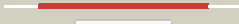
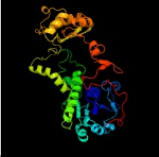

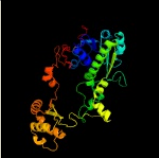
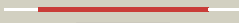








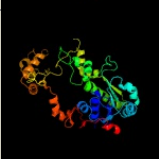





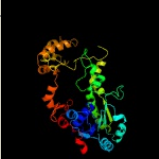


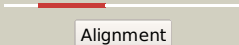













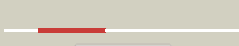




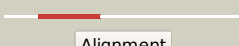
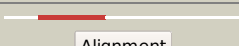

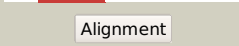
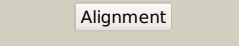




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0855_(far)_951635_952714
Date	Fri Jul 26 01:50:44 BST 2019
Unique Job ID	3483886e710fe137

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2g04B_	 Alignment		100.0	100	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
2	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
3	c4hl6D_	 Alignment		100.0	28	PDB header: transferase Chain: D; PDB Molecule: uncharacterized protein yfde; PDBTitle: yfde from escherichia coli
4	d1x74a1	 Alignment		100.0	58	Fold: CoA-transferase family III (CaiB/BaiF) Superfamily: CoA-transferase family III (CaiB/BaiF) Family: CoA-transferase family III (CaiB/BaiF)
5	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
6	d1xk7a1	 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)
7	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
8	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
9	d2vjma1	 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)
10	d1q7ea_	 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)
11	d1l7da1	 Alignment		96.5	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain

12	c3p2yA_	 Alignment		96.3	19	PDB header: oxidoreductase Chain: A: PDB Molecule: alanine dehydrogenase/pyridine nucleotide transhydrogenase; PDBTitle: crystal structure of alanine dehydrogenase/pyridine nucleotide2 transhydrogenase from mycobacterium smegmatis
13	c2bruB_	 Alignment		96.2	20	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
14	c2eezG_	 Alignment		95.9	17	PDB header: oxidoreductase Chain: G: PDB Molecule: alanine dehydrogenase; PDBTitle: crystal structure of alanine dehydrogenase from themus thermophilus
15	c117eC_	 Alignment		95.9	19	PDB header: oxidoreductase Chain: C: PDB Molecule: nicotinamide nucleotide transhydrogenase, PDBTitle: crystal structure of r. rubrum transhydrogenase domain i2 with bound nadh
16	c3dhyC_	 Alignment		95.6	18	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
17	c5hm8C_	 Alignment		95.5	19	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.
18	c1pjcA_	 Alignment		95.4	19	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (l-alanine dehydrogenase); PDBTitle: l-alanine dehydrogenase complexed with nad
19	c6ih2B_	 Alignment		95.2	17	PDB header: oxidoreductase Chain: B: PDB Molecule: phosphite dehydrogenase; PDBTitle: crystal structure of phosphite dehydrogenase from ralstonia sp. 4506
20	c4xa8A_	 Alignment		95.1	18	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	c4dioB_	 Alignment	not modelled	95.1	20	PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p) transhydrogenase subunit alpha part 1; PDBTitle: the crystal structure of transhydrogenase from sinorhizobium meliloti
22	c5j23D_	 Alignment	not modelled	94.9	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- adp-ribose
23	c3bazA_	 Alignment	not modelled	94.9	14	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyphenylpyruvate reductase; PDBTitle: structure of hydroxyphenylpyruvate reductase from coleus blumei in2 complex with nadp+
24	c4cukA_	 Alignment	not modelled	94.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: structure of salmonella d-lactate dehydrogenase in complex2 with nadh
25	c2vhyB_	 Alignment	not modelled	94.8	16	PDB header: oxidoreductase Chain: B: PDB Molecule: alanine dehydrogenase; PDBTitle: crystal structure of apo l-alanine dehydrogenase from mycobacterium2 tuberculosis
26	d1pjca1	 Alignment	not modelled	94.7	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
27	c4g2nA_	 Alignment	not modelled	94.5	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
		 Alignment				PDB header: oxidoreductase Chain: A: PDB Molecule: nad-dependent dehydrogenase;

28	c4wegA	Alignment	not modelled	94.4	19	PDBTitle: crystal structure of nadph-dependent glyoxylate/hydroxypyruvate2 reductase smc02828 (smghra) from sinorhizobium meliloti in complex3 with nadp and sulfate
29	c3gvxA	Alignment	not modelled	94.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerate dehydrogenase related protein; PDBTitle: crystal structure of glycerate dehydrogenase related2 protein from thermoplasma acidophilum
30	d2ldla1	Alignment	not modelled	94.4	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
31	c3x2fA	Alignment	not modelled	94.3	20	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: a thermophilic s-adenosylhomocysteine hydrolase
32	c3kboB	Alignment	not modelled	94.3	10	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	c3n58D	Alignment	not modelled	94.2	20	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
34	c3wnvA	Alignment	not modelled	94.2	21	PDB header: oxidoreductase Chain: A: PDB Molecule: glyoxylate reductase; PDBTitle: crystal structure of a glyoxylate reductase from paecilomyces2 thermophila
35	c3gvpB	Alignment	not modelled	94.1	14	PDB header: hydrolase Chain: B: PDB Molecule: adenosylhomocysteinase 3; PDBTitle: human sahh-like domain of human adenosylhomocysteinase 3
36	c2rirA	Alignment	not modelled	94.1	20	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase, a chain; PDBTitle: crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
37	c1v8bA	Alignment	not modelled	94.1	19	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of a hydrolase
38	c3oneA	Alignment	not modelled	94.0	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
39	c2gcbB	Alignment	not modelled	93.9	17	PDB header: oxidoreductase Chain: B: PDB Molecule: glyoxylate reductase/hydroxypyruvate reductase; PDBTitle: ternary crystal structure of human glyoxylate2 reductase/hydroxypyruvate reductase
40	c6aphA	Alignment	not modelled	93.8	16	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of adenosylhomocysteinase from elizabethkingia2 anophelis nuhp1 in complex with nad and adenosine
41	c4izhA	Alignment	not modelled	93.6	22	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
42	c4zgsE	Alignment	not modelled	93.5	16	PDB header: oxidoreductase Chain: E: PDB Molecule: putative d-lactate dehydrogenase; PDBTitle: identification of the pyruvate reductase of chlamydomonas reinhardtii
43	c1d4fD	Alignment	not modelled	93.5	15	PDB header: hydrolase Chain: D: PDB Molecule: s-adenosylhomocysteine hydrolase; PDBTitle: crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
44	c1gdhA	Alignment	not modelled	93.5	8	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
45	c3d64A	Alignment	not modelled	93.5	22	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
46	d2naca1	Alignment	not modelled	93.4	9	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
47	d1gdha1	Alignment	not modelled	93.4	9	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
48	d1li4a1	Alignment	not modelled	93.3	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
49	c4n18A	Alignment	not modelled	93.2	15	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
50	d1qp8a1	Alignment	not modelled	93.1	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
51	c3evtA	Alignment	not modelled	93.1	16	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoglycerate dehydrogenase; PDBTitle: crystal structure of phosphoglycerate dehydrogenase from lactobacillus2 plantarum
52	c4xdyB	Alignment	not modelled	93.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: structure of nadh-preferring ketol-acid reductoisomerase from an2 uncultured archaean PDB header: oxidoreductase

53	c2dbqA	Alignment	not modelled	92.9	11	Chain: A: PDB Molecule: glyoxylate reductase; PDBTitle: crystal structure of glyoxylate reductase (ph0597) from pyrococcus2 horikoshii ot3, complexed with nadp (i41)
54	c2pi1C	Alignment	not modelled	92.8	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
55	c5v96A	Alignment	not modelled	92.8	19	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
56	d1j4aa1	Alignment	not modelled	92.7	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
57	c6f3oC	Alignment	not modelled	92.7	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
58	c1wwkA	Alignment	not modelled	92.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoglycerate dehydrogenase; PDBTitle: crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
59	c1luaA	Alignment	not modelled	92.6	21	PDB header: oxidoreductase Chain: A: PDB Molecule: methylene tetrahydromethanopterin dehydrogenase; PDBTitle: structure of methylene-tetrahydromethanopterin dehydrogenase from2 methylobacterium extorquens am1 complexed with nadp
60	c4zqbB	Alignment	not modelled	92.3	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
61	d1ygya1	Alignment	not modelled	92.2	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
62	c3wwzB	Alignment	not modelled	92.1	20	PDB header: oxidoreductase Chain: B: PDB Molecule: d-lactate dehydrogenase (fermentative); PDBTitle: the crystal structure of d-lactate dehydrogenase from pseudomonas2 aeruginosa
63	c3d4oA	Alignment	not modelled	91.9	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
64	d1mx3a1	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
65	d1dxya1	Alignment	not modelled	91.8	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
66	c2eklA	Alignment	not modelled	91.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: structure of st1218 protein from sulfolobus tokodaii
67	c2g76A	Alignment	not modelled	91.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of human 3-phosphoglycerate dehydrogenase
68	c1j4aA	Alignment	not modelled	91.5	14	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
69	c3hg7A	Alignment	not modelled	91.4	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
70	d1np3a2	Alignment	not modelled	91.2	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
71	c2omeA	Alignment	not modelled	90.9	10	PDB header: oxidoreductase Chain: A: PDB Molecule: c-terminal-binding protein 2; PDBTitle: crystal structure of human ctbp2 dehydrogenase complexed with nad(h)
72	d1pg5a2	Alignment	not modelled	90.8	14	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
73	c5mh5A	Alignment	not modelled	90.8	20	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)
74	c1np3B	Alignment	not modelled	90.7	22	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of class i acetohydroxy acid isomeroreductase from2 pseudomonas aeruginosa
75	c4prkB	Alignment	not modelled	90.4	13	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-phosphoerythronate dehydrogenase; PDBTitle: crystal structure of d-lactate dehydrogenase (d-ldh) from2 lactobacillus jensenii
76	d1sc6a1	Alignment	not modelled	90.0	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
77	c4e5kC	Alignment	not modelled	89.8	19	PDB header: oxidoreductase Chain: C: PDB Molecule: phosphite dehydrogenase (thermostable variant); PDBTitle: thermostable phosphite dehydrogenase in complex with

						nad and sulfite
78	c2j6iC_	Alignment	not modelled	89.8	14	PDB header: oxidoreductase Chain: C: PDB Molecule: formate dehydrogenase; PDBTitle: candida boidinii formate dehydrogenase (fdh) c-terminal mutant
79	c3wwyA_	Alignment	not modelled	89.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: the crystal structure of d-lactate dehydrogenase from fusobacterium2 nucleatum subsp. nucleatum
80	c4xcvA_	Alignment	not modelled	89.2	19	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
81	c4lswA_	Alignment	not modelled	89.0	19	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
82	c2p2gD_	Alignment	not modelled	89.0	20	PDB header: transferase Chain: D: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
83	c5nngA_	Alignment	not modelled	88.9	13	PDB header: transferase Chain: A: PDB Molecule: ctatc; PDBTitle: aspartate transcarbamoylase from chaetomium thermophilum cad-like2 bound to carbamoyl phosphate
84	d1vlva2	Alignment	not modelled	88.7	18	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
85	c2cukC_	Alignment	not modelled	88.5	19	PDB header: oxidoreductase Chain: C: PDB Molecule: glycerate dehydrogenase/glyoxylate reductase; PDBTitle: crystal structure of tt0316 protein from thermus thermophilus hb8
86	d1v8ba1	Alignment	not modelled	88.5	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
87	c4njmA_	Alignment	not modelled	88.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase, putative; PDBTitle: crystal structure of phosphoglycerate bound 3-phosphoglycerate2 dehydrogenase in entamoeba histolytica
88	c4xdzB_	Alignment	not modelled	88.3	19	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: holo structure of ketol-acid reductoisomerase from ignisphaera2 aggregans
89	c4s1vD_	Alignment	not modelled	88.2	22	PDB header: oxidoreductase Chain: D: PDB Molecule: d-3-phosphoglycerate dehydrogenase-related protein; PDBTitle: crystal structure of phosphoglycerate oxidoreductase from vibrio2 cholerae o395
90	c1xdwA_	Alignment	not modelled	87.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: nad+-dependent (r)-2-hydroxyglutarate PDBTitle: nad+-dependent (r)-2-hydroxyglutarate dehydrogenase from2 acidaminococcus fermentans
91	c4xkjA_	Alignment	not modelled	87.3	20	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: a novel d-lactate dehydrogenase from sporolactobacillus sp
92	c1a1sA_	Alignment	not modelled	87.0	20	PDB header: transcarbamylase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: ornithine carbamoyltransferase from pyrococcus furiosus
93	d1to3a_	Alignment	not modelled	86.9	40	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
94	c4kqxB_	Alignment	not modelled	86.8	21	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
95	c4hy3D_	Alignment	not modelled	86.7	16	PDB header: oxidoreductase Chain: D: PDB Molecule: phosphoglycerate oxidoreductase; PDBTitle: crystal structure of a phosphoglycerate oxidoreductase from rhizobium2 etli
96	c6aqjB_	Alignment	not modelled	86.6	22	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.
97	c4mozC_	Alignment	not modelled	86.3	33	PDB header: lyase Chain: C: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: fructose-bisphosphate aldolase from slackia heliotrinireducens dsm2 20476
98	c3n7uD_	Alignment	not modelled	86.0	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
99	c5tx7A_	Alignment	not modelled	85.9	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 from desulfovibrio vulgaris
100	c4f2gA_	Alignment	not modelled	84.8	16	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase 1; PDBTitle: the crystal structure of ornithine carbamoyltransferase from2 burkholderia thailandensis e264
101	c1dxyA_	Alignment	not modelled	84.3	18	PDB header: oxidoreductase Chain: A: PDB Molecule: d-2-hydroxyisocaproate dehydrogenase; PDBTitle: structure of d-2-hydroxyisocaproate dehydrogenase
						PDB header: oxidoreductase

102	c3gg9C_	Alignment	not modelled	83.9	20	Chain: C: PDB Molecule: d-3-phosphoglycerate dehydrogenase oxidoreductase protein; PDBTitle: crystal structure of putative d-3-phosphoglycerate dehydrogenase2 oxidoreductase from ralstonia solanacearum
103	d1c1da1	Alignment	not modelled	83.8	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
104	c1e5IA_	Alignment	not modelled	83.4	22	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine reductase; PDBTitle: apo saccharopine reductase from magnaporthe grisea
105	c4ypoB_	Alignment	not modelled	83.3	26	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of mycobacterium tuberculosis ketol-acid2 reductoisomerase in complex with mg2+
106	c5xj2C_	Alignment	not modelled	82.9	15	PDB header: transferase/rna Chain: C: PDB Molecule: uncharacterized rna methyltransferase sp_1029; PDBTitle: structure of sprlmcid with u747 rna
107	c2yq4C_	Alignment	not modelled	82.2	10	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
108	d1ekxa2	Alignment	not modelled	82.0	13	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
109	c4tskA_	Alignment	not modelled	81.5	19	PDB header: oxidoreductase, isomerase Chain: A: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: ketol-acid reductoisomerase from alicyclobacillus acidocaldarius
110	c5tueB_	Alignment	not modelled	81.2	23	PDB header: oxidoreductase Chain: B: PDB Molecule: tetracycline destructase tet(50); PDBTitle: crystal structure of tetracycline destructase tet(50)
111	c2d0iC_	Alignment	not modelled	80.3	20	PDB header: oxidoreductase Chain: C: PDB Molecule: dehydrogenase; PDBTitle: crystal structure ph0520 protein from pyrococcus horikoshii ot3
112	c2ef0A_	Alignment	not modelled	79.9	24	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from thermus2 thermophilus
113	d2jfga1	Alignment	not modelled	79.2	16	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
114	c1v1vA_	Alignment	not modelled	79.2	19	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase (tm1097) from2 thermotoga maritima at 2.25 a resolution
115	c3oetF_	Alignment	not modelled	79.1	19	PDB header: oxidoreductase Chain: F: PDB Molecule: erythronate-4-phosphate dehydrogenase; PDBTitle: d-erythronate-4-phosphate dehydrogenase complexed with nad
116	d1luaa1	Alignment	not modelled	79.1	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
117	c2xagA_	Alignment	not modelled	79.0	42	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
118	c2v1dA_	Alignment	not modelled	79.0	42	PDB header: oxidoreductase/repressor Chain: A: PDB Molecule: lysine-specific histone demethylase 1; PDBTitle: structural basis of lsd1-corest selectivity in histone h32 recognition
119	c5I78A_	Alignment	not modelled	78.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-aminoadipic semialdehyde synthase, mitochondrial; PDBTitle: crystal structure of human aminoadipate semialdehyde synthase,2 saccharopine dehydrogenase domain (in nad+ bound form)
120	c2w2kB_	Alignment	not modelled	78.7	16	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.