





















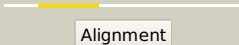



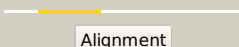

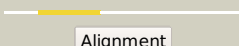

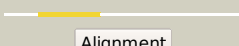

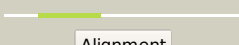







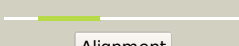
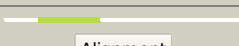


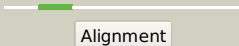
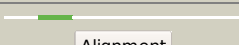




# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD0319\_(pcp)\_387148\_387816  
 Date Tue Jul 23 14:50:38 BST 2019  
 Unique Job ID 7193c96c211fc03a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1a2za_</a>	 Alignment		100.0	35	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) <b>Family:</b> Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
2	<a href="#">c4gxhC_</a>	 Alignment		100.0	39	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> pyrrolidone-carboxylate peptidase; <b>PDBTitle:</b> crystal structure of a pyrrolidone-carboxylate peptidase 1 (target id2 nysgrc-012831) from xenorhabdus bovienii ss-2004
3	<a href="#">d1iofa_</a>	 Alignment		100.0	37	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) <b>Family:</b> Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
4	<a href="#">d1auga_</a>	 Alignment		100.0	36	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) <b>Family:</b> Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
5	<a href="#">c3giuA_</a>	 Alignment		100.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrrolidone-carboxylate peptidase; <b>PDBTitle:</b> 1.25 angstrom crystal structure of pyrrolidone-carboxylate peptidase2 (pcp) from staphylococcus aureus
6	<a href="#">d1iu8a_</a>	 Alignment		100.0	37	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) <b>Family:</b> Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
7	<a href="#">c5z47A_</a>	 Alignment		100.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrrolidone-carboxylate peptidase; <b>PDBTitle:</b> crystal structure of pyrrolidone carboxylate peptidase i with2 disordered loop a from deinococcus radiodurans r1
8	<a href="#">c3lacA_</a>	 Alignment		100.0	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrrolidone-carboxylate peptidase; <b>PDBTitle:</b> crystal structure of bacillus anthracis pyrrolidone-carboxylate2 peptidase, pcp
9	<a href="#">c2ebjB_</a>	 Alignment		100.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> pyrrolidone carboxyl peptidase; <b>PDBTitle:</b> crystal structure of pyrrolidone carboxyl peptidase from thermus2 thermophilus
10	<a href="#">c3wmwB_</a>	 Alignment		86.8	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nad dependent epimerase/dehydratase; <b>PDBTitle:</b> gale-like l-threonine dehydrogenase from cupriavidus necator (apo2 form)
11	<a href="#">c4b8wB_</a>	 Alignment		84.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> gdp-l-fucose synthase; <b>PDBTitle:</b> crystal structure of human gdp-l-fucose synthase with bound nadp and2 gdp, tetragonal crystal form

12	<a href="#">c2i5bC_</a>	 Alignment		79.6	17	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> phosphomethylpyrimidine kinase; <b>PDBTitle:</b> the crystal structure of an adp complex of bacillus subtilis pyridoxal2 kinase provides evidence for the parralel emergence of enzyme3 activity during evolution
13	<a href="#">c3sc6F_</a>	 Alignment		79.3	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F; <b>PDB Molecule:</b> ddtp-4-dehydrorhamnose reductase; <b>PDBTitle:</b> 2.65 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 reductase (rfbd) from bacillus anthracis str. ames in complex with3 nadp
14	<a href="#">c4wpgA_</a>	 Alignment		78.5	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> ddtp-4-dehydrorhamnose reductase; <b>PDBTitle:</b> group a streptococcus gaca is an essential dtdp-4-dehydrorhamnose2 reductase (rmlD)
15	<a href="#">c2ydyA_</a>	 Alignment		76.3	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> methionine adenosyltransferase 2 subunit beta; <b>PDBTitle:</b> crystal structure of human s-adenosylmethionine synthetase 2, beta2 subunit in orthorhombic crystal form
16	<a href="#">d1jja_</a>	 Alignment		71.5	20	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
17	<a href="#">c6aaqD_</a>	 Alignment		68.9	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D; <b>PDB Molecule:</b> gdp-l-fucose synthetase; <b>PDBTitle:</b> crystal structure of a gdp-l-fucose synthetase from naegleria fowleri
18	<a href="#">d1db3a_</a>	 Alignment		67.0	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
19	<a href="#">c4josA_</a>	 Alignment		63.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> adenosylhomocysteine nucleosidase; <b>PDBTitle:</b> crystal structure of a putative 5'-methylthioadenosine/s-2 adenosylhomocysteine nucleosidase from francisella philomiragia atcc3 25017 (target nysgrc-029335)
20	<a href="#">d2f7wa1</a>	 Alignment		62.6	9	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
21	<a href="#">c1z45A_</a>	 Alignment	not modelled	61.5	26	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> gal10 bifunctional protein; <b>PDBTitle:</b> crystal structure of the gal10 fusion protein galactose2 mutarotase/udp-galactose 4-epimerase from saccharomyces cerevisiae3 complexed with nad, udp-glucose, and galactose
22	<a href="#">c2qq1A_</a>	 Alignment	not modelled	60.7	14	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> molybdenum cofactor biosynthesis mog; <b>PDBTitle:</b> crystal structure of molybdenum cofactor biosynthesis2 (aq_061) other form from aquifex aeolicus vf5
23	<a href="#">d1n2sa_</a>	 Alignment	not modelled	59.7	10	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
24	<a href="#">c4jgbB_</a>	 Alignment	not modelled	56.8	38	<b>PDB header:</b> protein binding <b>Chain:</b> B; <b>PDB Molecule:</b> putative exported protein; <b>PDBTitle:</b> crystal structure of putative exported protein from burkholderia2 pseudomallei
25	<a href="#">d1bxka_</a>	 Alignment	not modelled	56.7	63	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
26	<a href="#">c5b6kA_</a>	 Alignment	not modelled	55.3	50	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein cgkr1; <b>PDBTitle:</b> crystal strucutre of ketoreductase 1 from candida glabrata
27	<a href="#">c4dqvA_</a>	 Alignment	not modelled	55.1	22	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> probable peptide synthetase nrp (peptide synthase); <b>PDBTitle:</b> crystal structure of reductase (r) domain of non-ribosomal peptide2 synthetase from mycobacterium tuberculosis
28	<a href="#">d1jysa_</a>	 Alignment	not modelled	54.8	16	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases

29	<a href="#">d1vl0a_</a>	Alignment	not modelled	54.4	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
30	<a href="#">c2is8A_</a>	Alignment	not modelled	54.2	13	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin biosynthesis enzyme, moab; <b>PDBTitle:</b> crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus thermophilus hb8
31	<a href="#">c5l9aB_</a>	Alignment	not modelled	54.0	75	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> l-threonine 3-dehydrogenase; <b>PDBTitle:</b> l-threonine dehydrogenase from trypanosoma brucei.
32	<a href="#">c2q1wC_</a>	Alignment	not modelled	54.0	63	<b>PDB header:</b> sugar binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> putative nucleotide sugar epimerase/dehydratase; <b>PDBTitle:</b> crystal structure of the bordetella bronchiseptica enzyme wbmh in2 complex with nad+
33	<a href="#">c3rfxB_</a>	Alignment	not modelled	52.6	63	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> uronate dehydrogenase; <b>PDBTitle:</b> crystal structure of uronate dehydrogenase from agrobacterium2 tumefaciens, y136a mutant complexed with nad
34	<a href="#">d1oc2a_</a>	Alignment	not modelled	51.3	38	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
35	<a href="#">c3dhnA_</a>	Alignment	not modelled	51.2	25	<b>PDB header:</b> isomerase, lyase <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent epimerase/dehydratase; <b>PDBTitle:</b> crystal structure of the putative epimerase q89z24_bactn from2 bacteroides thetaiotaomicron. northeast structural genomics3 consortium target btr310.
36	<a href="#">c4jwTA_</a>	Alignment	not modelled	51.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> methylthioadenosine nucleosidase; <b>PDBTitle:</b> crystal structure of a putative 5'-methylthioadenosine/s-2 adenosylhomocysteine nucleosidase from sulfurimonas denitrificans dsm3 1251 (target nysgrc-029304 )
37	<a href="#">c4l0mA_</a>	Alignment	not modelled	50.1	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative 5'-methylthioadenosine/s-adenosylhomocysteine <b>PDBTitle:</b> crystal structure of a putative 5'-methylthioadenosine/s-2 adenosylhomocysteine nucleosidase from borrelia burgdorferi b31 bound3 to adenine (target nysgrc-029268 )
38	<a href="#">c4kn5A_</a>	Alignment	not modelled	49.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> methylthioadenosine nucleosidase; <b>PDBTitle:</b> crystal structure of a putative methylthioadenosine nucleosidase from2 weissella paramesenteroides atcc 33313 (target nysgrc-029342 )
39	<a href="#">c6po4A_</a>	Alignment	not modelled	48.1	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 5'-methylthioadenosine/s-adenosylhomocysteine nucleosidase; <b>PDBTitle:</b> 2.1 angstrom resolution crystal structure of 5'-methylthioadenosine/s-2 adenosylhomocysteine nucleosidase (mtmn) from haemophilus influenzae3 pittii.
40	<a href="#">d2c5aa1</a>	Alignment	not modelled	47.9	38	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
41	<a href="#">c5b7pB_</a>	Alignment	not modelled	46.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mta/sah nucleosidase; <b>PDBTitle:</b> structures and functional analysis of periplasmic 5-2 methylthioadenosine/s-adenosylhomocysteine nucleosidase from3 aeromonas hydrophila
42	<a href="#">c6g1nB_</a>	Alignment	not modelled	46.3	14	<b>PDB header:</b> antitoxin <b>Chain:</b> B: <b>PDB Molecule:</b> antitoxin hicb; <b>PDBTitle:</b> crystal structure of the burkholderia pseudomallei antitoxin hicb
43	<a href="#">c5wqnD_</a>	Alignment	not modelled	45.1	50	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> probable dehydrogenase; <b>PDBTitle:</b> crystal structure of a carbonyl reductase from pseudomonas aeruginosa2 pao1 (condition ii)
44	<a href="#">c3c1oA_</a>	Alignment	not modelled	44.0	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> eugenol synthase; <b>PDBTitle:</b> the multiple phenylpropene synthases in both clarkia2 breweri and petunia hybrida represent two distinct lineages
45	<a href="#">d1f0ka_</a>	Alignment	not modelled	43.7	22	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Peptidoglycan biosynthesis glycosyltransferase MurG
46	<a href="#">c3ay3C_</a>	Alignment	not modelled	43.0	50	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nad-dependent epimerase/dehydratase; <b>PDBTitle:</b> crystal structure of glucuronic acid dehydrogeanse from2 chromohalobacter salexigens
47	<a href="#">c3dp9A_</a>	Alignment	not modelled	43.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mta/sah nucleosidase; <b>PDBTitle:</b> crystal structure of vibrio cholerae 5'-methylthioadenosine/s-adenosyl2 homocysteine nucleosidase (mtan) complexed with butylthio-dadme-3 immucillin a
48	<a href="#">d1kewa_</a>	Alignment	not modelled	41.9	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
49	<a href="#">c4qezC_</a>	Alignment	not modelled	41.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> 5'-methylthioadenosine/s-adenosylhomocysteine nucleosidase; <b>PDBTitle:</b> crystal structure of 5'-methylthioadenosine/s-adenosylhomocysteine2 nucleosidase from bacillus anthracis
50	<a href="#">c1zosE_</a>	Alignment	not modelled	41.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> 5'-methylthioadenosine / s-adenosylhomocysteine <b>PDBTitle:</b> structure of 5'-methylthioadenosine/s-adenosylhomocysteine2 nucleosidase from s. pneumoniae with a transition-state inhibitor mt-3 imma
51	<a href="#">c4bmvH_</a>	Alignment	not modelled	40.8	50	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> short-chain dehydrogenase; <b>PDBTitle:</b> short-chain dehydrogenase from sphingobium yanoikuyae

						in2 complex with nadph
52	<a href="#">c5msuC_</a>	Alignment	not modelled	40.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> carboxylic acid reductase; <b>PDBTitle:</b> structure of the r domain of carboxylic acid reductase (car) from2 mycobacterium marinum in complex with nadp, p21 form
53	<a href="#">d2vbaa1</a>	Alignment	not modelled	40.4	40	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
54	<a href="#">c6if8D_</a>	Alignment	not modelled	40.2	24	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> 5'-methylthioadenosine/s-adenosylhomocysteine nucleosidase; <b>PDBTitle:</b> aeromonas hydrophila mtan-2 complexed with adenine
55	<a href="#">c3l6eA_</a>	Alignment	not modelled	39.9	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, short-chain dehydrogenase/reductase family; <b>PDBTitle:</b> crystal structure of putative short chain dehydrogenase/reductase2 family oxidoreductase from aeromonas hydrophila subsp. hydrophila3 atcc 7966
56	<a href="#">c3gpiA_</a>	Alignment	not modelled	39.9	50	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent epimerase/dehydratase; <b>PDBTitle:</b> structure of putative nad-dependent epimerase/dehydratase from2 methylobacillus flagellatus
57	<a href="#">c1gsoA_</a>	Alignment	not modelled	39.0	60	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (glycinamide ribonucleotide synthetase); <b>PDBTitle:</b> glycinamide ribonucleotide synthetase (gar-syn) from e.2 coli.
58	<a href="#">c5dk6A_</a>	Alignment	not modelled	38.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 5'-methylthioadenosine/s-adenosylhomocysteine nucleosidase; <b>PDBTitle:</b> crystal structure of a 5'-methylthioadenosine/s-adenosylhomocysteine2 (mta/sah) nucleosidase (mtan) from colwellia psychrerythraea 34h3 (cps_4743, target psi-029300) in complex with adenine at 2.27 a4 resolution
59	<a href="#">c4qjiB_</a>	Alignment	not modelled	37.2	24	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphopantothenate--cysteine ligase; <b>PDBTitle:</b> crystal structure of the c-terminal ctp-binding domain of a2 phosphopantothenylcysteine decarboxylase/phosphopantothenate-3 cysteine ligase with bound ctp from mycobacterium smegmatis
60	<a href="#">d1hdoa_</a>	Alignment	not modelled	37.1	25	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
61	<a href="#">d1di6a_</a>	Alignment	not modelled	36.9	17	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
62	<a href="#">c2b7lD_</a>	Alignment	not modelled	36.1	25	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glycerol-3-phosphate cytidyltransferase; <b>PDBTitle:</b> crystal structure of ctp:glycerol-3-phosphate2 cytidyltransferase from staphylococcus aureus
63	<a href="#">d1e6ua_</a>	Alignment	not modelled	36.0	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
64	<a href="#">d2g2ca1</a>	Alignment	not modelled	35.6	22	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
65	<a href="#">c3eeiA_</a>	Alignment	not modelled	35.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-methylthioadenosine nucleosidase/s-adenosylhomocysteine <b>PDBTitle:</b> crystal structure of 5'-methylthioadenosine/s-adenosylhomocysteine2 nucleosidase from neisseria meningitidis in complex with methylthio-3 immucillin-a
66	<a href="#">c5ldwA_</a>	Alignment	not modelled	34.9	50	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr; <b>PDBTitle:</b> crystal structure of an oxidoreductase from burkholderia vietnamiensis2 in complex with nadp
67	<a href="#">c3ia7A_</a>	Alignment	not modelled	33.9	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> calg4; <b>PDBTitle:</b> crystal structure of calg4, the calicheamicin glycosyltransferase
68	<a href="#">c4xcwF_</a>	Alignment	not modelled	33.8	16	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> molybdopterin adenyltransferase; <b>PDBTitle:</b> crystal structure of molybdenum cofactor biosynthesis protein moga2 from helicobacter pylori str. j99
69	<a href="#">c4g41A_</a>	Alignment	not modelled	33.7	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mta/sah nucleosidase; <b>PDBTitle:</b> crystal structure of s-adenosylhomocysteine nucleosidase from2 streptococcus pyogenes in complex with 5-methylthiotubercidin
70	<a href="#">c5u9cC_</a>	Alignment	not modelled	33.5	19	<b>PDB header:</b> hydrolase,oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> ddtp-4-dehydrorhamnose reductase; <b>PDBTitle:</b> 1.9 angstrom resolution crystal structure of ddtp-4-dehydrorhamnose2 reductase from yersinia enterocolitica
71	<a href="#">c3eywA_</a>	Alignment	not modelled	33.4	42	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> c-terminal domain of glutathione-regulated potassium-efflux <b>PDBTitle:</b> crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
72	<a href="#">c5yrzC_</a>	Alignment	not modelled	33.2	14	<b>PDB header:</b> antitoxin/hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> hicb; <b>PDBTitle:</b> toxin-antitoxin complex from streptococcus pneumoniae
73	<a href="#">c3rfqC_</a>	Alignment	not modelled	32.8	23	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C: <b>PDB Molecule:</b> pterin-4-alpha-carbinolamine dehydratase moab2; <b>PDBTitle:</b> crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
74	<a href="#">c3nrzD_</a>	Alignment	not modelled	32.7	23	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> udp-n-acetylglucosamine 4,6-dehydratase;

74	<a href="#">c3pvzD</a>	Alignment	not modelled	32.7	43	<b>PDBTitle:</b> udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri <b>PDB header:</b> oxidoreductase
75	<a href="#">c4w4tA</a>	Alignment	not modelled	31.7	18	<b>Chain:</b> A; <b>PDB Molecule:</b> mxaa; <b>PDBTitle:</b> the crystal structure of the terminal r domain from the myxalamid pks-2 nrps biosynthetic pathway
76	<a href="#">d1vpxa</a>	Alignment	not modelled	30.7	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
77	<a href="#">c2buiC</a>	Alignment	not modelled	30.4	40	<b>PDB header:</b> synthase <b>Chain:</b> C; <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] synthase i; <b>PDBTitle:</b> e.coli beta-ketoacyl (acyl carrier protein) synthase i in2 complex with octanoic acid, 120k
78	<a href="#">c5xvsA</a>	Alignment	not modelled	29.8	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> gdp/udp-n,n'-diacetylbacillosamine 2-epimerase <b>PDBTitle:</b> crystal structure of udp-glcnac 2-epimerase neuc complexed with udp
79	<a href="#">d1uuya</a>	Alignment	not modelled	29.5	18	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
80	<a href="#">d1ub0a</a>	Alignment	not modelled	29.5	11	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Thiamin biosynthesis kinases
81	<a href="#">c4qqrB</a>	Alignment	not modelled	29.5	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> 3,5-epimerase/4-reductase; <b>PDBTitle:</b> structural insight into nucleotide rhamnose synthase/epimerase-2 reductase from arabidopsis thaliana
82	<a href="#">c3fryB</a>	Alignment	not modelled	28.5	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> probable copper-exporting p-type atpase a; <b>PDBTitle:</b> crystal structure of the copa c-terminal metal binding domain
83	<a href="#">c2el7A</a>	Alignment	not modelled	28.3	40	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of tryptophanyl-trna synthetase from thermus2 thermophilus
84	<a href="#">c4pr3A</a>	Alignment	not modelled	28.1	35	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> 5'-methylthioadenosine nucleosidase / s- <b>PDBTitle:</b> crystal structure of brucella melitensis 5'-methylthioadenosine/s-2 adenosylhomocysteine nucleosidase
85	<a href="#">c3bl6A</a>	Alignment	not modelled	28.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> 5'-methylthioadenosine nucleosidase/s- <b>PDBTitle:</b> crystal structure of staphylococcus aureus 5'-2 methylthioadenosine/s-adenosylhomocysteine nucleosidase in3 complex with formycin a
86	<a href="#">d1j3na1</a>	Alignment	not modelled	27.4	60	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related
87	<a href="#">c2h8gA</a>	Alignment	not modelled	27.3	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> 5'-methylthioadenosine nucleosidase; <b>PDBTitle:</b> 5'-methylthioadenosine nucleosidase from arabidopsis2 thaliana
88	<a href="#">c2a5hC</a>	Alignment	not modelled	26.6	10	<b>PDB header:</b> isomerase <b>Chain:</b> C; <b>PDB Molecule:</b> l-lysine 2,3-aminomutase; <b>PDBTitle:</b> 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate).
89	<a href="#">d1fjha</a>	Alignment	not modelled	26.5	38	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
90	<a href="#">d1iira</a>	Alignment	not modelled	26.3	26	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Gtf glycosyltransferase
91	<a href="#">c2kkhA</a>	Alignment	not modelled	26.1	19	<b>PDB header:</b> metal transport <b>Chain:</b> A; <b>PDB Molecule:</b> putative heavy metal transporter; <b>PDBTitle:</b> structure of the zinc binding domain of the atpase hma4
92	<a href="#">c2qx7A</a>	Alignment	not modelled	25.3	63	<b>PDB header:</b> plant protein <b>Chain:</b> A; <b>PDB Molecule:</b> eugenol synthase 1; <b>PDBTitle:</b> structure of eugenol synthase from ocimum basilicum
93	<a href="#">c4p7dA</a>	Alignment	not modelled	25.2	11	<b>PDB header:</b> toxin <b>Chain:</b> A; <b>PDB Molecule:</b> antitoxin hicb3; <b>PDBTitle:</b> antitoxin hicb3 crystal structure
94	<a href="#">d1udca</a>	Alignment	not modelled	24.8	71	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
95	<a href="#">c6aytD</a>	Alignment	not modelled	24.1	9	<b>PDB header:</b> hydrolase, transferase <b>Chain:</b> D; <b>PDB Molecule:</b> 5'-methylthioadenosine/s-adenosylhomocysteine nucleosidase; <b>PDBTitle:</b> crystal structure of campylobacter jejuni 5'-methylthioadenosine/s-2 adenosyl homocysteine nucleosidase (mtan) complexed with3 pyrazinylthio-dadme-immucillin-a
96	<a href="#">d1fmta2</a>	Alignment	not modelled	24.0	17	<b>Fold:</b> Formyltransferase <b>Superfamily:</b> Formyltransferase <b>Family:</b> Formyltransferase
97	<a href="#">c3l77A</a>	Alignment	not modelled	23.8	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> short-chain alcohol dehydrogenase; <b>PDBTitle:</b> x-ray structure alcohol dehydrogenase from archaeon thermococcus2 sibiricus complexed with 5-hydroxy-nadp
98	<a href="#">d1coza</a>	Alignment	not modelled	23.7	38	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Cytidyl transferase
						<b>Fold:</b> NAD(P)-binding Rossmann-fold domains



99	<a href="#">d1r6da_</a>	Alignment	not modelled	23.5	57	<b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
100	<a href="#">c3icpA_</a>	Alignment	not modelled	23.5	43	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent epimerase/dehydratase; <b>PDBTitle:</b> crystal structure of udp-galactose 4-epimerase
101	<a href="#">d2blla1</a>	Alignment	not modelled	23.4	43	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
102	<a href="#">c5mx6C_</a>	Alignment	not modelled	23.4	7	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> purine nucleoside phosphorylase deod-type; <b>PDBTitle:</b> crystal structure of h. pylori purine nucleoside phosphorylase from2 clinical isolate hppnp-2
103	<a href="#">c5intB_</a>	Alignment	not modelled	23.2	25	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphopantothenate--cysteine ligase; <b>PDBTitle:</b> crystal structure of the c-terminal domain of coenzyme a biosynthesis2 bifunctional protein coabc
104	<a href="#">d2q46a1</a>	Alignment	not modelled	23.0	36	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
105	<a href="#">c3bsfB_</a>	Alignment	not modelled	23.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> at4g34840; <b>PDBTitle:</b> crystal structure of the mta/sah nucleosidase
106	<a href="#">c4zrmB_</a>	Alignment	not modelled	22.9	57	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-glucose 4-epimerase; <b>PDBTitle:</b> crystal structure of udp-glucose 4-epimerase (tm0509) from2 hyperthermophilic eubacterium thermotoga maritima
107	<a href="#">c1z34A_</a>	Alignment	not modelled	22.7	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> purine nucleoside phosphorylase; <b>PDBTitle:</b> crystal structure of trichomonas vaginalis purine nucleoside2 phosphorylase complexed with 2-fluoro-2'-deoxyadenosine
108	<a href="#">c3lrfA_</a>	Alignment	not modelled	22.6	60	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-ketoacyl synthase; <b>PDBTitle:</b> crystal structure of beta-ketoacyl synthase from brucella2 melitensis
109	<a href="#">c3s2uA_</a>	Alignment	not modelled	22.5	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine--n-acetylmuramyl-(pentapeptide) <b>PDBTitle:</b> crystal structure of the pseudomonas aeruginosa murg:udp-glcna2 substrate complex
110	<a href="#">c2pk3B_</a>	Alignment	not modelled	22.4	43	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> gdp-6-deoxy-d-lyxo-4-hexulose reductase; <b>PDBTitle:</b> crystal structure of a gdp-4-keto-6-deoxy-d-mannose reductase
111	<a href="#">c4pvcB_</a>	Alignment	not modelled	22.4	43	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadph-dependent methylglyoxal reductase gre2; <b>PDBTitle:</b> crystal structure of yeast methylglyoxal/ isovaleraldehyde reductase2 gre2
112	<a href="#">c6bwIA_</a>	Alignment	not modelled	22.1	71	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> pal; <b>PDBTitle:</b> x-ray structure of pal from bacillus thuringiensis
113	<a href="#">d1gy8a_</a>	Alignment	not modelled	22.0	57	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
114	<a href="#">c1k82D_</a>	Alignment	not modelled	21.8	11	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> D: <b>PDB Molecule:</b> formamidopyrimidine-dna glycosylase; <b>PDBTitle:</b> crystal structure of e.coli formamidopyrimidine-dna2 glycosylase (fpg) covalently trapped with dna
115	<a href="#">c3m2pD_</a>	Alignment	not modelled	21.8	57	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> udp-n-acetylglucosamine 4-epimerase; <b>PDBTitle:</b> the crystal structure of udp-n-acetylglucosamine 4-epimerase2 from bacillus cereus
116	<a href="#">d1d8wa_</a>	Alignment	not modelled	21.5	32	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> L-rhamnose isomerase
117	<a href="#">d1i24a_</a>	Alignment	not modelled	21.5	28	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
118	<a href="#">c2pzlB_</a>	Alignment	not modelled	21.4	43	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative nucleotide sugar epimerase/dehydratase; <b>PDBTitle:</b> crystal structure of the bordetella bronchiseptica enzyme wbmj in2 complex with nad and udp
119	<a href="#">c2x4gA_</a>	Alignment	not modelled	21.3	43	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoside-diphosphate-sugar epimerase; <b>PDBTitle:</b> crystal structure of pa4631, a nucleoside-diphosphate-sugar epimerase2 from pseudomonas aeruginosa
120	<a href="#">c4yl5A_</a>	Alignment	not modelled	21.1	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphomethylpyrimidine kinase; <b>PDBTitle:</b> structure of a putative phosphomethylpyrimidine kinase from2 acinetobacter baumannii