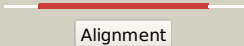

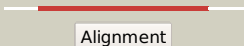

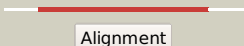
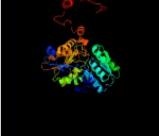






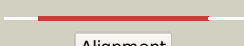
















Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0848_cysK2_944941_946059
 Date Fri Jul 26 01:50:43 BST 2019
 Unique Job ID 75fcb173cbf77535

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5ohxB_	 Alignment		100.0	25	PDB header: lyase Chain: B; PDB Molecule: cystathionine beta-synthase; PDBTitle: structure of active cystathionine b-synthase from apis mellifera
2	c3pc3A_	 Alignment		100.0	23	PDB header: lyase Chain: A; PDB Molecule: cg1753, isoform a; PDBTitle: full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacylate
3	c4l3vB_	 Alignment		100.0	27	PDB header: lyase Chain: B; PDB Molecule: cystathionine beta-synthase; PDBTitle: crystal structure of delta516-525 human cystathionine beta-synthase
4	d1jbqa_	 Alignment		100.0	29	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
5	c1jbqD_	 Alignment		100.0	29	PDB header: lyase Chain: D; PDB Molecule: cystathionine beta-synthase; PDBTitle: structure of human cystathionine beta-synthase: a unique pyridoxal 5'-2 phosphate dependent hemeprotein
6	c6c2qA_	 Alignment		100.0	27	PDB header: lyase Chain: A; PDB Molecule: cystathionine beta-synthase; PDBTitle: crystal structures of cystathionine beta-synthase from saccharomyces2 cerevisiae: the structure of the plp-l-serine intermediate
7	c5d87A_	 Alignment		100.0	32	PDB header: biosynthetic protein Chain: A; PDB Molecule: probable siderophore biosynthesis protein sbna; PDBTitle: staphyloferrin b precursor biosynthetic enzyme sbna y152f/s185g2 variant
8	c5i7wA_	 Alignment		100.0	27	PDB header: transferase Chain: A; PDB Molecule: cysteine synthase a; PDBTitle: crystal structure of a cysteine synthase from brucella suis
9	c2pqaA_	 Alignment		100.0	26	PDB header: lyase Chain: A; PDB Molecule: cysteine synthase; PDBTitle: crystal structure of cysteine synthase (oass) from entamoeba2 histolytica at 1.86 a resolution
10	c3dwgA_	 Alignment		100.0	31	PDB header: transferase Chain: A; PDB Molecule: cysteine synthase b; PDBTitle: crystal structure of a sulfur carrier protein complex found in the2 cysteine biosynthetic pathway of mycobacterium tuberculosis
11	c3x43F_	 Alignment		100.0	28	PDB header: transferase Chain: F; PDB Molecule: o-ureido-l-serine synthase; PDBTitle: crystal structure of o-ureido-l-serine synthase

12	dlz7wa1	Alignment		100.0	28	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
13	c3vbeA	Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: beta-cyanoalanine synthase; PDBTitle: crystal structure of beta-cyanoalanine synthase in soybean
14	c4aecB	Alignment		100.0	29	PDB header: lyase Chain: B: PDB Molecule: cysteine synthase, mitochondrial; PDBTitle: crystal structure of the arabidopsis thaliana o-acetylserine-(thiol)-2 lyase c
15	c4lmaA	Alignment		100.0	27	PDB header: transferase Chain: A: PDB Molecule: cysteine synthase; PDBTitle: crystal structure analysis of o-acetylserine sulfhydrylase cysk1 from2 microcystis aeruginosa 7806
16	c5b1iC	Alignment		100.0	31	PDB header: lyase Chain: C: PDB Molecule: cystathionine beta-synthase; PDBTitle: crystal structure of k42a mutant of cystathionine beta-synthase from2 lactobacillus plantarum in a complex with l-methionine
17	c4airB	Alignment		100.0	24	PDB header: transferase Chain: B: PDB Molecule: cysteine synthase; PDBTitle: leishmania major cysteine synthase
18	c4ilxA	Alignment		100.0	28	PDB header: transferase Chain: A: PDB Molecule: cysteine synthase; PDBTitle: crystal structure of cysteine synthase from helicobacter pylori 26695
19	d1wkvA1	Alignment		100.0	20	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
20	c5xenB	Alignment		100.0	27	PDB header: transferase Chain: B: PDB Molecule: cysteine synthase; PDBTitle: crystal structure of a hydrogen sulfide-producing enzyme (fn1220) from2 fusobacterium nucleatum in complex with l-serine-plp schiff base
21	d1ve1a1	Alignment	not modelled	100.0	35	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
22	d1y7la1	Alignment	not modelled	100.0	25	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
23	d2bhsa1	Alignment	not modelled	100.0	29	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
24	c2q3bA	Alignment	not modelled	100.0	27	PDB header: transferase Chain: A: PDB Molecule: cysteine synthase a; PDBTitle: 1.8 a resolution crystal structure of o-acetylserine sulfhydrylase2 (oass) holoenzyme from mycobacterium tuberculosis
25	c5xa2B	Alignment	not modelled	100.0	30	PDB header: transferase Chain: B: PDB Molecule: cysteine synthase; PDBTitle: crystal structure of o-acetylserine sulfhydrylase from planctomyces2 limnophila
26	c4ql4A	Alignment	not modelled	100.0	31	PDB header: lyase Chain: A: PDB Molecule: o-acetylserine lyase; PDBTitle: crystal structure of o-acetylserine sulfhydrylase from bacillus2 anthracis
27	c2eguA	Alignment	not modelled	100.0	30	PDB header: transferase Chain: A: PDB Molecule: cysteine synthase; PDBTitle: crystal structure of o-acetylserine sulfhydrase from geobacillus2 kaustophilus hta426
28	c6hulB	Alignment	not modelled	100.0	19	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase beta chain 1;

						PDBTitle: sulfolobus solfataricus tryptophan synthase ab complex
29	c3l6cA_	Alignment	not modelled	100.0	20	PDB header: isomerase Chain: A: PDB Molecule: serine racemase; PDBTitle: x-ray crystal structure of rat serine racemase in complex with2 malonate a potent inhibitor
30	d1o58a_	Alignment	not modelled	100.0	31	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
31	d1pwha_	Alignment	not modelled	100.0	23	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
32	c2d1fA_	Alignment	not modelled	100.0	16	PDB header: lyase Chain: A: PDB Molecule: threonine synthase; PDBTitle: structure of mycobacterium tuberculosis threonine synthase
33	c1tdja_	Alignment	not modelled	100.0	19	PDB header: allostery Chain: A: PDB Molecule: biosynthetic threonine deaminase; PDBTitle: threonine deaminase (biosynthetic) from e. coli
34	d1fcja_	Alignment	not modelled	100.0	25	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
35	d1v7ca_	Alignment	not modelled	100.0	18	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
36	c6cggA_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: A: PDB Molecule: threonine synthase; PDBTitle: threonine synthase from bacillus subtilis atcc 6633 with plp and plp-2 ala
37	c1p5ja_	Alignment	not modelled	100.0	20	PDB header: lyase Chain: A: PDB Molecule: l-serine dehydratase; PDBTitle: crystal structure analysis of human serine dehydratase
38	d1p5ja_	Alignment	not modelled	100.0	20	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
39	c3iauA_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: A: PDB Molecule: threonine deaminase; PDBTitle: the structure of the processed form of threonine deaminase isoform 22 from solanum lycopersicum
40	c2gn0A_	Alignment	not modelled	100.0	16	PDB header: lyase Chain: A: PDB Molecule: threonine dehydratase catabolic; PDBTitle: 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)
41	c2zsjB_	Alignment	not modelled	100.0	16	PDB header: lyase Chain: B: PDB Molecule: threonine synthase; PDBTitle: crystal structure of threonine synthase from aquifex aeolicus vf5
42	c1x1qA_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase beta chain; PDBTitle: crystal structure of tryptophan synthase beta chain from thermus2 thermophilus hb8
43	c4qysA_	Alignment	not modelled	100.0	16	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase beta chain 2; PDBTitle: trpb2 enzymes
44	c4negA_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase beta chain; PDBTitle: the crystal structure of tryptophan synthase subunit beta from2 bacillus anthracis str. 'ames ancestor'
45	c5c3uA_	Alignment	not modelled	100.0	20	PDB header: lyase Chain: A: PDB Molecule: l-serine ammonia-lyase; PDBTitle: crystal structure of a fungal l-serine ammonia-lyase from rhizomucor2 miehei
46	c5b54D_	Alignment	not modelled	100.0	27	PDB header: transferase Chain: D: PDB Molecule: cysteine synthase; PDBTitle: crystal structure of hydrogen sulfide-producing enzyme (fn1055) from2 fusobacterium nucleatum: lysine-dimethylated form
47	c3r0za_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: A: PDB Molecule: d-serine dehydratase; PDBTitle: crystal structure of apo d-serine deaminase from salmonella2 typhimurium
48	d1v8za1	Alignment	not modelled	100.0	20	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
49	d1v71a1	Alignment	not modelled	100.0	19	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
50	d1tdja1	Alignment	not modelled	100.0	19	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
51	c5ybwA_	Alignment	not modelled	100.0	19	PDB header: isomerase Chain: A: PDB Molecule: aspartate racemase; PDBTitle: crystal structure of pyridoxal 5'-phosphate-dependent aspartate2 racemase

52	d1qopb_	Alignment	not modelled	100.0	19	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
53	c5cvcB_	Alignment	not modelled	100.0	19	PDB header: isomerase Chain: B: PDB Molecule: serine racemase; PDBTitle: structure of maize serine racemase
54	d1ve5a1	Alignment	not modelled	100.0	20	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
55	c2o2jA_	Alignment	not modelled	100.0	20	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase beta chain; PDBTitle: mycobacterium tuberculosis tryptophan synthase beta chain dimer2 (apofrom)
56	c2rkbE_	Alignment	not modelled	100.0	24	PDB header: lyase Chain: E: PDB Molecule: serine dehydratase-like; PDBTitle: serine dehydratase like-1 from human cancer cells
57	c5tchH_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: H: PDB Molecule: tryptophan synthase beta chain; PDBTitle: crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant
58	c5kinD_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: D: PDB Molecule: tryptophan synthase beta chain; PDBTitle: crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
59	c4d9gA_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: A: PDB Molecule: putative diaminopropionate ammonia-lyase; PDBTitle: crystal structure of selenomethionine incorporated holo2 diaminopropionate ammonia lyase from escherichia coli
60	c5ygrA_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: A: PDB Molecule: diaminopropionate ammonia lyase; PDBTitle: crystal structure of plp bound diaminopropionate ammonia lyase from2 salmonella typhimurium
61	d1e5xa_	Alignment	not modelled	100.0	12	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
62	d1j0aa_	Alignment	not modelled	100.0	18	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
63	d1f2da_	Alignment	not modelled	100.0	16	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
64	c4d8tC_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: C: PDB Molecule: d-cysteine desulphydrase; PDBTitle: crystal structure of d-cysteine desulphydrase from salmonella2 typhimurium at 2.2 a resolution
65	d1tyza_	Alignment	not modelled	100.0	19	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
66	c3v7nA_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: A: PDB Molecule: threonine synthase; PDBTitle: crystal structure of threonine synthase (thrc) from burkholderia2 thailandensis
67	d1vb3a1	Alignment	not modelled	100.0	19	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
68	c4f4fB_	Alignment	not modelled	100.0	14	PDB header: lyase Chain: B: PDB Molecule: threonine synthase; PDBTitle: x-ray crystal structure of plp bound threonine synthase from brucella2 melitensis
69	d1kl7a_	Alignment	not modelled	99.9	14	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
70	d1vp8a_	Alignment	not modelled	95.9	24	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: MTH1675-like
71	c3zu3A_	Alignment	not modelled	94.3	22	PDB header: oxidoreductase Chain: A: PDB Molecule: putative reductase ypo4104/y4119/yp_4011; PDBTitle: structure of the enoyl-acp reductase fabv from yersinia pestis with2 the cofactor nadh (mr, cleaved histag)
72	d1c1da1	Alignment	not modelled	94.2	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
73	d1o89a2	Alignment	not modelled	94.1	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
74	d1kola2	Alignment	not modelled	93.5	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
75	d1o8ca2	Alignment	not modelled	93.4	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain

76	c4pz0A_	Alignment	not modelled	92.6	11	PDB header: sugar binding protein Chain: A: PDB Molecule: sugar abc transporter, sugar-binding protein; PDBTitle: the crystal structure of a solute binding protein from bacillus2 anthracis str. ames in complex with quorum-sensing signal3 autoinducer-2 (ai-2)
77	c3eywA_	Alignment	not modelled	92.3	12	PDB header: transport protein Chain: A: PDB Molecule: c-terminal domain of glutathione-regulated potassium-efflux PDBTitle: crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
78	d1lua2	Alignment	not modelled	92.3	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
79	c4pe6B_	Alignment	not modelled	92.3	11	PDB header: solute-binding protein Chain: B: PDB Molecule: putative abc transporter; PDBTitle: crystal structure of abc transporter solute binding protein from2 thermobispora bispora dsm 43833
80	d1p0fa2	Alignment	not modelled	92.2	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
81	d1tjya_	Alignment	not modelled	91.8	13	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
82	d1cdoa2	Alignment	not modelled	91.7	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
83	c2x7xA_	Alignment	not modelled	90.8	13	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: fructose binding periplasmic domain of hybrid two component system2 bt1754
84	c3krtC_	Alignment	not modelled	90.8	19	PDB header: oxidoreductase Chain: C: PDB Molecule: crotonyl coa reductase; PDBTitle: crystal structure of putative crotonyl coa reductase from streptomyces2 coelicolor a3(2)
85	d1jx6a_	Alignment	not modelled	90.5	11	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
86	c3widC_	Alignment	not modelled	90.5	18	PDB header: oxidoreductase Chain: C: PDB Molecule: glucose 1-dehydrogenase; PDBTitle: structure of a glucose dehydrogenase t277f mutant in complex with nadp
87	d1xa0a2	Alignment	not modelled	90.4	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
88	c4gi2B_	Alignment	not modelled	90.3	12	PDB header: oxidoreductase Chain: B: PDB Molecule: crotonyl-coa carboxylase/reductase; PDBTitle: crotonyl-coa carboxylase/reductase
89	d1d1ta2	Alignment	not modelled	89.8	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
90	d1bg6a2	Alignment	not modelled	89.4	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
91	c4wzzA_	Alignment	not modelled	89.3	11	PDB header: transport protein Chain: A: PDB Molecule: putative sugar abc transporter, substrate-binding protein; PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from clostridium phytofermentas (cphy_0583, target efi-3 511148) with bound l-rhamnose
92	c3h75A_	Alignment	not modelled	89.1	15	PDB header: sugar binding protein Chain: A: PDB Molecule: periplasmic sugar-binding domain protein; PDBTitle: crystal structure of a periplasmic sugar-binding protein from the2 pseudomonas fluorescens
93	c5xi0B_	Alignment	not modelled	88.9	19	PDB header: oxidoreductase Chain: B: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nadh]; PDBTitle: crystal structure of fabv, a new class of enyl-acyl carrier protein2 reductase from vibrio fischeri
94	c3iupB_	Alignment	not modelled	87.7	22	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nadph:quinone oxidoreductase; PDBTitle: crystal structure of putative nadph:quinone oxidoreductase2 (yp_296108.1) from ralstonia eutropha jmp134 at 1.70 a resolution
95	d1t57a_	Alignment	not modelled	87.6	26	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: MTH1675-like
96	d1tt7a2	Alignment	not modelled	87.2	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
97	c4euhA_	Alignment	not modelled	86.1	12	PDB header: oxidoreductase Chain: A: PDB Molecule: putative reductase ca_c0462; PDBTitle: crystal structure of clostridium acetobutulicum trans-2-enoyl-coa2 reductase apo form
98	c3orgA_	Alignment	not modelled	85.8	23	PDB header: ligase,biosynthetic protein Chain: A: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide synthetase; PDBTitle: crystal structure of n5-carboxyaminoimidazole synthetase from2 staphylococcus aureus complexed with adp
99	c4izhA_	Alignment	not modelled	85.3	14	PDB header: oxidoreductase Chain: A: PDB Molecule: nad/nadp transhydrogenase alpha subunit 1; PDBTitle: crystal structure of the alpha1 dimer of thermus thermophilus2 transhydrogenase in p6 PDB header: solute-binding protein

100	c4y9tA_	Alignment	not modelled	85.2	10	Chain: A: PDB Molecule: abc transporter, solute binding protein; PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from agrobacterium vitis s4 (avi_5305, target efi-511224)3 with bound alpha-d-glucosamine
101	d1ykfa2	Alignment	not modelled	84.5	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
102	d1l7da1	Alignment	not modelled	83.4	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
103	c4a10A_	Alignment	not modelled	83.2	14	PDB header: oxidoreductase Chain: A: PDB Molecule: octenoyl-coa reductase/carboxylase; PDBTitle: apo-structure of 2-octenoyl-coa carboxylase reductase cinf from2 streptomyces sp.
104	c6dspB_	Alignment	not modelled	82.8	15	PDB header: signaling protein Chain: B: PDB Molecule: autoinducer 2-binding protein lsrb; PDBTitle: lsrb from clostridium saccharobutylicum in complex with ai-2
105	c2qioA_	Alignment	not modelled	82.2	12	PDB header: unknown function Chain: A: PDB Molecule: enoyl-(acyl-carrier-protein) reductase; PDBTitle: x-ray structure of enoyl-acyl carrier protein reductase from bacillus2 anthracis with triclosan
106	d1u3wa2	Alignment	not modelled	82.2	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
107	d1rjwa2	Alignment	not modelled	82.1	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
108	d1ml4a2	Alignment	not modelled	81.5	26	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
109	c4fq5B_	Alignment	not modelled	81.4	16	PDB header: isomerase Chain: B: PDB Molecule: maleate cis-trans isomerase; PDBTitle: crystal structure of the maleate isomerase iso(c200a) from pseudomonas2 putida s16 with maleate
110	d1piwa2	Alignment	not modelled	80.5	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
111	c6hnuA_	Alignment	not modelled	80.4	11	PDB header: transferase Chain: A: PDB Molecule: aromatic amino acid aminotransferase i; PDBTitle: crystal structure of the aminotransferase aro8 from c. albicans with2 ligands
112	d1vlva2	Alignment	not modelled	79.8	9	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
113	c1m6yA_	Alignment	not modelled	79.3	14	PDB header: transferase Chain: A: PDB Molecule: s-adenosyl-methyltransferase mraw; PDBTitle: crystal structure analysis of tm0872, a putative sam-dependent2 methyltransferase, complexed with sah
114	d1iz0a2	Alignment	not modelled	79.3	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
115	c5l53A_	Alignment	not modelled	79.3	20	PDB header: oxidoreductase Chain: A: PDB Molecule: (-)-menthone:(+)-neomenthol reductase; PDBTitle: menthone neomenthol reductase from mentha piperita in complex with2 nadp
116	c3d02A_	Alignment	not modelled	77.6	14	PDB header: sugar binding protein Chain: A: PDB Molecule: putative lacI-type transcriptional regulator; PDBTitle: crystal structure of periplasmic sugar-binding protein2 (yp_001338366.1) from klebsiella pneumoniae subsp. pneumoniae mgh3 78578 at 1.30 a resolution
117	d1e3ia2	Alignment	not modelled	77.5	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
118	c6hyhA_	Alignment	not modelled	77.3	14	PDB header: sugar binding protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of msmeg_1712 from mycobacterium smegmatis in2 complex with beta-d-fucofuranose
119	c3s8mA_	Alignment	not modelled	77.2	11	PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl-accp reductase; PDBTitle: the crystal structure of fabv
120	c5dkvD_	Alignment	not modelled	77.1	15	PDB header: sugar binding protein Chain: D: PDB Molecule: abc transporter substrate binding protein (ribose); PDBTitle: crystal structure of an abc transporter solute binding protein from2 agrobacterium vitis(avis_5339, target efi-511225) bound with alpha-d-3 tagatopyranose