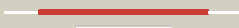



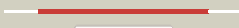

























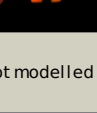


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1q7ea_	 Alignment		100.0	98	Fold: CoA-transferase family III (CaiB/BaiF) Superfamily: CoA-transferase family III (CaiB/BaiF) Family: CoA-transferase family III (CaiB/BaiF)
2	d2vjma1	 Alignment		100.0	60	Fold: CoA-transferase family III (CaiB/BaiF) Superfamily: CoA-transferase family III (CaiB/BaiF) Family: CoA-transferase family III (CaiB/BaiF)
3	d1xk7a1	 Alignment		100.0	24	Fold: CoA-transferase family III (CaiB/BaiF) Superfamily: CoA-transferase family III (CaiB/BaiF) Family: CoA-transferase family III (CaiB/BaiF)
4	c1xa3B_	 Alignment		100.0	24	PDB header: transferase Chain: B: PDB Molecule: crotonobetainyl-coa:carnitine coa-transferase; PDBTitle: crystal structure of caib, a type iii coa transferase in2 carnitine metabolism
5	d1x74a1	 Alignment		100.0	26	Fold: CoA-transferase family III (CaiB/BaiF) Superfamily: CoA-transferase family III (CaiB/BaiF) Family: CoA-transferase family III (CaiB/BaiF)
6	c2g04B_	 Alignment		100.0	24	PDB header: isomerase Chain: B: PDB Molecule: probable fatty-acid-coa racemase far; PDBTitle: crystal structure of fatty acid-coa racemase from mycobacterium2 tuberculosis h37rv
7	c3p2yA_	 Alignment		95.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: alanine dehydrogenase/pyridine nucleotide transhydrogenase; PDBTitle: crystal structure of alanine dehydrogenase/pyridine nucleotide2 transhydrogenase from mycobacterium smegmatis
8	d1ygya1	 Alignment		94.3	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
9	c3kboB_	 Alignment		94.1	11	PDB header: oxidoreductase Chain: B: PDB Molecule: glyoxylate/hydroxypyruvate reductase a; PDBTitle: 2.14 angstrom crystal structure of putative oxidoreductase (ycdw) from2 salmonella typhimurium in complex with nadp
10	c2g76A_	 Alignment		93.9	11	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of human 3-phosphoglycerate dehydrogenase
11	c2dbqA_	 Alignment		93.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: glyoxylate reductase; PDBTitle: crystal structure of glyoxylate reductase (ph0597) from pyrococcus2 horikoshii ot3, complexed with nadp (i41)

12	c1wwkA	Alignment		93.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoglycerate dehydrogenase; PDBTitle: crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
13	d2dlda1	Alignment		93.8	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
14	d1l7da1	Alignment		93.8	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
15	c3dhyC	Alignment		93.5	31	PDB header: hydrolase Chain: C: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structures of mycobacterium tuberculosis s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and3 inhibitors
16	d1gdha1	Alignment		93.4	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
17	d2naca1	Alignment		93.4	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
18	c1v8bA	Alignment		93.1	20	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of a hydrolase
19	d1qp8a1	Alignment		93.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
20	c3oneA	Alignment		92.9	27	PDB header: hydrolase/hydrolase substrate Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of lupinus luteus s-adenosyl-l-homocysteine2 hydrolase in complex with adenine
21	c2omeA	Alignment	not modelled	92.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: c-terminal-binding protein 2; PDBTitle: crystal structure of human ctbp2 dehydrogenase complexed with nad(h)
22	d1pjca1	Alignment	not modelled	92.7	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
23	c3gvpB	Alignment	not modelled	92.6	23	PDB header: hydrolase Chain: B: PDB Molecule: adenosylhomocysteinase 3; PDBTitle: human sahh-like domain of human adenosylhomocysteinase 3
24	c2bruB	Alignment	not modelled	92.5	17	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
25	c1gdhA	Alignment	not modelled	92.5	11	PDB header: oxidoreductase(choh (d)-nad(p)+ (a)) Chain: A: PDB Molecule: d-glycerate dehydrogenase; PDBTitle: crystal structure of a nad-dependent d-glycerate2 dehydrogenase at 2.4 angstroms resolution
26	c3bazaA	Alignment	not modelled	92.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyphenylpyruvate reductase; PDBTitle: structure of hydroxyphenylpyruvate reductase from coleus blumei in2 complex with nadp+
27	d1dxya1	Alignment	not modelled	92.3	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
28	c1pjca	Alignment	not modelled	92.1	18	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (l-alanine dehydrogenase); PDBTitle: l-alanine dehydrogenase complexed with nad
						Fold: NAD(P)-binding Rossmann-fold domains

29	d1j4aa1	Alignment	not modelled	92.0	16	Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
30	c3gvxA	Alignment	not modelled	92.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerate dehydrogenase related protein; PDBTitle: crystal structure of glycerate dehydrogenase related2 protein from thermoplasma acidophilum
31	c2gcgB	Alignment	not modelled	91.5	14	PDB header: oxidoreductase Chain: B: PDB Molecule: glyoxylate reductase/hydroxypyruvate reductase; PDBTitle: ternary crystal structure of human glyoxylate2 reductase/hydroxypyruvate reductase
32	d1mx3a1	Alignment	not modelled	91.5	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
33	c1luaA	Alignment	not modelled	91.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: methylene tetrahydromethanopterin dehydrogenase; PDBTitle: structure of methylene-tetrahydromethanopterin dehydrogenase from2 methylobacterium extorquens am1 complexed with nadp
34	c2rirA	Alignment	not modelled	90.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase, a chain; PDBTitle: crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
35	c2eklA	Alignment	not modelled	90.7	11	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: structure of st1218 protein from sulfolobus tokodaii
36	c3hg7A	Alignment	not modelled	90.7	23	PDB header: oxidoreductase Chain: A: PDB Molecule: d-isomer specific 2-hydroxyacid dehydrogenase family PDBTitle: crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 family protein from aeromonas salmonicida subsp. salmonicida a449
37	c1l7eC	Alignment	not modelled	90.7	20	PDB header: oxidoreductase Chain: C: PDB Molecule: nicotinamide nucleotide transhydrogenase, PDBTitle: crystal structure of r. rubrum transhydrogenase domain i2 with bound nadh
38	c2pi1C	Alignment	not modelled	90.5	15	PDB header: oxidoreductase Chain: C: PDB Molecule: d-lactate dehydrogenase; PDBTitle: crystal structure of d-lactate dehydrogenase from aquifex2 aeolicus complexed with nad and lactic acid
39	d1li4a1	Alignment	not modelled	90.4	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
40	c1j4aA	Alignment	not modelled	90.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: insights into domain closure, substrate specificity and2 catalysis of d-lactate dehydrogenase from lactobacillus3 bulgaricus
41	c2cukC	Alignment	not modelled	90.2	20	PDB header: oxidoreductase Chain: C: PDB Molecule: glycerate dehydrogenase/glyoxylate reductase; PDBTitle: crystal structure of tt0316 protein from thermus thermophilus hb8
42	c2eezG	Alignment	not modelled	90.0	19	PDB header: oxidoreductase Chain: G: PDB Molecule: alanine dehydrogenase; PDBTitle: crystal structure of alanine dehydrogenase from themus thermophilus
43	c3d64A	Alignment	not modelled	89.8	22	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
44	d1np3a2	Alignment	not modelled	89.4	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
45	d1m1na	Alignment	not modelled	88.9	19	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
46	c2j6iC	Alignment	not modelled	88.3	16	PDB header: oxidoreductase Chain: C: PDB Molecule: formate dehydrogenase; PDBTitle: candida boidinii formate dehydrogenase (fdh) c-terminal2 mutant
47	d1to3a	Alignment	not modelled	87.2	36	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
48	c3evtA	Alignment	not modelled	87.2	21	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoglycerate dehydrogenase; PDBTitle: crystal structure of phosphoglycerate dehydrogenase from2 lactobacillus plantarum
49	d1pg5a2	Alignment	not modelled	87.0	14	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
50	c3d4oA	Alignment	not modelled	86.8	16	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	c1xdwA	Alignment	not modelled	86.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: nad+-dependent (r)-2-hydroxyglutarate PDBTitle: nad+-dependent (r)-2-hydroxyglutarate dehydrogenase from2 acidaminococcus fermentans
52	c2xdoC	Alignment	not modelled	86.3	25	PDB header: oxidoreductase Chain: C: PDB Molecule: teb2 protein; PDBTitle: structure of the tetracycline degrading monooxygenase teb2 from2 bacteroides thetaiotaomicron
53	c1d4fD	Alignment	not modelled	86.1	26	PDB header: hydrolase Chain: D: PDB Molecule: s-adenosylhomocysteine hydrolase;

53	c1u4tD	Alignment	not modelled	86.1	20	PDBTitle: crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase PDB header: oxidoreductase
54	c2vhyB	Alignment	not modelled	85.4	15	Chain: B: PDB Molecule: alanine dehydrogenase; PDBTitle: crystal structure of apo l-alanine dehydrogenase from2 mycobacterium tuberculosis
55	c3gg9C	Alignment	not modelled	85.1	18	PDB header: oxidoreductase Chain: C: PDB Molecule: d-3-phosphoglycerate dehydrogenase oxidoreductase protein; PDBTitle: crystal structure of putative d-3-phosphoglycerate dehydrogenase2 oxidoreductase from ralstonia solanacearum
56	c2p2gD	Alignment	not modelled	84.9	10	PDB header: transferase Chain: D: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
57	c1qp8A	Alignment	not modelled	84.9	24	PDB header: oxidoreductase Chain: A: PDB Molecule: formate dehydrogenase; PDBTitle: crystal structure of a putative formate dehydrogenase from2 pyrobaculum aerophilum
58	d1vlva2	Alignment	not modelled	84.6	14	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
59	c1np3B	Alignment	not modelled	83.3	18	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of class i acetohydroxy acid isomeroreductase from2 pseudomonas aeruginosa
60	c3n58D	Alignment	not modelled	82.8	26	PDB header: hydrolase Chain: D: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from brucella2 melitensis in ternary complex with nad and adenosine, orthorhombic3 form
61	d1sc6a1	Alignment	not modelled	81.6	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
62	c3n7uD	Alignment	not modelled	81.4	15	PDB header: oxidoreductase Chain: D: PDB Molecule: formate dehydrogenase; PDBTitle: nad-dependent formate dehydrogenase from higher-plant arabidopsis2 thaliana in complex with nad and azide
63	d1v8ba1	Alignment	not modelled	80.0	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
64	c3pdiG	Alignment	not modelled	79.9	22	PDB header: protein binding Chain: G: PDB Molecule: nitrogenase mofe cofactor biosynthesis protein nife; PDBTitle: precursor bound nifen
65	c1u5tA	Alignment	not modelled	79.8	14	PDB header: transport protein Chain: A: PDB Molecule: appears to be functionally related to snf7; PDBTitle: structure of the escrt-ii endosomal trafficking complex
66	c1ygyA	Alignment	not modelled	77.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
67	d1dxha2	Alignment	not modelled	77.4	18	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
68	d2ngra3	Alignment	not modelled	77.0	18	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
69	d1ekxa2	Alignment	not modelled	76.8	16	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
70	d1li4a2	Alignment	not modelled	76.7	24	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: S-adenosylhomocystein hydrolase
71	d1qh8a	Alignment	not modelled	76.4	18	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
72	d1u7za	Alignment	not modelled	75.9	21	Fold: Ribokinase-like Superfamily: CoaB-like Family: CoaB-like
73	c2vouA	Alignment	not modelled	75.6	33	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,6-dihydroxypyridine hydroxylase; PDBTitle: structure of 2,6-dihydroxypyridine-3-hydroxylase from2 arthrobacter nicotinovorans
74	c2qjhH	Alignment	not modelled	74.9	30	PDB header: lyase Chain: H: PDB Molecule: putative aldolase mj0400; PDBTitle: m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
75	d1v8ba2	Alignment	not modelled	74.6	17	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: S-adenosylhomocystein hydrolase
76	c3nlcA	Alignment	not modelled	74.5	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein vp0956; PDBTitle: crystal structure of the vp0956 protein from vibrio parahaemolyticus.2 northeast structural genomics consortium target vpr147
77	c2w2kB	Alignment	not modelled	73.4	12	PDB header: oxidoreductase Chain: B: PDB Molecule: d-mandelate dehydrogenase; PDBTitle: crystal structure of the apo forms of rhodotorula graminis2 d-mandelate dehydrogenase at 1.8a.
78	c1dxyA	Alignment	not modelled	72.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: d-2-hydroxysicaproate dehydrogenase; PDBTitle: structure of d-2-hydroxysicaproate dehydrogenase PDB header: oxidoreductase

79	c3aIIA_	Alignment	not modelled	71.8	23	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
80	c2acZA_	Alignment	not modelled	71.7	11	PDB header: oxidoreductase/electron transport Chain: A: PDB Molecule: succinate dehydrogenase flavoprotein subunit; PDBTitle: complex ii (succinate dehydrogenase) from e. coli with atpenin a52 inhibitor co-crystallized at the ubiquinone binding site
81	dlseza1	Alignment	not modelled	71.5	23	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
82	dlc1da1	Alignment	not modelled	71.0	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
83	clqo8A_	Alignment	not modelled	70.8	22	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c3 fumarate reductase; PDBTitle: the structure of the open conformation of a flavocytochrome2 c3 fumarate reductase
84	c2d0iC_	Alignment	not modelled	70.5	18	PDB header: oxidoreductase Chain: C: PDB Molecule: dehydrogenase; PDBTitle: crystal structure ph0520 protein from pyrococcus horikoshii ot3
85	c2vdcl_	Alignment	not modelled	70.0	13	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.
86	c2xagA_	Alignment	not modelled	68.5	34	PDB header: transcription Chain: A: PDB Molecule: lysine-specific histone demethylase 1; PDBTitle: crystal structure of lsd1-corest in complex with para-bromo-2 (-)-trans-2-phenylcyclopropyl-1-amine
87	c2v1dA_	Alignment	not modelled	68.5	34	PDB header: oxidoreductase/repressor Chain: A: PDB Molecule: lysine-specific histone demethylase 1; PDBTitle: structural basis of lsd1-corest selectivity in histone h32 recognition
88	clf8sA_	Alignment	not modelled	68.3	27	PDB header: oxidoreductase Chain: A: PDB Molecule: l-amino acid oxidase; PDBTitle: crystal structure of l-amino acid oxidase from calloselasma2 rhodostoma, complexed with three molecules of o-aminobenzoate.
89	cljrxA_	Alignment	not modelled	67.7	30	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c; PDBTitle: crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
90	c3ka7A_	Alignment	not modelled	66.6	23	PDB header: oxidoreductase Chain: A: PDB Molecule: oxi doreductase; PDBTitle: crystal structure of an oxidoreductase from methanosarcina2 mazei. northeast structural genomics consortium target id3 mar208
91	d2dw4a2	Alignment	not modelled	66.5	34	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
92	dluz5a3	Alignment	not modelled	65.9	22	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
93	dli8ta1	Alignment	not modelled	65.2	20	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: UDP-galactopyranose mutase, N-terminal domain
94	c3d8xB_	Alignment	not modelled	65.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase 1; PDBTitle: crystal structure of saccharomyces cerevisiae nadph dependent2 thioredoxin reductase 1
95	cld4cB_	Alignment	not modelled	63.9	24	PDB header: oxidoreductase Chain: B: PDB Molecule: flavocytochrome c fumarate reductase; PDBTitle: crystal structure of the uncomplexed form of the2 flavocytochrome c fumarate reductase of shewanella3 putrefaciens strain mr-1
96	c2nacA_	Alignment	not modelled	63.1	16	PDB header: oxidoreductase(al dehyde(d),nad+(a)) Chain: A: PDB Molecule: nad-dependent formate dehydrogenase; PDBTitle: high resolution structures of holo and apo formate dehydrogenase
97	c2jb1B_	Alignment	not modelled	62.3	23	PDB header: oxidoreductase Chain: B: PDB Molecule: l-amino acid oxidase; PDBTitle: the l-amino acid oxidase from rhodococcus opacus in complex2 with l-alanine
98	d1ml4a2	Alignment	not modelled	61.9	14	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
99	clzx9A_	Alignment	not modelled	61.8	23	PDB header: oxidoreductase Chain: A: PDB Molecule: mercuric reductase; PDBTitle: crystal structure of tn501 mera
100	clf6mF_	Alignment	not modelled	61.2	17	PDB header: oxidoreductase Chain: F: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of a complex between thioredoxin2 reductase, thioredoxin, and the nadp+ analog, aadp+
101	d1duvg2	Alignment	not modelled	60.9	14	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
102	c3i3lA_	Alignment	not modelled	60.1	31	PDB header: hydrolase Chain: A: PDB Molecule: alkylhalidase cmls; PDBTitle: crystal structure of cmls, a flavin-dependent halogenase
103	clvdcA_	Alignment	not modelled	59.3	7	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dependent thioredoxin reductase; PDBTitle: structure of nadph dependent thioredoxin reductase
						PDB header: oxidoreductase

104	c2e1mA	Alignment	not modelled	59.1	24	Chain: A: PDB Molecule: l-glutamate oxidase; PDBTitle: crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
105	c1sezA	Alignment	not modelled	58.9	23	PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase, mitochondrial; PDBTitle: crystal structure of protoporphyrinogen ix oxidase
106	c1yvvB	Alignment	not modelled	58.5	19	PDB header: oxidoreductase Chain: B: PDB Molecule: amine oxidase, flavin-containing; PDBTitle: x-ray structurure of p. syringae q888a4 oxidoreductase at2 resolution 2.5a. northeast structural genomics consortium3 target psr10.
107	c2a87A	Alignment	not modelled	58.3	13	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of m. tuberculosis thioredoxin reductase
108	c2yg4B	Alignment	not modelled	58.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: putrescine oxidase; PDBTitle: structure-based redesign of cofactor binding in putrescine2 oxidase: wild type bound to putrescine
109	c2hkoA	Alignment	not modelled	57.6	29	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific histone demethylase 1; PDBTitle: crystal structure of lsd1
110	d1g6q1	Alignment	not modelled	57.6	27	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Arginine methyltransferase
111	c3ihmB	Alignment	not modelled	57.4	13	PDB header: oxidoreductase Chain: B: PDB Molecule: styrene monooxygenase a; PDBTitle: structure of the oxygenase component of a pseudomonas styrene2 monooxygenase
112	c2gk4A	Alignment	not modelled	57.3	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: the crystal structure of the dna/pantothenate metabolism flavoprotein2 from streptococcus pneumoniae
113	c3f8rD	Alignment	not modelled	57.1	10	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
114	d1neka2	Alignment	not modelled	56.7	11	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
115	d2naca2	Alignment	not modelled	56.6	15	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
116	c1ybaC	Alignment	not modelled	56.3	11	PDB header: oxidoreductase Chain: C: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: the active form of phosphoglycerate dehydrogenase
117	c2r6zA	Alignment	not modelled	56.0	26	PDB header: transferase Chain: A: PDB Molecule: upf0341 protein in rsp 3' region; PDBTitle: crystal structure of the sam-dependent methyltransferase2 ngo1261 from neisseria gonorrhoeae, northeast structural3 genomics consortium target ngr48
118	d2ivda1	Alignment	not modelled	55.8	26	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
119	c3ctyA	Alignment	not modelled	55.7	21	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of t. acidophilum thioredoxin reductase
120	c2g4rB	Alignment	not modelled	55.5	16	PDB header: biosynthetic protein Chain: B: PDB Molecule: molybdopterin biosynthesis mog protein; PDBTitle: anomalous substructure of moga