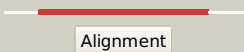

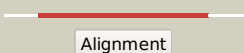

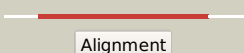

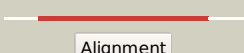


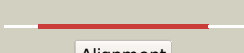



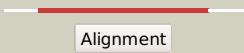



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1612_(trpB)_1811134_1812366
Date	Fri Aug 2 13:30:20 BST 2019
Unique Job ID	4f9231618fb213ca

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5tchH_</a>	 Alignment		100.0	100	<b>PDB header:</b> lyase <b>Chain:</b> H: <b>PDB Molecule:</b> tryptophan synthase beta chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant
2	<a href="#">c5kinD_</a>	 Alignment		100.0	58	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> tryptophan synthase beta chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
3	<a href="#">d1qopb_</a>	 Alignment		100.0	55	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
4	<a href="#">c1x1qA_</a>	 Alignment		100.0	56	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase beta chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase beta chain from thermus2 thermophilus hb8
5	<a href="#">d1v8za1</a>	 Alignment		100.0	59	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
6	<a href="#">c2o2jA_</a>	 Alignment		100.0	100	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase beta chain; <b>PDBTitle:</b> mycobacterium tuberculosis tryptophan synthase beta chain dimer2 (apofrom)
7	<a href="#">c4negA_</a>	 Alignment		100.0	57	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase beta chain; <b>PDBTitle:</b> the crystal structure of tryptophan synthase subunit beta from2 bacillus anthracis str. 'ames ancestor'
8	<a href="#">c6hulB_</a>	 Alignment		100.0	30	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan synthase beta chain 1; <b>PDBTitle:</b> sulfolobus solfataricus tryptophan synthase ab complex
9	<a href="#">c4qysA_</a>	 Alignment		100.0	29	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase beta chain 2; <b>PDBTitle:</b> trpb2 enzymes
10	<a href="#">d1wkva1</a>	 Alignment		100.0	21	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
11	<a href="#">c1tdjA_</a>	 Alignment		100.0	22	<b>PDB header:</b> allostery <b>Chain:</b> A: <b>PDB Molecule:</b> biosynthetic threonine deaminase; <b>PDBTitle:</b> threonine deaminase (biosynthetic) from e. coli

12	<a href="#">c3iauA_</a>	Alignment		100.0	23	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> threonine deaminase; <b>PDBTitle:</b> the structure of the processed form of threonine deaminase isoform 22 from solanum lycopersicum
13	<a href="#">c4d9gA_</a>	Alignment		100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative diaminopropionate ammonia-lyase; <b>PDBTitle:</b> crystal structure of selenomethionine incorporated holo2 diaminopropionate ammonia lyase from escherichia coli
14	<a href="#">c4l3vB_</a>	Alignment		100.0	24	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> cystathionine beta-synthase; <b>PDBTitle:</b> crystal structure of delta516-525 human cystathionine beta-synthase
15	<a href="#">c5ohxB_</a>	Alignment		100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> cystathionine beta-synthase; <b>PDBTitle:</b> structure of active cystathionine b-synthase from apis mellifera
16	<a href="#">d1v71a1</a>	Alignment		100.0	19	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
17	<a href="#">c3pc3A_</a>	Alignment		100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> cg1753, isoform a; <b>PDBTitle:</b> full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
18	<a href="#">c5ygrA_</a>	Alignment		100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopropionate ammonia lyase; <b>PDBTitle:</b> crystal structure of plp bound diaminopropionate ammonia lyase from2 salmonella typhimurium
19	<a href="#">d1jbqa_</a>	Alignment		100.0	25	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
20	<a href="#">c1jbqD_</a>	Alignment		100.0	25	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> cystathionine beta-synthase; <b>PDBTitle:</b> structure of human cystathionine beta-synthase: a unique pyridoxal 5'-2 phosphate dependent hemeprotein
21	<a href="#">d1pwha_</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
22	<a href="#">c6c2qA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> cystathionine beta-synthase; <b>PDBTitle:</b> crystal structures of cystathionine beta-synthase from saccharomyces2 cerevisiae: the structure of the plp-l-serine intermediate
23	<a href="#">d1tdja1</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
24	<a href="#">c2gn0A_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> threonine dehydratase catabolic; <b>PDBTitle:</b> crystal structure of dimeric biodegradative threonine deaminase (tdcb)2 from salmonella typhimurium at 1.7 a resolution (triclinic form with3 one complete subunit built in alternate conformation)
25	<a href="#">c3r0zA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> d-serine dehydratase; <b>PDBTitle:</b> crystal structure of apo d-serine deaminase from salmonella2 typhimurium
26	<a href="#">c5i7wA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine synthase a; <b>PDBTitle:</b> crystal structure of a cysteine synthase from brucella suis
27	<a href="#">c5d87A_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable siderophore biosynthesis protein sbna; <b>PDBTitle:</b> staphyloferrin b precursor biosynthetic enzyme sbna

						y152f/s185g2 variant
28	<a href="#">d1ve1a1</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
29	<a href="#">d1z7wa1</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
30	<a href="#">c1p5jA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> l-serine dehydratase; <b>PDBTitle:</b> crystal structure analysis of human serine dehydratase
31	<a href="#">d1p5ja</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
32	<a href="#">c3l6cA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> serine racemase; <b>PDBTitle:</b> x-ray crystal structure of rat serine racemase in complex with2 malonate a potent inhibitor
33	<a href="#">d1ve5a1</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
34	<a href="#">c4aecB</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> cysteine synthase, mitochondrial; <b>PDBTitle:</b> crystal structure of the arabidopsis thaliana o-acetylserine-(thiol)-2 lyase c
35	<a href="#">c5cvcB</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> serine racemase; <b>PDBTitle:</b> structure of maize serine racemase
36	<a href="#">c4lmaA</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine synthase; <b>PDBTitle:</b> crystal structure analysis of o-acetylserine sulfhydrylase cysk1 from2 microcystis aeruginosa 7806
37	<a href="#">c3x43F</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> o-ureido-l-serine synthase; <b>PDBTitle:</b> crystal structure of o-ureido-l-serine synthase
38	<a href="#">c3vbeA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-cyanoalanine synthase; <b>PDBTitle:</b> crystal structure of beta-cyanoalanine synthase in soybean
39	<a href="#">c3dwgA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine synthase b; <b>PDBTitle:</b> crystal structure of a sulfur carrier protein complex found in the2 cysteine biosynthetic pathway of mycobacterium tuberculosis
40	<a href="#">c5b1iC</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> cystathionine beta-synthase; <b>PDBTitle:</b> crystal structure of k42a mutant of cystathionine beta-synthase from2 lactobacillus plantarum in a complex with l-methionine
41	<a href="#">d2bhsa1</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
42	<a href="#">c2d1fA</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> threonine synthase; <b>PDBTitle:</b> structure of mycobacterium tuberculosis threonine synthase
43	<a href="#">c2pqmA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine synthase; <b>PDBTitle:</b> crystal structure of cysteine synthase (oass) from entamoeba2 histolytica at 1.86 a resolution
44	<a href="#">c2zsjB</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> threonine synthase; <b>PDBTitle:</b> crystal structure of threonine synthase from aquifex aeolicus vf5
45	<a href="#">c5c3uA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> l-serine ammonia-lyase; <b>PDBTitle:</b> crystal structure of a fungal l-serine ammonia-lyase from rhizomucor2 miehei
46	<a href="#">c4i1xA</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine synthase; <b>PDBTitle:</b> crystal structure of cysteine synthase from helicobacter pylori 26695
47	<a href="#">d1o58a</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
48	<a href="#">c5ybwA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate racemase; <b>PDBTitle:</b> crystal structure of pyridoxal 5'-phosphate-dependent aspartate2 racemase
49	<a href="#">d1y7la1</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
50	<a href="#">d1v7ca</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
						<b>PDB header:</b> lyase

51	<a href="#">c2rkbE_</a>	Alignment	not modelled	100.0	22	<b>Chain:</b> E: <b>PDB Molecule:</b> serine dehydratase-like; <b>PDBTitle:</b> serine dehydratase like-1 from human cancer cells
52	<a href="#">c4airB_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cysteine synthase; <b>PDBTitle:</b> leishmania major cysteine synthase
53	<a href="#">c4ql4A_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> o-acetylserine lyase; <b>PDBTitle:</b> crystal structure of o-acetylserine sulfhydrylase from bacillus2 anthracis
54	<a href="#">d1e5xa_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
55	<a href="#">c2q3bA_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine synthase a; <b>PDBTitle:</b> 1.8 a resolution crystal structure of o-acetylserine sulfhydrylase2 (oass) holoenzyme from mycobacterium tuberculosis
56	<a href="#">c6cggA_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> threonine synthase; <b>PDBTitle:</b> threonine synthase from bacillus subtilis atcc 6633 with plp and plp-2 ala
57	<a href="#">c2eguA_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine synthase; <b>PDBTitle:</b> crystal structure of o-acetylserine sulfhydrase from geobacillus2 kaustophilus hta426
58	<a href="#">c5xenB_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cysteine synthase; <b>PDBTitle:</b> crystal structure of a hydrogen sulfide-producing enzyme (fn1220) from2 fusobacterium nucleatum in complex with l-serine-plp schiff base
59	<a href="#">c5xa2B_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cysteine synthase; <b>PDBTitle:</b> crystal structure of o-acetylserine sulfhydrylase from planctomyces2 limnophila
60	<a href="#">d1fcja_</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
61	<a href="#">c4d8tC_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> d-cysteine desulfhydrase; <b>PDBTitle:</b> crystal structure of d-cysteine desulfhydrase from salmonella2 typhimurium at 2.2 a resolution
62	<a href="#">d1f2da_</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
63	<a href="#">d1j0aa_</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
64	<a href="#">d1tyza_</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
65	<a href="#">c5b54D_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> cysteine synthase; <b>PDBTitle:</b> crystal structure of hydrogen sulfide-producing enzyme (fn1055) from2 fusobacterium nucleatum: lysine-dimethylated form
66	<a href="#">d1vb3a1</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
67	<a href="#">c3v7nA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> threonine synthase; <b>PDBTitle:</b> crystal structure of threonine synthase (thrc) from from burkholderia2 thailandensis
68	<a href="#">c4f4fB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> threonine synthase; <b>PDBTitle:</b> x-ray crystal structure of plp bound threonine synthase from brucella2 melitensis
69	<a href="#">d1kl7a_</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
70	<a href="#">d1vp8a_</a>	Alignment	not modelled	96.1	14	<b>Fold:</b> Pyruvate kinase C-terminal domain-like <b>Superfamily:</b> PK C-terminal domain-like <b>Family:</b> MTH1675-like
71	<a href="#">d1im5a_</a>	Alignment	not modelled	88.9	23	<b>Fold:</b> Isochorismatase-like hydrolases <b>Superfamily:</b> Isochorismatase-like hydrolases <b>Family:</b> Isochorismatase-like hydrolases
72	<a href="#">c3iupB_</a>	Alignment	not modelled	88.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative nadph:quinone oxidoreductase; <b>PDBTitle:</b> crystal structure of putative nadph:quinone oxidoreductase2 (yp_296108.1) from ralstonia eutropha jmp134 at 1.70 a resolution
73	<a href="#">d1t57a_</a>	Alignment	not modelled	88.4	10	<b>Fold:</b> Pyruvate kinase C-terminal domain-like <b>Superfamily:</b> PK C-terminal domain-like <b>Family:</b> MTH1675-like
74	<a href="#">d1hyua1</a>	Alignment	not modelled	87.5	23	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
						<b>Fold:</b> NAD(P)-binding Rossmann-fold domains

75	<a href="#">d1bg6a2</a>	Alignment	not modelled	85.1	24	<b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
76	<a href="#">d1yaca</a>	Alignment	not modelled	84.3	19	<b>Fold:</b> Isochorismatase-like hydrolases <b>Superfamily:</b> Isochorismatase-like hydrolases <b>Family:</b> Isochorismatase-like hydrolases
77	<a href="#">c3gbcA</a>	Alignment	not modelled	81.2	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrazinamidase/nicotinamidase pnca; <b>PDBTitle:</b> determination of the crystal structure of the pyrazinamidase from <i>M. tuberculosis</i> : a structure-function analysis for prediction3 resistance to pyrazinamide
78	<a href="#">d1o8ca2</a>	Alignment	not modelled	80.8	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
79	<a href="#">d1c1da1</a>	Alignment	not modelled	80.5	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
80	<a href="#">d1l7da1</a>	Alignment	not modelled	80.0	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
81	<a href="#">c4izhA</a>	Alignment	not modelled	78.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad/nadp transhydrogenase alpha subunit 1; <b>PDBTitle:</b> crystal structure of the alpha1 dimer of thermus thermophilus2 transhydrogenase in p6
82	<a href="#">c3hu5B</a>	Alignment	not modelled	78.6	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> isochorismatase family protein; <b>PDBTitle:</b> crystal structure of isochorismatase family protein from <i>Desulfovibrio2 vulgaris</i> subsp. <i>vulgaris</i> str. <i>hildenborough</i>
83	<a href="#">d1fl2a1</a>	Alignment	not modelled	77.6	26	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
84	<a href="#">c6de6B</a>	Alignment	not modelled	75.8	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> histamine dehydrogenase; <b>PDBTitle:</b> 2.1 a resolution structure of histamine dehydrogenase from <i>Rhizobium2</i> sp. 4-9
85	<a href="#">c3o93A</a>	Alignment	not modelled	74.1	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinamidase; <b>PDBTitle:</b> high resolution crystal structures of streptococcus pneumoniae2 nicotinamidase with trapped intermediates provide insights into3 catalytic mechanism and inhibition by aldehydes
86	<a href="#">d2i0za1</a>	Alignment	not modelled	73.9	22	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> HI0933 N-terminal domain-like
87	<a href="#">c2bryA</a>	Alignment	not modelled	73.8	29	<b>PDB header:</b> transport <b>Chain:</b> A: <b>PDB Molecule:</b> nedd9 interacting protein with calponin homology <b>PDBTitle:</b> crystal structure of the native monooxygenase domain of2 mical at 1.45 a resolution
88	<a href="#">c2ywlA</a>	Alignment	not modelled	73.6	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase related protein; <b>PDBTitle:</b> crystal structure of thioredoxin reductase-related protein ttha03702 from thermus thermophilus hb8
89	<a href="#">d1trba1</a>	Alignment	not modelled	73.6	26	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
90	<a href="#">c5wxvl</a>	Alignment	not modelled	73.2	9	<b>PDB header:</b> lyase <b>Chain:</b> L: <b>PDB Molecule:</b> isochorismate lyase; <b>PDBTitle:</b> the crystal structure of vabb-icl domain from <i>Vibrio anguillarum</i> 775
91	<a href="#">c3allA</a>	Alignment	not modelled	72.8	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-methyl-3-hydroxypyridine-5-carboxylic acid oxygenase; <b>PDBTitle:</b> crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic acid2 oxygenase, mutant y270a
92	<a href="#">d3lada1</a>	Alignment	not modelled	72.3	33	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
93	<a href="#">d1vdca1</a>	Alignment	not modelled	72.1	19	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
94	<a href="#">c3d4oA</a>	Alignment	not modelled	71.9	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dipicolinate synthase subunit a; <b>PDBTitle:</b> crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from <i>Bacillus halodurans</i> at 2.10 a resolution
95	<a href="#">d1ryia1</a>	Alignment	not modelled	70.9	21	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
96	<a href="#">c5x68B</a>	Alignment	not modelled	70.7	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> kynurenine 3-monooxygenase; <b>PDBTitle:</b> crystal structure of human kmo
97	<a href="#">c5eowA</a>	Alignment	not modelled	70.3	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-hydroxynicotinate 3-monooxygenase; <b>PDBTitle:</b> crystal structure of 6-hydroxynicotinic acid 3-monooxygenase from2 <i>Pseudomonas putida</i> kt2440
98	<a href="#">d1dxa1</a>	Alignment	not modelled	70.2	26	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
99	<a href="#">c5bulA</a>	Alignment	not modelled	69.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> flavin-dependent halogenase triple mutant; <b>PDBTitle:</b> structure of flavin-dependent brominase bmp2 triple mutant y302s f306v2 a345w
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-methyl-3-hydroxypyridine-5-carboxylic

100	<a href="#">c3gmbB_</a>	Alignment	not modelled	69.8	30	acid oxygenase; <b>PDBTitle:</b> crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic acid2 oxygenase
101	<a href="#">c4j33B_</a>	Alignment	not modelled	69.6	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> kynurenine 3-monooxygenase; <b>PDBTitle:</b> crystal structure of kynurenine 3-monooxygenase (kmo-394)
102	<a href="#">c2b34C_</a>	Alignment	not modelled	69.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> mar1 ribonuclease; <b>PDBTitle:</b> structure of mar1 ribonuclease from caenorhabditis elegans
103	<a href="#">c3d3kD_</a>	Alignment	not modelled	68.8	12	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> enhancer of mrna-decapping protein 3; <b>PDBTitle:</b> crystal structure of human edc3p
104	<a href="#">d1seza1</a>	Alignment	not modelled	68.8	34	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
105	<a href="#">d2cula1</a>	Alignment	not modelled	68.8	30	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> GidA-like
106	<a href="#">d1ml4a2</a>	Alignment	not modelled	68.6	21	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
107	<a href="#">c3f8rD_</a>	Alignment	not modelled	68.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> thioredoxin reductase (trxb-3); <b>PDBTitle:</b> crystal structure of sulfobolus solfataricus thioredoxin2 reductase b3 in complex with two nadp molecules
108	<a href="#">d1ebda1</a>	Alignment	not modelled	67.9	33	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
109	<a href="#">c1gl9B_</a>	Alignment	not modelled	67.4	13	<b>PDB header:</b> topoisomerase <b>Chain:</b> B: <b>PDB Molecule:</b> reverse gyrase; <b>PDBTitle:</b> archaeoglobus fulgidus reverse gyrase complexed with adpnp
110	<a href="#">d1nbaa_</a>	Alignment	not modelled	67.0	15	<b>Fold:</b> Isochorismatase-like hydrolases <b>Superfamily:</b> Isochorismatase-like hydrolases <b>Family:</b> Isochorismatase-like hydrolases
111	<a href="#">c4dioB_</a>	Alignment	not modelled	66.1	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nad(p) transhydrogenase subunit alpha part 1; <b>PDBTitle:</b> the crystal structure of transhydrogenase from sinorhizobium meliloti
112	<a href="#">c3orgA_</a>	Alignment	not modelled	66.1	24	<b>PDB header:</b> ligase,biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> n5-carboxyaminoimidazole ribonucleotide synthetase; <b>PDBTitle:</b> crystal structure of n5-carboxyaminoimidazole synthetase from2 staphylococcus aureus complexed with adp
113	<a href="#">c3r2jC_</a>	Alignment	not modelled	65.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> alpha/beta-hydrolase-like protein; <b>PDBTitle:</b> crystal structure of pnc1 from l. infantum in complex with nicotinate
114	<a href="#">d1ohta1</a>	Alignment	not modelled	65.1	33	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
115	<a href="#">c6aqjB_</a>	Alignment	not modelled	64.9	33	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase (nadp(+)); <b>PDBTitle:</b> crystal structures of staphylococcus aureus ketol-acid2 reductoisomerase in complex with two transition state analogs that3 have biocidal activity.
116	<a href="#">d1lvla1</a>	Alignment	not modelled	64.8	26	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
117	<a href="#">c3g05B_</a>	Alignment	not modelled	64.1	26	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl modification enzyme <b>PDBTitle:</b> crystal structure of n-terminal domain (2-550) of e.coli mnmg
118	<a href="#">c2bruB_</a>	Alignment	not modelled	62.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nad(p) transhydrogenase subunit alpha; <b>PDBTitle:</b> complex of the domain i and domain iii of escherichia coli2 transhydrogenase
119	<a href="#">c5tukC_</a>	Alignment	not modelled	62.8	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> tetracycline destructase tet(51); <b>PDBTitle:</b> crystal structure of tetracycline destructase tet(51)
120	<a href="#">c3cgvA_</a>	Alignment	not modelled	62.3	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranyl reductase related protein; <b>PDBTitle:</b> crystal structure of geranylgeranyl bacteriochlorophyll reductase-like2 fixc homolog (np_393992.1) from thermoplasma acidophilum at 1.60 a3 resolution