




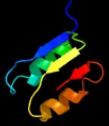
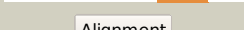

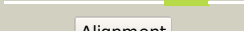










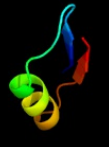

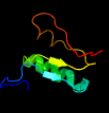


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD2899c\_(fdhD)\_3208586\_3209416  
 Date Thu Aug 8 16:20:05 BST 2019  
 Unique Job ID d734f043d8943f7d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4pdeA_</a>	 Alignment		100.0	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein fdhd; <b>PDBTitle:</b> crystal structure of fdhd in complex with gdp
2	<a href="#">d2pw9a1</a>	 Alignment		100.0	25	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> FdhD/NarQ
3	<a href="#">d2nu7a1</a>	 Alignment		89.1	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
4	<a href="#">d1oi7a1</a>	 Alignment		88.9	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
5	<a href="#">c6hxqA_</a>	 Alignment		68.3	19	<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
6	<a href="#">c3mwdB_</a>	 Alignment		65.9	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> atp-citrate synthase; <b>PDBTitle:</b> truncated human atp-citrate lyase with citrate bound
7	<a href="#">c3evnA_</a>	 Alignment		64.6	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
8	<a href="#">c2duwA_</a>	 Alignment		62.6	19	<b>PDB header:</b> ligand binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative coa-binding protein; <b>PDBTitle:</b> solution structure of putative coa-binding protein of2 klebsiella pneumoniae
9	<a href="#">d1iuKa_</a>	 Alignment		60.3	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
10	<a href="#">c1y88A_</a>	 Alignment		56.4	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein af1548; <b>PDBTitle:</b> crystal structure of protein of unknown function af1548
11	<a href="#">c4h3vA_</a>	 Alignment		53.6	27	<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 flvida

12	<a href="#">c3ff4A_</a>	Alignment		52.8	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein chu_1412
13	<a href="#">c3dtyA_</a>	Alignment		52.6	14	<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 pseudomonas2 syringae
14	<a href="#">d1y88a2</a>	Alignment		51.8	22	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> MRR-like
15	<a href="#">d2csua1</a>	Alignment		51.5	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
16	<a href="#">d1y81a1</a>	Alignment		50.8	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
17	<a href="#">c4xb1B_</a>	Alignment		50.4	24	<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
18	<a href="#">c5yeeA_</a>	Alignment		45.9	24	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of lokiprofilin1/rabbit actin complex
19	<a href="#">d1j5pa4</a>	Alignment		44.0	11	<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
20	<a href="#">c1oi7A_</a>	Alignment		43.2	25	<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
21	<a href="#">d2zdra2</a>	Alignment	not modelled	42.5	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> NeuB-like
22	<a href="#">d1q3qa2</a>	Alignment	not modelled	41.8	19	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> GroEL apical domain-like <b>Family:</b> Group II chaperonin (CCT, TRIC), apical domain
23	<a href="#">c1y4hA_</a>	Alignment	not modelled	41.8	7	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine protease; <b>PDBTitle:</b> wild type staphopain-staphostatin complex
24	<a href="#">c3euwB_</a>	Alignment	not modelled	41.4	16	<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
25	<a href="#">d1mxsa_</a>	Alignment	not modelled	41.3	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
26	<a href="#">d1vlia2</a>	Alignment	not modelled	40.3	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> NeuB-like
27	<a href="#">c2v4iA_</a>	Alignment	not modelled	40.2	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate n-acetyltransferase 2 alpha chain; <b>PDBTitle:</b> structure of a novel n-acyl-enzyme intermediate of an n-2 terminal nucleophile (ntn) hydrolase, oat2
28	<a href="#">c4gmfD_</a>	Alignment	not modelled	39.6	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> yersiniabactin biosynthetic protein ybtu; <b>PDBTitle:</b> apo structure of a thiazolinyli imine reductase from yersinia2 enterocolitica (irp3) <b>PDB header:</b> lyase

29	<a href="#">c6daoB</a>	Alignment	not modelled	39.2	6	<b>Chain:</b> B: <b>PDB Molecule:</b> trans-o-hydroxybenzylidenepyruvate hydratase-aldolase; <b>PDBTitle:</b> nahe wt selenomethionine
30	<a href="#">c2hwgA</a>	Alignment	not modelled	39.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate-protein phosphotransferase; <b>PDBTitle:</b> structure of phosphorylated enzyme i of the phosphoenolpyruvate:sugar2 phosphotransferase system
31	<a href="#">d1lassa</a>	Alignment	not modelled	38.6	19	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> GroEL apical domain-like <b>Family:</b> Group II chaperonin (CCT, TRIC), apical domain
32	<a href="#">c6oviA</a>	Alignment	not modelled	38.3	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> keto-deoxy-phosphogluconate aldolase; <b>PDBTitle:</b> crystal structure of kdpq aldolase from legionella pneumophila with2 pyruvate captured at low ph as a covalent carbinolamine intermediate
33	<a href="#">c1xuzA</a>	Alignment	not modelled	37.9	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> polysialic acid capsule biosynthesis protein siaC; <b>PDBTitle:</b> crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
34	<a href="#">d2d59a1</a>	Alignment	not modelled	37.7	27	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
35	<a href="#">d1gmla</a>	Alignment	not modelled	37.5	16	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> GroEL apical domain-like <b>Family:</b> Group II chaperonin (CCT, TRIC), apical domain
36	<a href="#">d1kzyc2</a>	Alignment	not modelled	37.4	17	<b>Fold:</b> BRCT domain <b>Superfamily:</b> BRCT domain <b>Family:</b> 53BP1
37	<a href="#">c3oa0B</a>	Alignment	not modelled	37.4	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> lipopolysaccharide biosynthesis protein wbbp; <b>PDBTitle:</b> crystal structure of the wlba (wbbp) dehydrogenase from thermus2 thermophilus in complex with nad and udp-glcnaC
38	<a href="#">c3g8rA</a>	Alignment	not modelled	36.8	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable spore coat polysaccharide biosynthesis protein e; <b>PDBTitle:</b> crystal structure of putative spore coat polysaccharide biosynthesis2 protein e from chromobacterium violaceum atcc 12472
39	<a href="#">c3f4f</a>	Alignment	not modelled	36.0	30	<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
40	<a href="#">c2hmcA</a>	Alignment	not modelled	35.3	32	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
41	<a href="#">d1e0ta2</a>	Alignment	not modelled	35.0	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Pyruvate kinase
42	<a href="#">d1g8ma2</a>	Alignment	not modelled	34.6	25	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
43	<a href="#">c4qccA</a>	Alignment	not modelled	34.2	18	<b>PDB header:</b> structural protein, lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxy-6-phosphogalactonate aldolase, peptidyl- <b>PDBTitle:</b> structure of a cube-shaped, highly porous protein cage designed by2 fusing symmetric oligomeric domains
44	<a href="#">c6iauB</a>	Alignment	not modelled	33.9	21	<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
45	<a href="#">c2qneA</a>	Alignment	not modelled	33.5	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase; <b>PDBTitle:</b> crystal structure of putative methyltransferase (zp_00558420.1) from2 desulfitobacterium hafniense y51 at 2.30 a resolution
46	<a href="#">d1h6da1</a>	Alignment	not modelled	33.3	21	<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
47	<a href="#">d1euca1</a>	Alignment	not modelled	32.8	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
48	<a href="#">c3ip3D</a>	Alignment	not modelled	32.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> oxidoreductase, putative; <b>PDBTitle:</b> structure of putative oxidoreductase (tm_0425) from thermotoga2 maritima
49	<a href="#">d1wpga2</a>	Alignment	not modelled	32.1	24	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Meta-cation ATPase, catalytic domain P
50	<a href="#">c3oa2B</a>	Alignment	not modelled	32.1	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> wbbp; <b>PDBTitle:</b> crystal structure of the wlba (wbbp) dehydrogenase from pseudomonas2 aeruginosa in complex with nad at 1.5 angstrom resolution
51	<a href="#">c6ncsB</a>	Alignment	not modelled	32.0	21	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> n-acetylneuraminic acid (sialic acid) synthetase; <b>PDBTitle:</b> crystal structure of n-acetylneuraminic acid (sialic acid) synthetase2 from leptospira borgpetersenii serovar hardjo-bovis in complex with3 citrate
						<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> 4-hydroxy-2-oxoglutarate aldolase/2-

52	<a href="#">c2yw3E_</a>	Alignment	not modelled	31.9	33	deydro-3- <b>PDBTitle:</b> crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 deydro-3-deoxyphosphogluconate aldolase from tthb1
53	<a href="#">c5uibA_</a>	Alignment	not modelled	31.7	27	<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
54	<a href="#">c3wb9A_</a>	Alignment	not modelled	31.6	24	<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
55	<a href="#">c2o48X_</a>	Alignment	not modelled	31.0	20	<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
56	<a href="#">d1cv8a_</a>	Alignment	not modelled	31.0	4	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
57	<a href="#">c5b3uB_</a>	Alignment	not modelled	29.7	18	<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
58	<a href="#">c5av0A_</a>	Alignment	not modelled	29.3	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> crystal structure of the reduced form of homoserine dehydrogenase from2 sulfobolus tokodaii.
59	<a href="#">c3lciA_</a>	Alignment	not modelled	28.9	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylneuraminate lyase; <b>PDBTitle:</b> the d-sialic acid aldolase mutant v251w
60	<a href="#">c6jnkA_</a>	Alignment	not modelled	28.8	16	<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)
61	<a href="#">d2a6na1</a>	Alignment	not modelled	28.8	28	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
62	<a href="#">c3e82A_</a>	Alignment	not modelled	28.7	20	<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
63	<a href="#">c5kt0A_</a>	Alignment	not modelled	28.7	14	<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.
64	<a href="#">c5uf2A_</a>	Alignment	not modelled	28.6	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of ribose 5 phosphate isomerase a from neisseria2 gonorrhoeae
65	<a href="#">c1j3wB_</a>	Alignment	not modelled	28.6	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> giding protein-mglb; <b>PDBTitle:</b> structure of gliding protein-mglb from thermus thermophilus hb8
66	<a href="#">c2fpgA_</a>	Alignment	not modelled	28.5	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
67	<a href="#">d1a6db2</a>	Alignment	not modelled	28.3	22	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> GroEL apical domain-like <b>Family:</b> Group II chaperonin (CCT, TRIC), apical domain
68	<a href="#">c3wycB_</a>	Alignment	not modelled	28.0	9	<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
69	<a href="#">c3e0fA_</a>	Alignment	not modelled	27.8	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative metal-dependent phosphoesterase; <b>PDBTitle:</b> crystal structure of a putative metal-dependent phosphoesterase2 (bad_1165) from bifidobacterium adolescentis atcc 15703 at 2.40 a3 resolution
70	<a href="#">c3aq1B_</a>	Alignment	not modelled	27.8	20	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> thermosome subunit; <b>PDBTitle:</b> open state monomer of a group ii chaperonin from methanococoides2 burtonii
71	<a href="#">c4mxeA_</a>	Alignment	not modelled	27.3	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetyltransferase esco1; <b>PDBTitle:</b> human esco1 (eco1/ctf7 ortholog), acetyltransferase domain in complex2 with acetyl-coa
72	<a href="#">c2glxD_</a>	Alignment	not modelled	26.9	27	<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
73	<a href="#">c3u3xj_</a>	Alignment	not modelled	26.8	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> J: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase from sinorhizobium2 melliloti 1021
74	<a href="#">c3p9ee_</a>	Alignment	not modelled	26.7	18	<b>PDB header:</b> chaperone <b>Chain:</b> E: <b>PDB Molecule:</b> <b>PDBTitle:</b> the crystal structure of yeast cct reveals intrinsic asymmetry of2 eukaryotic cytosolic chaperonins
75	<a href="#">c4fb5A_</a>	Alignment	not modelled	26.5	21	<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
76	<a href="#">c2nu8D_</a>	Alignment	not modelled	26.4	19	<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 <b>PDB header:</b> oxidoreductase

77	<a href="#">c4hktA</a>	Alignment	not modelled	26.4	14	<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)
78	<a href="#">c1zh8B</a>	Alignment	not modelled	25.9	20	<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
79	<a href="#">c3nt5B</a>	Alignment	not modelled	25.8	21	<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
80	<a href="#">c2ia5C</a>	Alignment	not modelled	25.2	29	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> polynucleotide kinase; <b>PDBTitle:</b> t4 polynucleotide kinase/phosphatase with bound sulfate and magnesium.
81	<a href="#">d1vz6a</a>	Alignment	not modelled	25.2	21	<b>Fold:</b> DmpA/Argj-like <b>Superfamily:</b> DmpA/Argj-like <b>Family:</b> Argj-like
82	<a href="#">d1hl2a</a>	Alignment	not modelled	25.1	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
83	<a href="#">c2ixaA</a>	Alignment	not modelled	24.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-n-acetylgalactosaminidase; <b>PDBTitle:</b> a-zyme, n-acetylgalactosaminidase
84	<a href="#">c6o6dA</a>	Alignment	not modelled	24.6	35	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor if-3; <b>PDBTitle:</b> n-terminal domain of translation initiation factor if-3 from2 helicobacter pylori
85	<a href="#">c4hbrD</a>	Alignment	not modelled	24.5	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> putative periplasmic protein; <b>PDBTitle:</b> crystal structure of a putative periplasmic proteins (bacegg_01429)2 from bacteroides eggerthii dsm 20697 at 2.40 a resolution
86	<a href="#">c6hxbB</a>	Alignment	not modelled	24.5	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> atp-citrate lyase alpha-subunit; <b>PDBTitle:</b> structure of atp citrate lyase from chlorobium limicola in complex2 with citrate and coenzyme a.
87	<a href="#">d1f74a</a>	Alignment	not modelled	24.2	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
88	<a href="#">c5yabD</a>	Alignment	not modelled	24.0	24	<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
89	<a href="#">d1ebfa1</a>	Alignment	not modelled	23.7	15	<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
90	<a href="#">c3oqbF</a>	Alignment	not modelled	23.7	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of putative oxidoreductase from bradyrhizobium2 japonicum usda 110
91	<a href="#">c3e18A</a>	Alignment	not modelled	23.6	21	<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
92	<a href="#">d2ioja1</a>	Alignment	not modelled	23.6	15	<b>Fold:</b> MurF and HprK N-domain-like <b>Superfamily:</b> HprK N-terminal domain-like <b>Family:</b> DRTGG domain
93	<a href="#">d2nvwa1</a>	Alignment	not modelled	23.3	15	<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
94	<a href="#">c1xeaD</a>	Alignment	not modelled	23.3	24	<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
95	<a href="#">c1lc3A</a>	Alignment	not modelled	23.2	25	<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
96	<a href="#">c1vliA</a>	Alignment	not modelled	22.9	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> spore coat polysaccharide biosynthesis protein spse; <b>PDBTitle:</b> crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
97	<a href="#">c3fkaA</a>	Alignment	not modelled	22.9	9	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> l-2-keto-3-deoxyarabonate dehydratase; <b>PDBTitle:</b> structure of l-2-keto-3-deoxyarabonate dehydratase
98	<a href="#">c4i7vD</a>	Alignment	not modelled	22.8	25	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> D: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> agrobacterium tumefaciens dhps with pyruvate
99	<a href="#">c5z2fA</a>	Alignment	not modelled	22.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> nadph/pda bound dihydrodipicolinate reductase from paenissporosarcina2 sp. tg-14
100	<a href="#">d1lc0a1</a>	Alignment	not modelled	22.8	25	<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
101	<a href="#">c2ehhE</a>	Alignment	not modelled	22.7	20	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus



102	<a href="#">c5n1wA_</a>	Alignment	not modelled	22.5	22	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> xeco2; <b>PDBTitle:</b> structure of xeco2 acetyltransferase domain bound to k105-coa2 conjugate
103	<a href="#">c3e9mC_</a>	Alignment	not modelled	22.4	21	<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
104	<a href="#">c4hadD_</a>	Alignment	not modelled	22.2	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
105	<a href="#">c6hxiD_</a>	Alignment	not modelled	22.2	23	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> succinyl-coa ligase (adp-forming) subunit alpha; <b>PDBTitle:</b> structure of atp citrate lyase from methanothrix soehngenii in complex2 with citrate and coenzyme a
106	<a href="#">c3pueA_</a>	Alignment	not modelled	22.2	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of the complex of dhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
107	<a href="#">c2v9dB_</a>	Alignment	not modelled	22.0	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> yage; <b>PDBTitle:</b> crystal structure of yage, a prophage protein belonging to2 the dihydrodipicolinic acid synthase family from e. coli3 k12
108	<a href="#">c3bt3B_</a>	Alignment	not modelled	21.7	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxalase-related enzyme, arac type; <b>PDBTitle:</b> crystal structure of a glyoxalase-related enzyme from clostridium2 phytofermentans
109	<a href="#">c3cprB_</a>	Alignment	not modelled	21.6	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthetase; <b>PDBTitle:</b> the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
110	<a href="#">c3ec7C_</a>	Alignment	not modelled	21.4	16	<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
111	<a href="#">c4ah7C_</a>	Alignment	not modelled	21.2	19	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> n-acetylneuraminate lyase; <b>PDBTitle:</b> structure of wild type stapylococcus aureus n-acetylneuraminic acid2 lyase in complex with pyruvate
112	<a href="#">c1m0sA_</a>	Alignment	not modelled	20.7	21	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> northeast structural genomics consortium (nesg id ir21)
113	<a href="#">c5ui3C_</a>	Alignment	not modelled	20.4	13	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dhds from chlamydomonas reinhardtii
114	<a href="#">c3kyeC_</a>	Alignment	not modelled	20.4	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> roadblock/lc7 domain, robl lc7; <b>PDBTitle:</b> crystal structure of roadblock/lc7 domain from streptomyces2 avermitilis