



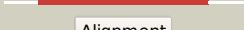

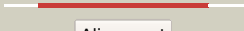









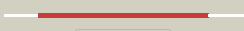













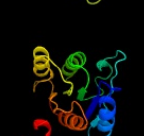


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2773c_(dapB)_3081614_3082351
Date	Wed Aug 7 12:50:43 BST 2019
Unique Job ID	3dcd0234ffd8e675

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1yl7F_</a>	Alignment 		100.0	100	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F; <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> the crystal structure of mycobacterium tuberculosis2 dihydrodipicolinate reductase (rv2773c) in complex with nadh (crystal3 form c)
2	<a href="#">c5eesA_</a>	Alignment 		100.0	66	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate reductase; <b>PDBTitle:</b> crystal structure of dapb in complex with nadp+ from corynebacterium2 glutamicum
3	<a href="#">c3ijpA_</a>	Alignment 		100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate reductase from bartonella2 henselae at 2.0a resolution
4	<a href="#">c5wo1A_</a>	Alignment 		100.0	45	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate reductase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate reductase dapb from coxiella2 burnetii
5	<a href="#">c5us6L_</a>	Alignment 		100.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> L; <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate reductase; <b>PDBTitle:</b> structure of dihydrodipicolinate reductase from vibrio vulnificus2 bound to nadh and 2,6 pyridine dicarboxylic acid with intact3 polyhistidine tag
6	<a href="#">c5ugjC_</a>	Alignment 		100.0	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate reductase; <b>PDBTitle:</b> crystal structure of htpa reductase from neisseria meningitidis
7	<a href="#">c5tenH_</a>	Alignment 		100.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H; <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate reductase; <b>PDBTitle:</b> structure of 4-hydroxy-tetrahydrodipicolinate reductase from vibrio2 vulnificus with 2,5 furan dicarboxylic and nadh with intact3 polyhistidine tag
8	<a href="#">c5kt0A_</a>	Alignment 		100.0	46	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate reductase; <b>PDBTitle:</b> dihydrodipicolinate reductase from the industrial and evolutionarily2 important cyanobacteria anabaena variabilis.
9	<a href="#">c4f3yA_</a>	Alignment 		100.0	34	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> x-ray crystal structure of dihydrodipicolinate reductase from2 burkholderia thailandensis
10	<a href="#">c1drwA_</a>	Alignment 		100.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> escherichia coli dhpr/nhdh complex
11	<a href="#">c4ywjB_</a>	Alignment 		100.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate reductase; <b>PDBTitle:</b> crystal structure of 4-hydroxy-tetrahydrodipicolinate reductase (htpa2 reductase) from pseudomonas aeruginosa

12	<a href="#">c3qy9C_</a>	Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> the crystal structure of dihydrodipicolinate reductase from2 staphylococcus aureus
13	<a href="#">c5z2fA_</a>	Alignment		100.0	46	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> nadph/pda bound dihydrodipicolinate reductase from paenisporsarcina2 sp. tg-14
14	<a href="#">c1vm6B_</a>	Alignment		100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate reductase (tm1520) from2 thermotoga maritima at 2.27 a resolution
15	<a href="#">c5ua0B_</a>	Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate reductase 2, <b>PDBTitle:</b> dimeric crystal structure of htpa reductase from arabidopsis thaliana
16	<a href="#">c5u5iA_</a>	Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> htpa reductase; <b>PDBTitle:</b> the dimeric crystal structure of the selenomethionine derivative of2 htpa reductase from sellaginella moellendorffii
17	<a href="#">c3bioB_</a>	Alignment		100.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family; <b>PDBTitle:</b> crystal structure of oxidoreductase (gfo/idh/moca family member) from2 porphyromonas gingivalis w83
18	<a href="#">d1yl7a1</a>	Alignment		100.0	82	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
19	<a href="#">d1yl7a2</a>	Alignment		100.0	100	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> Dihydrodipicolinate reductase-like
20	<a href="#">d1diha1</a>	Alignment		100.0	28	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
21	<a href="#">d1diha2</a>	Alignment	not modelled	100.0	33	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> Dihydrodipicolinate reductase-like
22	<a href="#">c3wb9A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate dehydrogenase; <b>PDBTitle:</b> crystal structures of meso-diaminopimelate dehydrogenase from2 symbiobacterium thermophilum
23	<a href="#">d1vm6a3</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
24	<a href="#">d1vm6a2</a>	Alignment	not modelled	100.0	38	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> Dihydrodipicolinate reductase-like
25	<a href="#">c6g1mA_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> amine dehydrogenase from petrotoga mobilis; open and closed form
26	<a href="#">c3wgzB_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> meso-diaminopimelate dehydrogenase; <b>PDBTitle:</b> crystal structure of meso-dapdh q154l/t173i/r199m/p248s/h249n/n276s2 mutant with d-leucine of from clostridium tetani e88
27	<a href="#">d1j5pa4</a>	Alignment	not modelled	99.4	14	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
28	<a href="#">c6iaqA_</a>	Alignment	not modelled	99.3	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate reductase n-terminus domain-containing

					<b>PDBTitle:</b> structure of amine dehydrogenase from mycobacterium smegmatis
29	<a href="#">c2dc1A</a>	Alignment	not modelled	99.2	19 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-aspartate dehydrogenase; <b>PDBTitle:</b> crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
30	<a href="#">d2czca2</a>	Alignment	not modelled	99.2	23 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
31	<a href="#">dloi7a1</a>	Alignment	not modelled	99.1	18 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
32	<a href="#">d2nu7a1</a>	Alignment	not modelled	99.1	18 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
33	<a href="#">d1euca1</a>	Alignment	not modelled	99.1	19 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
34	<a href="#">c6iauB</a>	Alignment	not modelled	99.1	15 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> amine dehydrogenase; <b>PDBTitle:</b> amine dehydrogenase from cystobacter fuscus in complex with nadp+ and2 cyclohexylamine
35	<a href="#">c1oi7A</a>	Alignment	not modelled	99.0	21 <b>PDB header:</b> synthetase <b>Chain:</b> A: <b>PDB Molecule:</b> succinyl-coa synthetase alpha chain; <b>PDBTitle:</b> the crystal structure of succinyl-coa synthetase alpha2 subunit from thermus thermophilus
36	<a href="#">c2yv1A</a>	Alignment	not modelled	98.9	17 <b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> succinyl-coa ligase [adp-forming] subunit alpha; <b>PDBTitle:</b> crystal structure of succinyl-coa synthetase alpha chain from2 methanocaldococcus jannaschii dsm 2661
37	<a href="#">c6me1A</a>	Alignment	not modelled	98.9	21 <b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> succinate--coa ligase subunit alpha; <b>PDBTitle:</b> succinyl-coa synthase from campylobacter jejuni
38	<a href="#">c3wycB</a>	Alignment	not modelled	98.8	12 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> meso-diaminopimelate d-dehydrogenase; <b>PDBTitle:</b> structure of a meso-diaminopimelate dehydrogenase in complex with nadp
39	<a href="#">c1j5pA</a>	Alignment	not modelled	98.8	16 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate dehydrogenase; <b>PDBTitle:</b> crystal structure of aspartate dehydrogenase (tm1643) from thermotoga2 maritima at 1.9 a resolution
40	<a href="#">d1ydwa1</a>	Alignment	not modelled	98.8	17 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
41	<a href="#">c3e18A</a>	Alignment	not modelled	98.7	19 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of nad-binding protein from listeria innocua
42	<a href="#">c5b3uB</a>	Alignment	not modelled	98.7	14 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> biliverdin reductase; <b>PDBTitle:</b> crystal structure of biliverdin reductase in complex with nadp+ from2 synechocystis sp. pcc 6803
43	<a href="#">c4mkzA</a>	Alignment	not modelled	98.7	13 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inositol dehydrogenase; <b>PDBTitle:</b> crystal structure of apo scyllo-inositol dehydrogenase from2 lactobacillus casei at 77k
44	<a href="#">c2ho3D</a>	Alignment	not modelled	98.7	15 <b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family; <b>PDBTitle:</b> crystal structure of oxidoreductase, gfo/idh/moca family from2 streptococcus pneumoniae
45	<a href="#">c2yv2A</a>	Alignment	not modelled	98.7	24 <b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> succinyl-coa synthetase alpha chain; <b>PDBTitle:</b> crystal structure of succinyl-coa synthetase alpha chain from2 aeropyrum pernix k1
46	<a href="#">c5uibA</a>	Alignment	not modelled	98.7	12 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase protein; <b>PDBTitle:</b> crystal structure of an oxidoreductase from agrobacterium radiobacter2 in complex with nad+, l-tartaric acid and magnesium
47	<a href="#">c3euwB</a>	Alignment	not modelled	98.7	19 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> myo-inositol dehydrogenase; <b>PDBTitle:</b> crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
48	<a href="#">c3evnA</a>	Alignment	not modelled	98.7	15 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family; <b>PDBTitle:</b> crystal structure of putative oxidoreductase from streptococcus2 agalactiae 2603v/r
49	<a href="#">c3ezyB</a>	Alignment	not modelled	98.7	17 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> dehydrogenase; <b>PDBTitle:</b> crystal structure of probable dehydrogenase tm_0414 from thermotoga2 maritima
50	<a href="#">c2nu8D</a>	Alignment	not modelled	98.7	17 <b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> succinyl-coa ligase [adp-forming] subunit alpha; <b>PDBTitle:</b> c123at mutant of e. coli succinyl-coa synthetase
51	<a href="#">c2z2vA</a>	Alignment	not modelled	98.7	22 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph1688; <b>PDBTitle:</b> crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
52	<a href="#">c2glxD</a>	Alignment	not modelled	98.7	17 <b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 1,5-anhydro-d-fructose reductase; <b>PDBTitle:</b> crystal structure analysis of bacterial 1,5-af reductase
53	<a href="#">c3dapB</a>	Alignment	not modelled	98.6	16 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> diaminopimelic acid dehydrogenase; <b>PDBTitle:</b> c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline

54	<a href="#">c4hktA</a>	Alignment	not modelled	98.6	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inositol 2-dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative myo-inositol dehydrogenase from2 sinorhizobium meliloti 1021 (target psi-012312)
55	<a href="#">c3ec7C</a>	Alignment	not modelled	98.6	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative dehydrogenase; <b>PDBTitle:</b> crystal structure of putative dehydrogenase from salmonella2 typhimurium lt2
56	<a href="#">d1f06a1</a>	Alignment	not modelled	98.6	14	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
57	<a href="#">c3upyB</a>	Alignment	not modelled	98.6	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of the brucella abortus enzyme catalyzing the first2 committed step of the methylerythritol 4-phosphate pathway.
58	<a href="#">c3e82A</a>	Alignment	not modelled	98.6	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase from2 klebsiella pneumoniae
59	<a href="#">c3db2C</a>	Alignment	not modelled	98.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative nadph-dependent oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative nadph-dependent oxidoreductase2 (dhaf_2064) from desulfitobacterium hafniense dcb-2 at 1.70 a3 resolution
60	<a href="#">c3fd8A</a>	Alignment	not modelled	98.6	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family; <b>PDBTitle:</b> crystal structure of an oxidoreductase from enterococcus2 faecalis
61	<a href="#">c3fhlC</a>	Alignment	not modelled	98.6	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase from bacteroides2 fragilis nctc 9343
62	<a href="#">c4xb1B</a>	Alignment	not modelled	98.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 319aa long hypothetical homoserine dehydrogenase; <b>PDBTitle:</b> hyperthermophilic archaeal homoserine dehydrogenase in complex with2 nadph
63	<a href="#">c2o48X</a>	Alignment	not modelled	98.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X: <b>PDB Molecule:</b> dimeric dihydrodiol dehydrogenase; <b>PDBTitle:</b> crystal structure of mammalian dimeric dihydrodiol dehydrogenase
64	<a href="#">c3kuxA</a>	Alignment	not modelled	98.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> structure of the ypo2259 putative oxidoreductase from yersinia pestis
65	<a href="#">c3do5A</a>	Alignment	not modelled	98.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> crystal structure of putative homoserine dehydrogenase (np_069768.1)2 from archaeoglobus fulgidus at 2.20 a resolution
66	<a href="#">c2axqA</a>	Alignment	not modelled	98.6	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine dehydrogenase; <b>PDBTitle:</b> apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
67	<a href="#">c4pg8B</a>	Alignment	not modelled	98.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> crystal structure of s. aureus homoserine dehydrogenase at ph8.5
68	<a href="#">c3e9mC</a>	Alignment	not modelled	98.6	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family; <b>PDBTitle:</b> crystal structure of an oxidoreductase from enterococcus2 faecalis
69	<a href="#">c2q4eB</a>	Alignment	not modelled	98.5	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable oxidoreductase at4g09670; <b>PDBTitle:</b> ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at4g09670
70	<a href="#">c1xeaD</a>	Alignment	not modelled	98.5	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family; <b>PDBTitle:</b> crystal structure of a gfo/idh/moca family oxidoreductase2 from vibrio cholerae
71	<a href="#">c2ixaA</a>	Alignment	not modelled	98.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-n-acetylgalactosaminidase; <b>PDBTitle:</b> a-zyme, n-acetylgalactosaminidase
72	<a href="#">c4miyB</a>	Alignment	not modelled	98.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; <b>PDBTitle:</b> crystal structure of myo-inositol dehydrogenase from lactobacillus2 casei in complex with nad and myo-inositol
73	<a href="#">c2czcD</a>	Alignment	not modelled	98.5	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 pyrococcus horikoshii ot3
74	<a href="#">c3gfgB</a>	Alignment	not modelled	98.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized oxidoreductase yvaa; <b>PDBTitle:</b> structure of putative oxidoreductase yvaa from bacillus subtilis in2 triclinic form
75	<a href="#">c5a06E</a>	Alignment	not modelled	98.5	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> aldose-aldose oxidoreductase; <b>PDBTitle:</b> crystal structure of aldose-aldose oxidoreductase from2 caulobacter crescentus complexed with sorbitol
76	<a href="#">c4gqaC</a>	Alignment	not modelled	98.5	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nad binding oxidoreductase; <b>PDBTitle:</b> crystal structure of nad binding oxidoreductase from klebsiella2 pneumoniae
77	<a href="#">d1cf2o1</a>	Alignment	not modelled	98.5	29	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain

78	<a href="#">c3rbvA</a>	Alignment	not modelled	98.5	12	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar 3-ketoreductase; <b>PDBTitle:</b> crystal structure of kjid10, a 3-ketoreductase from actinomadura2 kijaniata incomplex with nadp
79	<a href="#">c4hadD</a>	Alignment	not modelled	98.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> probable oxidoreductase protein; <b>PDBTitle:</b> crystal structure of probable oxidoreductase protein from rhizobium2 etli cfn 42
80	<a href="#">c3c1aB</a>	Alignment	not modelled	98.5	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase (zp_00056571.1) from2 magnetospirillum magnetotacticum ms-1 at 1.85 a resolution
81	<a href="#">c3f4fF</a>	Alignment	not modelled	98.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> putative oxidoreductase yhhx; <b>PDBTitle:</b> crystal structure of a probable oxidoreductase yhhx in2 triclinic form. northeast structural genomics target er647
82	<a href="#">c5i78A</a>	Alignment	not modelled	98.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-aminoadipic semialdehyde synthase, mitochondrial; <b>PDBTitle:</b> crystal structure of human aminoadipate semialdehyde synthase,2 saccharopine dehydrogenase domain (in nad+ bound form)
83	<a href="#">c3m2tA</a>	Alignment	not modelled	98.5	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable dehydrogenase; <b>PDBTitle:</b> the crystal structure of dehydrogenase from chromobacterium2 violaceum
84	<a href="#">c6norB</a>	Alignment	not modelled	98.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative nad dependent dehydrogenase; <b>PDBTitle:</b> crystal structure of gend2 from gentamicin a biosynthesis in complex2 with nad
85	<a href="#">c3v5nA</a>	Alignment	not modelled	98.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> the crystal structure of oxidoreductase from sinorhizobium melloti
86	<a href="#">c3nt5B</a>	Alignment	not modelled	98.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; <b>PDBTitle:</b> crystal structure of myo-inositol dehydrogenase from bacillus subtilis2 with bound cofactor and product inosose
87	<a href="#">c3ceaA</a>	Alignment	not modelled	98.4	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> myo-inositol 2-dehydrogenase; <b>PDBTitle:</b> crystal structure of myo-inositol 2-dehydrogenase (np_786804.1) from2 lactobacillus plantarum at 2.40 a resolution
88	<a href="#">c3moiA</a>	Alignment	not modelled	98.4	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable dehydrogenase; <b>PDBTitle:</b> the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50
89	<a href="#">c2fpgA</a>	Alignment	not modelled	98.4	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> succinyl-coa ligase [gdp-forming] alpha-chain, <b>PDBTitle:</b> crystal structure of pig gtp-specific succinyl-coa synthetase in2 complex with gdp
90	<a href="#">c1h6dL</a>	Alignment	not modelled	98.4	10	<b>PDB header:</b> protein translocation <b>Chain:</b> L: <b>PDB Molecule:</b> precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol
91	<a href="#">c1evjC</a>	Alignment	not modelled	98.4	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glucose-fructose oxidoreductase; <b>PDBTitle:</b> crystal structure of glucose-fructose oxidoreductase (gfor)2 delta1-22 s64d
92	<a href="#">c1ofgF</a>	Alignment	not modelled	98.4	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> glucose-fructose oxidoreductase; <b>PDBTitle:</b> glucose-fructose oxidoreductase
93	<a href="#">c1zh8B</a>	Alignment	not modelled	98.4	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
94	<a href="#">c3uuwB</a>	Alignment	not modelled	98.4	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase with nad(p)-binding rossmann-fold <b>PDBTitle:</b> 1.63 angstrom resolution crystal structure of dehydrogenase (mvim)2 from clostridium difficile.
95	<a href="#">c3ic5A</a>	Alignment	not modelled	98.4	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative saccharopine dehydrogenase; <b>PDBTitle:</b> n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
96	<a href="#">c6hxaA</a>	Alignment	not modelled	98.4	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> citryl-coa synthetase small subunit; <b>PDBTitle:</b> structure of citryl-coa synthetase from hydrogenobacter thermophilus
97	<a href="#">c3mtjA</a>	Alignment	not modelled	98.4	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
98	<a href="#">c6jnkA</a>	Alignment	not modelled	98.3	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-arabinose 1-dehydrogenase (nad(p)(+)); <b>PDBTitle:</b> crystal structure of azospirillum brasilense l-arabinose 1-2 dehydrogenase (nadp-bound form)
99	<a href="#">c5yabD</a>	Alignment	not modelled	98.3	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> scyllo-inositol dehydrogenase with l-glucose dehydrogenase <b>PDBTitle:</b> crystal structure of scyllo-inositol dehydrogenase with l-glucose2 dehydrogenase activity
100	<a href="#">c1ys4A</a>	Alignment	not modelled	98.3	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate-semialdehyde dehydrogenase; <b>PDBTitle:</b> structure of aspartate-semialdehyde dehydrogenase from methanococcus2 jannaschii
101	<a href="#">c2ejwB</a>	Alignment	not modelled	98.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> homoserine dehydrogenase from thermus thermophilus hb8



102	<a href="#">c1cf2Q_</a>	Alignment	not modelled	98.3	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> Q: <b>PDB Molecule:</b> protein (glyceraldehyde-3-phosphate dehydrogenase); <b>PDBTitle:</b> three-dimensional structure of d-glyceraldehyde-3-phosphate2 dehydrogenase from the hyperthermophilic archaeon methanothermus3 fervidus
103	<a href="#">c3q2kB_</a>	Alignment	not modelled	98.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of the wiba dehydrogenase from bordetella pertussis2 in complex with nadh and udp-glcna
104	<a href="#">c4ew6A_</a>	Alignment	not modelled	98.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-galactose-1-dehydrogenase protein; <b>PDBTitle:</b> crystal structure of d-galactose-1-dehydrogenase protein from2 rhizobium etli
105	<a href="#">c2ep5B_</a>	Alignment	not modelled	98.3	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 350aa long hypothetical aspartate-semialdehyde <b>PDBTitle:</b> structural study of project id st1242 from sulfobolus tokodaii strain7
106	<a href="#">c1lc3A_</a>	Alignment	not modelled	98.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> biliverdin reductase a; <b>PDBTitle:</b> crystal structure of a biliverdin reductase enzyme-cofactor2 complex
107	<a href="#">d1tltA1</a>	Alignment	not modelled	98.3	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
108	<a href="#">d1xeaa1</a>	Alignment	not modelled	98.2	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
109	<a href="#">c1tltB_</a>	Alignment	not modelled	98.2	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase (virulence factor mvim homolog); <b>PDBTitle:</b> crystal structure of a putative oxidoreductase (virulence factor mvim2 homolog)
110	<a href="#">c1b7gO_</a>	Alignment	not modelled	98.2	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> protein (glyceraldehyde 3-phosphate dehydrogenase); <b>PDBTitle:</b> glyceraldehyde 3-phosphate dehydrogenase
111	<a href="#">c2p2sA_</a>	Alignment	not modelled	98.2	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of putative oxidoreductase (yp_050235.1) from2 erwinia carotovora atroseptica scri1043 at 1.25 a resolution
112	<a href="#">c4dpkB_</a>	Alignment	not modelled	98.2	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> malonyl-coa/succinyl-coa reductase; <b>PDBTitle:</b> structure of malonyl-coenzyme a reductase from crenarchaeota
113	<a href="#">c4gmfD_</a>	Alignment	not modelled	98.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> yersiniabactin biosynthetic protein ybtu; <b>PDBTitle:</b> apo structure of a thiazolanyl imine reductase from yersinia2 enterocolitica (irp3)
114	<a href="#">c4fb5A_</a>	Alignment	not modelled	98.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable oxidoreductase protein; <b>PDBTitle:</b> crystal structure of a probable oxidoreductase protein
115	<a href="#">c1e5IA_</a>	Alignment	not modelled	98.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine reductase; <b>PDBTitle:</b> apo saccharopine reductase from magnaporthe grisea
116	<a href="#">c4h3vA_</a>	Alignment	not modelled	98.2	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase domain protein; <b>PDBTitle:</b> crystal structure of oxidoreductase domain protein from kribbella2 flavida
117	<a href="#">c1s7cA_</a>	Alignment	not modelled	98.2	29	<b>PDB header:</b> structural genomics, oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase a; <b>PDBTitle:</b> crystal structure of mes buffer bound form of glyceraldehyde 3-2 phosphate dehydrogenase from escherichia coli
118	<a href="#">c6dzsD_</a>	Alignment	not modelled	98.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> mycobacterial homoserine dehydrogenase thra in complex with nadp
119	<a href="#">c5cefA_</a>	Alignment	not modelled	98.1	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate-semialdehyde dehydrogenase; <b>PDBTitle:</b> cystal structure of aspartate semialdehyde dehydrogenase from2 cryptococcus neoformans
120	<a href="#">c1ebuA_</a>	Alignment	not modelled	98.1	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> homoserine dehydrogenase complex with nad analogue and l-2 homoserine