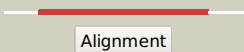

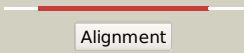


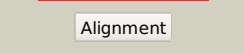



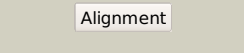

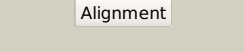


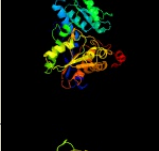
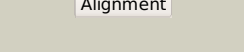

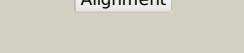

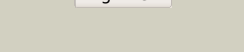
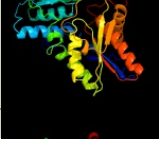








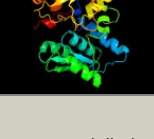


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3684 (- )_4125617_4126657
Date	Fri Aug 9 18:20:37 BST 2019
Unique Job ID	6acfc1e3bf853ed2

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3pc3A_</a>	 Alignment		100.0	26	<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
2	<a href="#">c5ohxB_</a>	 Alignment		100.0	26	<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="#">c4l3vB_</a>	 Alignment		100.0	26	<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
4	<a href="#">d1jbqa_</a>	 Alignment		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
5	<a href="#">c1jbqD_</a>	 Alignment		100.0	26	<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
6	<a href="#">c6c2qA_</a>	 Alignment		100.0	23	<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
7	<a href="#">c3x43F_</a>	 Alignment		100.0	26	<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
8	<a href="#">c5i7wA_</a>	 Alignment		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
9	<a href="#">c2pqaA_</a>	 Alignment		100.0	21	<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
10	<a href="#">c5d87A_</a>	 Alignment		100.0	24	<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
11	<a href="#">c3dwaA_</a>	 Alignment		100.0	26	<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

12	<a href="#">dlz7wa1</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
13	<a href="#">c3vbeA_</a>	Alignment		100.0	22	<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
14	<a href="#">c4aecB_</a>	Alignment		100.0	22	<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
15	<a href="#">c4airB_</a>	Alignment		100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cysteine synthase; <b>PDBTitle:</b> leishmania major cysteine synthase
16	<a href="#">dlwkva1</a>	Alignment		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
17	<a href="#">c5b1iC_</a>	Alignment		100.0	28	<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
18	<a href="#">c4lmaA_</a>	Alignment		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
19	<a href="#">dlve1a1</a>	Alignment		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
20	<a href="#">d2bhsa1</a>	Alignment		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
21	<a href="#">dl1y7la1</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
22	<a href="#">c4i1xA_</a>	Alignment	not modelled	100.0	25	<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
23	<a href="#">c5xa2B_</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> crystal structure of o-acetylserine sulfhydrylase from planctomyces2 limnophila
24	<a href="#">c5xenB_</a>	Alignment	not modelled	100.0	23	<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
25	<a href="#">c2q3bA_</a>	Alignment	not modelled	100.0	25	<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
26	<a href="#">dlpwaha_</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
27	<a href="#">c2eguA_</a>	Alignment	not modelled	100.0	25	<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
28	<a href="#">c3l6cA_</a>	Alignment	not modelled	100.0	20	<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
29	<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
30	<a href="#">c6hulB_</a>	Alignment	not modelled	100.0	16	<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
31	<a href="#">c4ql4A_</a>	Alignment	not modelled	100.0	24	<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
32	<a href="#">c1tdjA_</a>	Alignment	not modelled	100.0	21	<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="#">c2d1fA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> threonine synthase; <b>PDBTitle:</b> structure of mycobacterium tuberculosis threonine synthase
34	<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
35	<a href="#">d1p5ja_</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
36	<a href="#">c1p5jA_</a>	Alignment	not modelled	100.0	20	<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
37	<a href="#">c5c3uA_</a>	Alignment	not modelled	100.0	22	<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
38	<a href="#">d1fcja_</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
39	<a href="#">c2gn0A_</a>	Alignment	not modelled	100.0	18	<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)
40	<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
41	<a href="#">d1v71a1</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
42	<a href="#">c3r0zA_</a>	Alignment	not modelled	100.0	16	<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
43	<a href="#">c3iauA_</a>	Alignment	not modelled	100.0	18	<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
44	<a href="#">d1qopb_</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
45	<a href="#">c4qysA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase beta chain 2; <b>PDBTitle:</b> trpb2 enzymes
46	<a href="#">c1x1qA_</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> crystal structure of tryptophan synthase beta chain from thermus2 thermophilus hb8
47	<a href="#">c6cggA_</a>	Alignment	not modelled	100.0	20	<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
48	<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
49	<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
50	<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
51	<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'

52	<a href="#">c5b54D</a>	Alignment	not modelled	100.0	29	<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) from <i>2 fusobacterium nucleatum</i> : lysine-dimethylated form
53	<a href="#">c5ybwA</a>	Alignment	not modelled	100.0	18	<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
54	<a href="#">c2rkbE</a>	Alignment	not modelled	100.0	20	<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
55	<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
56	<a href="#">c4d9gA</a>	Alignment	not modelled	100.0	18	<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 <i>escherichia coli</i>
57	<a href="#">c5tchH</a>	Alignment	not modelled	100.0	19	<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 <i>m. tuberculosis</i> -2 ligand-free form, trpa-g66v mutant
58	<a href="#">c5kinD</a>	Alignment	not modelled	100.0	17	<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 from <i>2 streptococcus pneumoniae</i>
59	<a href="#">c2o2jA</a>	Alignment	not modelled	100.0	22	<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)
60	<a href="#">c5ygrA</a>	Alignment	not modelled	100.0	18	<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 from <i>2 salmonella typhimurium</i>
61	<a href="#">d1e5xa</a>	Alignment	not modelled	100.0	16	<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	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
63	<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 <i>salmonella2 typhimurium</i> at 2.2 a resolution
64	<a href="#">d1tyza</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
65	<a href="#">d1j0aa</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
66	<a href="#">d1vb3a1</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
67	<a href="#">c3v7nA</a>	Alignment	not modelled	100.0	17	<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 <i>from burkholderia2 thailandensis</i>
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 <i>brucella2 melitensis</i>
69	<a href="#">d1kl7a</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
70	<a href="#">d1c1da1</a>	Alignment	not modelled	94.9	18	<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
71	<a href="#">d1kola2</a>	Alignment	not modelled	94.3	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
72	<a href="#">c3iupB</a>	Alignment	not modelled	94.3	12	<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 <i>ralstonia eutropha jmp134</i> at 1.70 a resolution
73	<a href="#">d1o89a2</a>	Alignment	not modelled	93.6	17	<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
74	<a href="#">d1o8ca2</a>	Alignment	not modelled	92.9	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
75	<a href="#">c3widC</a>	Alignment	not modelled	91.3	16	<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

76	<a href="#">d1cdoa2</a>	Alignment	not modelled	90.9	12	<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="#">d1m4a2</a>	Alignment	not modelled	90.3	9	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
78	<a href="#">d1vp8a</a>	Alignment	not modelled	90.2	15	<b>Fold:</b> Pyruvate kinase C-terminal domain-like <b>Superfamily:</b> PK C-terminal domain-like <b>Family:</b> MTH1675-like
79	<a href="#">d1lua2</a>	Alignment	not modelled	89.7	15	<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
80	<a href="#">d1p0fa2</a>	Alignment	not modelled	88.7	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
81	<a href="#">d1tt7a2</a>	Alignment	not modelled	88.5	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
82	<a href="#">c3krtC</a>	Alignment	not modelled	87.1	18	<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)
83	<a href="#">d1ykfa2</a>	Alignment	not modelled	86.7	11	<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="#">d1ekxa2</a>	Alignment	not modelled	86.5	23	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
85	<a href="#">c1m4A</a>	Alignment	not modelled	86.2	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate transcarbamoylase; <b>PDBTitle:</b> the pala-liganded aspartate transcarbamoylase catalytic subunit from2 pyrococcus abyssi
86	<a href="#">d1xa0a2</a>	Alignment	not modelled	86.1	15	<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
87	<a href="#">c4gi2B</a>	Alignment	not modelled	85.5	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> crotonyl-coa carboxylase/reductase; <b>PDBTitle:</b> crotonyl-coa carboxylase/reductase
88	<a href="#">d1l7da1</a>	Alignment	not modelled	84.5	18	<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
89	<a href="#">c4effA</a>	Alignment	not modelled	83.6	12	<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
90	<a href="#">c5intB</a>	Alignment	not modelled	83.0	18	<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
91	<a href="#">d1bg6a2</a>	Alignment	not modelled	81.0	21	<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
92	<a href="#">d1u7za</a>	Alignment	not modelled	80.9	15	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> CoaB-like <b>Family:</b> CoaB-like
93	<a href="#">d1u3wa2</a>	Alignment	not modelled	80.8	13	<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="#">d1rjwa2</a>	Alignment	not modelled	79.3	17	<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
95	<a href="#">d1d1ta2</a>	Alignment	not modelled	79.2	13	<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
96	<a href="#">c4k2bA</a>	Alignment	not modelled	78.9	25	<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
97	<a href="#">c3orgA</a>	Alignment	not modelled	78.3	15	<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
98	<a href="#">c3p2yA</a>	Alignment	not modelled	75.7	8	<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
99	<a href="#">d1piwa2</a>	Alignment	not modelled	75.5	9	<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
100	<a href="#">d1qora2</a>	Alignment	not modelled	75.5	10	<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
101	<a href="#">d1hyua1</a>	Alignment	not modelled	75.5	22	<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="#">d1mv8a2</a>	Alignment	not modelled	75.1	25	<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



103	<a href="#">d1fl2a1</a>	Alignment	not modelled	75.0	22	<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
104	<a href="#">c3q98A</a>	Alignment	not modelled	74.2	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transcarbamylyase; <b>PDBTitle:</b> structure of ygew encoded protein from e. coli
105	<a href="#">d1otha2</a>	Alignment	not modelled	73.8	18	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
106	<a href="#">c3pduF</a>	Alignment	not modelled	73.5	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> 3-hydroxyisobutyrate dehydrogenase family protein; <b>PDBTitle:</b> crystal structure of gamma-hydroxybutyrate dehydrogenase from2 geobacter sulfurreducens in complex with nadp+
107	<a href="#">d1trba1</a>	Alignment	not modelled	73.3	22	<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
108	<a href="#">c3s8mA</a>	Alignment	not modelled	73.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-acyl reductase; <b>PDBTitle:</b> the crystal structure of fabv
109	<a href="#">c4qjB</a>	Alignment	not modelled	73.0	12	<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 phosphopantothenoylcysteine decarboxylase/phosphopantothenate-3 cysteine ligase with bound ctp from mycobacterium smegmatis
110	<a href="#">c4oh7B</a>	Alignment	not modelled	72.8	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ornithine carbamoyltransferase; <b>PDBTitle:</b> crystal structure of ornithine carbamoyltransferase from brucella2 melitensis
111	<a href="#">c4nimA</a>	Alignment	not modelled	72.6	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> versicolorin reductase; <b>PDBTitle:</b> crystal structure of a short chain dehydrogenase from brucella2 melitensis
112	<a href="#">c1r0ID</a>	Alignment	not modelled	72.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 1-deoxy-d-xylulose 5-phosphate reductoisomerase; <b>PDBTitle:</b> 1-deoxy-d-xylulose 5-phosphate reductoisomerase from zymomonas mobilis2 in complex with nadph
113	<a href="#">d1pg5a2</a>	Alignment	not modelled	72.3	9	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
114	<a href="#">d1pl8a2</a>	Alignment	not modelled	72.2	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
115	<a href="#">c3zu3A</a>	Alignment	not modelled	71.7	14	<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-acyl reductase fabv from yersinia pestis with2 the cofactor nadh (mr, cleaved histag)
116	<a href="#">d1e3ia2</a>	Alignment	not modelled	71.0	13	<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
117	<a href="#">c5y8mA</a>	Alignment	not modelled	71.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable 3-hydroxyisobutyrate dehydrogenase; <b>PDBTitle:</b> mycobacterium tuberculosis 3-hydroxyisobutyrate dehydrogenase2 (mthibadh) + nad + (r)-3-hydroxyisobutyrate (r-hiba)
118	<a href="#">c3qp9C</a>	Alignment	not modelled	69.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> type i polyketide synthase pikaii; <b>PDBTitle:</b> the structure of a c2-type ketoreductase from a modular polyketide2 synthase
119	<a href="#">d1vdca1</a>	Alignment	not modelled	69.0	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
120	<a href="#">c2vhyB</a>	Alignment	not modelled	68.3	17	<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