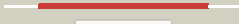



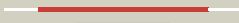










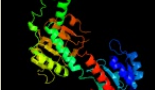








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0728c_(serA2)_820499_821479
Date	Fri Jul 26 01:50:30 BST 2019
Unique Job ID	a2129c17c4c4fbda

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ygyA_	 Alignment		100.0	37	PDB header: oxidoreductase Chain: A; PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of d-3-phosphoglycerate dehydrogenase from <i>Mycobacterium tuberculosis</i>
2	c2d0iC_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: C; PDB Molecule: dehydrogenase; PDBTitle: crystal structure of d-3-phosphoglycerate dehydrogenase from <i>Pyrococcus horikoshii</i> OT3
3	c2dbqA_	 Alignment		100.0	34	PDB header: oxidoreductase Chain: A; PDB Molecule: glyoxylate reductase; PDBTitle: crystal structure of glyoxylate reductase (ph0597) from <i>Pyrococcus horikoshii</i> OT3, complexed with NADP (i41)
4	c1ybaC_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: C; PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: the active form of phosphoglycerate dehydrogenase
5	c1gdhA_	 Alignment		100.0	27	PDB header: oxidoreductase (choh (d)-nad(p)+ (a)) Chain: A; PDB Molecule: d-glycerate dehydrogenase; PDBTitle: crystal structure of a nad-dependent d-glycerate 2 dehydrogenase at 2.4 angstroms resolution
6	c4e5kC_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: C; PDB Molecule: phosphite dehydrogenase (thermostable variant); PDBTitle: thermostable phosphite dehydrogenase in complex with nad and sulfite
7	c4g2nA_	 Alignment		100.0	31	PDB header: oxidoreductase Chain: A; PDB Molecule: d-isomer specific 2-hydroxyacid dehydrogenase, nad-binding; PDBTitle: crystal structure of putative d-isomer specific 2-hydroxyacid 2 dehydrogenase, nad-binding from <i>Polaromonas</i> sp. js6 66
8	c4lswA_	 Alignment		100.0	26	PDB header: hydrolase Chain: A; PDB Molecule: d-2-hydroxyacid dehydrogenase protein; PDBTitle: crystallization and structural analysis of 2-hydroxyacid dehydrogenase 2 from <i>Ketogulonicigenium vulgare</i> y25
9	c6ih2B_	 Alignment		100.0	29	PDB header: oxidoreductase Chain: B; PDB Molecule: phosphite dehydrogenase; PDBTitle: crystal structure of phosphite dehydrogenase from <i>Ralstonia</i> sp. 4506
10	c2gcbB_	 Alignment		100.0	30	PDB header: oxidoreductase Chain: B; PDB Molecule: glyoxylate reductase/hydroxypyruvate reductase; PDBTitle: ternary crystal structure of human glyoxylate 2 reductase/hydroxypyruvate reductase
11	c2omeA_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: A; PDB Molecule: c-terminal-binding protein 2; PDBTitle: crystal structure of human ctbp2 dehydrogenase complexed with nad(h)

12	c5tx7A_	Alignment		100.0	31	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
13	c3k5pA_	Alignment		100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of amino acid-binding act: d-isomer specific 2-2 hydroxyacid dehydrogenase catalytic domain from brucella melitensis
14	c3n7uD_	Alignment		100.0	23	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
15	c3gg9C_	Alignment		100.0	27	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
16	c5j23D_	Alignment		100.0	29	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- adp-ribose
17	c2yq4C_	Alignment		100.0	29	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
18	c2cukC_	Alignment		100.0	39	PDB header: oxidoreductase Chain: C: PDB Molecule: glycerate dehydrogenase/glyoxylate reductase; PDBTitle: crystal structure of tt0316 protein from thermus thermophilus hb8
19	c3wnvA_	Alignment		100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: glyoxylate reductase; PDBTitle: crystal structure of a glyoxylate reductase from paecilomyces2 thermophila
20	c2w2kB_	Alignment		100.0	27	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.
21	c3bazA_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyphenylpyruvate reductase; PDBTitle: structure of hydroxyphenylpyruvate reductase from coleus blumei in2 complex with nadp+
22	c4xkjA_	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: a novel d-lactate dehydrogenase from sporolactobacillus sp
23	c3fn4A_	Alignment	not modelled	100.0	24	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
24	c3wwyA_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: the crystal structure of d-lactate dehydrogenase from fusobacterium2 nucleatum subsp. nucleatum
25	c1j4aA_	Alignment	not modelled	100.0	23	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
26	c4prkB_	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-phosphoerythronate dehydrogenase; PDBTitle: crystal structure of d-lactate dehydrogenase (d-ldh) from2 lactobacillus jensenii
27	c4xcvA_	Alignment	not modelled	100.0	24	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
28	c2g76A_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of human 3-phosphoglycerate dehydrogenase
						PDB header: oxidoreductase

29	c4zgsE_	Alignment	not modelled	100.0	28	Chain: E; PDB Molecule: putative d-lactate dehydrogenase; PDBTitle: identification of the pyruvate reductase of chlamydomonas reinhardtii
30	c3wwzB_	Alignment	not modelled	100.0	34	PDB header: oxidoreductase Chain: B; PDB Molecule: d-lactate dehydrogenase (fermentative); PDBTitle: the crystal structure of d-lactate dehydrogenase from pseudomonas2 aeruginosa
31	c2eklA_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: A; PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: structure of st1218 protein from sulfolobus tokodaii
32	c4cukA_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: A; PDB Molecule: d-lactate dehydrogenase; PDBTitle: structure of salmonella d-lactate dehydrogenase in complex2 with nadh
33	c1wwkA_	Alignment	not modelled	100.0	35	PDB header: oxidoreductase Chain: A; PDB Molecule: phosphoglycerate dehydrogenase; PDBTitle: crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
34	c2nacA_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase(aldehyde(d),nad+(a)) Chain: A; PDB Molecule: nad-dependent formate dehydrogenase; PDBTitle: high resolution structures of holo and apo formate dehydrogenase
35	c1dxvA_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A; PDB Molecule: d-2-hydroxyisocaproate dehydrogenase; PDBTitle: structure of d-2-hydroxyisocaproate dehydrogenase
36	c2j6iC_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: C; PDB Molecule: formate dehydrogenase; PDBTitle: candida boidinii formate dehydrogenase (fdh) c-terminal mutant
37	c3evtA_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A; PDB Molecule: phosphoglycerate dehydrogenase; PDBTitle: crystal structure of phosphoglycerate dehydrogenase from lactobacillus2 plantarum
38	c1xdwA_	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: A; PDB Molecule: nad+-dependent (r)-2-hydroxyglutarate PDBTitle: nad+-dependent (r)-2-hydroxyglutarate dehydrogenase from2 acidaminococcus fermentans
39	c2pi1C_	Alignment	not modelled	100.0	25	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
40	c1qp8A_	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: A; PDB Molecule: formate dehydrogenase; PDBTitle: crystal structure of a putative formate dehydrogenase from2 pyrobaculum aerophilum
41	c4zqbB_	Alignment	not modelled	100.0	24	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
42	c4n18A_	Alignment	not modelled	100.0	24	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
43	c4s1vD_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: D; PDB Molecule: d-3-phosphoglycerate dehydrogenase-related protein; PDBTitle: crystal structure of phosphoglycerate oxidoreductase from vibrio2 cholerae o395
44	c4weqA_	Alignment	not modelled	100.0	21	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
45	c5mh5A_	Alignment	not modelled	100.0	26	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)
46	c3hg7A_	Alignment	not modelled	100.0	20	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
47	c4njmA_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: A; PDB Molecule: d-3-phosphoglycerate dehydrogenase, putative; PDBTitle: crystal structure of phosphoglycerate bound 3-phosphoglycerate2 dehydrogenase in entamoeba histolytica
48	c4hy3D_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: D; PDB Molecule: phosphoglycerate oxidoreductase; PDBTitle: crystal structure of a phosphoglycerate oxidoreductase from rhizobium2 etli
49	c3kboB_	Alignment	not modelled	100.0	21	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
50	c4xa8A_	Alignment	not modelled	100.0	23	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
51	c3gvxA_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: A; PDB Molecule: glycerate dehydrogenase related protein; PDBTitle: crystal structure of glycerate dehydrogenase related2 protein from thermoplasma acidophilum
52	c2o4cB_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: B; PDB Molecule: erythronate-4-phosphate dehydrogenase; PDBTitle: crystal structure of d-erythronate-4-phosphate dehydrogenase complexed2 with nad

53	c5dt9A	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: erythronate-4-phosphate dehydrogenase; PDBTitle: crystal structure of a putative d-erythronate-4-phosphate2 dehydrogenase from vibrio cholerae
54	c4dgsA	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase; PDBTitle: the crystals structure of dehydrogenase from rhizobium meliloti
55	c3oetF	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: F: PDB Molecule: erythronate-4-phosphate dehydrogenase; PDBTitle: d-erythronate-4-phosphate dehydrogenase complexed with nad
56	d1mx3a1	Alignment	not modelled	100.0	33	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
57	d1vgya1	Alignment	not modelled	100.0	45	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
58	d1gdha1	Alignment	not modelled	100.0	33	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
59	d1j4aa1	Alignment	not modelled	100.0	30	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
60	d2naca1	Alignment	not modelled	100.0	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
61	d2dda1	Alignment	not modelled	100.0	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
62	d1dxya1	Alignment	not modelled	100.0	35	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
63	d1qp8a1	Alignment	not modelled	100.0	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
64	d1sc6a1	Alignment	not modelled	100.0	34	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
65	c1l7eC	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: C: PDB Molecule: nicotinamide nucleotide transhydrogenase, PDBTitle: crystal structure of r. rubrum transhydrogenase domain i2 with bound nadh
66	c6f3oC	Alignment	not modelled	100.0	17	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
67	c1pjca	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (l-alanine dehydrogenase); PDBTitle: l-alanine dehydrogenase complexed with nad
68	c2eezG	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: G: PDB Molecule: alanine dehydrogenase; PDBTitle: crystal structure of alanine dehydrogenase from thermophilus
69	c5v96A	Alignment	not modelled	100.0	18	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
70	c2brub	Alignment	not modelled	100.0	15	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
71	c2vhyB	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: alanine dehydrogenase; PDBTitle: crystal structure of apo l-alanine dehydrogenase from mycobacterium2 tuberculosis
72	c3gvpB	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: adenosylhomocysteinase 3; PDBTitle: human sahh-like domain of human adenosylhomocysteinase 3
73	d1v8ba1	Alignment	not modelled	100.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
74	c1d4fD	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: D: PDB Molecule: s-adenosylhomocysteine hydrolase; PDBTitle: crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
75	c4izhA	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: nad/nadp transhydrogenase alpha subunit 1; PDBTitle: crystal structure of the alpha1 dimer of thermophilus2 transhydrogenase in p6
76	c3dhyC	Alignment	not modelled	100.0	17	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
77	c5hm8C	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: C: PDB Molecule: adenosylhomocysteinase; PDBTitle: 2.85 angstrom crystal structure of s-adenosylhomocysteinase from2 cryptosporidium parvum in complex with adenosine and nad. PDB header: hydrolase

78	c3n58D	Alignment	not modelled	100.0	17	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
79	c3oneA	Alignment	not modelled	100.0	17	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
80	c6aphA	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of adenosylhomocysteinase from elizabethkingia2 anophelis nuhp1 in complex with nad and adenosine
81	c3p2yA	Alignment	not modelled	99.9	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
82	c1v8bA	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of a hydrolase
83	c3x2fA	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: a thermophilic s-adenosylhomocysteine hydrolase
84	c4dioB	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p) transhydrogenase subunit alpha part 1; PDBTitle: the crystal structure of transhydrogenase from sinorhizobium meliloti
85	d1vgya2	Alignment	not modelled	99.9	24	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
86	d1l4a1	Alignment	not modelled	99.9	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
87	d1leha1	Alignment	not modelled	99.9	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
88	d1sc6a2	Alignment	not modelled	99.9	16	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
89	c3d64A	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
90	d1np3a2	Alignment	not modelled	99.9	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
91	d1gdha2	Alignment	not modelled	99.9	17	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
92	c3d4oA	Alignment	not modelled	99.9	12	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
93	d1pjca1	Alignment	not modelled	99.9	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
94	c5uscB	Alignment	not modelled	99.9	11	PDB header: hydrolase Chain: B: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase tyra from bacillus2 anthracis in complex with nad and l-tyrosine
95	c2rirA	Alignment	not modelled	99.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase, a chain; PDBTitle: crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
96	d1dxya2	Alignment	not modelled	99.8	15	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
97	d1mx3a2	Alignment	not modelled	99.8	20	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
98	c5b37A	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: tryptophan dehydrogenase; PDBTitle: crystal structure of l-tryptophan dehydrogenase from nostoc2 punctiforme
99	d2naca2	Alignment	not modelled	99.7	13	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
100	d1j4aa2	Alignment	not modelled	99.7	9	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
101	c1lehB	Alignment	not modelled	99.7	13	PDB header: oxidoreductase Chain: B: PDB Molecule: leucine dehydrogenase; PDBTitle: leucine dehydrogenase from bacillus sphaericus

102	d1c1da1	Alignment	not modelled	99.6	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
103	d2dlda2	Alignment	not modelled	99.6	10	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
104	d1l7da1	Alignment	not modelled	99.6	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
105	c3oj0A_	Alignment	not modelled	99.4	19	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamyl-trna reductase; PDBTitle: crystal structure of glutamyl-trna reductase from thermoplasma2 volcanium (nucleotide binding domain)
106	c6aaqjB_	Alignment	not modelled	99.4	17	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.
107	c4ypoB_	Alignment	not modelled	99.4	19	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of mycobacterium tuberculosis ketol-acid2 reductoisomerase in complex with mg2+
108	c4kqxB_	Alignment	not modelled	99.3	24	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	c4tskA_	Alignment	not modelled	99.3	13	PDB header: oxidoreductase, isomerase Chain: A: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: ketol-acid reductoisomerase from alicyclobacillus acidocaldarius
110	d3cuma2	Alignment	not modelled	99.3	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
111	c4xdzB_	Alignment	not modelled	99.3	24	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: holo structure of ketol-acid reductoisomerase from ignisphaera2 aggregans
112	d2g5ca2	Alignment	not modelled	99.3	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
113	c5yeqB_	Alignment	not modelled	99.3	18	PDB header: isomerase Chain: B: PDB Molecule: ketol-acid reductoisomerase (nadp(+)); PDBTitle: the structure of sac-kari protein
114	c1np3B_	Alignment	not modelled	99.3	18	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of class i acetoxy acid isomerase from pseudomonas aeruginosa
115	c6jczL_	Alignment	not modelled	99.3	18	PDB header: isomerase Chain: L: PDB Molecule: putative ketol-acid reductoisomerase 2; PDBTitle: cryo-em structure of sulfobolus solfataricus ketol-acid2 reductoisomerase (sso-kari) in complex with mg2+, nadph, and cpd at3 ph7.5
116	d2f1ka2	Alignment	not modelled	99.2	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
117	d1v9la1	Alignment	not modelled	99.2	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
118	d1vpda2	Alignment	not modelled	99.2	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
119	c4xdyB_	Alignment	not modelled	99.2	18	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: structure of nadh-preferring ketol-acid reductoisomerase from an2 uncultured archean
120	c4gjbB_	Alignment	not modelled	99.2	13	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase nad-binding; PDBTitle: crystal structure of nad-binding 6-phosphogluconate dehydrogenase from2 dyadobacter fermentans