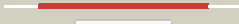



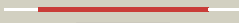



















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1336_(cysM)_1503400_1504371
Date	Wed Jul 31 22:05:43 BST 2019
Unique Job ID	0ef706a00c27581f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3dwgA_</a>	 Alignment		100.0	100	<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
2	<a href="#">c5ohxB_</a>	 Alignment		100.0	36	<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
3	<a href="#">c3pc3A_</a>	 Alignment		100.0	35	<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
4	<a href="#">c4l3vB_</a>	 Alignment		100.0	34	<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
5	<a href="#">d1jbqa_</a>	 Alignment		100.0	35	<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="#">c1jbqD_</a>	 Alignment		100.0	35	<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
7	<a href="#">c6c2qA_</a>	 Alignment		100.0	35	<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
8	<a href="#">c2pqmA_</a>	 Alignment		100.0	34	<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
9	<a href="#">c4aecB_</a>	 Alignment		100.0	36	<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-acetyl-serine-(thiol)-2 lyase c
10	<a href="#">c3x43F_</a>	 Alignment		100.0	40	<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
11	<a href="#">d1z7wa1</a>	 Alignment		100.0	36	<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

12	<a href="#">c5d87A_</a>	Alignment		100.0	36	<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
13	<a href="#">c4lmaA_</a>	Alignment		100.0	34	<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
14	<a href="#">c5b1iC_</a>	Alignment		100.0	35	<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
15	<a href="#">c3vbeA_</a>	Alignment		100.0	37	<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
16	<a href="#">c4i1xA_</a>	Alignment		100.0	31	<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
17	<a href="#">d2bhsa1</a>	Alignment		100.0	42	<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
18	<a href="#">c4airB_</a>	Alignment		100.0	35	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cysteine synthase; <b>PDBTitle:</b> leishmania major cysteine synthase
19	<a href="#">c5i7wA_</a>	Alignment		100.0	33	<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
20	<a href="#">c5xa2B_</a>	Alignment		100.0	39	<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
21	<a href="#">c4q14A_</a>	Alignment	not modelled	100.0	38	<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
22	<a href="#">c2q3bA_</a>	Alignment	not modelled	100.0	39	<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
23	<a href="#">d1ve1a1</a>	Alignment	not modelled	100.0	46	<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="#">d1y7la1</a>	Alignment	not modelled	100.0	35	<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
25	<a href="#">c5xenB_</a>	Alignment	not modelled	100.0	37	<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
26	<a href="#">d1wkv1</a>	Alignment	not modelled	100.0	29	<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
27	<a href="#">c2eguA_</a>	Alignment	not modelled	100.0	43	<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
						<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent

28	<a href="#">d1fcja_</a>	Alignment	not modelled	100.0	38	enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
29	<a href="#">d1o58a_</a>	Alignment	not modelled	100.0	42	<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="#">c3l6cA_</a>	Alignment	not modelled	100.0	21	<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
31	<a href="#">c6hulB_</a>	Alignment	not modelled	100.0	20	<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
32	<a href="#">c1tdja_</a>	Alignment	not modelled	100.0	19	<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
33	<a href="#">d1pwha_</a>	Alignment	not modelled	100.0	26	<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="#">c4qysA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase beta chain 2; <b>PDBTitle:</b> trpb2 enzymes
35	<a href="#">c2d1fA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> threonine synthase; <b>PDBTitle:</b> structure of mycobacterium tuberculosis threonine synthase
36	<a href="#">c4negA_</a>	Alignment	not modelled	100.0	19	<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'
37	<a href="#">d1v71a1</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
38	<a href="#">c2gn0A_</a>	Alignment	not modelled	100.0	16	<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)
39	<a href="#">c1x1qA_</a>	Alignment	not modelled	100.0	21	<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
40	<a href="#">c3iauA_</a>	Alignment	not modelled	100.0	17	<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
41	<a href="#">c5ybwA_</a>	Alignment	not modelled	100.0	17	<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
42	<a href="#">d1tdja1</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
43	<a href="#">c1p5ja_</a>	Alignment	not modelled	100.0	22	<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
44	<a href="#">d1p5ja_</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
45	<a href="#">c5b54D_</a>	Alignment	not modelled	100.0	35	<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
46	<a href="#">d1v8za1</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
47	<a href="#">d1qopb_</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
48	<a href="#">d1v7ca_</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
49	<a href="#">c5cvcB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> serine racemase; <b>PDBTitle:</b> structure of maize serine racemase
50	<a href="#">c3r0zA_</a>	Alignment	not modelled	100.0	19	<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
51	<a href="#">d1ve5a1</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
52	<a href="#">c5tchH</a>	Alignment	not modelled	100.0	21	<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
53	<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
54	<a href="#">c2o2jA</a>	Alignment	not modelled	100.0	23	<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 (apoform)
55	<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
56	<a href="#">c2zsjB</a>	Alignment	not modelled	100.0	18	<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
57	<a href="#">c5kinD</a>	Alignment	not modelled	100.0	21	<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
58	<a href="#">c4d9gA</a>	Alignment	not modelled	100.0	19	<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
59	<a href="#">c2rkbE</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> serine dehydratase-like; <b>PDBTitle:</b> serine dehydratase like-1 from human cancer cells
60	<a href="#">c5ygrA</a>	Alignment	not modelled	100.0	19	<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
61	<a href="#">d1e5xa</a>	Alignment	not modelled	100.0	15	<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
62	<a href="#">d1f2da</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
63	<a href="#">d1j0aa</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
64	<a href="#">c4d8tC</a>	Alignment	not modelled	100.0	17	<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
65	<a href="#">d1tyza</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
66	<a href="#">c3v7nA</a>	Alignment	not modelled	100.0	18	<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 burkholderia2 thailandensis
67	<a href="#">d1vb3a1</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
68	<a href="#">c4f4fB</a>	Alignment	not modelled	100.0	16	<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	99.9	14	<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="#">d1bg6a2</a>	Alignment	not modelled	93.8	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
71	<a href="#">d1c1da1</a>	Alignment	not modelled	92.8	26	<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
72	<a href="#">d1kola2</a>	Alignment	not modelled	92.7	20	<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
73	<a href="#">c3iupB</a>	Alignment	not modelled	91.5	20	<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
74	<a href="#">d1vp8a</a>	Alignment	not modelled	91.4	19	<b>Fold:</b> Pyruvate kinase C-terminal domain-like <b>Superfamily:</b> PK C-terminal domain-like <b>Family:</b> MTH1675-like
75	<a href="#">d1o8ca2</a>	Alignment	not modelled	91.4	21	<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

76	<a href="#">d1o89a2</a>	Alignment	not modelled	90.8	19	<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
77	<a href="#">c3widC</a>	Alignment	not modelled	87.4	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glucose 1-dehydrogenase; <b>PDBTitle:</b> structure of a glucose dehydrogenase t277f mutant in complex with nadp
78	<a href="#">c3zu3A</a>	Alignment	not modelled	87.3	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative reductase ypo4104/y4119/yp_4011; <b>PDBTitle:</b> structure of the enoyl-acp reductase fabv from yersinia pestis with2 the cofactor nadh (mr, cleaved histag)
79	<a href="#">c3s8mA</a>	Alignment	not modelled	84.1	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-acp reductase; <b>PDBTitle:</b> the crystal structure of fabv
80	<a href="#">d1lua2</a>	Alignment	not modelled	82.7	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
81	<a href="#">c2douA</a>	Alignment	not modelled	82.1	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable n-succinyldiaminopimelate aminotransferase; <b>PDBTitle:</b> probable n-succinyldiaminopimelate aminotransferase (ttha0342) from2 thermus thermophilus hb8
82	<a href="#">d1ml4a2</a>	Alignment	not modelled	81.2	22	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
83	<a href="#">d1tt7a2</a>	Alignment	not modelled	80.7	20	<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
84	<a href="#">c3p2yA</a>	Alignment	not modelled	80.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alanine dehydrogenase/pyridine nucleotide transhydrogenase; <b>PDBTitle:</b> crystal structure of alanine dehydrogenase/pyridine nucleotide2 transhydrogenase from mycobacterium smegmatis
85	<a href="#">c1m67A</a>	Alignment	not modelled	78.6	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of leishmania mexicana gpdh complexed with inhibitor2 2-bromo-6-hydroxy-purine
86	<a href="#">c5ijzH</a>	Alignment	not modelled	78.1	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> nadp-specific glutamate dehydrogenase; <b>PDBTitle:</b> crystal structure of glutamate dehydrogenase(gdh) from corynebacterium2 glutamicum
87	<a href="#">d1ykfa2</a>	Alignment	not modelled	77.1	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
88	<a href="#">d1cdoa2</a>	Alignment	not modelled	76.6	16	<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
89	<a href="#">d1l7da1</a>	Alignment	not modelled	75.4	19	<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
90	<a href="#">c4gi2B</a>	Alignment	not modelled	75.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> crotonyl-coa carboxylase/reductase; <b>PDBTitle:</b> crotonyl-coa carboxylase/reductase
91	<a href="#">d1p0fa2</a>	Alignment	not modelled	74.9	14	<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
92	<a href="#">d1rjwa2</a>	Alignment	not modelled	74.5	16	<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
93	<a href="#">d1xa0a2</a>	Alignment	not modelled	73.9	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
94	<a href="#">c3krtC</a>	Alignment	not modelled	73.8	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> crotonyl coa reductase; <b>PDBTitle:</b> crystal structure of putative crotonyl coa reductase from streptomyces2 coelicolor a3(2)
95	<a href="#">c3r3jC</a>	Alignment	not modelled	72.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glutamate dehydrogenase; <b>PDBTitle:</b> kinetic and structural characterization of plasmodium falciparum2 glutamate dehydrogenase 2
96	<a href="#">c3orqA</a>	Alignment	not modelled	72.3	23	<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
97	<a href="#">c4k2bA</a>	Alignment	not modelled	69.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ntd biosynthesis operon protein ntda; <b>PDBTitle:</b> crystal structure of ntda from bacillus subtilis in complex with the2 internal aldimine
98	<a href="#">d1jq5a</a>	Alignment	not modelled	67.0	18	<b>Fold:</b> Dehydroquinase synthase-like <b>Superfamily:</b> Dehydroquinase synthase-like <b>Family:</b> Iron-containing alcohol dehydrogenase
99	<a href="#">c4euhA</a>	Alignment	not modelled	66.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative reductase ca_c0462; <b>PDBTitle:</b> crystal structure of clostridium acetobutlicum trans-2-enoyl-coa2 reductase apo form
100	<a href="#">d1hyua1</a>	Alignment	not modelled	65.4	30	<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
101	<a href="#">d1fl2a1</a>	Alignment	not modelled	65.4	30	<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



102	<a href="#">d1ekxa2</a>	Alignment	not modelled	64.5	18	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
103	<a href="#">c4ak9A_</a>	Alignment	not modelled	64.3	12	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cpfts; <b>PDBTitle:</b> structure of chloroplast ftsy from physcomitrella patens
104	<a href="#">d2q7wa1</a>	Alignment	not modelled	64.1	7	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
105	<a href="#">d1trba1</a>	Alignment	not modelled	64.0	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
106	<a href="#">d1y6ja1</a>	Alignment	not modelled	63.9	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
107	<a href="#">c5ajtA_</a>	Alignment	not modelled	63.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribohydrolase lonely guy; <b>PDBTitle:</b> crystal structure of ligand-free phosphoribohydrolase lonely guy from2 claviceps purpurea
108	<a href="#">c2vq3B_</a>	Alignment	not modelled	63.7	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> metalloreductase steap3; <b>PDBTitle:</b> crystal structure of the membrane proximal oxidoreductase2 domain of human steap3, the dominant ferric reductase of3 the erythroid transferrin cycle
109	<a href="#">d1o69a_</a>	Alignment	not modelled	63.6	12	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
110	<a href="#">c4wd2A_</a>	Alignment	not modelled	63.1	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aromatic-amino-acid transaminase tyrb; <b>PDBTitle:</b> crystal structure of an aromatic amino acid aminotransferase from2 burkholderia cenocepacia j2315
111	<a href="#">c3f0hA_</a>	Alignment	not modelled	60.8	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution
112	<a href="#">c4effA_</a>	Alignment	not modelled	60.6	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aromatic-amino-acid aminotransferase; <b>PDBTitle:</b> crystal structure of aromatic-amino-acid aminotransferase from2 burkholderia pseudomallei
113	<a href="#">c3getA_</a>	Alignment	not modelled	60.1	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histidinol-phosphate aminotransferase; <b>PDBTitle:</b> crystal structure of putative histidinol-phosphate aminotransferase2 (np_281508.1) from campylobacter jejuni at 2.01 a resolution
114	<a href="#">c2vhyB_</a>	Alignment	not modelled	59.5	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alanine dehydrogenase; <b>PDBTitle:</b> crystal structure of apo l-alanine dehydrogenase from mycobacterium2 tuberculosis
115	<a href="#">c4ggoA_</a>	Alignment	not modelled	59.5	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trans-2-enoyl-coa reductase; <b>PDBTitle:</b> crystal structure of trans-2-enoyl-coa reductase from treponema2 denticola
116	<a href="#">d1vdca1</a>	Alignment	not modelled	58.9	15	<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="#">c3grkE_</a>	Alignment	not modelled	58.7	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> enoyl-(acyl-carrier-protein) reductase (nadh); <b>PDBTitle:</b> crystal structure of short chain dehydrogenase reductase2 sdr glucose-ribitol dehydrogenase from brucella melitensis
118	<a href="#">c4g56C_</a>	Alignment	not modelled	58.4	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> hsl7 protein; <b>PDBTitle:</b> crystal structure of full length prmt5/mep50 complexes from xenopus2 laevis
119	<a href="#">c6hnuA_</a>	Alignment	not modelled	58.3	6	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aromatic amino acid aminotransferase i; <b>PDBTitle:</b> crystal structure of the aminotransferase aro8 from c. albicans with2 ligands
120	<a href="#">c3e2yB_</a>	Alignment	not modelled	58.0	9	<b>PDB header:</b> transferase, lyase <b>Chain:</b> B: <b>PDB Molecule:</b> kynurenine-oxoglutarate transaminase 3; <b>PDBTitle:</b> crystal structure of mouse kynurenine aminotransferase iii in complex2 with glutamine