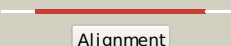
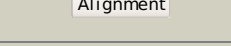
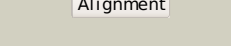
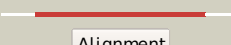
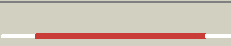
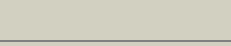
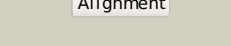
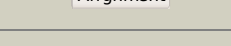
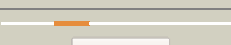
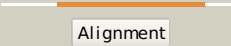
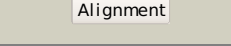


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dlqopb_	 Alignment		100.0	97	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
2	clx1qA_	 Alignment		100.0	54	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase beta chain; PDBTitle: crystal structure of tryptophan synthase beta chain from thermus2 thermophilus hb8
3	dlv8za1	 Alignment		100.0	59	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
4	c2o2jA_	 Alignment		100.0	59	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase beta chain; PDBTitle: mycobacterium tuberculosis tryptophan synthase beta chain2 dimer (apoform)
5	dlwkva1	 Alignment		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
6	cltdjA_	 Alignment		100.0	21	PDB header: allostery Chain: A: PDB Molecule: biosynthetic threonine deaminase; PDBTitle: threonine deaminase (biosynthetic) from e. coli
7	c3iauA_	 Alignment		100.0	22	PDB header: lyase Chain: A: PDB Molecule: threonine deaminase; PDBTitle: the structure of the processed form of threonine deaminase isoform 22 from solanum lycopersicum
8	c3pc3A_	 Alignment		100.0	21	PDB header: lyase Chain: A: PDB Molecule: cg1753, isoform a; PDBTitle: full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
9	dlv71a1	 Alignment		100.0	22	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
10	dljbqa_	 Alignment		100.0	22	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
11	cljbqD_	 Alignment		100.0	22	PDB header: lyase Chain: D: PDB Molecule: cystathionine beta-synthase; PDBTitle: structure of human cystathionine beta-synthase: a unique pyridoxal 5'-2 phosphate dependent hemeoprotein

12	c2gn0A_	Alignment		100.0	20	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)
13	dlz7wa1	Alignment		100.0	22	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
14	dlpwah_	Alignment		100.0	22	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
15	d1tdja1	Alignment		100.0	21	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
16	c3r0zA_	Alignment		100.0	16	PDB header: lyase Chain: A: PDB Molecule: d-serine dehydratase; PDBTitle: crystal structure of apo d-serine deaminase from salmonella2 typhimurium
17	c3l6cA_	Alignment		100.0	19	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
18	dlve5a1	Alignment		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
19	clp5ja_	Alignment		100.0	21	PDB header: lyase Chain: A: PDB Molecule: l-serine dehydratase; PDBTitle: crystal structure analysis of human serine dehydratase
20	dlp5ja_	Alignment		100.0	21	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
21	dlve1a1	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
22	c2pqmA_	Alignment	not modelled	100.0	21	PDB header: lyase Chain: A: PDB Molecule: cysteine synthase; PDBTitle: crystal structure of cysteine synthase (oass) from entamoeba2 histolytica at 1.86 a resolution
23	d2bhsa1	Alignment	not modelled	100.0	24	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	c3dwgA_	Alignment	not modelled	100.0	22	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
25	dlv7la1	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
26	c2q3bA_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: cysteine synthase a; PDBTitle: 1.8 a resolution crystal structure of o-acetylserine sulphydrylase2 (oass) holoenzyme from mycobacterium tuberculosis

27	c2d1fA_	 Alignment	not modelled	100.0	20	PDB header: lyase Chain: A: PDB Molecule: threonine synthase; PDBTitle: structure of mycobacterium tuberculosis threonine synthase
28	d1v7ca_	 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
29	c2zsjB_	 Alignment	not modelled	100.0	19	PDB header: lyase Chain: B: PDB Molecule: threonine synthase; PDBTitle: crystal structure of threonine synthase from aquifex aeolicus vf5
30	d1o58a_	 Alignment	not modelled	100.0	24	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	c2rkbE_	 Alignment	not modelled	100.0	20	PDB header: lyase Chain: E: PDB Molecule: serine dehydratase-like; PDBTitle: serine dehydratase like-1 from human cancer cells
32	c2eguA_	 Alignment	not modelled	100.0	25	PDB header: transferase Chain: A: PDB Molecule: cysteine synthase; PDBTitle: crystal structure of o-acetylserine sulfhydrase from geobacillus2 kaustophilus hta426
33	d1fcja_	 Alignment	not modelled	100.0	22	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
34	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
35	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
36	d1e5xa_	 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
37	d1tyza_	 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
38	d1vb3a1	 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
39	d1kl7a_	 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
40	d1vp8a_	 Alignment	not modelled	95.2	16	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: MTH1675-like
41	c3iupB_	 Alignment	not modelled	92.1	14	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
42	d1c1da1	 Alignment	not modelled	86.7	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
43	c3o93A_	 Alignment	not modelled	85.7	13	PDB header: hydrolase Chain: A: PDB Molecule: nicotinamidase; PDBTitle: high resolution crystal structures of streptococcus pneumoniae2 nicotinamidase with trapped intermediates provide insights into3 catalytic mechanism and inhibition by aldehydes
44	d1bg6a2	 Alignment	not modelled	85.5	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
45	d1hyua1	 Alignment	not modelled	84.4	23	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
46	c3krtC_	 Alignment	not modelled	84.0	19	PDB header: oxidoreductase Chain: C: PDB Molecule: crotonyl coa reductase; PDBTitle: crystal structure of putative crotonyl coa reductase from streptomyces2 coelicolor a3(2)
47	d1o8ca2	 Alignment	not modelled	84.0	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain

48	dl17da1	Alignment	not modelled	83.7	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
49	dlnbaa	Alignment	not modelled	83.4	12	Fold: Isochorismatase-like hydrolases Superfamily: Isochorismatase-like hydrolases Family: Isochorismatase-like hydrolases
50	c3d4oA	Alignment	not modelled	80.6	29	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase subunit a; PDBTitle: crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
51	c3k30B	Alignment	not modelled	80.3	16	PDB header: oxidoreductase Chain: B: PDB Molecule: histamine dehydrogenase; PDBTitle: histamine dehydrogenase from nocardioles simplex
52	dl1t57a	Alignment	not modelled	80.1	10	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: MTH1675-like
53	c2rghA	Alignment	not modelled	77.1	22	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-glycerophosphate oxidase; PDBTitle: structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
54	dl1f2a1	Alignment	not modelled	76.0	30	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
55	dlim5a	Alignment	not modelled	74.1	15	Fold: Isochorismatase-like hydrolases Superfamily: Isochorismatase-like hydrolases Family: Isochorismatase-like hydrolases
56	clboiA	Alignment	not modelled	73.3	29	PDB header: transferase Chain: A: PDB Molecule: rhodanese; PDBTitle: n-terminally truncated rhodanese
57	c3gbcA	Alignment	not modelled	73.3	17	PDB header: hydrolase Chain: A: PDB Molecule: pyrazinamidase/nicotinamidase pnca; PDBTitle: determination of the crystal structure of the pyrazinamidase from2 m.tuberculosis : a structure-function analysis for prediction3 resistance to pyrazinamide
58	c2bruB	Alignment	not modelled	70.6	21	PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p) transhydrogenase subunit alpha; PDBTitle: complex of the domain i and domain iii of escherichia coli2 transhydrogenase
59	c3oqpB	Alignment	not modelled	70.4	11	PDB header: hydrolase Chain: B: PDB Molecule: putative isochorismatase; PDBTitle: crystal structure of a putative isochorismatase (bx_e_a0706) from2 burkholderia xenovorans lb400 at 1.22 a resolution
60	dl1rba1	Alignment	not modelled	70.1	22	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
61	dlvdca1	Alignment	not modelled	69.1	22	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
62	c3gmbB	Alignment	not modelled	69.1	24	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-methyl-3-hydroxypyridine-5-carboxylic acid PDBTitle: crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic2 acid oxygenase
63	clgl9B	Alignment	not modelled	68.9	13	PDB header: topoisomerase Chain: B: PDB Molecule: reverse gyrase; PDBTitle: archaeoglobus fulgidus reverse gyrase complexed with adpnp
64	c2ywlA	Alignment	not modelled	68.4	33	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase related protein; PDBTitle: crystal structure of thioredoxin reductase-related protein ttha03702 from thermus thermophilus hb8
65	c2qx7A	Alignment	not modelled	68.3	18	PDB header: plant protein Chain: A: PDB Molecule: eugenol synthase 1; PDBTitle: structure of eugenol synthase from ocimum basilicum
66	dlseza1	Alignment	not modelled	68.1	28	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
67	c3da1A	Alignment	not modelled	68.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase; PDBTitle: x-ray structure of the glycerol-3-phosphate dehydrogenase2 from bacillus halodurans complexed with fad. northeast3 structural genomics consortium target bhr167.
68	d2i0za1	Alignment	not modelled	67.9	22	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
69	c3d3kD	Alignment	not modelled	67.5	9	PDB header: protein binding Chain: D: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: crystal structure of human edc3p
70	dlmv8a2	Alignment	not modelled	67.4	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
71	dl1t7a2	Alignment	not modelled	66.3	8	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
72	dlxgka	Alignment	not modelled	66.1	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
73	d3lada1	Alignment	not modelled	65.5	41	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain

73	c3raaA	Alignment	not modelled	65.5	41	Family: FAD/NAD-linked reductases, N-terminal and central domains PDB header: hydrolase Chain: A: PDB Molecule: putative isochorismatase; PDBTitle: crystal structure of a putative isochorismatase (bxe_a0706) from2 burkholderia xenovorans lb400 at 1.22 a resolution
74	c3oqaA	Alignment	not modelled	65.1	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
75	d1o89a2	Alignment	not modelled	64.7	17	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
76	d1ml4a2	Alignment	not modelled	64.3	12	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
77	d1dxa1	Alignment	not modelled	63.9	30	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
78	c3orgA	Alignment	not modelled	63.2	23	PDB header: hydrolase Chain: B: PDB Molecule: isochorismatase family protein; PDBTitle: crystal structure of isochorismatase family protein from desulfovibrio2 vulgaris subsp. vulgaris str. hildenborough
79	c3hu5B	Alignment	not modelled	63.0	15	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GidA-like
80	d2cula1	Alignment	not modelled	62.5	26	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
81	d1ebda1	Alignment	not modelled	62.4	37	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
82	d1lvla1	Alignment	not modelled	62.3	22	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
83	d3lada2	Alignment	not modelled	61.4	19	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
84	d1v59a2	Alignment	not modelled	61.3	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
85	c3eywA	Alignment	not modelled	60.9	15	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
86	c3ot4F	Alignment	not modelled	60.8	19	PDB header: hydrolase Chain: F: PDB Molecule: putative isochorismatase; PDBTitle: structure and catalytic mechanism of bordetella bronchiseptica nicf
87	c2rgoA	Alignment	not modelled	60.7	24	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-glycerophosphate oxidase; PDBTitle: structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
88	c1bg6A	Alignment	not modelled	60.5	20	PDB header: oxidoreductase Chain: A: PDB Molecule: n-(1-d-carboxylethyl)-l-norvaline dehydrogenase; PDBTitle: crystal structure of the n-(1-d-carboxylethyl)-l-norvaline2 dehydrogenase from arthrobacter sp. strain 1c
89	d1ryia1	Alignment	not modelled	60.5	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
90	c3allA	Alignment	not modelled	59.6	29	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-methyl-3-hydroxypyridine-5-carboxylic acid oxygenase; PDBTitle: crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic acid2 oxygenase, mutant y270a
91	c3p2yA	Alignment	not modelled	59.5	19	PDB header: oxidoreductase Chain: A: PDB Molecule: alanine dehydrogenase/pyridine nucleotide transhydrogenase; PDBTitle: crystal structure of alanine dehydrogenase/pyridine nucleotide2 transhydrogenase from mycobacterium smegmatis
92	d2gf3a1	Alignment	not modelled	58.7	30	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
93	d1onfa2	Alignment	not modelled	58.5	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
94	c1djbB	Alignment	not modelled	58.3	23	PDB header: oxidoreductase Chain: B: PDB Molecule: trimethylamine dehydrogenase; PDBTitle: structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylophilus methylotrophus (sp.3 w3a1)
95	c2vhyB	Alignment	not modelled	58.2	13	PDB header: oxidoreductase Chain: B: PDB Molecule: alanine dehydrogenase; PDBTitle: crystal structure of apo l-alanine dehydrogenase from2 mycobacterium tuberculosis
96	c2hk8B	Alignment	not modelled	57.7	15	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase from aquifex2 aeolicus at 2.35 angstrom resolution
97	c3c1aA	Alignment	not modelled	57.0	10	PDB header: oxidoreductase Chain: A: PDB Molecule: eugenol synthase;

97	c3c10A	Alignment	not modelled	57.0	19	PDBTitle: the multiple phenylpropene synthases in both clarkia2 breweri and petunia hybrida represent two distinct lineages PDB header: transferase/rna
98	c3eplA	Alignment	not modelled	56.9	15	Chain: A: PDB Molecule: trna isopentenyltransferase; PDBTitle: crystallographic snapshots of eukaryotic c2 dimethylallyltransferase acting on trna: insight into trna3 recognition and reaction mechanism
99	d1neka2	Alignment	not modelled	56.5	30	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
100	c2bryA	Alignment	not modelled	56.5	26	PDB header: transport Chain: A: PDB Molecule: nedd9 interacting protein with calponin homology PDBTitle: crystal structure of the native monooxygenase domain of 2 mical at 1.45 a resolution
101	c3k96B	Alignment	not modelled	56.0	37	PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad(p)+]; PDBTitle: 2.1 angstrom resolution crystal structure of glycerol-3-phosphate2 dehydrogenase (gpsa) from coxiella burnetii
102	c3g05B	Alignment	not modelled	55.2	26	PDB header: rna binding protein Chain: B: PDB Molecule: trna uridine 5-carboxymethylaminomethyl modification enzyme PDBTitle: crystal structure of n-terminal domain (2-550) of e.coli mnmg
103	d2iida1	Alignment	not modelled	55.0	22	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
104	c3fk4A	Alignment	not modelled	55.0	28	PDB header: isomerase Chain: A: PDB Molecule: rubisco-like protein; PDBTitle: crystal structure of rubisco-like protein from bacillus2 cereus atcc 14579
105	d1qyda	Alignment	not modelled	54.9	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
106	d1ojta1	Alignment	not modelled	54.7	37	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
107	c2xdoC	Alignment	not modelled	54.3	19	PDB header: oxidoreductase Chain: C: PDB Molecule: tex2 protein; PDBTitle: structure of the tetracycline degrading monooxygenase tex2 from2 bacteroides thetaiotaomicron
108	c3f8rD	Alignment	not modelled	53.8	28	PDB header: oxidoreductase Chain: D: PDB Molecule: thioredoxin reductase (trxb-3); PDBTitle: crystal structure of sulfolobus solfataricus thioredoxin2 reductase b3 in complex with two nadp molecules
109	d1lpfa1	Alignment	not modelled	53.7	37	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
110	c2ze5A	Alignment	not modelled	53.6	9	PDB header: transferase Chain: A: PDB Molecule: isopentenyl transferase; PDBTitle: crystal structure of adenosine phosphate-isopentenyltransferase
111	c3cumA	Alignment	not modelled	53.3	21	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
112	c3atrA	Alignment	not modelled	53.2	26	PDB header: oxidoreductase Chain: A: PDB Molecule: conserved archaeal protein; PDBTitle: geranylgeranyl reductase (ggr) from sulfolobus acidocaldarius co-2 crystallized with its ligand
113	c1hyuA	Alignment	not modelled	53.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: alkyl hydroperoxide reductase subunit f; PDBTitle: crystal structure of intact ahpf
114	c1pjca	Alignment	not modelled	52.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (l-alanine dehydrogenase); PDBTitle: l-alanine dehydrogenase complexed with nad
115	d2bs2a2	Alignment	not modelled	52.8	26	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
116	d1kja2	Alignment	not modelled	52.8	22	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
117	c2vdcl	Alignment	not modelled	52.5	28	PDB header: oxidoreductase Chain: I: PDB Molecule: glutamate synthase [nadh] small chain; PDBTitle: the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
118	c3d3ja	Alignment	not modelled	51.9	9	PDB header: protein binding Chain: A: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: crystal structure of human edc3p
119	c3cgva	Alignment	not modelled	51.8	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: geranylgeranyl reductase related protein; PDBTitle: crystal structure of geranylgeranyl bacteriochlorophyll reductase-like2 fixc homolog (np_393992.1) from thermoplasma acidophilum at 1.60 a3 resolution
120	c2gf2B	Alignment	not modelled	51.6	20	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of human hydroxyisobutyrate dehydrogenase