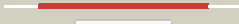



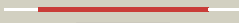








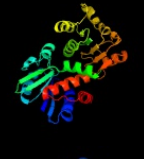



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2552c_aroE_2871216_2872025
Date	Wed Aug 7 12:50:19 BST 2019
Unique Job ID	15c032cfda6c089a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4xijA_	 Alignment		100.0	71	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of a shikimate 5-dehydrogenase from mycobacterium2 fortuitum determined by iodide sad phasing
2	c1vi2B_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate 5-dehydrogenase 2; PDBTitle: crystal structure of shikimate-5-dehydrogenase with nad
3	c1nvtA_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate 5'-dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase (aroE or2 mj1084) in complex with nadp+
4	c3tozA_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: 2.2 angstrom crystal structure of shikimate 5-dehydrogenase from2 listeria monocytogenes in complex with nad.
5	c2hk8B_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase from aquifex2 aeolicus at 2.35 angstrom resolution
6	c3pwzA_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase 3; PDBTitle: crystal structure of an ael1 enzyme from pseudomonas putida
7	c2ev9B_	 Alignment		100.0	31	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of shikimate 5-dehydrogenase (aroE) from thermus2 thermophilus hb8 in complex with nadp(h) and shikimate
8	c2eggA_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of shikimate 5-dehydrogenase (aroE) from geobacillus2 kaustophilus
9	c1nytC_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: C: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: shikimate dehydrogenase aroe complexed with nadp+
10	c4omuA_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase (aroE) from pseudomonas2 putida
11	c3o8qB_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate 5-dehydrogenase i alpha; PDBTitle: 1.45 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroE) from vibrio cholerae

12	c2nloA	Alignment		100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of the quinate dehydrogenase from corynebacterium2 glutamicum
13	c5swvC	Alignment		100.0	32	PDB header: lyase Chain: C: PDB Molecule: pentafunctional arom polypeptide; PDBTitle: dehydroquininate dehydratase and shikimate dehydrogenase from s. pombe2 arom
14	c3fbtB	Alignment		100.0	26	PDB header: oxidoreductase, lyase Chain: B: PDB Molecule: chorismate mutase and shikimate 5-dehydrogenase fusion PDBTitle: crystal structure of a chorismate mutase/shikimate 5-dehydrogenase2 fusion protein from clostridium acetobutylicum
15	c1p74B	Alignment		100.0	24	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase (aroe) from haemophilus2 influenzae
16	c2o7qA	Alignment		100.0	28	PDB header: oxidoreductase,transferase Chain: A: PDB Molecule: bifunctional 3-dehydroquininate dehydratase/shikimate PDBTitle: crystal structure of the a. thaliana dhq-dehydroshikimate-sdh-2 shikimate-nadp(h)
17	c5dzsA	Alignment		100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase (nadp(+)); PDBTitle: 1.5 angstrom crystal structure of shikimate dehydrogenase 1 from2 peptoclostridium difficile.
18	c1npyA	Alignment		100.0	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical shikimate 5-dehydrogenase-like protein hi0607; PDBTitle: structure of shikimate 5-dehydrogenase-like protein hi0607
19	c3donA	Alignment		100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase from staphylococcus2 epidermidis
20	c3tumA	Alignment		100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase family protein; PDBTitle: 2.15 angstrom resolution crystal structure of a shikimate2 dehydrogenase family protein from pseudomonas putida kt2440 in3 complex with nad+
21	c3pgjB	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate dehydrogenase; PDBTitle: 2.49 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae o1 biovar eltor str. n169613 in complex with shikimate
22	c3u62A	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase from thermotoga maritima
23	d1vi2a1	Alignment	not modelled	100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
24	d1nvtA1	Alignment	not modelled	100.0	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
25	d1npyA1	Alignment	not modelled	100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
26	d1nyta1	Alignment	not modelled	100.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
27	d1p77a1	Alignment	not modelled	100.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
28	d1vi2a2	Alignment	not modelled	100.0	33	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
						Fold: Aminoacid dehydrogenase-like, N-terminal domain

29	d1nvtA2	Alignment	not modelled	100.0	31	Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
30	d1p77a2	Alignment	not modelled	100.0	29	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
31	d1nyta2	Alignment	not modelled	100.0	36	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
32	d1npya2	Alignment	not modelled	100.0	26	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
33	c1luaA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: methylene tetrahydromethanopterin dehydrogenase; PDBTitle: structure of methylene-tetrahydromethanopterin dehydrogenase from2 methylobacterium extorquens am1 complexed with nadp
34	c1e5IA_	Alignment	not modelled	99.4	22	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine reductase; PDBTitle: apo saccharopine reductase from magnaporthe grisea
35	c2axqA_	Alignment	not modelled	99.4	23	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
36	d1luaa1	Alignment	not modelled	99.4	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
37	c1gpjA_	Alignment	not modelled	99.3	24	PDB header: reductase Chain: A: PDB Molecule: glutamyl-trna reductase; PDBTitle: glutamyl-trna reductase from methanopyrus kandleri
38	c4n7rB_	Alignment	not modelled	99.3	17	PDB header: oxidoreductase/protein binding Chain: B: PDB Molecule: glutamyl-trna reductase 1, chloroplastic; PDBTitle: crystal structure of arabidopsis glutamyl-trna reductase in complex2 with its binding protein
39	c5I78A_	Alignment	not modelled	99.2	21	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)
40	d1gpja2	Alignment	not modelled	99.2	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
41	c4mp6A_	Alignment	not modelled	99.2	13	PDB header: oxidoreductase Chain: A: PDB Molecule: putative ornithine cyclodeaminase; PDBTitle: staphyloferrin b precursor biosynthetic enzyme sbnb bound to citrate2 and nad+
42	c3oj0A_	Alignment	not modelled	99.1	13	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamyl-trna reductase; PDBTitle: crystal structure of glutamyl-trna reductase from thermoplasma2 volcanium (nucleotide binding domain)
43	c4rI6A_	Alignment	not modelled	99.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: crystal structure of the q04I03_strp2 protein from streptococcus2 pneumoniae. northeast structural genomics consortium target spr105
44	d1e5qa1	Alignment	not modelled	98.9	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
45	c2rirA_	Alignment	not modelled	98.9	25	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase, a chain; PDBTitle: crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
46	c5gzIB_	Alignment	not modelled	98.8	12	PDB header: lyase Chain: B: PDB Molecule: lysine cyclodeaminase; PDBTitle: cyclodeaminase_pa
47	c4a26B_	Alignment	not modelled	98.8	19	PDB header: oxidoreductase Chain: B: PDB Molecule: putative c-1-tetrahydrofolate synthase, cytoplasmic; PDBTitle: the crystal structure of leishmania major n5,n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase
48	c2i99A_	Alignment	not modelled	98.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: mu-crystallin homolog; PDBTitle: crystal structure of human mu_crystallin at 2.6 angstrom
49	d1x7da_	Alignment	not modelled	98.8	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Ornithine cyclodeaminase-like
50	c4a5oB_	Alignment	not modelled	98.8	22	PDB header: oxidoreductase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of pseudomonas aeruginosa n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
51	d1omoa_	Alignment	not modelled	98.7	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Ornithine cyclodeaminase-like
52	d1pjca1	Alignment	not modelled	98.7	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
53	c2eezG_	Alignment	not modelled	98.7	18	PDB header: oxidoreductase Chain: G: PDB Molecule: alanine dehydrogenase; PDBTitle: crystal structure of alanine dehydrogenase from themus thermophilus
54	c3d1aA_	Alignment	not modelled	98.7	27	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase subunit a;

54	c3u4vA	Alignment	not modelled	98.7	27	PDBTitle: crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution PDB header: oxidoreductase
55	c5tc4A	Alignment	not modelled	98.7	17	Chain: A: PDB Molecule: bifunctional methylenetetrahydrofolate PDBTitle: crystal structure of human mitochondrial methylenetetrahydrofolate2 dehydrogenase-cyclohydrolase (mthfd2) in complex with ly345899 and3 cofactors
56	c2z2vA	Alignment	not modelled	98.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein ph1688; PDBTitle: crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
57	c4inaA	Alignment	not modelled	98.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: crystal structure of the q7mss8_wolsu protein from wolinnella2 succinogenes. northeast structural genomics consortium target wsr35
58	c5nhsB	Alignment	not modelled	98.6	21	PDB header: oxidoreductase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: the crystal structure of xanthomonas albilineans n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
59	c3i07B	Alignment	not modelled	98.5	18	PDB header: oxidoreductase,hydrolase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella3 tularensis.
60	c1a4iB	Alignment	not modelled	98.5	18	PDB header: oxidoreductase Chain: B: PDB Molecule: methylenetetrahydrofolate dehydrogenase / PDBTitle: human tetrahydrofolate dehydrogenase / cyclohydrolase
61	c6apeA	Alignment	not modelled	98.5	19	PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of bifunctional protein fold from helicobacter2 pylori
62	d1b0aa1	Alignment	not modelled	98.4	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
63	c1b0aA	Alignment	not modelled	98.4	20	PDB header: oxidoreductase,hydrolase Chain: A: PDB Molecule: protein (fold bifunctional protein); PDBTitle: 5,10, methylene-tetrahydrofolate2 dehydrogenase/cyclohydrolase from e coli.
64	c2a9fB	Alignment	not modelled	98.4	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative malic enzyme ((s)-malate:nad+ oxidoreductase PDBTitle: crystal structure of a putative malic enzyme ((s)-malate:nad+2 oxidoreductase (decarboxylating))
65	d1a4ia1	Alignment	not modelled	98.3	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
66	d1i4a1	Alignment	not modelled	98.3	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
67	d1i7da1	Alignment	not modelled	98.3	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
68	c2vhyB	Alignment	not modelled	98.2	22	PDB header: oxidoreductase Chain: B: PDB Molecule: alanine dehydrogenase; PDBTitle: crystal structure of apo l-alanine dehydrogenase from mycobacterium2 tuberculosis
69	c3nglA	Alignment	not modelled	98.2	10	PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of bifunctional 5,10-methylenetetrahydrofolate2 dehydrogenase / cyclohydrolase from thermoplasma acidophilum
70	c3p2oB	Alignment	not modelled	98.1	15	PDB header: oxidoreductase, hydrolase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of fold bifunctional protein from campylobacter2 jejuni
71	c3p2oA	Alignment	not modelled	98.1	15	PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of fold bifunctional protein from campylobacter2 jejuni
72	c1pjca	Alignment	not modelled	98.1	22	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (l-alanine dehydrogenase); PDBTitle: l-alanine dehydrogenase complexed with nad
73	c4e21B	Alignment	not modelled	98.1	20	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase (decarboxylating); PDBTitle: the crystal structure of 6-phosphogluconate dehydrogenase from2 geobacter metallireducens
74	c2ph5A	Alignment	not modelled	98.1	16	PDB header: transferase Chain: A: PDB Molecule: homospermidine synthase; PDBTitle: crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54
75	c6fqzB	Alignment	not modelled	98.1	9	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: plasmodium falciparum 6-phosphogluconate dehydrogenase in its apo2 form, in complex with its cofactor nadp+ and in complex with its3 substrate 6-phosphogluconate
76	c3cumA	Alignment	not modelled	98.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
77	d1v8ba1	Alignment	not modelled	98.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain PDB header: oxidoreductase

78	c2f1kD_	Alignment	not modelled	98.0	15	Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of synechocystis arogenate dehydrogenase
79	c3ic5A_	Alignment	not modelled	98.0	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative saccharopine dehydrogenase; PDBTitle: n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
80	c3gt0A_	Alignment	not modelled	98.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: crystal structure of pyrroline 5-carboxylate reductase from bacillus2 cereus. northeast structural genomics consortium target bcr38b
81	c3hdiA_	Alignment	not modelled	98.0	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: probable ornithine cyclodeaminase; PDBTitle: the crystal structure of probable ornithine cyclodeaminase from2 bordetella pertussis tohama i
82	c3triB_	Alignment	not modelled	98.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: structure of a pyrroline-5-carboxylate reductase (proc) from coxiella2 burnetii
83	c2g5cD_	Alignment	not modelled	98.0	17	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from aquifex aeolicus
84	c1vpdA_	Alignment	not modelled	98.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: tartronate semialdehyde reductase; PDBTitle: x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2]
85	d2pgda2	Alignment	not modelled	98.0	9	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
86	c3x2fA_	Alignment	not modelled	98.0	23	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: a thermophilic s-adenosylhomocysteine hydrolase
87	c4plpB_	Alignment	not modelled	97.9	16	PDB header: transferase Chain: B: PDB Molecule: homospermidine synthase; PDBTitle: crystal structure of the homospermidine synthase (hss) from2 blastochloris viridis in complex with nad
88	c2ahrB_	Alignment	not modelled	97.9	10	PDB header: oxidoreductase Chain: B: PDB Molecule: putative pyrroline carboxylate reductase; PDBTitle: crystal structures of 1-pyrroline-5-carboxylate reductase from human2 pathogen streptococcus pyogenes
89	c4xdzB_	Alignment	not modelled	97.9	21	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: holo structure of ketol-acid reductoisomerase from ignisphaera2 aggregans
90	d3cuma2	Alignment	not modelled	97.9	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
91	c5t57A_	Alignment	not modelled	97.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: semialdehyde dehydrogenase nad-binding protein; PDBTitle: crystal structure of a semialdehyde dehydrogenase nad-binding protein2 from cupriavidus necator in complex with calcium and nad
92	c1v6C_	Alignment	not modelled	97.9	17	PDB header: oxidoreductase Chain: C: PDB Molecule: malate oxidoreductase; PDBTitle: crystal structure of nad-dependent malic enzyme (tm0542) from2 thermotoga maritima at 2.61 a resolution
93	c1pgiA_	Alignment	not modelled	97.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei
94	c4dlIB_	Alignment	not modelled	97.9	24	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-hydroxy-3-oxopropionate reductase; PDBTitle: crystal structure of a 2-hydroxy-3-oxopropionate reductase from2 polaromonas sp. js666
95	c4kqxB_	Alignment	not modelled	97.9	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
96	d1yqqa2	Alignment	not modelled	97.9	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
97	c4oqzA_	Alignment	not modelled	97.9	25	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase yfjr; PDBTitle: streptomyces aurantiacus imine reductase
98	c6aphA_	Alignment	not modelled	97.9	19	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of adenosylhomocysteinase from elizabethkingia2 anophelis nuhp1 in complex with nad and adenosine
99	d1c1da1	Alignment	not modelled	97.9	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
100	c2ag8A_	Alignment	not modelled	97.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: nadp complex of pyrroline-5-carboxylate reductase from neisseria2 meningitidis
101	c1np3B_	Alignment	not modelled	97.9	25	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of class i acetoxyhydroxy acid isomeroreductase from2 pseudomonas aeruginosa
102	c2cvzD_	Alignment	not modelled	97.8	23	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: structure of hydroxyisobutyrate dehydrogenase from thermus2 thermophilus hb8
103	c1z82A_	Alignment	not modelled	97.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase; PDBTitle: crystal structure of glycerol-3-phosphate dehydrogenase

					(tm0378) from <i>Thermotoga maritima</i> at 2.00 Å resolution
104	c5g4kB_	Alignment	not modelled	97.8	19 PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase PDBTitle: phloroglucinol reductase from <i>Clostridium</i> sp. apo-form
105	c3ktdC_	Alignment	not modelled	97.8	19 PDB header: oxidoreductase Chain: C: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of a putative prephenate dehydrogenase (cg10226)2 from <i>Corynebacterium glutamicum</i> atcc 13032 at 2.60 Å resolution
106	c6iauB_	Alignment	not modelled	97.8	14 PDB header: oxidoreductase Chain: B: PDB Molecule: amine dehydrogenase; PDBTitle: amine dehydrogenase from <i>Cystobacter fuscus</i> in complex with nadp+ and 2 cyclohexylamine
107	c3b1fA_	Alignment	not modelled	97.8	12 PDB header: oxidoreductase Chain: A: PDB Molecule: putative prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from <i>Streptococcus</i> 2 mutans
108	d1bdba_	Alignment	not modelled	97.8	14 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
109	c2bruB_	Alignment	not modelled	97.8	15 PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p) transhydrogenase subunit alpha; PDBTitle: complex of the domain i and domain iii of <i>Escherichia coli</i> 2 transhydrogenase
110	c3wtcB_	Alignment	not modelled	97.8	19 PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of gox2036
111	c5u9pB_	Alignment	not modelled	97.8	31 PDB header: oxidoreductase Chain: B: PDB Molecule: gluconate 5-dehydrogenase; PDBTitle: crystal structure of a gluconate 5-dehydrogenase from <i>Burkholderia</i> 2 cenocepacia j2315 in complex with nadp and tartrate
112	c4nbvA_	Alignment	not modelled	97.8	13 PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase putative short- PDBTitle: crystal structure of fabg from <i>Cupriavidus taiwanensis</i>
113	c3gvpB_	Alignment	not modelled	97.8	13 PDB header: hydrolase Chain: B: PDB Molecule: adenosylhomocysteinase 3; PDBTitle: human sahh-like domain of human adenosylhomocysteinase 3
114	c5h5xH_	Alignment	not modelled	97.8	22 PDB header: oxidoreductase Chain: H: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of nadh bound carbonyl reductase from <i>Streptomyces</i> 2 coelicolor
115	c2iz1C_	Alignment	not modelled	97.8	13 PDB header: oxidoreductase Chain: C: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: 6pdh complexed with pex inhibitor synchrotron data
116	c3imfA_	Alignment	not modelled	97.8	13 PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: 1.99 Å resolution crystal structure of a short chain 2 dehydrogenase from <i>Bacillus anthracis</i> str. 'Ames ancestor'
117	c4trrH_	Alignment	not modelled	97.8	22 PDB header: oxidoreductase Chain: H: PDB Molecule: putative d-beta-hydroxybutyrate dehydrogenase; PDBTitle: crystal structure of a putative putative d-beta-hydroxybutyrate 2 dehydrogenase from <i>Burkholderia cenocepacia</i> j2315
118	c3fwnB_	Alignment	not modelled	97.8	11 PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: dimeric 6-phosphogluconate dehydrogenase complexed with 6-2 phosphogluconate and 2'-monophosphoadenosine-5'-diphosphate
119	d1jaya_	Alignment	not modelled	97.8	26 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
120	c5yeqB_	Alignment	not modelled	97.8	18 PDB header: isomerase Chain: B: PDB Molecule: ketol-acid reductoisomerase (nadp(+)); PDBTitle: the structure of sac-kari protein