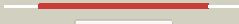

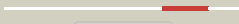




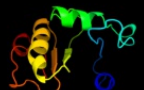





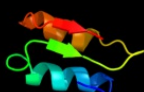







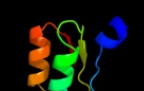


# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P32177
Date	Thu Jan 5 11:49:54 GMT 2012
Unique Job ID	0f80e69fb230b9a3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2pw9a1</a>	 Alignment		100.0	28	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> FdhD/NarQ
2	<a href="#">d2nu7a1</a>	 Alignment		91.4	12	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
3	<a href="#">d1oi7a1</a>	 Alignment		88.0	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
4	<a href="#">c3evnA_</a>	 Alignment		70.7	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, gfo/ldh/moca family; <b>PDBTitle:</b> crystal structure of putative oxidoreductase from streptococcus2 agalactiae 2603v/r
5	<a href="#">c1y88A_</a>	 Alignment		68.0	19	<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
6	<a href="#">c3dtyA_</a>	 Alignment		67.3	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, gfo/ldh/moca family; <b>PDBTitle:</b> crystal structure of an oxidoreductase from pseudomonas2 syringae
7	<a href="#">c2duwA_</a>	 Alignment		66.6	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 of 2 klebsiella pneumoniae
8	<a href="#">d1iuka_</a>	 Alignment		65.9	3	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
9	<a href="#">d1y88a2</a>	 Alignment		63.5	19	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> MRR-like
10	<a href="#">d1gvfa_</a>	 Alignment		63.4	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class II FBP aldolase
11	<a href="#">d2d59a1</a>	 Alignment		63.2	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain

12	<a href="#">c3ff4A_</a>	Alignment		63.0	9	<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="#">c3euwB_</a>	Alignment		61.6	9	<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
14	<a href="#">d1y81a1</a>	Alignment		61.6	9	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
15	<a href="#">d2csua1</a>	Alignment		58.8	15	<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="#">c3f41F_</a>	Alignment		53.8	20	<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
17	<a href="#">d1g8ma2</a>	Alignment		53.7	26	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> ALCAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
18	<a href="#">d1j5pa4</a>	Alignment		49.9	8	<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="#">c3e82A_</a>	Alignment		48.7	9	<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
20	<a href="#">c2o48X_</a>	Alignment		48.5	16	<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
21	<a href="#">c2glxD_</a>	Alignment	not modelled	47.3	20	<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
22	<a href="#">c2v4iA_</a>	Alignment	not modelled	46.7	17	<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
23	<a href="#">d1h6da1</a>	Alignment	not modelled	46.3	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
24	<a href="#">d1q3qa2</a>	Alignment	not modelled	45.0	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
25	<a href="#">d2zdra2</a>	Alignment	not modelled	44.4	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> NeuB-like
26	<a href="#">c3mwdB_</a>	Alignment	not modelled	43.3	11	<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
27	<a href="#">d1assa_</a>	Alignment	not modelled	43.1	17	<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
28	<a href="#">d1kzyc2</a>	Alignment	not modelled	43.0	4	<b>Fold:</b> BRCT domain <b>Superfamily:</b> BRCT domain <b>Family:</b> 53BP1
						<b>PDB header:</b> hydrolase/hydrolase inhibitor

29	<a href="#">c1y4hA_</a>	Alignment	not modelled	42.3	16	<b>Chain:</b> A: <b>PDB Molecule:</b> cysteine protease; <b>PDBTitle:</b> wild type staphopain-staphostatin complex
30	<a href="#">d2nvwa1</a>	Alignment	not modelled	41.8	16	<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="#">d1euca1</a>	Alignment	not modelled	41.6	9	<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="#">d1gmla_</a>	Alignment	not modelled	41.0	14	<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
33	<a href="#">c3ec7C_</a>	Alignment	not modelled	40.8	13	<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
34	<a href="#">c3e18A_</a>	Alignment	not modelled	40.6	18	<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
35	<a href="#">d1vlia2</a>	Alignment	not modelled	40.5	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> NeuB-like
36	<a href="#">c3g8rA_</a>	Alignment	not modelled	40.4	7	<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
37	<a href="#">c3oqbF_</a>	Alignment	not modelled	40.2	12	<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
38	<a href="#">c3nt5B_</a>	Alignment	not modelled	39.4	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
39	<a href="#">c1xuzA_</a>	Alignment	not modelled	39.1	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 mannosaminol
40	<a href="#">d2ioja1</a>	Alignment	not modelled	38.8	15	<b>Fold:</b> MurF and HprK N-domain-like <b>Superfamily:</b> HprK N-terminal domain-like <b>Family:</b> DRTGG domain
41	<a href="#">d1mxsa_</a>	Alignment	not modelled	38.6	7	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
42	<a href="#">c3ip3D_</a>	Alignment	not modelled	38.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> oxidoreductase, putative; <b>PDBTitle:</b> structure of putative oxidoreductase (tm_0425) from2 thermotoga maritima
43	<a href="#">c2iswB_</a>	Alignment	not modelled	37.9	23	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative fructose-1,6-bisphosphate aldolase; <b>PDBTitle:</b> structure of giardia fructose-1,6-bisphosphate aldolase in2 complex with phosphoglycolohydroxamate
44	<a href="#">c2hmcA_</a>	Alignment	not modelled	37.8	24	<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
45	<a href="#">c3q2kB_</a>	Alignment	not modelled	37.7	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of the wlbA dehydrogenase from bordetella pertussis2 in complex with nadh and udp-glcnaa
46	<a href="#">c2ixaA_</a>	Alignment	not modelled	37.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-n-acetyl galactosaminidase; <b>PDBTitle:</b> a-zyme, n-acetyl galactosaminidase
47	<a href="#">c3e9mC_</a>	Alignment	not modelled	37.5	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> oxidoreductase, gfo/ldh/moa family; <b>PDBTitle:</b> crystal structure of an oxidoreductase from enterococcus2 faecalis
48	<a href="#">c1oi7A_</a>	Alignment	not modelled	37.2	16	<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
49	<a href="#">c3aq1B_</a>	Alignment	not modelled	36.9	23	<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 methanococcus2 burtonii
50	<a href="#">c2fpgA_</a>	Alignment	not modelled	36.4	13	<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-coa2 synthetase in complex with gdp
51	<a href="#">d1lc0a1</a>	Alignment	not modelled	36.2	16	<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
52	<a href="#">c3gfgB_</a>	Alignment	not modelled	36.1	14	<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
53	<a href="#">c1evjC_</a>	Alignment	not modelled	35.8	14	<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
54	<a href="#">c3oa2B_</a>	Alignment	not modelled	35.4	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
55	<a href="#">d1vz6a_</a>	Alignment	not modelled	35.2	17	<b>Fold:</b> DmpA/ArgJ-like <b>Superfamily:</b> DmpA/ArgJ-like <b>Family:</b> ArgJ-like
56	<a href="#">c1zh8B_</a>	Alignment	not modelled	34.8	18	<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
57	<a href="#">d1e0ta2</a>	Alignment	not modelled	34.4	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Pyruvate kinase
58	<a href="#">c3c1aB_</a>	Alignment	not modelled	34.2	14	<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
59	<a href="#">d1cv8a_</a>	Alignment	not modelled	33.3	17	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
60	<a href="#">c3dmyA_</a>	Alignment	not modelled	33.0	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein fdra; <b>PDBTitle:</b> crystal structure of a predicated acyl-coa synthetase from e.coli
61	<a href="#">c3ceaA_</a>	Alignment	not modelled	33.0	8	<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
62	<a href="#">c3p9ee_</a>	Alignment	not modelled	32.8	14	<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
63	<a href="#">d1a6db2</a>	Alignment	not modelled	32.3	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
64	<a href="#">d1ryda1</a>	Alignment	not modelled	32.2	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
65	<a href="#">c1m0sA_</a>	Alignment	not modelled	31.8	10	<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)
66	<a href="#">c3fd8A_</a>	Alignment	not modelled	31.4	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, gfo/ldh/moca family; <b>PDBTitle:</b> crystal structure of an oxidoreductase from enterococcus2 faecalis
67	<a href="#">c2yw3E_</a>	Alignment	not modelled	31.0	31	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> 4-hydroxy-2-oxoglutarate aldolase/2-dehydro-3- <b>PDBTitle:</b> crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 dehydro-3-deoxyphosphogluconate aldolase from tthb1
68	<a href="#">c3v5nA_</a>	Alignment	not modelled	30.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> the crystal structure of oxidoreductase from sinorhizobium meliloti
69	<a href="#">d1ydwa1</a>	Alignment	not modelled	29.4	19	<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
70	<a href="#">c2q4eB_</a>	Alignment	not modelled	28.8	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
71	<a href="#">d2a6na1</a>	Alignment	not modelled	28.4	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
72	<a href="#">c3oa0B_</a>	Alignment	not modelled	28.4	15	<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
73	<a href="#">c1xeaD_</a>	Alignment	not modelled	28.3	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> oxidoreductase, gfo/ldh/moca family; <b>PDBTitle:</b> crystal structure of a gfo/ldh/moca family oxidoreductase2 from vibrio cholerae
74	<a href="#">c3lciA_</a>	Alignment	not modelled	27.8	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
75	<a href="#">c3fhIC_</a>	Alignment	not modelled	27.8	16	<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
76	<a href="#">c1lc3A_</a>	Alignment	not modelled	27.6	16	<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
77	<a href="#">c3n2xB_</a>	Alignment	not modelled	27.5	10	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein yage; <b>PDBTitle:</b> crystal structure of yage, a prophage protein belonging to the2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable nadp-dependent mannitol

78	<a href="#">c3gdfA_</a>	Alignment	not modelled	27.2	18	dehydrogenase; <b>PDBTitle:</b> crystal structure of the nadp-dependent mannitol dehydrogenase from2 cladosporium herbarum.
79	<a href="#">c2nu8D_</a>	Alignment	not modelled	27.0	6	<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
80	<a href="#">d1pkxa2</a>	Alignment	not modelled	27.0	20	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> AlCAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
81	<a href="#">c3rbvA_</a>	Alignment	not modelled	26.9	20	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar 3-ketoreductase; <b>PDBTitle:</b> crystal structure of kijd10, a 3-ketoreductase from actinomadura2 kijaniata incomplex with nadp
82	<a href="#">c3moiA_</a>	Alignment	not modelled	26.3	17	<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
83	<a href="#">c3kuxA_</a>	Alignment	not modelled	26.1	20	<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
84	<a href="#">c3sz8D_</a>	Alignment	not modelled	26.0	15	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphoactonate aldolase 2; <b>PDBTitle:</b> crystal structure of 2-dehydro-3-deoxyphosphoactonate aldolase from2 burkholderia pseudomallei
85	<a href="#">c2csuB_</a>	Alignment	not modelled	26.0	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> 457aa long hypothetical protein; <b>PDBTitle:</b> crystal structure of ph0766 from pyrococcus horikoshii ot3
86	<a href="#">d1wzca1</a>	Alignment	not modelled	25.9	11	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
87	<a href="#">c1j3wB_</a>	Alignment	not modelled	25.8	10	<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
88	<a href="#">c2okkA_</a>	Alignment	not modelled	25.0	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate decarboxylase 2; <b>PDBTitle:</b> the x-ray crystal structure of the 65kda isoform of glutamic acid2 decarboxylase (gad65)
89	<a href="#">d1wpqa2</a>	Alignment	not modelled	24.6	12	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Meta-cation ATPase, catalytic domain P
90	<a href="#">c3ezyB_</a>	Alignment	not modelled	24.6	18	<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 from2 thermotoga maritima
91	<a href="#">d1j5ya2</a>	Alignment	not modelled	24.5	15	<b>Fold:</b> HPr-like <b>Superfamily:</b> Putative transcriptional regulator TM1602, C-terminal domain <b>Family:</b> Putative transcriptional regulator TM1602, C-terminal domain
92	<a href="#">d1ebfa1</a>	Alignment	not modelled	24.4	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
93	<a href="#">c1vliA_</a>	Alignment	not modelled	24.3	17	<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
94	<a href="#">d1j4aa2</a>	Alignment	not modelled	23.9	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Formate/glycerate dehydrogenase catalytic domain-like <b>Family:</b> Formate/glycerate dehydrogenases, substrate-binding domain
95	<a href="#">c1ezaA_</a>	Alignment	not modelled	23.4	10	<b>PDB header:</b> phosphotransferase <b>Chain:</b> A: <b>PDB Molecule:</b> enzyme i; <b>PDBTitle:</b> amino terminal domain of enzyme i from escherichia coli nmr,2 restrained regularized mean structure
96	<a href="#">d1nmpa_</a>	Alignment	not modelled	23.0	13	<b>Fold:</b> NIF3 (NKG1p interacting factor 3)-like <b>Superfamily:</b> NIF3 (NKG1p interacting factor 3)-like <b>Family:</b> NIF3 (NKG1p interacting factor 3)-like
97	<a href="#">d1zcza2</a>	Alignment	not modelled	22.8	17	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> AlCAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
98	<a href="#">d1nvmb1</a>	Alignment	not modelled	22.5	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
99	<a href="#">d1hl2a_</a>	Alignment	not modelled	22.3	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
100	<a href="#">d1f74a_</a>	Alignment	not modelled	22.2	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
101	<a href="#">c3fkka_</a>	Alignment	not modelled	21.9	13	<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
102	<a href="#">c3bt3B_</a>	Alignment	not modelled	21.9	8	<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 <b>PDB header:</b> lyase

103	<a href="#">c2v9dB_</a>	Alignment	not modelled	21.5	9	<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
104	<a href="#">c3d0cB_</a>	Alignment	not modelled	21.1	9	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2 oceanobacillus iheyensis at 1.9 a resolution
105	<a href="#">c2v82A_</a>	Alignment	not modelled	20.6	13	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; <b>PDBTitle:</b> kdpgal complexed to kdpgal
106	<a href="#">c3pueA_</a>	Alignment	not modelled	20.5	19	<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