





















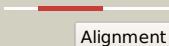


























# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1143_(mcr)_1270067_1271149
Date	Wed Jul 31 22:05:22 BST 2019
Unique Job ID	7311897596427fc5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1x74a1</a>	 Alignment		100.0	99	<b>Fold:</b> CoA-transferase family III (CaiB/BaiF) <b>Superfamily:</b> CoA-transferase family III (CaiB/BaiF) <b>Family:</b> CoA-transferase family III (CaiB/BaiF)
2	<a href="#">c4ed9A</a>	 Alignment		100.0	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> caib/baif family protein; <b>PDBTitle:</b> crystal structure of a caib/baif family protein from brucella suis
3	<a href="#">c4hl6D</a>	 Alignment		100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein yfde; <b>PDBTitle:</b> yfde from escherichia coli
4	<a href="#">c3ubmB</a>	 Alignment		100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> formyl-coa:oxalate coa-transferase; <b>PDBTitle:</b> formyl-coa:oxalate coa-transferase from acetobacter aceti
5	<a href="#">d1xk7a1</a>	 Alignment		100.0	25	<b>Fold:</b> CoA-transferase family III (CaiB/BaiF) <b>Superfamily:</b> CoA-transferase family III (CaiB/BaiF) <b>Family:</b> CoA-transferase family III (CaiB/BaiF)
6	<a href="#">c2g04B</a>	 Alignment		100.0	58	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> probable fatty-acid-coa racemase far; <b>PDBTitle:</b> crystal structure of fatty acid-coa racemase from mycobacterium2 tuberculosis h37rv
7	<a href="#">c1xa3B</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> crotonobetainyl-coa:carnitine coa-transferase; <b>PDBTitle:</b> crystal structure of caib, a type iii coa transferase in2 carnitine metabolism
8	<a href="#">d2vjma1</a>	 Alignment		100.0	25	<b>Fold:</b> CoA-transferase family III (CaiB/BaiF) <b>Superfamily:</b> CoA-transferase family III (CaiB/BaiF) <b>Family:</b> CoA-transferase family III (CaiB/BaiF)
9	<a href="#">c5yx6D</a>	 Alignment		100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein rv3272; <b>PDBTitle:</b> crystal structure of rv3272 from m. tuberculosis orthorhombic form
10	<a href="#">d1q7ea</a>	 Alignment		100.0	25	<b>Fold:</b> CoA-transferase family III (CaiB/BaiF) <b>Superfamily:</b> CoA-transferase family III (CaiB/BaiF) <b>Family:</b> CoA-transferase family III (CaiB/BaiF)
11	<a href="#">d1gdha1</a>	 Alignment		96.0	9	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain

12	<a href="#">c2bruB</a>	 Alignment		95.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> nad(p) transhydrogenase subunit alpha; <b>PDBTitle:</b> complex of the domain i and domain iii of escherichia coli2 transhydrogenase
13	<a href="#">c6ih2B</a>	 Alignment		95.5	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> phosphite dehydrogenase; <b>PDBTitle:</b> crystal structure of phosphite dehydrogenase from ralstonia sp. 4506
14	<a href="#">c5j23D</a>	 Alignment		95.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D; <b>PDB Molecule:</b> 2-hydroxyacid dehydrogenase; <b>PDBTitle:</b> crystal structure of nadph-dependent glyoxylate/hydroxypyruvate2 reductase smc04462 (smghrb) from sinorhizobium mellioti in complex3 with 2'-phospho- adp-ribose
15	<a href="#">d1ygya1</a>	 Alignment		95.0	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
16	<a href="#">c3gvxA</a>	 Alignment		94.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> glycerate dehydrogenase related protein; <b>PDBTitle:</b> crystal structure of glycerate dehydrogenase related2 protein from thermoplasma acidophilum
17	<a href="#">c2eezG</a>	 Alignment		94.8	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G; <b>PDB Molecule:</b> alanine dehydrogenase; <b>PDBTitle:</b> crystal structure of alanine dehydrogenase from thermophilus
18	<a href="#">c1pjcA</a>	 Alignment		94.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> protein (l-alanine dehydrogenase); <b>PDBTitle:</b> l-alanine dehydrogenase complexed with nad
19	<a href="#">c1gdhA</a>	 Alignment		94.7	11	<b>PDB header:</b> oxidoreductase(choh (d)-nad(p)+ (a)) <b>Chain:</b> A; <b>PDB Molecule:</b> d-glycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of a nad-dependent d-glycerate2 dehydrogenase at 2.4 angstroms resolution
20	<a href="#">c2g76A</a>	 Alignment		94.7	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of human 3-phosphoglycerate dehydrogenase
21	<a href="#">c3p2yA</a>	 Alignment	not modelled	94.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> alanine dehydrogenase/pyridine nucleotide transhydrogenase; <b>PDBTitle:</b> crystal structure of alanine dehydrogenase/pyridine nucleotide2 transhydrogenase from mycobacterium smegmatis
22	<a href="#">c3bazA</a>	 Alignment	not modelled	94.6	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> hydroxyphenylpyruvate reductase; <b>PDBTitle:</b> structure of hydroxyphenylpyruvate reductase from coleus blumei in2 complex with nadp+
23	<a href="#">c2cukC</a>	 Alignment	not modelled	94.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> glycerate dehydrogenase/glyoxylate reductase; <b>PDBTitle:</b> crystal structure of tt0316 protein from thermophilus hb8
24	<a href="#">d2naca1</a>	 Alignment	not modelled	94.6	12	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
25	<a href="#">c4cukA</a>	 Alignment	not modelled	94.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> d-lactate dehydrogenase; <b>PDBTitle:</b> structure of salmonella d-lactate dehydrogenase in complex2 with nadh
26	<a href="#">c4izhA</a>	 Alignment	not modelled	94.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> nad/nadp transhydrogenase alpha subunit 1; <b>PDBTitle:</b> crystal structure of the alpha1 dimer of thermophilus2 transhydrogenase in p6
27	<a href="#">c4xa8A</a>	 Alignment	not modelled	94.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> d-isomer specific 2-hydroxyacid dehydrogenase nad-binding; <b>PDBTitle:</b> crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 from xanthobacter autotrophicus py2 <b>PDB header:</b> hydrolase

28	<a href="#">c5hm8C</a>	Alignment	not modelled	94.4	19	<b>Chain:</b> C; <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> 2.85 angstrom crystal structure of s-adenosylhomocysteinase from2 cryptosporidium parvum in complex with adenosine and nad.
29	<a href="#">c4g2nA</a>	Alignment	not modelled	94.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> d-isomer specific 2-hydroxyacid dehydrogenase, nad-binding; <b>PDBTitle:</b> crystal structure of putative d-isomer specific 2-hydroxyacid2 dehydrogenase, nad-binding from polaromonas sp. js6 66
30	<a href="#">c4dioB</a>	Alignment	not modelled	94.4	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> nad(p) transhydrogenase subunit alpha part 1; <b>PDBTitle:</b> the crystal structure of transhydrogenase from sinorhizobium melliloti
31	<a href="#">d1l7da1</a>	Alignment	not modelled	94.4	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
32	<a href="#">c2rirA</a>	Alignment	not modelled	94.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> dipicolinate synthase, a chain; <b>PDBTitle:</b> crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
33	<a href="#">d1dxya1</a>	Alignment	not modelled	94.3	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
34	<a href="#">c2gqcB</a>	Alignment	not modelled	94.3	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> glyoxylate reductase/hydroxypyruvate reductase; <b>PDBTitle:</b> ternary crystal structure of human glyoxylate2 reductase/hydroxypyruvate reductase
35	<a href="#">c3kboB</a>	Alignment	not modelled	94.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> glyoxylate/hydroxypyruvate reductase a; <b>PDBTitle:</b> 2.14 angstrom crystal structure of putative oxidoreductase (ycdw) from2 salmonella typhimurium in complex with nadp
36	<a href="#">c2omeA</a>	Alignment	not modelled	94.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> c-terminal-binding protein 2; <b>PDBTitle:</b> crystal structure of human ctbp2 dehydrogenase complexed with nad(h)
37	<a href="#">d1j4aa1</a>	Alignment	not modelled	94.0	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
38	<a href="#">d1li4a1</a>	Alignment	not modelled	93.7	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
39	<a href="#">c1l7eC</a>	Alignment	not modelled	93.7	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> nicotinamide nucleotide transhydrogenase, <b>PDBTitle:</b> crystal structure of r. rubrum transhydrogenase domain i2 with bound nadh
40	<a href="#">c1wwkA</a>	Alignment	not modelled	93.6	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
41	<a href="#">d1mx3a1</a>	Alignment	not modelled	93.5	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
42	<a href="#">c3dhyC</a>	Alignment	not modelled	93.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structures of mycobacterium tuberculosis s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and3 inhibitors
43	<a href="#">c1xdwA</a>	Alignment	not modelled	93.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> nad+-dependent (r)-2-hydroxyglutarate <b>PDBTitle:</b> nad+-dependent (r)-2-hydroxyglutarate dehydrogenase from2 acidaminococcus fermentans
44	<a href="#">c4lswA</a>	Alignment	not modelled	93.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> d-2-hydroxyacid dehydrogenase protein; <b>PDBTitle:</b> crystallization and structural analysis of 2-hydroxyacid dehydrogenase2 from ketogulonigenium vulgare y25
45	<a href="#">c3wnvA</a>	Alignment	not modelled	93.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> glyoxylate reductase; <b>PDBTitle:</b> crystal structure of a glyoxylate reductase from paecilomyces2 thermophila
46	<a href="#">d1qp8a1</a>	Alignment	not modelled	93.4	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
47	<a href="#">c3d64A</a>	Alignment	not modelled	93.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
48	<a href="#">c4zgsE</a>	Alignment	not modelled	93.4	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E; <b>PDB Molecule:</b> putative d-lactate dehydrogenase; <b>PDBTitle:</b> identification of the pyruvate reductase of chlamydomonas reinhardtii
49	<a href="#">d2dlda1</a>	Alignment	not modelled	93.2	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
50	<a href="#">c1luaA</a>	Alignment	not modelled	93.1	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> methylene tetrahydromethanopterin dehydrogenase; <b>PDBTitle:</b> structure of methylene-tetrahydromethanopterin dehydrogenase from2 methylobacterium extorquens am1 complexed with nadp
51	<a href="#">c4weqA</a>	Alignment	not modelled	93.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> nad-dependent dehydrogenase; <b>PDBTitle:</b> crystal structure of nadph-dependent glyoxylate/hydroxypyruvate2 reductase smc02828 (smghra) from

						sinorhizobium melloti in complex3 with nadp and sulfate <b>PDB header:</b> hydrolase/hydrolase substrate <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of lupinus luteus s-adenosyl-l-homocysteine2 hydrolase in complex with adenine
52	<a href="#">c3oneA_</a>	Alignment	not modelled	93.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> formate dehydrogenase; <b>PDBTitle:</b> nad-dependent formate dehydrogenase from higher-plant arabidopsis2 thaliana in complex with nad and azide
53	<a href="#">c3n7uD_</a>	Alignment	not modelled	93.1	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
54	<a href="#">d1pjca1</a>	Alignment	not modelled	93.1	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-isomer specific 2-hydroxyacid dehydrogenase family <b>PDBTitle:</b> crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 family protein from klebsiella pneumoniae 342
55	<a href="#">c4n18A_</a>	Alignment	not modelled	93.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of a hydrolase
56	<a href="#">c1v8bA_</a>	Alignment	not modelled	93.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> formate dehydrogenase; <b>PDBTitle:</b> candida boidinii formate dehydrogenase (fdh) c-terminal mutant
57	<a href="#">c2j6iC_</a>	Alignment	not modelled	93.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ornithine carbamoyltransferase 1; <b>PDBTitle:</b> the crystal structure of ornithine carbamoyltransferase from2 burkholderia thailandensis e264
58	<a href="#">c4f2gA_</a>	Alignment	not modelled	92.7	12	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
59	<a href="#">d1sc6a1</a>	Alignment	not modelled	92.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> adenosylhomocysteinase 3; <b>PDBTitle:</b> human sahh-like domain of human adenosylhomocysteinase 3
60	<a href="#">c3gvpB_</a>	Alignment	not modelled	92.3	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> d-lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of d-lactate dehydrogenase from aquifex2 aeolicus complexed with nad and lactic acid
61	<a href="#">c2pi1C_</a>	Alignment	not modelled	92.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase; <b>PDBTitle:</b> structure of nadh-preferring ketol-acid reductoisomerase from an2 uncultured archaean
62	<a href="#">c4xdyB_</a>	Alignment	not modelled	92.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-lactate dehydrogenase; <b>PDBTitle:</b> the crystal structure of d-lactate dehydrogenase from fusobacterium2 nucleatum subsp. nucleatum
63	<a href="#">c3wwyA_</a>	Alignment	not modelled	92.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-lactate dehydrogenase; <b>PDBTitle:</b> insights into domain closure, substrate specificity and2 catalysis of d-lactate dehydrogenase from lactobacillus3 bulgaricus
64	<a href="#">c1j4aA_</a>	Alignment	not modelled	92.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dipicolinate synthase subunit a; <b>PDBTitle:</b> crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
65	<a href="#">c3d4oA_</a>	Alignment	not modelled	92.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-2-hydroxyacid dehydrogenase; <b>PDBTitle:</b> d-2-hydroxyacid dehydrogenases (d2-hdh) from haloferax mediterranei in2 complex with 2-keto-hexanoic acid and nadp+ (1.4 a resolution)
66	<a href="#">c5mh5A_</a>	Alignment	not modelled	92.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-isomer specific 2-hydroxyacid dehydrogenase family <b>PDBTitle:</b> crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 family protein from aeromonas salmonicida subsp. salmonicida a449
67	<a href="#">c3hg7A_</a>	Alignment	not modelled	91.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-lactate dehydrogenase; <b>PDBTitle:</b> a novel d-lactate dehydrogenase from sporolactobacillus sp
68	<a href="#">c4xkja_</a>	Alignment	not modelled	91.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxylate reductase; <b>PDBTitle:</b> crystal structure of glyoxylate reductase (ph0597) from pyrococcus2 horikoshii ot3, complexed with nadp (i41)
69	<a href="#">c2dbqA_</a>	Alignment	not modelled	91.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadp-dependent dehydrogenase; <b>PDBTitle:</b> crystal structure of nadp-dependent dehydrogenase from2 rhodobactersphaeroides in complex with nadp and sulfate
70	<a href="#">c4zqbB_</a>	Alignment	not modelled	91.5	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase, putative; <b>PDBTitle:</b> crystal structure of phosphoglycerate bound 3-phosphoglycerate2 dehydrogenase in entamoeba histolytica
71	<a href="#">c4njmA_</a>	Alignment	not modelled	91.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of adenosylhomocysteinase from elizabethkingia2 anophelis nuhp1 in complex with nad and adenosine
72	<a href="#">c6aphA_</a>	Alignment	not modelled	91.0	21	<b>PDB header:</b> oxidoreductase, biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycerate dehydrogenase; <b>PDBTitle:</b> acyclic imino acid reductase (bsp5) in complex with nadph and d-arg
73	<a href="#">c6p2ia_</a>	Alignment	not modelled	90.9	10	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
74	<a href="#">d1m1na_</a>	Alignment	not modelled	90.6	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-phosphoerythronate dehydrogenase; <b>PDBTitle:</b> crystal structure of d-lactate dehydrogenase (d-ldh) from2 lactobacillus jensenii
75	<a href="#">c4prkB_</a>	Alignment	not modelled	90.6	15	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase (nadp(+));

76	<a href="#">c6aqjB_</a>	Alignment	not modelled	90.6	23	<b>PDBTitle:</b> crystal structures of staphylococcus aureus ketol-acid2 reductoisomerase in complex with two transition state analogs that3 have biocidal activity.
77	<a href="#">c2eklA_</a>	Alignment	not modelled	90.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> structure of st1218 protein from sulfolobus tokodaii
78	<a href="#">c3wvzB_</a>	Alignment	not modelled	90.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> d-lactate dehydrogenase (fermentative); <b>PDBTitle:</b> the crystal structure of d-lactate dehydrogenase from pseudomonas2 aeruginosa
79	<a href="#">d1pg5a2</a>	Alignment	not modelled	90.5	15	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
80	<a href="#">c1d4fD_</a>	Alignment	not modelled	90.4	14	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> s-adenosylhomocysteine hydrolase; <b>PDBTitle:</b> crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
81	<a href="#">c5v96A_</a>	Alignment	not modelled	90.3	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosyl-l-homocysteine hydrolase; <b>PDBTitle:</b> crystal structure of s-adenosyl-l-homocysteine hydrolase from2 naegleria fowleri with bound nad and adenosine
82	<a href="#">c4e5kC_</a>	Alignment	not modelled	90.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphite dehydrogenase (thermostable variant); <b>PDBTitle:</b> thermostable phosphite dehydrogenase in complex with nad and sulfite
83	<a href="#">c4qjiB_</a>	Alignment	not modelled	89.9	22	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphopantothenate--cysteine ligase; <b>PDBTitle:</b> crystal structure of the c-terminal ctp-binding domain of a2 phosphopantothenoylcysteine decarboxylase/phosphopantothenate-3 cysteine ligase with bound ctp from mycobacterium smegmatis
84	<a href="#">c3evtA_</a>	Alignment	not modelled	89.6	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of phosphoglycerate dehydrogenase from lactobacillus2 plantarum
85	<a href="#">c1qp8A_</a>	Alignment	not modelled	89.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> formate dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative formate dehydrogenase from2 pyrobaculum aerophilum
86	<a href="#">c4xcvA_</a>	Alignment	not modelled	89.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadp-dependent 2-hydroxyacid dehydrogenase; <b>PDBTitle:</b> probable 2-hydroxyacid dehydrogenase from rhizobium etli cfn 42 in2 complex with nadph
87	<a href="#">c3x2fA_</a>	Alignment	not modelled	89.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> a thermophilic s-adenosylhomocysteine hydrolase
88	<a href="#">c4hy3D_</a>	Alignment	not modelled	89.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoglycerate oxidoreductase; <b>PDBTitle:</b> crystal structure of a phosphoglycerate oxidoreductase from rhizobium2 etli
89	<a href="#">d1to3a_</a>	Alignment	not modelled	89.1	29	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
90	<a href="#">d1v8ba1</a>	Alignment	not modelled	89.0	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
91	<a href="#">c4s1vD_</a>	Alignment	not modelled	88.7	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase-related protein; <b>PDBTitle:</b> crystal structure of phosphoglycerate oxidoreductase from vibrio2 cholerae o395
92	<a href="#">d1np3a2</a>	Alignment	not modelled	88.5	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
93	<a href="#">c1dxyA_</a>	Alignment	not modelled	88.5	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-2-hydroxyisocaproate dehydrogenase; <b>PDBTitle:</b> structure of d-2-hydroxyisocaproate dehydrogenase
94	<a href="#">c4xdzB_</a>	Alignment	not modelled	88.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase; <b>PDBTitle:</b> holo structure of ketol-acid reductoisomerase from ignisphaera2 aggregans
95	<a href="#">c2yq4C_</a>	Alignment	not modelled	88.2	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> d-isomer specific 2-hydroxyacid dehydrogenase; <b>PDBTitle:</b> crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 from lactobacillus delbrueckii ssp. bulgaricus
96	<a href="#">c2p2gD_</a>	Alignment	not modelled	88.2	22	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> ornithine carbamoyltransferase; <b>PDBTitle:</b> crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
97	<a href="#">c3gg9C_</a>	Alignment	not modelled	88.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase oxidoreductase protein; <b>PDBTitle:</b> crystal structure of putative d-3-phosphoglycerate dehydrogenase2 oxidoreductase from ralstonia solanacearum
98	<a href="#">d2jfga1</a>	Alignment	not modelled	88.0	20	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
99	<a href="#">c3n58D_</a>	Alignment	not modelled	87.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of s-adenosyl-l-homocysteine hydrolase from brucella2 melitensis in ternary complex with nad and adenosine, orthorhombic3 form
100	<a href="#">c2nacA_</a>	Alignment	not modelled	87.8	12	<b>PDB header:</b> oxidoreductase(aldehyde(d),nad+(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent formate dehydrogenase;



100	<a href="#">c2haaA</a>	Alignment	not modelled	87.8	12	<b>PDBTitle:</b> high resolution structures of holo and apo formate dehydrogenase <b>PDB header:</b> oxidoreductase
101	<a href="#">c3fn4A</a>	Alignment	not modelled	87.7	13	<b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent formate dehydrogenase; <b>PDBTitle:</b> apo-form of nad-dependent formate dehydrogenase from bacterium2 moraxella sp.c-1 in closed conformation
102	<a href="#">c6f3oC</a>	Alignment	not modelled	87.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of s-adenosyl-l-homocysteine hydrolase from2 pseudomonas aeruginosa complexed with adenine, k+ and zn2+ cations
103	<a href="#">c2vhyB</a>	Alignment	not modelled	87.1	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alanine dehydrogenase; <b>PDBTitle:</b> crystal structure of apo l-alanine dehydrogenase from mycobacterium2 tuberculosis
104	<a href="#">c2d0iC</a>	Alignment	not modelled	87.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dehydrogenase; <b>PDBTitle:</b> crystal structure ph0520 protein from pyrococcus horikoshii ot3
105	<a href="#">c4tskA</a>	Alignment	not modelled	86.9	22	<b>PDB header:</b> oxidoreductase,isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ketol-acid reductoisomerase; <b>PDBTitle:</b> ketol-acid reductoisomerase from alicyclobacillus acidocaldarius
106	<a href="#">c1np3B</a>	Alignment	not modelled	85.7	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase; <b>PDBTitle:</b> crystal structure of class i acetohydroxy acid isomereoreductase from2 pseudomonas aeruginosa
107	<a href="#">c2w2kB</a>	Alignment	not modelled	85.5	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> d-mandelate dehydrogenase; <b>PDBTitle:</b> crystal structure of the apo forms of rhodoturla graminis2 d-mandelate dehydrogenase at 1.8a.
108	<a href="#">c2xdoC</a>	Alignment	not modelled	85.5	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> tetx2 protein; <b>PDBTitle:</b> structure of the tetracycline degrading monooxygenase tetx2 from2 bacteroides thetaiotaomicron
109	<a href="#">d1vlva2</a>	Alignment	not modelled	85.4	13	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
110	<a href="#">c1e5IA</a>	Alignment	not modelled	85.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine reductase; <b>PDBTitle:</b> apo saccharopine reductase from magnaporthe grisea
111	<a href="#">c4mozC</a>	Alignment	not modelled	85.3	19	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> fructose-bisphosphate aldolase; <b>PDBTitle:</b> fructose-bisphosphate aldolase from slackia heliotrinireducens dsm2 20476
112	<a href="#">c5tx7A</a>	Alignment	not modelled	85.3	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-isomer specific 2-hydroxyacid dehydrogenase family <b>PDBTitle:</b> crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 from desulfovibrio vulgaris
113	<a href="#">c3pdiG</a>	Alignment	not modelled	85.1	18	<b>PDB header:</b> protein binding <b>Chain:</b> G: <b>PDB Molecule:</b> nitrogenase mofe cofactor biosynthesis protein nife; <b>PDBTitle:</b> precursor bound nifen
114	<a href="#">c4oh7B</a>	Alignment	not modelled	85.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ornithine carbamoyltransferase; <b>PDBTitle:</b> crystal structure of ornithine carbamoyltransferase from brucella2 melitensis
115	<a href="#">d1b0aa1</a>	Alignment	not modelled	84.9	25	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
116	<a href="#">d1u7za</a>	Alignment	not modelled	84.7	16	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> CoaB-like <b>Family:</b> CoaB-like
117	<a href="#">c2qjhH</a>	Alignment	not modelled	84.5	26	<b>PDB header:</b> lyase <b>Chain:</b> H: <b>PDB Molecule:</b> putative aldolase mj0400; <b>PDBTitle:</b> m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
118	<a href="#">c2gk4A</a>	Alignment	not modelled	83.9	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> the crystal structure of the dna/pantothenate metabolism flavoprotein2 from streptococcus pneumoniae
119	<a href="#">c4nk4E</a>	Alignment	not modelled	83.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> enoyl-[acyl-carrier-protein] reductase [nadh]; <b>PDBTitle:</b> crystal structure of fabi from candidatus liberibacter asiaticus
120	<a href="#">d1ekxa2</a>	Alignment	not modelled	83.1	13	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase