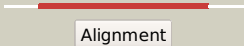

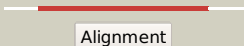

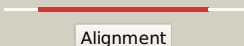







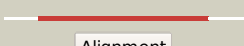











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3248c_sahH_3628157_3629644
Date	Thu Aug 8 16:20:45 BST 2019
Unique Job ID	d0d647a0db6e55ea

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3dhyC_</a>	 Alignment		100.0	100	<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 and 3 inhibitors
2	<a href="#">c5v96A_</a>	 Alignment		100.0	61	<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 from 2 naegleria fowleri with bound nad and adenosine
3	<a href="#">c3oneA_</a>	 Alignment		100.0	62	<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-homocysteine 2 hydrolase in complex with adenine
4	<a href="#">c5hm8C_</a>	 Alignment		100.0	52	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> 2.85 angstrom crystal structure of s-adenosylhomocysteinase from 2 cryptosporidium parvum in complex with adenosine and nad.
5	<a href="#">c1v8bA_</a>	 Alignment		100.0	58	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of a hydrolase
6	<a href="#">c3n58D_</a>	 Alignment		100.0	64	<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 2 brucella 2 melitensis in ternary complex with nad and adenosine, orthorhombic 3 form
7	<a href="#">c3d64A_</a>	 Alignment		100.0	61	<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 from 2 burkholderia pseudomallei
8	<a href="#">c6f3oC_</a>	 Alignment		100.0	57	<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 from 2 pseudomonas aeruginosa complexed with adenine, k+ and zn2+ cations
9	<a href="#">c6aphA_</a>	 Alignment		100.0	62	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of adenosylhomocysteinase from elizabethkingia 2 anophelis nuhp1 in complex with nad and adenosine
10	<a href="#">c1d4fD_</a>	 Alignment		100.0	63	<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
11	<a href="#">c3gvpB_</a>	 Alignment		100.0	51	<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

12	<a href="#">c3x2fA_</a>	Alignment		100.0	41	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> a thermophilic s-adenosylhomocysteine hydrolase
13	<a href="#">d1v8ba2</a>	Alignment		100.0	60	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Formate/glycerate dehydrogenase catalytic domain-like <b>Family:</b> S-adenosylhomocystein hydrolase
14	<a href="#">d1l4a2</a>	Alignment		100.0	66	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Formate/glycerate dehydrogenase catalytic domain-like <b>Family:</b> S-adenosylhomocystein hydrolase
15	<a href="#">d1l4a1</a>	Alignment		100.0	59	<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="#">d1v8ba1</a>	Alignment		100.0	62	<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
17	<a href="#">c1ygyA_</a>	Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
18	<a href="#">c2g76A_</a>	Alignment		100.0	18	<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
19	<a href="#">c1ybaC_</a>	Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> the active form of phosphoglycerate dehydrogenase
20	<a href="#">c1j4aA_</a>	Alignment		100.0	18	<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
21	<a href="#">c4e5kC_</a>	Alignment	not modelled	100.0	17	<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
22	<a href="#">c1gdhA_</a>	Alignment	not modelled	100.0	12	<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
23	<a href="#">c2eklA_</a>	Alignment	not modelled	100.0	16	<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
24	<a href="#">c6ih2B_</a>	Alignment	not modelled	100.0	20	<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
25	<a href="#">c2gcbB_</a>	Alignment	not modelled	100.0	18	<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
26	<a href="#">c2w2kB_</a>	Alignment	not modelled	100.0	14	<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 rhodotorula graminis2 d-mandelate dehydrogenase at 1.8a.
27	<a href="#">c1wwkA_</a>	Alignment	not modelled	100.0	18	<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
28	<a href="#">c3n7uD_</a>	Alignment	not modelled	100.0	12	<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
29	<a href="#">c3k5pA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of amino acid-binding act: d-isomer specific 2-2 hydroxyacid dehydrogenase catalytic domain from brucella melitensis
30	<a href="#">c4xkjA</a>	Alignment	not modelled	100.0	21	<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
31	<a href="#">c3evtA</a>	Alignment	not modelled	100.0	17	<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
32	<a href="#">c2omeA</a>	Alignment	not modelled	100.0	17	<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)
33	<a href="#">c4prkB</a>	Alignment	not modelled	100.0	18	<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
34	<a href="#">c2dbqA</a>	Alignment	not modelled	100.0	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)
35	<a href="#">c3fn4A</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> oxidoreductase <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
36	<a href="#">c2cukC</a>	Alignment	not modelled	99.9	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 thermus thermophilus hb8
37	<a href="#">c2nacA</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> oxidoreductase(aldehyde(d),nad+(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent formate dehydrogenase; <b>PDBTitle:</b> high resolution structures of holo and apo formate dehydrogenase
38	<a href="#">c3wzwB</a>	Alignment	not modelled	99.9	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
39	<a href="#">c5tx7A</a>	Alignment	not modelled	99.9	17	<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
40	<a href="#">c4g2nA</a>	Alignment	not modelled	99.9	17	<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
41	<a href="#">c4njmA</a>	Alignment	not modelled	99.9	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
42	<a href="#">c5j23D</a>	Alignment	not modelled	99.9	15	<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 melloti in complex3 with 2'-phospho- <small>adp</small> -ribose
43	<a href="#">c2d0iC</a>	Alignment	not modelled	99.9	18	<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
44	<a href="#">c3bazA</a>	Alignment	not modelled	99.9	20	<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+
45	<a href="#">c3gg9C</a>	Alignment	not modelled	99.9	14	<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
46	<a href="#">c3wnvA</a>	Alignment	not modelled	99.9	21	<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
47	<a href="#">c2j6iC</a>	Alignment	not modelled	99.9	16	<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
48	<a href="#">c5mh5A</a>	Alignment	not modelled	99.9	17	<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)
49	<a href="#">c4zgsE</a>	Alignment	not modelled	99.9	21	<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
50	<a href="#">c4cukA</a>	Alignment	not modelled	99.9	16	<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
51	<a href="#">c6p2iA</a>	Alignment	not modelled	99.9	16	<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
						<b>PDB header:</b> oxidoreductase

52	<a href="#">c2yq4C</a>	Alignment	not modelled	99.9	17	<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
53	<a href="#">c3wwyA</a>	Alignment	not modelled	99.9	23	<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
54	<a href="#">c2pi1C</a>	Alignment	not modelled	99.9	14	<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
55	<a href="#">c1dxyA</a>	Alignment	not modelled	99.9	17	<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
56	<a href="#">c4zqbB</a>	Alignment	not modelled	99.9	14	<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
57	<a href="#">c1xdwA</a>	Alignment	not modelled	99.9	18	<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
58	<a href="#">c4lswA</a>	Alignment	not modelled	99.9	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
59	<a href="#">c4slvD</a>	Alignment	not modelled	99.9	15	<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
60	<a href="#">c4n18A</a>	Alignment	not modelled	99.9	14	<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
61	<a href="#">c3gvxA</a>	Alignment	not modelled	99.9	15	<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
62	<a href="#">c3kboB</a>	Alignment	not modelled	99.9	14	<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
63	<a href="#">c3hg7A</a>	Alignment	not modelled	99.9	16	<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
64	<a href="#">c4xcvA</a>	Alignment	not modelled	99.9	14	<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
65	<a href="#">c5dt9A</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> erythronate-4-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative d-erythronate-4-phosphate2 dehydrogenase from vibrio cholerae
66	<a href="#">c4xa8A</a>	Alignment	not modelled	99.9	16	<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
67	<a href="#">c3oetF</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F; <b>PDB Molecule:</b> erythronate-4-phosphate dehydrogenase; <b>PDBTitle:</b> d-erythronate-4-phosphate dehydrogenase complexed with nad
68	<a href="#">c2o4cB</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> erythronate-4-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of d-erythronate-4-phosphate dehydrogenase complexed2 with nad
69	<a href="#">c4weqA</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> nad-dependent dehydrogenase; <b>PDBTitle:</b> crystal structure of nadp-dependent glyoxylate/hydroxypyruvate2 reductase smc02828 (smghra) from sinorhizobium meliloti in complex3 with nadp and sulfate
70	<a href="#">c4hy3D</a>	Alignment	not modelled	99.9	16	<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
71	<a href="#">c1qp8A</a>	Alignment	not modelled	99.9	18	<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
72	<a href="#">d1ygya1</a>	Alignment	not modelled	99.9	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
73	<a href="#">d1gdha1</a>	Alignment	not modelled	99.9	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
74	<a href="#">d1mx3a1</a>	Alignment	not modelled	99.9	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
75	<a href="#">d2naca1</a>	Alignment	not modelled	99.9	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

76	<a href="#">d1dxya1</a>	Alignment	not modelled	99.9	18	<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
77	<a href="#">d1j4aa1</a>	Alignment	not modelled	99.9	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
78	<a href="#">d2dlda1</a>	Alignment	not modelled	99.9	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
79	<a href="#">d1sc6a1</a>	Alignment	not modelled	99.9	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
80	<a href="#">c2rirA</a>	Alignment	not modelled	99.9	16	<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
81	<a href="#">d1qp8a1</a>	Alignment	not modelled	99.9	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
82	<a href="#">c4dgsA</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dehydrogenase; <b>PDBTitle:</b> the crystals structure of dehydrogenase from rhizobium meliloti
83	<a href="#">c3d4oA</a>	Alignment	not modelled	99.8	18	<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
84	<a href="#">c1l7eC</a>	Alignment	not modelled	99.7	18	<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
85	<a href="#">c3p2yA</a>	Alignment	not modelled	99.6	21	<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
86	<a href="#">d1np3a2</a>	Alignment	not modelled	99.6	23	<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
87	<a href="#">c2bruB</a>	Alignment	not modelled	99.6	19	<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
88	<a href="#">d1pjca1</a>	Alignment	not modelled	99.6	21	<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
89	<a href="#">c1pjca</a>	Alignment	not modelled	99.6	21	<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
90	<a href="#">c2eezG</a>	Alignment	not modelled	99.5	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> alanine dehydrogenase; <b>PDBTitle:</b> crystal structure of alanine dehydrogenase from thermus thermophilus
91	<a href="#">c4izhA</a>	Alignment	not modelled	99.5	19	<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 thermus thermophilus2 transhydrogenase in p6
92	<a href="#">c5uscB</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of prephenate dehydrogenase tyra from bacillus2 anthracis in complex with nad and l-tyrosine
93	<a href="#">c4dioB</a>	Alignment	not modelled	99.5	23	<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 meliloti
94	<a href="#">d1c1da1</a>	Alignment	not modelled	99.5	18	<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
95	<a href="#">d1l7da1</a>	Alignment	not modelled	99.5	21	<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
96	<a href="#">d1leha1</a>	Alignment	not modelled	99.5	18	<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
97	<a href="#">c5b37A</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan dehydrogenase; <b>PDBTitle:</b> crystal structure of l-tryptophan dehydrogenase from nostoc2 punctiforme
98	<a href="#">c6jczL</a>	Alignment	not modelled	99.3	21	<b>PDB header:</b> isomerase <b>Chain:</b> L: <b>PDB Molecule:</b> putative ketol-acid reductoisomerase 2; <b>PDBTitle:</b> cryo-em structure of sulfolobus solfataricus ketol-acid2 reductoisomerase (sso-kari) in complex with mg2+, nadph, and cpd at3 ph7.5
99	<a href="#">d1a4ia1</a>	Alignment	not modelled	99.3	22	<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
100	<a href="#">c4tskA</a>	Alignment	not modelled	99.3	21	<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
						<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase (nadp(+));



101	<a href="#">c6aqjB_</a>	Alignment	not modelled	99.3	28	<b>PDBTitle:</b> crystal structures of staphylococcus aureus ketol-acid2 reductoisomerase in complex with two transition state analogs that have biocidal activity.
102	<a href="#">c2vhyB_</a>	Alignment	not modelled	99.3	27	<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
103	<a href="#">d1b0aa1</a>	Alignment	not modelled	99.3	17	<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
104	<a href="#">c1lehB_</a>	Alignment	not modelled	99.2	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> leucine dehydrogenase; <b>PDBTitle:</b> leucine dehydrogenase from bacillus sphaericus
105	<a href="#">c4a26B_</a>	Alignment	not modelled	99.2	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative c-1-tetrahydrofolate synthase, cytoplasmic; <b>PDBTitle:</b> the crystal structure of leishmania major n5,n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase
106	<a href="#">c1a4iB_</a>	Alignment	not modelled	99.2	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> methylenetetrahydrofolate dehydrogenase / <b>PDBTitle:</b> human tetrahydrofolate dehydrogenase / cyclohydrolase
107	<a href="#">c1bxgA_</a>	Alignment	not modelled	99.2	18	<b>PDB header:</b> amino acid dehydrogenase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylalanine dehydrogenase; <b>PDBTitle:</b> phenylalanine dehydrogenase structure in ternary complex2 with nad+ and beta-phenylpropionate
108	<a href="#">c5yeqB_</a>	Alignment	not modelled	99.2	27	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase (nadp(+)); <b>PDBTitle:</b> the structure of sac-kari protein
109	<a href="#">c6apeA_</a>	Alignment	not modelled	99.2	30	<b>PDB header:</b> oxidoreductase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> crystal structure of bifunctional protein fold from helicobacter2 pylori
110	<a href="#">c4a5oB_</a>	Alignment	not modelled	99.2	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
111	<a href="#">c5tc4A_</a>	Alignment	not modelled	99.1	22	<b>PDB header:</b> oxidoreductase <b>PDBTitle:</b> crystal structure of human mitochondrial methylenetetrahydrofolate2 dehydrogenase-cyclohydrolase (mthfd2) in complex with ly345899 and3 cofactors
112	<a href="#">c4ypoB_</a>	Alignment	not modelled	99.1	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis ketol-acid2 reductoisomerase in complex with mg2+
113	<a href="#">c3p2oB_</a>	Alignment	not modelled	99.1	22	<b>PDB header:</b> oxidoreductase, hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> crystal structure of fold bifunctional protein from campylobacter2 jejuni
114	<a href="#">c3i07B_</a>	Alignment	not modelled	99.1	21	<b>PDB header:</b> oxidoreductase,hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella3 tularensis.
115	<a href="#">c3p2oA_</a>	Alignment	not modelled	99.1	22	<b>PDB header:</b> oxidoreductase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> crystal structure of fold bifunctional protein from campylobacter2 jejuni
116	<a href="#">c3oj0A_</a>	Alignment	not modelled	99.1	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna reductase; <b>PDBTitle:</b> crystal structure of glutamyl-trna reductase from thermoplasma2 volcanium (nucleotide binding domain)
117	<a href="#">c4xdzB_</a>	Alignment	not modelled	99.1	26	<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
118	<a href="#">c4kqxB_</a>	Alignment	not modelled	99.1	23	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase; <b>PDBTitle:</b> mutant slackia exigua kari ddv in complex with nad and an inhibitor
119	<a href="#">c1np3B_</a>	Alignment	not modelled	99.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase; <b>PDBTitle:</b> crystal structure of class i acetoxy acid isomeroreductase from2 pseudomonas aeruginosa
120	<a href="#">c4xdyB_</a>	Alignment	not modelled	99.0	22	<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 archean