSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILSGG
 SGGWMEWDREINNYTSLIHSLIEESQNNQEKNEQELLGGSGGSGIVQQQNNLLRAIEAQQ
 HLLQLTVWGIKQLQARIL
 >3KWRA 97 XRAY 1.45 0.164 0.181 no Putative RNA-binding protein <UNP Q8W58_LACPL>
 [LACTOBACILLUS PLANTARUM]
 GMNHNYVEVKYPAIFRDEGTWYDVRFPDVPAAQTFGASVQVAADNAANALALFEQSLP
 PASDPQYWRLASTEFVWITMADVQFGPGADTPEPMN
 >3DSBA 157 XRAY 1.48 0.170 0.205 no Putative acetyltransferase <UNP Q185U9_CLOD6>
 [CLOSTRIDIUM DIFFICILE]
 SNAEELIEIREARMDDLDTIAKFNYNLAKETEGKELDMDLTKGVKALLDERKGKYHVY
 TVFDKVVQIMYTYEWSWRNGNFLWISVYVDKEYRRKGIFNYLFNYIKNICDKDENIV
 GMRLYVEKENINAKATYESLNMYECDYNMYEYEVHS
 >1Z72A 225 XRAY 1.45 0.152 0.167 no transcriptional regulator, putative <UNP Q97RS7_STRPN>
 [STREPTOCOCCUS PNEUMONIAE] SNAMETQDYAFQPLTVGELLKSSQKDWQAANHRFVKELFAGTIENKVLKDYLIQDYHF
 FDAFLSMLGACVAHADKLESKLRFAKQLGFLEADEDGYFQKAFKELKVAENDYLEVTLHP
 VTKAFQDLMYSAVASSDYAHLVMLVIAEGLYLDWGSKDLDALPEVYIHSEWINLHRGPFF
 AEWWQFLVDELNRVGKNREDLTEQQRWNAVALELAFFDIGYDV
 >2W79A 241 XRAY 1.85 0.206 0.267 no 1-(5-PHOSPHORIBOSYL)-5-[(5-PHOSPHORIBOSYLAMINO)
 METHYLIDENEAMINO] IMIDAZOLE-4-CARBOXAMIDE ISOMERASE <UNP HIS4_THEMA> [THERMOTOGA MARITIMA]

MLVVPAILDFRGKVARMIKGRKENTIFYEKDPVELVEKLIIEGFTLIHVVDLSNAIENSG
ENLPVLEKLSEFAEYIQIGGGIRSLDYAEKLRKLGYYRRQIVSSKVLDPSSLKSLREIDV
EPVFSLVTRGGVAFKGLAAEEIDPVSLKRLKEYGLEEIVHTEIEKVGTLQEHDFSLT
KKIAIEAEVKVLAAGGISSENSLKTAKVHTETNGLLGKGVIVGRAFLEGILTVEVMKRYA
R
>4EGTA 357 XRAY 2.00 0.201 0.232 no Major capsid protein VP60 <UNP Q3HNQ1_RHDV> [RABBIT
HEMORRHAGIC DISEASE VIRUS]
GPLGSAPSSKTVDSISPAGLLTTPVLTVGVNDNRWNGQIVRLQVPVGGFSTCNRHWNLNG
STYGWSSPRFADIDHRRGSASYSGNSSTNVLQFWYANAGSAIDNPISQVAPDGFPMDSFV
PFNSPNIPTAGWVGFGGIWNSNNGAPAATTQAYELGFATGAPNNLQPTTNTSGAQTVAK
SIYAVVTGTNQPTGLFVMASGVISTPNASAVTYTPQPDRIVTTPGTPAAAPVGKNTPIIM
FASVVRTGDVNAAAGSTNGTQYGTGSQPLVPTIGLSLNNYSSALMPGQFFVWQLTFASG
FMEIGLSVDGYFYAGTEASTLIDLTELIDVRPVGPRPSKSTLVFNLGTTNGFSYV
>1UZKA 162 XRAY 1.35 0.202 0.261 no FIBRILLIN-1 <UNP FBN1_HUMAN> [HOMO SAPIENS]
TDVNECLDPTTCISGNCVNTPGSYICDPPDFELNPTRVGCVDTRSGNCYLDIRPRGDNG
DTACSNEIGVGVSASCCCSLGAWGTPEMCPAVNTSEYKILCPGGEGFRPNPITVILE
DIDECQELPGLCQGGKCINTFGSFQCRCPGTGYLNEEDTRVCD
>3HHFA 213 XRAY 2.30 0.204 0.258 no Transcriptional regulator, LysR family <UNP Q9JXW7_NEIMB>
[NEISSERIA MENINGITIDIS SEROGROUP B]
GPEIPQGVLSVDSAMPVHLHLLAPLAAKFNERYPHIRLSLVSSSEGYINLIERKVDIALRA
GELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQSTEELAGHQCLGFTEPGSLNTWAVLD
AQGNPYKISPHTASSGEILRSLCLSGCGIVCLSDFLVDNDIAEGKLIPLLAEQTSKTH
PFNAVYYSDKAVNLRVFLDFLVEELGNNLCG
>2VK2A 306 XRAY 1.20 0.179 0.190 no ABC TRANSPORTER PERIPLASMIC-BINDING PROTEIN YTFQ
<PDB 2VK2> [ESCHERICHIA COLI]
APLTVGFSQVGSESGWRAAETNVAKSEAEKRGITLKIADGQQKQENQIKAVRSFVAQGV
AIFIAPVVATGWEPVLKEAKDAEIPVFLDRSIDVKDSLYMTTVTADNILEGKLIGDWL
VKEVNGKPCNVVELQGTVGASVAIDRKKGF AEAIKNAPNIKIIRSQSGDFTRSKGKEVME
SFKAENNGKNICMVYAHNDMDVIGAIQAIKEAGLKPGKDILTGSIDGVPDIYKAMMDGE
ANASVELTPNMAGPAFDAL EKYKKGDTMPEKLT LTKSTLYLPDTAKEELEKKKNMGYLEH
HHHHHH
>1Y6ZA 263 XRAY 1.88 0.208 0.268 no heat shock protein, putative <UNP Q8IL32_PLAF7>
[PLASMODIUM FALCIPARUM]
GHQLPIWKQDEKSLTENDYYSFYKNTFKAYDDPLAYVHFVNEGQISFNSILYIPGSLPWE
LSKNMFDEESRGIRLYVKRVFINDKFSESIPRWLTLRGIVDSENLPNVGREILQKSKM
LSIINKRIVLKSISMMKGLKETGGDKWTKFLNTFGKYLKIGVVEDKENQEEIASLVEFY
INSGDKKTDLSYIENMKEDQKCIYYISGENKKT AQNSPSLEKLKALNYDVLFSLEPIDE FCLSSLTVNKYKGYEVL DVNKAD
>2YNMD 530 XRAY 2.10 0.201 0.233 no LIGHT-INDEPENDENT PROTOCHLOROPHYLLIDE REDUCTASE SUBUNIT
B <UNP CHLB_PROMA> [PROCHLOROCOCCUS MARINUS]
MELTLWTYEGPPHIGAMRIATSMKGLHYVLHAPQGDYADLLFTMIERRGSRPPVYTTTF
QARDLGGDTAELVKGHIFEAVERFKPEALLVGESCTAELIQDQPGSLAKGMGLNIPIVSL
ELPAYSKKENWGASETFYQLIRGLLKEISEDSSNNAKQSWQEEGRRPRVNLGPSLLGFR
CRDDVLEIQKILGENGIDINVIAPLGASPSDL MRLPKADANVCLYPEIAESTCLWLERNF
KTPFTKVVPIGVKATQDFLEELYELLGMEVSNSISNSDQSKLPWYSKSVDSNYLTGKRVF

IFGDGTHVLAAARIANEELGFEVVGIGTYSREMARKVRAAATELGLEALITNDYLEVEES
 IKECAPELVLGTQMERHSAKRLGIPCAVISTPMHVQDVPARYSPQMGWEGANVIFDDWVH
 PLMMGLEEHLIGMFRHDFEFTDGHQSHLGHLGGHASETKTSSKGINQSPNNHSPAGESIH
 WTSEGESELAkipFFVRGKVRRNTEKYARQAGCREIDGETLLDAKAHFGA
 >3S84A 273 XRAY 2.40 0.202 0.229 no Apolipoprotein A-IV <UNP APOA4_HUMAN> [HOMO SAPIENS]
 GATELHERLAKDSEKLKEEIGKELEELRARLLPHANEVSKIGDNLRELQQRLPYADQL
 RTQVNTQAEQLRRQLTPYAQRMERVLRENADSLQASLRPHADELKAKIDQNVEELKGRLT
 PYADEFKVKIDQTVEELRRSLAPYAQDTQEKLNHQLEGLTFQMKNAEELKARISASAE
 LRQLAPLAEDVRGNLRGNTTEGLQKSLAELGGHLDQQVEEFRRRVEPYGENFNKALVQQM
 EQLRQKLGPAGDVEGHLSFLEKDLRDKVNSFF
 >3FIJA 254 XRAY 2.30 0.240 0.269 no Lin1909 protein <UNP Q92AL3_LISIN> [LISTERIA INNOCUA]
 MSLKPVIGITGNRLVKGVDFYGHVITYTQQRYVDALQKVGGFPIALPIDDPSTAVQAIS
 LVDGLLLTGGQDITPQLYLEEPSQEIGAYFPPRDSYEIALVRAALDAGKPIFAICRGMQL
 VNVALGGTLYQDISQVETKALQHLQRVDEQLGSHITDIEPTSELAKHHPNKKLVNSLHHQ
 FIKKLAPSFKVITARTADGMIEAVEGDNLPWYLGWVQWHELMFQTDPESEQLFQALVDES
 KKTVMKEGHHHHHH
 >1NEPA 130 XRAY 1.70 0.195 0.212 no Epididymal secretory protein E1 <UNP NPC2_BOVIN> [BOS TAURUS]
 EPVKFKDCGSWVGVIKEVNVSPCPTQPCKLHRGQSYSVNVTFTSNTQSQSSKAVVHGIVM
 GIPVPFPIPEDGCKSGIRCPIDKTYNYVKNLPVKNEYPSIKVVVEWELTDDKNQRFF
 CWQIPIEVEA
 >1XLYA 234 XRAY 1.95 0.206 0.241 no SHE2p <UNP YKNO_YEAST> [SACCHAROMYCES CEREVISIAE]
 DIKVTPGTSELVEQILALLSRYLSSYIHVLNKFISHLRRVATLRFERTTLIKFVKKLRFY
 NDSVLSYNASEFINEGKNELDPEADSFQVILPIASMFVKSVEFDLLNYYLTQSLQKEI
 LSKTLNEDLTLAESILAIIDDTYNHFVKFSQWMIESLRIGSNLLDLEVQFAIKSADEG
 TNIGETDNIFLQELPVSSEEFQTLAAWHSILDGKLSALDEEFDVVATKWH
 >1ISPA 181 XRAY 1.30 0.192 0.232 no lipase <UNP LIP_BACSU> [BACILLUS SUBTILIS]
 AEHNPVVMVHGIGGASFNFAGIKSYLVSQGWSRDKLYAVDFWDKGTNYNNGPVLSRFVQ
 KVLDETGAKKVDIVAHSMGGANTLYYIKNLDGGNKVANVTLGGANRLTTGKALPGTDPN
 QKILYTSIYSSADMIVMNYLSRLDGARNVQIHGVGHIGLLYSSQVNSLIKEGLNGGGQNT
 N
 >1H8UA 117 XRAY 1.80 0.234 0.264 no EOSINOPHIL GRANULE MAJOR BASIC PROTEIN 1 <UNP EMBP_HUMAN>
 [HOMO SAPIENS]
 TCRYLLVRSLSQTFQAWFTCRRCYRGNLVSINFNINRYIQCSVSALNQGQVWIGGRITG
 SGRCRRFQWVDGSRWNFAYWAAHQPSRGGHCVALCTRGYWRRAHCLRLPFICSY
 >3LMAA 347 XRAY 1.99 0.170 0.211 no Stage V sporulation protein AD (SpoVAD) <UNP Q65HU8_BACLD>
 [BACILLUS LICHENIFORMIS]
 MKLTGKQTWEFENPLFVNSSGTAVGPKEKEGPLGHLFDKSYDEMHCNQKNWEMAERKLME
 DAVQSALSQKQNKEDIDIFLAGDLLNQNTANYVARHLKIPFLCLFGACSTSMESIAIS
 SALIDGGFAKRALAATSSHNAERQFRYPTEYGGQKPGTATSTVTGSGAVVLSQQPGGI
 KITSATVGRVIDLGITDSQDMGSAMAPAAADTIKQHLEDLGRTPDDYDLILTGDLSGVGS
 PILKDLLKEEINVGTKHNDCLMIYTPDQQVFAGGSGCACSAVVTFHIFKEIEAGRLN
 RVLVVATGALLSPTIIQQKESIPCIAHGTVFERAERGNALHHHHHH
 >3W54A 329 XRAY 2.30 0.188 0.227 no Alternative oxidase, mitochondrial <UNP AOX_TRYBB>

[TRYPANOSOMA BRUCEI BRUCEI]

MFRNHASRTAAAPWVLRTACRQKSDAKTPVWGHTQLNRLSFLETVPVPLRVSDASSE
DRPTWSPDIENVAITHKKPNGLVDTLAYRSVRTCRWLFDTFSLYRFGSITESKVISRCL
FLETVAGVPGMVGMLRHLSSLRYMTRDKGWINTLLVEAENERMHLMTFIELRQPGLPLR
VSIIITQAIMYLFLLVAYVISPRFVHRFVGYLEEEAVITYTGMRAIDEGRLRPTKNDVP
EVARVYWNLSKNATFRDLINVIRADEAEHRVNVHTFADMHEKRLQNSVNPFFVLKKNPEE
MYSNQPSGKTRTDFGSEGAKTASNKNHV

>107JA 327 XRAY 1.00 0.110 0.128 no L-ASPARAGINASE <UNP ASPG_ERWCH> [ERWINIA CHRYSANTHEMI]

ADKLPNIVILATGGTIAGSAATGTQTTGYKAGALGVDTLINAVPEVKLANVKGEQFSNM
ASENMTGDVVLKLSQRVNELLARDDVDGVVITHGTDTEESAYFLHLTVKSDKPVVFVAA
MRPATAISADGPMNLLEAVRVAGDKQSRGRGVMVINDRIGSARYITKTASTLDTFRAN
EEGYLGVIIGNRIYYQNRIDKLHTTRSVFDVRGLTSLPKVDILYGYQDDPEYLYDAAIQH
GVKGIVYAGMGAGSVSVRG IAGMRKALEKGVVVMRSTRTGNGIVPPDEELPGLVSDSLNP
AHARILLMLALTRTSDPKV IQEYFHTY

>2EHWA 120 XRAY 2.22 0.220 0.284 no Hypothetical protein TTHB059 <UNP Q53WA3_THET8> [THERMUS

THERMOPHILUS] MACHELSALRIAIGELLEKEAHDLLHEREELAPVLGQRPELKRLAEAKTLPAL EEALREA
LLHLEERAAQEPEEPYWRG LLLAVEAMEGRKALRAEAEALYQDL DALHGRHLRFLP RRR

>1WDEA 294 XRAY 2.00 0.199 0.244 no Probable diphthine synthase <UNP DPHB_AERPE> [AEROPYRUM
PERNIX]

MARGREAVTLLLVGWGYAPGMQTLEALDAVRRADV VYVESYTMPGSSWLYKSVVEAAGEA
RVVEASRRDLEERSREIVSRALDAVVAVVTAGDPMVATTHSSLAAEAEAGAVRYIPGV
SGVQAARGATMLSFYRFGGTVTLPGPWVGVTPI SVARRIYLNLCAGLHTTALLDVDERGV
QLSPGQGVSLLEADREYAREAGAPALLARLPSVLVEAGAGGGHRVLYWSSLERLSTADV
EGGVYSIVIPARLSGVEEWLLAAASGQRRPLEYDRSVYETVEENCKKG VMEPV

>2NR4A 213 XRAY 1.85 0.223 0.256 no Conserved hypothetical protein <UNP Q8PVV4_METMA>

[METHANOSARCINA MAZEI]

SLIGFLSDRQGFEKQYHDIDLSSFGIREGISEIIASTGFEHPNAAPIGIVMKGERPFVRL
FKGSHTWENVLKEKCLASN VVYDPILFVRSTFSDLPSEFEYVDAGEFKFPVLKEAIAWV
VFECINLRNTDQSLVADLVPLNAGFNERNIKELPVPN RGFNAVLEATVHATRYQLTGEEK
YLELIRHYESLASKCGDAEKKAMKLIYEALGL

>2I9CA 123 XRAY 2.00 0.176 0.202 no Hypothetical protein RPA1889 <UNP Q6N8L4_RHOPA>

[RHODOPSEUDOMONAS PALUSTRIS]

MSKLDLHQMTTQDLVALFAKVTEQDDALLGNQISRFRNLFGVMAEIADELKARDGDQRT
ALLSLFEYPNMQVRLQAAKLTAVAPVKAREQLEAIVSSKWFPQAGDAGMCLDLLDDGTF
KPK

>2EK0A 90 XRAY 1.90 0.229 0.255 no Stage V sporulation protein S (SpoVS) related protein
<UNP Q5SK02_THET8> [THERMUS THERMOPHILUS]

METLRVSSKSRPNSVAGAI AAMLRTKGEVEVQAIGPQAVNQAVKAIAIARGYIAPDNLDL
VVKPAFVKLELENEERTALKFSIKAHPLET

>3PHXA 185 XRAY 1.60 0.142 0.192 no RNA-directed RNA polymerase L <UNP L_CCHFI> [CRIMEAN-CONGO
HEMORRHAGIC FEVER VIRUS]

GPMDFLRSLDWTQVIAGQYVS NFRFNISDYFEIVRQPGDGNC FYHSIAELTMPNKTDHSY
HYIKRLTESAARKYYQEEPEARLVGLSLEDY LKRLSDNEWGSTLEASMLAKEMGITIII
WTVASDEVEAGIKFGDGDVFTAVNLLHSGQTHFDALRILPQFETDTREALSLMDRVIAV

DQLTS

>3LL2A 123 XRAY 0.97 0.144 0.155 no Griffithsin <UNP GRFIN_GRISQ> [GRIFFITHSIA]

SSTHRKFGSGGSPFSGSLSSIAVRSGSYLDAIIIDGVHHGSGGNLSPTFTFGSGEYI
SNMTIRSGDYIDNISFETNMGRRFPGPYGGSGGSANTLSNVKVIQINGSAGDYLDSLDIYY
EQY

>2BONA 332 XRAY 1.90 0.222 0.267 no LIPID KINASE <UNP YEGS_ECOLI> [ESCHERICHIA COLI]

MHHHHHHGSTSLYKKAGSETLYIQMAEFPASLLILNGKSTDNLPLREAIMLLREEGMTI
HVRVTWEKGDAARYVEEARKFGVATVIAGGGDGTINEVSTALIQCEGDDIPALGILPLGT
ANDFATSVGIPEALDKALKLAIAGDAIAIDMAQVKNQTCFINMATGGFGTRITTETPEKL
KAALGSVSYIIHGLMRMDTLQPDRCERGENFHWQGDALVIGIGNRQAGGGQQLCPNAL
INDGLLQLRIFTGDEILPALVSTLKSDEDNPNIEGASSWFDIQAPHDITFNLDGEPLSG
QNFHIEILPAALRCRLPPDCPLL RSTHHHHH

>2VDF 253 XRAY 1.95 0.227 0.272 no OUTER MEMBRANE PROTEIN <PDB 2VDF> [NEISSERIA MENINGITIDIS]

AQELQTANEFTVHTDLSSISSTRAFLKEKHAKHIGVRADIPFDANQGIRLEAGFGRSK
KNIINLETDENKLGKTKNVKLPTGVPENRIDLYTGYTYTQTLSDSLNFRVGAGLGFESSK
DSIKTTKHTLHSSRQSWLAKVHADLLSQLGNGWYINPWSEVKFDLNSRYKLNTGVTNLKK
DINQKTNGWGFGLGANIGKKLGESASIEAGPFYKQRTYKESGEFSVTTKSGDVSLTIPKT
SIREYGLRVGIKF

>4NKTA 341 XRAY 1.90 0.180 0.212 no Poly(A) RNA polymerase protein cid1 <UNP CID1_SCHPO>
[SCHIZOSACCHAROMYCES POMBE]

GDMSHKEFTKFCYEVYNEIKISDKEFKKRAALDTLRLCLKRISPDALVAFGSLESGLA
LKNSDMDLCVLMDSRVQSDTIALQFYEEELIAEGFEGKFLQARAPIIKLTSDTKNGFGAS
FQCAIGFNNRLAIHNTLLSSYTKLDARLKPMVLLVKHWAKRKQINSPYFGLTSSYGYVL
MVLYLIHVIKPPVFPNLLSPLKQEKIVDGFVDFDDKLEDIPPSQNYSSLGSLHGGFF
RFYAYKFEPREKVVTFRPPDGYLTQKEKGWTSATEHTGSADQIIKDRYILAIEDPFEISH
NVGRVTSSSGLYRIRGEFMAASRLNRSYPIPYDSLFEAA

>2HWKA 320 XRAY 2.45 0.208 0.242 no helicase nsP2 <UNP POLN_EEVVT> [VENEZUELAN EQUINE
ENCEPHALITIS VIRUS (STRAIN TC-83)]

DVFQNKANVCWAKALVPVLKTAGIDMTTEQWNTVDYFETDKAHSAEIVLNQLCVRFFGLD
LDGLFSAPTVPISIRNNHWDNSPSPNMYGLNKEVVRQLSRRYPQLPRAVATGRVYDMNT
GTLRNYDPRINLVPVNRRLPHALVLHHNEHPQSDFFSVSKLKGRTVLVVGKLSVPGKM
VDWLSDRPEATFRARLDLGIPODVPKYDIIIFVNVRTYPKYHHYQQCEDHAIKLSMLTKKA
CLHLNPGGTCVSIQGYADRASESIIGAIARQFKFSRVCKPKSSLEETEVLVVFVIGYDRK
ARTHNPYKLSSTLTNIYTG

>2Q18X 293 XRAY 2.10 0.202 0.219 no 2-keto-3-deoxy-D-arabinonate dehydratase <UNP
Q97UA0_SULSO> [SULFOLOBUS SOLFATARICUS]

MKLFRVVKRGYYISYAILDNSTIIRLDEDPIKALMRYSENKEVLGDRVTGIDYQSLLKSF
QINDIRITKPIDPPEVWGSGISYEMARERYSEENVAKILGKTIYEKVDARPEIFFKAT
PNRCVGHGEAIAVRSDSEWTLPEPELAVVLDNSGKILGYTIMDDVSARDLEAENPLYLPQ
SKIYAGCCAFGPVIVTSDEIKNPYSLDITLKIVREGRVFFEGSVNTNKMRRKIEEQIYQL
IRDNPIDGTILTTGTAIVPGRDKGLKDEDIVEITISNIGTLITPVKKRRKIT

>2JE6B 250 XRAY 1.60 0.216 0.249 no EXOSOME COMPLEX EXONUCLEASE 1 <PDB 2JE6> [SULFOLOBUS
SOLFATARICUS]

GHMREMLQVERPKLILDDGKRTDGRKPDELRSIKIELGVLKNADGSAIFEMGNTKAI AAV
YGPKEMHPRHLSLPDRAVLRVRYHMTPTFSTDERKNPAPSRREIELSKVIREALES AVLVE
LFPRTAIDVFTEILQADAGSRLVSLMAASLALADAGIPMRDLIAGVAVGKADGVIIIDLN
ETEAMWGEADMPIAMMPSLNQVTLFQLNGSMTPTDEFQAFDLAVKGINIIYNLEREALKS
KYVEFKKEGV

>2B06A 155 XRAY 1.40 0.190 0.219 no MutT/nudix family protein <GB AAK75341> [STREPTOCOCCUS
PNEUMONIAE] MSRSQTLTILTNICLIEDLETQRVVMQYRAPENNRWSGYAFPGGHVENDEAFAESVIREIY
EETGLTIQNPQLVGIKNWPLDTGGRIYIVICYKATEFSGTLQSSEEGEVSWVQKDQIPNLN
LAYDMLPLMEMMEAPDKSEFFYPRTTEDDWEKKIF

>2WLRA 423 XRAY 1.45 0.176 0.196 no PUTATIVE THIOSULFATE SULFURTRANSFERASE YNJE <UNP
YNJE_ECOLI> [ESCHERICHIA COLI]
MASAELAKPLTLDQLQQQNGKAIDTRPSAFYNGWPQTLNGPSGHELAALNLSASWLDKMS
TEQLNAWIKQHNLKTDAPVALYGNKDVDVAVKTRLQKAGLTHISILSDALSEPSRLQKLP
HFEQLVYPQWLHDLQQGKEVTAKPAGDWKVEIAAWGAPKLYLISHIPGADYIDTNEVESE
PLWNKVSDEQLKAMLAKHGIRHDTTVILYGRDVYAAARVAQIMLYAGVKDVRLLDGGWQT
WSDAGLPVERGTPPKVKAEPDFGVKIPAPQLMLDMEQARGLLHRQDASLVSIRSWPEFI
GTTSGYSYIKPKGEIAGARWGHAGSDSTHMEDFHNPDGTMRSADDITAMWKAWNKPEQQ
VSFYCGTGWRASETFMYARAMGWKNVSVYDGGWYEWSSDPKNPVATGERGPDSSKLEHHH
HHH

>2W7VA 95 XRAY 2.30 0.216 0.256 no GENERAL SECRETION PATHWAY PROTEIN L <UNP Q87TC9_VIBPA>
[VIBRIO PARAHAEMOLYTICUS] MSGGSTDVAMLSWLAALPATLGQVKDEITTSFKYDQGRGEVRIHARSSDFQPFQARVKL
AEKFNVEQQQLNRSNDNVMGSFVLKRQLEHHHHHHH

>1M2XA 223 XRAY 1.50 0.190 0.208 no class B carbapenemase BlaB-1 <UNP BLAB1_FLAME>
[ELIZABETHKINGIA MENINGOSEPTICA]
DVKIEKLKDNLYVYTTYNTFNKGTYAANAVYLVTDKGVVVIDCPWGDKFKSFTDEIYKK
HGKKVIMNIATHSHDDRAGGLEIFGKIGAKTYSTKMTDSLAKENKPRAQYTFDNNKSFK
VGKSEFQVYYPGKGHTADNVVWFPEKVLVGGCIKSADSKDLGYIGEAYVNDWTQSVH
NIQQKFSGAQYVVAGHDDWKDQRSIQHTLDLINEYQQKQKASN

>3C9UA 342 XRAY 1.48 0.201 0.219 no Thiamine monophosphate kinase <UNP O67883_AQUAE> [AQUIFEX
AEOLICUS]
MGSHHHHHHDITSLYKKAGSAAAVLEENLYFQGSFTMRLKELGEFGLIDLIKKTLESKVI
GDDTAPVEYCSKLLLTDTVLNEG VHFLRSYIPEAVGWKAISVNVSDVIANGGLPKWALI
SLNLPEDLEVS YVERFYIGVKRACEFYKCEVVGNI SKSEKIGISVFLVGETERFVGRDG
ARLGDSV FVSGTLGDSRAGLELLMEKEEYEPFELALIQRHLRPTARIDYVKHIQKYANA
SMDISDGLVADANHLAQRSGVKIEILSEKLPLSNELKMYCEKYGNPIEYALFGGEDYQL
LFTHPKERWNPFLDMTEIGRVEEGEGVFVDGKKVEPKGWKHF

>2ANXA 146 XRAY 1.04 0.117 0.150 no Lysozyme <UNP LYS_BPP22> [ENTEROBACTERIA PHAGE P22]
MMQISSNGITRLKREEGERLKAYSDSRGIPTIGVGHTGKVDGNSVASGMTITAEKSSELL
KEDLQWVEDAISSLRVPLNQNYDAMCSLIFNIGKSAFAGSTVLRQLNLKNYQAAADAF
LLWKKAGKDPDILLPRRRRERALFLS

>2HLRA 100 XRAY 1.20 0.221 0.229 no Bone morphogenetic protein receptor type-2 <UNP Q91WY9_RAT>
[OVIS ARIES] ALCAFKDPYQQDLGIGESRISHENG TILCSKGSTCYGLWEKSKGDINLVKQGCWSHIGDP
QECHYEECVVTTPPSIQNGTYRFCCSTDL CNVNFTENF

>4MOMA 756 XRAY 2.19 0.188 0.240 no Putative uncharacterized protein <UNP Q5ZSU4_LEGPH>

[LEGIONELLA PNEUMOPHILA SUBSP. PNEUMOPHILA]

SNAMSTSEKDVREQVKVTVLSFLGTGQHREKVHHILTSFHNTISEVNKDNPVTAMRMFD
GPGSEPKSGDSKDIPIGTIYNPKDNSKILISPVISQTITNAIQKLTGNLAGEGIEHLLF
EAVLYLNDIIEKNGGKLPETVNLHGFSRGADTCMRMANLLYQLYPDIKVNLFLIDQVGP
GKRDDPHSYTVPPNVEHFESTLMLHEYRPGFDPQHSGRYVIADPEKTKVVVKPYGGEHNT
GNRVTEDPNTNHTAILLNDDMNRFCRETGSLPSVGISPPIIARVGDKKEEVRTHSELSPE
KRFELLCGMKENEWGYAKLTKKYHERSILSKREDYVQDSRLFVNQEHRELFKQLYPKSFN
WFFEKNHGGQTKKEEIVELKSLSEDPRYEHFFSSLAKHFQINENNIAGTLPEPSGIDRD
EKSSFGQPPVRDRLSYLQHSLSIAANYHYHCDEKSSTNESVKNLLERVESRTKPDSE
AIKHLEQTMDEVQRILESKNEKGFLWQQINHISPNAQYCEQVKAALREHLEHNQVLSDT
QKEEIRKAMDRMDNIVNDSSKDSQQKYREIRREVIELNAKATTPEDDNQLTRSHFQKAYF
ELSGDTQKTLNLESLSQTLNQLSKAHYGETSMTDKITQRLDGYKNRNWFNSVKEVLNFF
NIPLPKLHSEVKEQIADKLKERLVDLKEKGMGNDVNAITRELKAREDLEHYKKTSKLE
MGELDKIINKSMEEELLVARKVTKDLVHEEVSQVKLN

>3PICA 375 XRAY 1.90 0.195 0.234 no Cip2 <UNP Q7Z9N1_TRIRE> [HYPOCREA JECORINA]

QQTSGAGGATCSALPGSITLRSNAKLNLFMTFNGDKVTTKDKFSCRQAEMSELIQRYEL
GTLPGRPSTLTASFSGNTLTINCGEAGKSISFTVTITYPSSGTAPYPAIIGYGGGSLPAP
AGVAMINFNNDNIAAQVNTGSRGQKGYDLYGSSHSAGAMTAWAGVSRVIDALELVGA
RIDTTKIGVTGCSRNGKGAMVAGAFEKRIVLTLPQESGAGGSACWRISDYLSQGANIQT
ASEIIGEDPWFSTTFNSYVNPVLPFDHHSALAIAPRGLFVIDNNIDWLGPQSCFGCM
TAAHMAWQALGVSDHMGYSQIGAHAHCAFPSNQSSQLTAFVQKFLLGQSTNTAIFQSDFS
ANQSQWIDWTTPTLS

>3R45C 81 XRAY 2.60 0.187 0.245 no Holliday junction recognition protein <UNP HJURP_HUMAN>
[HOMO SAPIENS]

SMLGTLRAMEGEDVEDDQLLQKLRRSRRFQRRMQRLIEKYNQPFEDTPVVQMATLTYET
PQGLRIWGGRLIKERNEGEIQ

>1ZIWA 680 XRAY 2.10 0.210 0.248 no Toll-like receptor 3 <UNP TLR3_HUMAN> [HOMO SAPIENS]

KCTVSHEVADCSHLKLTVPPDDLPTNITVLNLTHNQLRRLPAANFTRYSQLTSLDVGFN
ISKLEPELCQKLPMLKVLNLQHNELSQLSDKTFAFCTNLTELHLSNSIQIKNNPFVKQ
KNLITLDSLHNGLSSTKLGTQVQLENLQELLSNNKIQALKSEELDIFANSSKKLELSS
NQIKEFSPGCFHAIGRLFGLFLNNVQLGPSLTEKLCLELANTSIRNLSLSNSQLSTTSNT
TFLGLKWTNLTMLDSYNNLNNVGNSFAWLPQLEYFFLEYNNIQHLFSHSLHGLFNVR
LNLKRSFTKQISLASLPKIDDFSQWLKCLEHLNMEDNDIPGIKSNMFTGLINLKYSLS
SNSFTSLRTLNETFVSLAHSPLHILNLTKNKISKIESDAFSWLGHLEVLDLGLNEIGQE
LTGQEWGLENIFEIYLSYNKYLLQTRNSFALVPSLQRLMLRRVALKNVDSSPSPFQPLR
NLITLDLSNNNIANINDDMLEGLEKLEILDQLHNNLARLWKHANPGGPIYFLKGLSHLHI
LNLESNGFDEIPVEVFKDLFELKIDLGLNNLNTLPASVFNNQVSLKSLNLQKNLITSVE
KKVFGPAFRNLTELDMRFPDCTCESIAWVFNWINETHNTNIPELSSHYLCNTPPHYHGF
PVRLFDTSSCKDSAHHHHHH