



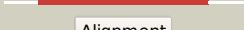

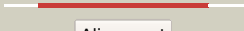









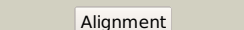

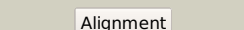

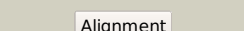

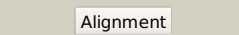

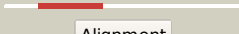















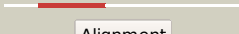
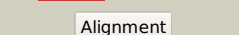
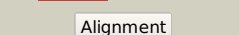







Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3272 (-)_3653445_3654629
Date	Thu Aug 8 16:20:48 BST 2019
Unique Job ID	7f287a16802571ee

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4ed9A_	 Alignment		100.0	32	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: caib/baif family protein; PDBTitle: crystal structure of a caib/baif family protein from brucella suis
2	c5yx6D_	 Alignment		100.0	100	PDB header: transferase Chain: D; PDB Molecule: uncharacterized protein rv3272; PDBTitle: crystal structure of rv3272 from m. tuberculosis orthorhombic form
3	c4hl6D_	 Alignment		100.0	29	PDB header: transferase Chain: D; PDB Molecule: uncharacterized protein yfde; PDBTitle: yfde from escherichia coli
4	c3ubmB_	 Alignment		100.0	28	PDB header: transferase Chain: B; PDB Molecule: formyl-coa:oxalate coa-transferase; PDBTitle: formyl-coa:oxalate coa-transferase from acetobacter aceti
5	d2vjma1	 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	d1xk7a1	 Alignment		100.0	20	Fold: CoA-transferase family III (CaiB/BaiF) Superfamily: CoA-transferase family III (CaiB/BaiF) Family: CoA-transferase family III (CaiB/BaiF)
7	c1xa3B_	 Alignment		100.0	21	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
8	d1q7ea_	 Alignment		100.0	25	Fold: CoA-transferase family III (CaiB/BaiF) Superfamily: CoA-transferase family III (CaiB/BaiF) Family: CoA-transferase family III (CaiB/BaiF)
9	d1x74a1	 Alignment		100.0	27	Fold: CoA-transferase family III (CaiB/BaiF) Superfamily: CoA-transferase family III (CaiB/BaiF) Family: CoA-transferase family III (CaiB/BaiF)
10	c2g04B_	 Alignment		100.0	30	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
11	c3p2yA_	 Alignment		94.7	17	PDB header: oxidoreductase Chain: A; PDB Molecule: alanine dehydrogenase/pyridine nucleotide transhydrogenase; PDBTitle: crystal structure of alanine dehydrogenase/pyridine nucleotide2 transhydrogenase from mycobacterium smegmatis

12	c3dhyC	 Alignment		94.6	20	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 and 3 inhibitors
13	c6ih2B	 Alignment		94.3	15	PDB header: oxidoreductase Chain: B; PDB Molecule: phosphite dehydrogenase; PDBTitle: crystal structure of phosphite dehydrogenase from ralstonia sp. 4506
14	c1v8bA	 Alignment		94.2	22	PDB header: hydrolase Chain: A; PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of a hydrolase
15	c2bruB	 Alignment		93.9	15	PDB header: oxidoreductase Chain: B; PDB Molecule: nad(p) transhydrogenase subunit alpha; PDBTitle: complex of the domain i and domain iii of escherichia coli 2 transhydrogenase
16	c5hm8C	 Alignment		93.9	22	PDB header: hydrolase Chain: C; PDB Molecule: adenosylhomocysteinase; PDBTitle: 2.85 angstrom crystal structure of s-adenosylhomocysteinase from 2 cryptosporidium parvum in complex with adenosine and nad.
17	c1pjcA	 Alignment		93.5	14	PDB header: oxidoreductase Chain: A; PDB Molecule: protein (l-alanine dehydrogenase); PDBTitle: l-alanine dehydrogenase complexed with nad
18	c4dioB	 Alignment		93.3	20	PDB header: oxidoreductase Chain: B; PDB Molecule: nad(p) transhydrogenase subunit alpha part 1; PDBTitle: the crystal structure of transhydrogenase from sinorhizobium mellioti
19	d1l7da1	 Alignment		93.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
20	c1l7eC	 Alignment		92.9	20	PDB header: oxidoreductase Chain: C; PDB Molecule: nicotinamide nucleotide transhydrogenase, PDBTitle: crystal structure of r. rubrum transhydrogenase domain i2 with bound nadh
21	c2rirA	 Alignment	not modelled	92.9	18	PDB header: oxidoreductase Chain: A; PDB Molecule: dipicolinate synthase, a chain; PDBTitle: crystal structure of dipicolinate synthase, a chain, from bacillus 2 subtilis
22	c6aphA	 Alignment	not modelled	92.9	18	PDB header: hydrolase Chain: A; PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of adenosylhomocysteinase from elizabethkingia 2 anophelis nuhp1 in complex with nad and adenosine
23	c2gcgB	 Alignment	not modelled	92.8	12	PDB header: oxidoreductase Chain: B; PDB Molecule: glyoxylate reductase/hydroxypyruvate reductase; PDBTitle: ternary crystal structure of human glyoxylate 2 reductase/hydroxypyruvate reductase
24	c4izhA	 Alignment	not modelled	92.6	20	PDB header: oxidoreductase Chain: A; PDB Molecule: nad/nadp transhydrogenase alpha subunit 1; PDBTitle: crystal structure of the alpha1 dimer of thermus thermophilus 2 transhydrogenase in p6
25	c3n58D	 Alignment	not modelled	92.5	25	PDB header: hydrolase Chain: D; PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from brucella 2 melitensis in ternary complex with nad and adenosine, orthorhombic 3 form
26	c4xa8A	 Alignment	not modelled	92.5	9	PDB header: oxidoreductase Chain: A; PDB Molecule: d-isomer specific 2-hydroxyacid dehydrogenase nad-binding; PDBTitle: crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase 2 from xanthobacter autotrophicus py2
27	c3d4oA	 Alignment	not modelled	92.4	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
		 Alignment				PDB header: oxidoreductase Chain: D; PDB Molecule: 2-hydroxyacid dehydrogenase;

28	c5j23D_	Alignment	not modelled	92.3	17	PDBTitle: crystal structure of nadph-dependent glyoxylate/hydroxypyruvate2 reductase smc04462 (smghrb) from sinorhizobium meliloti in complex3 with 2'-phospho- <small>adp-ribose</small>
29	c3gvpB_	Alignment	not modelled	92.3	18	PDB header: hydrolase Chain: B: PDB Molecule: adenosylhomocysteinase 3; PDBTitle: human sahh-like domain of human adenosylhomocysteinase 3
30	d2naca1	Alignment	not modelled	92.2	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
31	c1wwkA_	Alignment	not modelled	92.1	14	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoglycerate dehydrogenase; PDBTitle: crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
32	c3kboB_	Alignment	not modelled	92.0	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
33	c3d64A_	Alignment	not modelled	91.9	24	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
34	d1m1na_	Alignment	not modelled	91.9	19	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
35	c1gdhA_	Alignment	not modelled	91.8	7	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
36	d2dda1	Alignment	not modelled	91.8	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
37	c1d4fD_	Alignment	not modelled	91.5	19	PDB header: hydrolase Chain: D: PDB Molecule: s-adenosylhomocysteine hydrolase; PDBTitle: crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
38	d1gdha1	Alignment	not modelled	91.5	9	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
39	c3gvxA_	Alignment	not modelled	91.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerate dehydrogenase related protein; PDBTitle: crystal structure of glycerate dehydrogenase related2 protein from thermoplasma acidophilum
40	c3x2fA_	Alignment	not modelled	91.4	23	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: a thermophilic s-adenosylhomocysteine hydrolase
41	c6f3oC_	Alignment	not modelled	91.4	19	PDB header: hydrolase Chain: C: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 pseudomonas aeruginosa complexed with adenine, k+ and zn2+ cations
42	c4cukA_	Alignment	not modelled	91.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: structure of salmonella d-lactate dehydrogenase in complex2 with nadh
43	c1luaA_	Alignment	not modelled	91.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: methylene tetrahydromethanopterin dehydrogenase; PDBTitle: structure of methylene-tetrahydromethanopterin dehydrogenase from2 methylobacterium extorquens am1 complexed with nadp
44	c3wnvA_	Alignment	not modelled	90.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: glyoxylate reductase; PDBTitle: crystal structure of a glyoxylate reductase from paecilomyces2 thermophila
45	d1ygya1	Alignment	not modelled	90.6	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
46	c4zqsE_	Alignment	not modelled	90.6	11	PDB header: oxidoreductase Chain: E: PDB Molecule: putative d-lactate dehydrogenase; PDBTitle: identification of the pyruvate reductase of chlamydomonas reinhardtii
47	c3oneA_	Alignment	not modelled	90.5	23	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
48	c2pi1C_	Alignment	not modelled	90.2	11	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
49	c2g76A_	Alignment	not modelled	90.1	8	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of human 3-phosphoglycerate dehydrogenase
50	d1pjca1	Alignment	not modelled	90.0	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
51	c4n18A_	Alignment	not modelled	89.9	12	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 klebsiella pneumoniae 342
52	d1li4a1	Alignment	not modelled	89.7	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
						PDB header: oxidoreductase

53	c4xdyB_	Alignment	not modelled	89.7	15	Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: structure of nadh-preferring ketol-acid reductoisomerase from an2 uncultured archaean
54	c3evtA_	Alignment	not modelled	89.5	18	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoglycerate dehydrogenase; PDBTitle: crystal structure of phosphoglycerate dehydrogenase from lactobacillus2 plantarum
55	c3hg7A_	Alignment	not modelled	89.4	19	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
56	c4g2nA_	Alignment	not modelled	89.1	19	PDB header: oxidoreductase Chain: A: PDB Molecule: d-isomer specific 2-hydroxyacid dehydrogenase, nad-binding; PDBTitle: crystal structure of putative d-isomer specific 2-hydroxyacid2 dehydrogenase, nad-binding from polaromonas sp. js6 66
57	c2omeA_	Alignment	not modelled	89.1	14	PDB header: oxidoreductase Chain: A: PDB Molecule: c-terminal-binding protein 2; PDBTitle: crystal structure of human ctbp2 dehydrogenase complexed with nad(h)
58	d1qp8a1	Alignment	not modelled	89.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
59	c5v96A_	Alignment	not modelled	88.8	23	PDB header: hydrolase Chain: A: PDB Molecule: s-adenosyl-l-homocysteine hydrolase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 naegleria fowleri with bound nad and adenosine
60	c3wwzB_	Alignment	not modelled	88.6	14	PDB header: oxidoreductase Chain: B: PDB Molecule: d-lactate dehydrogenase (fermentative); PDBTitle: the crystal structure of d-lactate dehydrogenase from pseudomonas2 aeruginosa
61	c2eezG_	Alignment	not modelled	88.4	17	PDB header: oxidoreductase Chain: G: PDB Molecule: alanine dehydrogenase; PDBTitle: crystal structure of alanine dehydrogenase from themus thermophilus
62	c4weqA_	Alignment	not modelled	88.1	13	PDB header: oxidoreductase Chain: A: PDB Molecule: nad-dependent dehydrogenase; PDBTitle: crystal structure of nadph-dependent glyoxylate/hydroxypyruvate2 reductase smc02828 (smghra) from sinorhizobium melloti in complex3 with nadp and sulfate
63	c2eklA_	Alignment	not modelled	88.1	15	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: structure of st1218 protein from sulfolobus tokodaii
64	d1dxya1	Alignment	not modelled	87.9	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
65	c4prkB_	Alignment	not modelled	87.9	12	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-phosphoerythronate dehydrogenase; PDBTitle: crystal structure of d-lactate dehydrogenase (d-ldh) from2 lactobacillus jensenii
66	c3bazA_	Alignment	not modelled	87.9	10	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyphenylpyruvate reductase; PDBTitle: structure of hydroxyphenylpyruvate reductase from coleus blumei in2 complex with nadp+
67	d1mx3a1	Alignment	not modelled	87.7	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
68	c4njmA_	Alignment	not modelled	87.5	11	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase, putative; PDBTitle: crystal structure of phosphoglycerate bound 3-phosphoglycerate2 dehydrogenase in entamoeba histolytica
69	c4zqbB_	Alignment	not modelled	86.8	15	PDB header: oxidoreductase Chain: B: PDB Molecule: nadp-dependent dehydrogenase; PDBTitle: crystal structure of nadp-dependent dehydrogenase from2 rhodobactersphaeroides in complex with nadp and sulfate
70	d1j4aa1	Alignment	not modelled	86.7	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
71	c5mh5A_	Alignment	not modelled	86.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: d-2-hydroxyacid dehydrogenase; PDBTitle: d-2-hydroxyacid dehydrogenases (d2-hdh) from haloferax mediterranei in2 complex with 2-keto-hexanoic acid and nadp+ (1.4 a resolution)
72	c4xkjA_	Alignment	not modelled	86.2	17	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: a novel d-lactate dehydrogenase from sporolactobacillus sp
73	d1qh8a_	Alignment	not modelled	86.2	19	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
74	c2vhyB_	Alignment	not modelled	86.0	14	PDB header: oxidoreductase Chain: B: PDB Molecule: alanine dehydrogenase; PDBTitle: crystal structure of apo l-alanine dehydrogenase from mycobacterium2 tuberculosis
75	c3n7uD_	Alignment	not modelled	85.9	11	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
76	c1xdwA_	Alignment	not modelled	85.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: nad+-dependent (r)-2-hydroxyglutarate PDBTitle: nad+-dependent (r)-2-hydroxyglutarate dehydrogenase from2 acidaminococcus fermentans
77	d1pg5a2	Alignment	not modelled	85.6	12	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase

						Family: Aspartate/ornithine carbamoyltransferase
78	c4lswA	Alignment	not modelled	85.4	15	PDB header: hydrolase Chain: A: PDB Molecule: d-2-hydroxyacid dehydrogenase protein; PDBTitle: crystallization and structural analysis of 2-hydroxyacid dehydrogenase2 from ketogulonigenium vulgare y25
79	c4ypoB	Alignment	not modelled	85.2	19	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of mycobacterium tuberculosis ketol-acid2 reductoisomerase in complex with mg2+
80	c2dbqA	Alignment	not modelled	85.1	14	PDB header: oxidoreductase Chain: A: PDB Molecule: glyoxylate reductase; PDBTitle: crystal structure of glyoxylate reductase (ph0597) from pyrococcus2 horikoshii ot3, complexed with nadp (i41)
81	d1np3a2	Alignment	not modelled	84.5	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
82	c4s1vD	Alignment	not modelled	84.5	17	PDB header: oxidoreductase Chain: D: PDB Molecule: d-3-phosphoglycerate dehydrogenase-related protein; PDBTitle: crystal structure of phosphoglycerate oxidoreductase from vibrio2 cholerae o395
83	c2cukC	Alignment	not modelled	84.3	17	PDB header: oxidoreductase Chain: C: PDB Molecule: glycerate dehydrogenase/glyoxylate reductase; PDBTitle: crystal structure of tt0316 protein from thermus thermophilus hb8
84	d1to3a	Alignment	not modelled	84.0	45	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
85	d1v8ba1	Alignment	not modelled	83.7	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
86	c3wwyA	Alignment	not modelled	83.7	12	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: the crystal structure of d-lactate dehydrogenase from fusobacterium2 nucleatum subsp. nucleatum
87	c2j6iC	Alignment	not modelled	83.3	13	PDB header: oxidoreductase Chain: C: PDB Molecule: formate dehydrogenase; PDBTitle: candida boidinii formate dehydrogenase (fdh) c-terminal mutant
88	c1j4aA	Alignment	not modelled	82.8	12	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
89	c4kqxB	Alignment	not modelled	81.6	19	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: mutant slackia exigua kari ddv in complex with nad and an inhibitor
90	d1sc6a1	Alignment	not modelled	81.6	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
91	c4xdzB	Alignment	not modelled	81.1	13	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: holo structure of ketol-acid reductoisomerase from ignisphaera2 aggregans
92	c3pdiG	Alignment	not modelled	81.0	28	PDB header: protein binding Chain: G: PDB Molecule: nitrogenase mofe cofactor biosynthesis protein nife; PDBTitle: precursor bound nifen
93	c4hy3D	Alignment	not modelled	80.8	14	PDB header: oxidoreductase Chain: D: PDB Molecule: phosphoglycerate oxidoreductase; PDBTitle: crystal structure of a phosphoglycerate oxidoreductase from rhizobium2 etli
94	d1vlva2	Alignment	not modelled	80.1	17	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
95	c3gg9C	Alignment	not modelled	80.0	16	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
96	c2yq4C	Alignment	not modelled	79.8	13	PDB header: oxidoreductase Chain: C: PDB Molecule: d-isomer specific 2-hydroxyacid dehydrogenase; PDBTitle: crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 from lactobacillus delbrueckii ssp. bulgaricus
97	c1np3B	Alignment	not modelled	79.8	21	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of class i acetoxy acid isomerase/reductase from2 pseudomonas aeruginosa
98	c1dxyA	Alignment	not modelled	79.5	15	PDB header: oxidoreductase Chain: A: PDB Molecule: d-2-hydroxyisocaproate dehydrogenase; PDBTitle: structure of d-2-hydroxyisocaproate dehydrogenase
99	c6p2iA	Alignment	not modelled	78.5	11	PDB header: oxidoreductase, biosynthetic protein Chain: A: PDB Molecule: glycerate dehydrogenase; PDBTitle: acyclic imino acid reductase (bsp5) in complex with nadph and d-arg
100	c5n6yD	Alignment	not modelled	78.3	15	PDB header: oxidoreductase Chain: D: PDB Molecule: nitrogenase vanadium-iron protein alpha chain; PDBTitle: azotobacter vinelandii vanadium nitrogenase
101	d1ekxa2	Alignment	not modelled	77.2	17	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
102	d1b0aa1	Alignment	not modelled	75.9	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain

103	c1qp8A_	Alignment	not modelled	75.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: formate dehydrogenase; PDBTitle: crystal structure of a putative formate dehydrogenase from2 pyrobaculum aerophilum
104	c4mozC_	Alignment	not modelled	75.5	36	PDB header: lyase Chain: C: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: fructose-bisphosphate aldolase from slackia heliotrinireducens dsm2 20476
105	c4qjiB_	Alignment	not modelled	74.7	21	PDB header: ligase Chain: B: PDB Molecule: phosphopantothenate--cysteine ligase; PDBTitle: crystal structure of the c-terminal ctp-binding domain of a2 phosphopantothenylcysteine decarboxylase/phosphopantothenate-3 cysteine ligase with bound ctp from mycobacterium smegmatis
106	c2p2gD_	Alignment	not modelled	73.7	23	PDB header: transferase Chain: D: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
107	c4tskA_	Alignment	not modelled	73.5	20	PDB header: oxidoreductase,isomerase Chain: A: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: ketol-acid reductoisomerase from alicyclobacillus acidocaldarius
108	c5tueB_	Alignment	not modelled	73.1	26	PDB header: oxidoreductase Chain: B: PDB Molecule: tetracycline destructase tet(50); PDBTitle: crystal structure of tetracycline destructase tet(50)
109	c5evyX_	Alignment	not modelled	72.6	22	PDB header: oxidoreductase Chain: X: PDB Molecule: salicylate hydroxylase; PDBTitle: salicylate hydroxylase substrate complex
110	c6aqjB_	Alignment	not modelled	72.3	18	PDB header: isomerase Chain: B: PDB Molecule: ketol-acid reductoisomerase (nadp(+)); PDBTitle: crystal structures of staphylococcus aureus ketol-acid2 reductoisomerase in complex with two transition state analogs that have biocidal activity.
111	c4xcvA_	Alignment	not modelled	71.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: nadp-dependent 2-hydroxyacid dehydrogenase; PDBTitle: probable 2-hydroxyacid dehydrogenase from rhizobium etli cfn 42 in2 complex with nadph
112	d1c1da1	Alignment	not modelled	71.6	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
113	c5tx7A_	Alignment	not modelled	71.5	18	PDB header: oxidoreductase Chain: A: PDB Molecule: d-isomer specific 2-hydroxyacid dehydrogenase family PDBTitle: crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 from desulfovibrio vulgaris
114	c2vouA_	Alignment	not modelled	71.4	27	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,6-dihydroxypyridine hydroxylase; PDBTitle: structure of 2,6-dihydroxypyridine-3-hydroxylase from2 arthrobacter nicotinovorans
115	d1a4ia1	Alignment	not modelled	71.1	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
116	c6bz5B_	Alignment	not modelled	70.8	22	PDB header: oxidoreductase Chain: B: PDB Molecule: salicylate hydroxylase; PDBTitle: structure and mechanism of salicylate hydroxylase from pseudomonas2 putida g7
117	c1a4iB_	Alignment	not modelled	70.3	13	PDB header: oxidoreductase Chain: B: PDB Molecule: methylenetetrahydrofolate dehydrogenase / PDBTitle: human tetrahydrofolate dehydrogenase / cyclohydrolase
118	c2vdcl_	Alignment	not modelled	69.0	21	PDB header: oxidoreductase Chain: I: PDB Molecule: glutamate synthase [nadph] small chain; PDBTitle: the 9.5 a resolution structure of glutamate synthase from cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications.
119	c5eowA_	Alignment	not modelled	68.9	20	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-hydroxynicotinate 3-monooxygenase; PDBTitle: crystal structure of 6-hydroxynicotinic acid 3-monooxygenase from2 pseudomonas putida kt2440
120	c4euhA_	Alignment	not modelled	68.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: putative reductase ca_c0462; PDBTitle: crystal structure of clostridium acetobutlicum trans-2-enoyl-coa2 reductase apo form