

























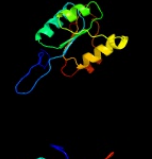
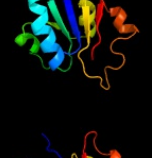

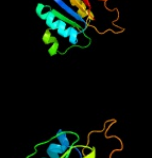
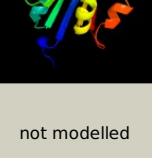


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1866 (-)_2113147_2115483
Date	Fri Aug 2 13:30:48 BST 2019
Unique Job ID	5a82a164ae8d3be0

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ubmB_	 Alignment		100.0	24	PDB header: transferase Chain: B; PDB Molecule: formyl-coa:oxalate coa-transferase; PDBTitle: formyl-coa:oxalate coa-transferase from acetobacter aceti
2	d2vjma1	 Alignment		100.0	22	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	21	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	22	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	d1q7ea_	 Alignment		100.0	22	Fold: CoA-transferase family III (CaiB/BaiF) Superfamily: CoA-transferase family III (CaiB/BaiF) Family: CoA-transferase family III (CaiB/BaiF)
6	c4ed9A_	 Alignment		100.0	29	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
7	c4hl6D_	 Alignment		100.0	26	PDB header: transferase Chain: D; PDB Molecule: uncharacterized protein yfde; PDBTitle: yfde from escherichia coli
8	c5yx6D_	 Alignment		100.0	29	PDB header: transferase Chain: D; PDB Molecule: uncharacterized protein rv3272; PDBTitle: crystal structure of rv3272 from m. tuberculosis orthorhombic form
9	d1x74a1	 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)
10	c2g04B_	 Alignment		100.0	20	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		94.3	16	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	c2bruB	Alignment		94.0	16	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
13	c6ih2B	Alignment		93.3	11	PDB header: oxidoreductase Chain: B; PDB Molecule: phosphite dehydrogenase; PDBTitle: crystal structure of phosphite dehydrogenase from ralstonia sp. 4506
14	c1wwkA	Alignment		93.1	18	PDB header: oxidoreductase Chain: A; PDB Molecule: phosphoglycerate dehydrogenase; PDBTitle: crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
15	c4dioB	Alignment		92.7	20	PDB header: oxidoreductase Chain: B; PDB Molecule: nad(p) transhydrogenase subunit alpha part 1; PDBTitle: the crystal structure of transhydrogenase from sinorhizobium melloti
16	d1l7da1	Alignment		92.7	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
17	c2omeA	Alignment		92.6	15	PDB header: oxidoreductase Chain: A; PDB Molecule: c-terminal-binding protein 2; PDBTitle: crystal structure of human ctbp2 dehydrogenase complexed with nad(h)
18	c1pjcA	Alignment		92.2	20	PDB header: oxidoreductase Chain: A; PDB Molecule: protein (l-alanine dehydrogenase); PDBTitle: l-alanine dehydrogenase complexed with nad
19	d1gdha1	Alignment		92.0	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
20	c4xa8A	Alignment		92.0	16	PDB header: oxidoreductase Chain: A; PDB Molecule: d-isomer specific 2-hydroxyacid dehydrogenase nad-binding; PDBTitle: crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 from xanthobacter autotrophicus py2
21	c4izhA	Alignment	not modelled	91.8	17	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
22	d1pg5a2	Alignment	not modelled	90.9	15	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
23	d2naca1	Alignment	not modelled	90.9	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
24	c3dhyC	Alignment	not modelled	90.8	16	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
25	c1l7eC	Alignment	not modelled	90.6	16	PDB header: oxidoreductase Chain: C; PDB Molecule: nicotinamide nucleotide transhydrogenase, PDBTitle: crystal structure of r. rubrum transhydrogenase domain i2 with bound nadh
26	c3kboB	Alignment	not modelled	90.2	12	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
27	c3gvxA	Alignment	not modelled	89.7	18	PDB header: oxidoreductase Chain: A; PDB Molecule: glycerate dehydrogenase related protein; PDBTitle: crystal structure of glycerate dehydrogenase related2 protein from thermoplasma acidophilum PDB header: hydrolase

28	c5hm8C	Alignment	not modelled	89.7	17	Chain: C: PDB Molecule: adenosylhomocysteinase; PDBTitle: 2.85 angstrom crystal structure of s-adenosylhomocysteinase from2 cryptosporidium parvum in complex with adenosine and nad.
29	c3bazA	Alignment	not modelled	89.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyphenylpyruvate reductase; PDBTitle: structure of hydroxyphenylpyruvate reductase from coleus blumei in2 complex with nadp+
30	c4g2nA	Alignment	not modelled	89.5	14	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
31	d1qp8a1	Alignment	not modelled	89.4	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
32	d1j4aa1	Alignment	not modelled	89.4	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
33	c3hg7A	Alignment	not modelled	88.8	17	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
34	c1luaA	Alignment	not modelled	88.6	18	PDB header: oxidoreductase Chain: A: PDB Molecule: methylene tetrahydromethanopterin dehydrogenase; PDBTitle: structure of methylene-tetrahydromethanopterin dehydrogenase from2 methylobacterium extorquens am1 complexed with nadp
35	d1m1na	Alignment	not modelled	88.5	19	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
36	c5j23D	Alignment	not modelled	88.5	17	PDB header: oxidoreductase Chain: D: PDB Molecule: 2-hydroxyacid dehydrogenase; PDBTitle: crystal structure of nadph-dependent glyoxylate/hydroxypyruvate2 reductase smc04462 (smghrb) from sinorhizobium meliloti in complex3 with 2'-phospho- <small>adp</small> -ribose
37	c1gdhA	Alignment	not modelled	88.4	9	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
38	c2g76A	Alignment	not modelled	88.3	14	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of human 3-phosphoglycerate dehydrogenase
39	d1pjca1	Alignment	not modelled	88.2	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
40	d1mx3a1	Alignment	not modelled	88.2	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
41	d1ygya1	Alignment	not modelled	88.2	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
42	c2rirA	Alignment	not modelled	88.1	21	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase, a chain; PDBTitle: crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
43	c3d64A	Alignment	not modelled	87.9	14	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
44	c2pi1C	Alignment	not modelled	87.6	14	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
45	c2gcgB	Alignment	not modelled	87.3	15	PDB header: oxidoreductase Chain: B: PDB Molecule: glyoxylate reductase/hydroxypyruvate reductase; PDBTitle: ternary crystal structure of human glyoxylate2 reductase/hydroxypyruvate reductase
46	d1vlva2	Alignment	not modelled	87.3	12	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
47	c2eezG	Alignment	not modelled	87.3	15	PDB header: oxidoreductase Chain: G: PDB Molecule: alanine dehydrogenase; PDBTitle: crystal structure of alanine dehydrogenase from thermophilus
48	c3oneA	Alignment	not modelled	87.2	18	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
49	d2dlda1	Alignment	not modelled	87.2	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
50	c2vhyB	Alignment	not modelled	87.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: alanine dehydrogenase; PDBTitle: crystal structure of apo l-alanine dehydrogenase from mycobacterium2 tuberculosis
51	c2cukC	Alignment	not modelled	86.8	20	PDB header: oxidoreductase Chain: C: PDB Molecule: glycerate dehydrogenase/glyoxylate reductase; PDBTitle: crystal structure of tt0316 protein from thermus thermophilus hb8

52	c3d4oA	Alignment	not modelled	86.6	20	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
53	c2dbqA	Alignment	not modelled	86.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: glyoxylate reductase; PDBTitle: crystal structure of glyoxylate reductase (ph0597) from pyrococcus2 horikoshii ot3, complexed with nadp (i41)
54	c1v8bA	Alignment	not modelled	86.5	14	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of a hydrolase
55	d1np3a2	Alignment	not modelled	86.4	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
56	d1l4a1	Alignment	not modelled	86.1	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
57	d1pvva2	Alignment	not modelled	85.9	13	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
58	c3wwyA	Alignment	not modelled	85.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: the crystal structure of d-lactate dehydrogenase from fusobacterium2 nucleatum subsp. nucleatum
59	c4cukA	Alignment	not modelled	85.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: structure of salmonella d-lactate dehydrogenase in complex2 with nadh
60	d1to3a	Alignment	not modelled	85.6	35	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
61	c4xdyB	Alignment	not modelled	85.4	15	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: structure of nadh-preferring ketol-acid reductoisomerase from an2 uncultured archaean
62	d1dxya1	Alignment	not modelled	85.3	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
63	c2eklA	Alignment	not modelled	85.1	16	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: structure of st1218 protein from sulfolobus tokodaii
64	d1ekxa2	Alignment	not modelled	85.0	13	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
65	c3wnvA	Alignment	not modelled	84.7	24	PDB header: oxidoreductase Chain: A: PDB Molecule: glyoxylate reductase; PDBTitle: crystal structure of a glyoxylate reductase from paecilomyces2 thermophila
66	c3evtA	Alignment	not modelled	84.5	20	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoglycerate dehydrogenase; PDBTitle: crystal structure of phosphoglycerate dehydrogenase from lactobacillus2 plantarum
67	c3gvpB	Alignment	not modelled	84.3	16	PDB header: hydrolase Chain: B: PDB Molecule: adenosylhomocysteinase 3; PDBTitle: human sahh-like domain of human adenosylhomocysteinase 3
68	c4zgsE	Alignment	not modelled	83.7	16	PDB header: oxidoreductase Chain: E: PDB Molecule: putative d-lactate dehydrogenase; PDBTitle: identification of the pyruvate reductase of chlamydomonas reinhardtii
69	c4qjB	Alignment	not modelled	83.7	10	PDB header: ligase Chain: B: PDB Molecule: phosphopantothenate--cysteine ligase; PDBTitle: crystal structure of the c-terminal ctp-binding domain of a2 phosphopantothenoylcysteine decarboxylase/phosphopantothenate-3 cysteine ligase with bound ctp from mycobacterium smegmatis
70	c6aphA	Alignment	not modelled	83.4	14	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of adenosylhomocysteinase from elizabethkingia2 anophelis nuhp1 in complex with nad and adenosine
71	c1a1sA	Alignment	not modelled	83.3	16	PDB header: transcarbamylase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: ornithine carbamoyltransferase from pyrococcus furiosus
72	d1dxha2	Alignment	not modelled	83.1	17	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
73	c2p2gD	Alignment	not modelled	82.9	12	PDB header: transferase Chain: D: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
74	c1np3B	Alignment	not modelled	82.7	15	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of class i acetohydroxy acid isomeroreductase from2 pseudomonas aeruginosa
75	c4weqA	Alignment	not modelled	82.7	15	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
76	c1xdwA	Alignment	not modelled	82.5	13	PDB header: oxidoreductase Chain: A: PDB Molecule: nad+-dependent (r)-2-hydroxyglutarate PDBTitle: nad+-dependent (r)-2-hydroxyglutarate dehydrogenase from2 acidaminococcus fermentans
77	c6f3oC	Alignment	not modelled	81.9	18	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
78	c4mozC	Alignment	not modelled	81.8	20	PDB header: lyase Chain: C: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: fructose-bisphosphate aldolase from slackia heliotrinireducens dsm2 20476
79	c4hy3D	Alignment	not modelled	81.8	20	PDB header: oxidoreductase Chain: D: PDB Molecule: phosphoglycerate oxidoreductase; PDBTitle: crystal structure of a phosphoglycerate oxidoreductase from rhizobium2 etli
80	c4njmA	Alignment	not modelled	81.7	9	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase, putative; PDBTitle: crystal structure of phosphoglycerate bound 3-phosphoglycerate2 dehydrogenase in entamoeba histolytica
81	c4n18A	Alignment	not modelled	81.5	14	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
82	c4tskA	Alignment	not modelled	80.7	27	PDB header: oxidoreductase, isomerase Chain: A: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: ketol-acid reductoisomerase from alicyclobacillus acidocaldarius
83	c5mh5A	Alignment	not modelled	80.2	17	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)
84	c3n7uD	Alignment	not modelled	79.7	13	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
85	c4zqbB	Alignment	not modelled	79.7	14	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
86	c4xkjA	Alignment	not modelled	79.3	26	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: a novel d-lactate dehydrogenase from sporolactobacillus sp
87	d1djqa2	Alignment	not modelled	79.0	19	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: C-terminal domain of adrenodoxin reductase-like
88	c3pdiG	Alignment	not modelled	78.2	25	PDB header: protein binding Chain: G: PDB Molecule: nitrogenase mofe cofactor biosynthesis protein nife; PDBTitle: precursor bound nifen
89	c5v96A	Alignment	not modelled	78.1	16	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
90	c2j6iC	Alignment	not modelled	78.1	18	PDB header: oxidoreductase Chain: C: PDB Molecule: formate dehydrogenase; PDBTitle: candida boidinii formate dehydrogenase (fdh) c-terminal mutant
91	c3wwzB	Alignment	not modelled	78.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: d-lactate dehydrogenase (fermentative); PDBTitle: the crystal structure of d-lactate dehydrogenase from pseudomonas2 aeruginosa
92	c6aqjB	Alignment	not modelled	77.8	16	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 that3 have biocidal activity.
93	d1u7za	Alignment	not modelled	77.0	18	Fold: Ribokinase-like Superfamily: CoaB-like Family: CoaB-like
94	d1v8ba1	Alignment	not modelled	76.8	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
95	c3n58D	Alignment	not modelled	76.8	13	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
96	c4prkB	Alignment	not modelled	76.5	16	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-phosphoerythronate dehydrogenase; PDBTitle: crystal structure of d-lactate dehydrogenase (d-ldh) from2 lactobacillus jensenii
97	c4lswA	Alignment	not modelled	76.4	22	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
98	d1ml4a2	Alignment	not modelled	76.4	14	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
99	c4s1vD	Alignment	not modelled	76.3	15	PDB header: oxidoreductase Chain: D: PDB Molecule: d-3-phosphoglycerate dehydrogenase-related protein; PDBTitle: crystal structure of phosphoglycerate oxidoreductase from vibrio2 cholerae o395
100	c1qp8A	Alignment	not modelled	76.1	19	PDB header: oxidoreductase Chain: A: PDB Molecule: formate dehydrogenase; PDBTitle: crystal structure of a putative formate dehydrogenase from2 pyrobaculum aerophilum
101	c1j4aA	Alignment	not modelled	75.6	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

102	d1sc6a1	Alignment	not modelled	75.5	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
103	c1d4fD	Alignment	not modelled	75.2	12	PDB header: hydrolase Chain: D: PDB Molecule: s-adenosylhomocysteine hydrolase; PDBTitle: crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
104	c5msuC	Alignment	not modelled	74.6	12	PDB header: oxidoreductase Chain: C: PDB Molecule: carboxylic acid reductase; PDBTitle: structure of the r domain of carboxylic acid reductase (car) from2 mycobacterium marinum in complex with nadp, p21 form
105	c1dxyA	Alignment	not modelled	74.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: d-2-hydroxyisocaproate dehydrogenase; PDBTitle: structure of d-2-hydroxyisocaproate dehydrogenase
106	c4ypoB	Alignment	not modelled	73.3	13	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of mycobacterium tuberculosis ketol-acid2 reductoisomerase in complex with mg2+
107	c6p2iA	Alignment	not modelled	73.1	18	PDB header: oxidoreductase, biosynthetic protein Chain: A: PDB Molecule: glycerate dehydrogenase; PDBTitle: acyclic imino acid reductase (bsp5) in complex with nadph and d-arg
108	c4kqxB	Alignment	not modelled	73.0	16	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
109	c4f2gA	Alignment	not modelled	72.6	9	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase 1; PDBTitle: the crystal structure of ornithine carbamoyltransferase from2 burkholderia thailandensis e264
110	c4e5kC	Alignment	not modelled	72.3	16	PDB header: oxidoreductase Chain: C: PDB Molecule: phosphite dehydrogenase (thermostable variant); PDBTitle: thermostable phosphite dehydrogenase in complex with nad and sulfite
111	c4xdzB	Alignment	not modelled	72.2	19	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: holo structure of ketol-acid reductoisomerase from ignisphaera2 aggregans
112	d1qh8a	Alignment	not modelled	70.3	25	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
113	c1u5tA	Alignment	not modelled	69.9	12	PDB header: transport protein Chain: A: PDB Molecule: appears to be functionally related to snf7; PDBTitle: structure of the escrt-ii endosomal trafficking complex
114	c3nlcA	Alignment	not modelled	69.1	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
115	c2qjhH	Alignment	not modelled	69.0	31	PDB header: lyase Chain: H: PDB Molecule: putative aldolase mj0400; PDBTitle: m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
116	c6bz5B	Alignment	not modelled	68.8	28	PDB header: oxidoreductase Chain: B: PDB Molecule: salicylate hydroxylase; PDBTitle: structure and mechanism of salicylate hydroxylase from pseudomonas2 putida g7
117	c3gg9C	Alignment	not modelled	68.5	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
118	c3bt7A	Alignment	not modelled	67.8	15	PDB header: transferase/rna Chain: A: PDB Molecule: trna (uracil-5-)-methyltransferase; PDBTitle: structure of e. coli 5-methyluridine methyltransferase trna in complex2 with 19 nucleotide t-arm analogue
119	c3fn4A	Alignment	not modelled	67.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: nad-dependent formate dehydrogenase; PDBTitle: apo-form of nad-dependent formate dehydrogenase from bacterium2 moraxella sp.c-1 in closed conformation
120	d1b0aa1	Alignment	not modelled	66.6	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain