Phyre2

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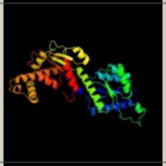
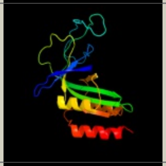
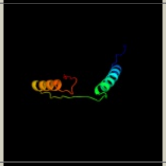
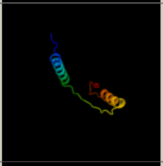
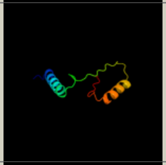
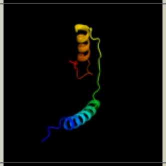
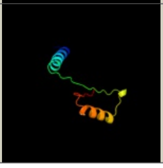
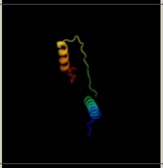
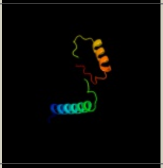
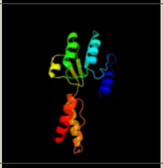
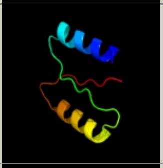
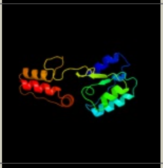
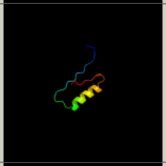
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2hxgB_	Alignment		100.0	99	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**l-arabinose isomerase; **PDBTitle:** crystal structure of mn2+ bound ecai
2	d2ajta2	Alignment		100.0	99	**Fold:**FucI/AraA N-terminal and middle domains **Superfamily:**FucI/AraA N-terminal and middle domains **Family:**AraA N-terminal and middle domain-like
3	d2ajta1	Alignment		100.0	99	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**FucI/AraA C-terminal domain-like **Family:**AraA C-terminal domain-like
4	d1fuia2	Alignment		100.0	12	**Fold:**FucI/AraA N-terminal and middle domains **Superfamily:**FucI/AraA N-terminal and middle domains **Family:**L-fucose isomerase, N-terminal and second domains
5	c1fuiB_	Alignment		100.0	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**l-fucose isomerase; **PDBTitle:** l-fucose isomerase from escherichia coli
6	c3a9rA_	Alignment		100.0	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**d-arabinose isomerase; **PDBTitle:** x-ray structures of bacillus pallidus d-arabinose2 isomerasecomplex with (4r)-2-methylpentane-2,4-diol
7	c2c2xB_	Alignment		87.2	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase- **PDBTitle:** three dimensional structure of bifunctional2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase3 from mycobacterium tuberculosis
8	d1a4ia2	Alignment		86.5	26	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Tetrahydrofolate dehydrogenase/cyclohydrolase
9	d1b0aa2	Alignment		84.7	23	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Tetrahydrofolate dehydrogenase/cyclohydrolase
10	c3p2oA_	Alignment		82.3	22	**PDB header:**oxidoreductase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of fold bifunctional protein from campylobacter2 jejuni
11	c3nglA_	Alignment		81.6	15	**PDB header:**oxidoreductase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of bifunctional 5,10-methylenetetrahydrofolate2 dehydrogenase / cyclohydrolase from thermoplasma acidophilum

12	c3p2oB_	Alignment		79.3	21	**PDB header:**oxidoreductase, hydrolase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of fold bifunctional protein from campylobacter2 jejuni
13	c1a4iB_	Alignment		77.9	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase / **PDBTitle:** human tetrahydrofolate dehydrogenase / cyclohydrolase
14	c1b0aA_	Alignment		74.8	23	**PDB header:**oxidoreductase,hydrolase **Chain:** A: **PDB Molecule:**protein (fold bifunctional protein); **PDBTitle:** 5,10, methylene-tetrahydropholate2 dehydrogenase/cyclohydrolase from e coli.
15	d1gcaa_	Alignment		74.7	12	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
16	d1fuia1	Alignment		68.2	15	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**FucI/AraA C-terminal domain-like **Family:**L-fucose isomerase, C-terminal domain
17	c4a5oB_	Alignment		67.3	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of pseudomonas aeruginosa n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
18	c3h5oB_	Alignment		65.2	10	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator gntr; **PDBTitle:** the crystal structure of transcription regulator gntr from2 chromobacterium violaceum
19	c4a26B_	Alignment		64.3	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative c-1-tetrahydrofolate synthase, cytoplasmic; **PDBTitle:** the crystal structure of leishmania major n5,n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase
20	c2p2gD_	Alignment		64.1	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
21	c3l07B_	Alignment	not modelled	63.4	17	**PDB header:**oxidoreductase,hydrolase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella3 tularensis.
22	c2x7xA_	Alignment	not modelled	61.2	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** fructose binding periplasmic domain of hybrid two component2 system bt1754
23	c3bblA_	Alignment	not modelled	60.5	12	**PDB header:**regulatory protein **Chain:** A: **PDB Molecule:**regulatory protein of laci family; **PDBTitle:** crystal structure of a regulatory protein of laci family from2 chloroflexus aggregans
24	c3oqbF_	Alignment	not modelled	57.9	19	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase from bradyrhizobium2 japonicum usda 110
25	c3v5nA_	Alignment	not modelled	56.2	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** the crystal structure of oxidoreductase from sinorhizobium meliloti
26	c3nt5B_	Alignment	not modelled	56.1	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; **PDBTitle:** crystal structure of myo-inositol dehydrogenase from bacillus subtilis2 with bound cofactor and product inosose
27	c3eafA_	Alignment	not modelled	54.3	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter, substrate binding protein; **PDBTitle:** crystal structure of abc transporter, substrate binding protein2 aeropyrum pernix
						Fold: Periplasmic binding protein-like I

28	d2dria_	Alignment	not modelled	53.8	14	**Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
29	c3kkeA_	Alignment	not modelled	51.4	12	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**laci family transcriptional regulator; **PDBTitle:** crystal structure of a laci family transcriptional regulator2 from mycobacterium smegmatis
30	c3e18A_	Alignment	not modelled	51.3	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of nad-binding protein from listeria innocua
31	c3ec7C_	Alignment	not modelled	51.2	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative dehydrogenase; **PDBTitle:** crystal structure of putative dehydrogenase from salmonella2 typhimurium lt2
32	d1skyb3	Alignment	not modelled	50.2	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
33	c3ksmA_	Alignment	not modelled	47.1	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc-type sugar transport system, periplasmic component; **PDBTitle:** crystal structure of abc-type sugar transport system, periplasmic2 component from hahella chejuensis
34	d2fvya1	Alignment	not modelled	46.5	14	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
35	c3d8uA_	Alignment	not modelled	45.6	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**purr transcriptional regulator; **PDBTitle:** the crystal structure of a purr family transcriptional regulator from2 vibrio parahaemolyticus rimd 2210633
36	c3moiA_	Alignment	not modelled	44.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable dehydrogenase; **PDBTitle:** the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50
37	c2xecD_	Alignment	not modelled	43.7	14	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative maleate isomerase; **PDBTitle:** nocardia farcinica maleate cis-trans isomerase bound to2 tris
38	c3hcwB_	Alignment	not modelled	43.0	8	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**maltose operon transcriptional repressor; **PDBTitle:** crystal structure of probable maltose operon transcriptional repressor2 malr from staphylococcus areus
39	c3ctpB_	Alignment	not modelled	41.9	11	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**periplasmic binding protein/laci transcriptional regulator; **PDBTitle:** crystal structure of periplasmic binding protein/laci transcriptional2 regulator from alkaliphilus metalliredigens qymf complexed with d-3 xylulofuranose
40	c3gfgB_	Alignment	not modelled	41.2	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**uncharacterized oxidoreductase yvaa; **PDBTitle:** structure of putative oxidoreductase yvaa from bacillus subtilis in2 triclinic form
41	d8abpa_	Alignment	not modelled	41.0	12	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
42	d1edza2	Alignment	not modelled	40.6	27	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Tetrahydrofolate dehydrogenase/cyclohydrolase
43	d1hcza2	Alignment	not modelled	40.3	28	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
44	c3l49D_	Alignment	not modelled	39.5	9	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**abc sugar (ribose) transporter, periplasmic **PDBTitle:** crystal structure of abc sugar transporter subunit from2 rhodobacter sphaeroides 2.4.1
45	d1dxha2	Alignment	not modelled	39.2	14	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
46	c3kuxA_	Alignment	not modelled	39.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** structure of the ypo2259 putative oxidoreductase from yersinia pestis
47	c1h6dL_	Alignment	not modelled	39.0	13	**PDB header:**protein translocation **Chain:** L: **PDB Molecule:**precursor form of glucose-fructose **PDBTitle:** oxidized precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol
48	d2jdia3	Alignment	not modelled	38.3	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
49	c3gr7A_	Alignment	not modelled	38.2	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph dehydrogenase; **PDBTitle:** structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
50	d1gg2g_	Alignment	not modelled	37.8	20	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Transducin (heterotrimeric G protein), gamma chain **Family:**Transducin (heterotrimeric G protein), gamma chain
51	c2r9vA_	Alignment	not modelled	37.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp synthase subunit alpha; **PDBTitle:** crystal structure of atp synthase subunit alpha (tm1612) from2 thermotoga maritima at 2.10 a resolution
52	c3c1aB_	Alignment	not modelled	37.1	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase (zp_00056571.1) from2 magnetospirillum magnetotacticum ms-1 at 1.85 a resolution

53	d2b7oa1	Alignment	not modelled	37.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class-II DAHP synthetase
54	c3ceaA_	Alignment	not modelled	35.0	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**myo-inositol 2-dehydrogenase; **PDBTitle:** crystal structure of myo-inositol 2-dehydrogenase (np_786804.1) from2 lactobacillus plantarum at 2.40 a resolution
55	d1omwg_	Alignment	not modelled	34.9	20	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Transducin (heterotrimeric G protein), gamma chain **Family:**Transducin (heterotrimeric G protein), gamma chain
56	c2qu7B_	Alignment	not modelled	34.4	5	**PDB header:**transcription **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of a putative transcription regulator2 from staphylococcus saprophyticus subsp. saprophyticus
57	c3oa2B_	Alignment	not modelled	34.3	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**wbpb; **PDBTitle:** crystal structure of the wlba (wbpb) dehydrogenase from pseudomonas2 aeruginosa in complex with nad at 1.5 angstrom resolution
58	c1ofgF_	Alignment	not modelled	34.2	18	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**glucose-fructose oxidoreductase; **PDBTitle:** glucose-fructose oxidoreductase
59	d1lc0a1	Alignment	not modelled	34.0	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
60	d1gqoa_	Alignment	not modelled	33.7	15	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
61	d2nu7b1	Alignment	not modelled	33.6	13	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
62	c3qk7C_	Alignment	not modelled	32.9	15	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulators; **PDBTitle:** crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
63	c1edzA_	Alignment	not modelled	32.6	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**5,10-methylenetetrahydrofolate dehydrogenase; **PDBTitle:** structure of the nad-dependent 5,10-2 methylenetetrahydrofolate dehydrogenase from saccharomyces3 cerevisiae
64	d2gm3a1	Alignment	not modelled	32.5	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
65	c1kxfA_	Alignment	not modelled	32.2	26	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**sindbis virus capsid protein; **PDBTitle:** sindbis virus capsid, (wild-type) residues 1-264,2 tetragonal crystal form (form ii)
66	d1auoa_	Alignment	not modelled	32.1	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
67	c3fd8A_	Alignment	not modelled	31.8	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from enterococcus2 faecalis
68	c2rjoA_	Alignment	not modelled	31.7	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**twin-arginine translocation pathway signal protein; **PDBTitle:** crystal structure of twin-arginine translocation pathway signal2 protein from burkholderia phytofirmans
69	d1ep5a_	Alignment	not modelled	31.5	28	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
70	c3lkbB_	Alignment	not modelled	31.4	10	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**probable branched-chain amino acid abc **PDBTitle:** crystal structure of a branched chain amino acid abc2 transporter from thermus thermophilus with bound valine
71	c1zq1B_	Alignment	not modelled	31.1	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit d; **PDBTitle:** structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi
72	c3oa0B_	Alignment	not modelled	30.8	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**lipopolysaccaride biosynthesis protein wbpb; **PDBTitle:** crystal structure of the wlba (wbpb) dehydrogenase from thermus2 thermophilus in complex with nad and udp-glcnaca
73	c3cn9B_	Alignment	not modelled	30.7	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**carboxylesterase; **PDBTitle:** crystal structure analysis of the carboxylesterase pa3859 from2 pseudomonas aeruginosa pao1- orthorhombic crystal form
74	c1zh8B_	Alignment	not modelled	30.7	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
75	d1wyka_	Alignment	not modelled	30.5	26	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
76	d1ci3m2	Alignment	not modelled	30.5	21	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
77	c1tltB_	Alignment	not modelled	29.3	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase (virulence factor mvim homolog); **PDBTitle:** crystal structure of a putative oxidoreductase (virulence

						factor mvim2 homolog)
78	c3f4lF_	Alignment	not modelled	29.3	14	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**putative oxidoreductase yhhx; **PDBTitle:** crystal structure of a probable oxidoreductase yhhx in2 triclinic form. northeast structural genomics target er647
79	d1e2wa2	Alignment	not modelled	29.2	32	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
80	d1fx0a3	Alignment	not modelled	28.7	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
81	c2uygF_	Alignment	not modelled	28.4	13	**PDB header:**lyase **Chain:** F: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** crystallographic structure of the typeii 3-dehydroquinase2 from thermus thermophilus
82	c3bdkB_	Alignment	not modelled	28.2	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**d-mannonate dehydratase; **PDBTitle:** crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
83	c2glxD_	Alignment	not modelled	28.0	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**1,5-anhydro-d-fructose reductase; **PDBTitle:** crystal structure analysis of bacterial 1,5-af reductase
84	d1gtza_	Alignment	not modelled	27.7	19	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
85	d1ekxa2	Alignment	not modelled	27.4	20	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
86	c3g85A_	Alignment	not modelled	27.3	9	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (laci family); **PDBTitle:** crystal structure of laci family transcription regulator from2 clostridium acetobutylicum
87	d1h6da1	Alignment	not modelled	27.1	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
88	c3ezyB_	Alignment	not modelled	27.0	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure of probable dehydrogenase tm_0414 from2 thermotoga maritima
89	d1ydwa1	Alignment	not modelled	26.8	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
90	c2pfsA_	Alignment	not modelled	26.7	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**universal stress protein; **PDBTitle:** crystal structure of universal stress protein from nitrosomonas2 europaea
91	d2g50a2	Alignment	not modelled	26.6	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
92	d1xima_	Alignment	not modelled	26.3	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
93	c2vc6A_	Alignment	not modelled	26.3	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of mosa from s. meliloti with pyruvate bound
94	c2p10D_	Alignment	not modelled	26.0	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mll9387 protein; **PDBTitle:** crystal structure of a putative phosphonopyruvate hydrolase (mll9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
95	c3sdoB_	Alignment	not modelled	25.9	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitrilotriacetate monooxygenase; **PDBTitle:** structure of a nitrilotriacetate monooxygenase from burkholderia2 pseudomallei
96	d2c4va1	Alignment	not modelled	25.2	19	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
97	d2h1ia1	Alignment	not modelled	25.2	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
98	c1jyeA_	Alignment	not modelled	25.0	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lactose operon repressor; **PDBTitle:** structure of a dimeric lac repressor with c-terminal deletion and k84l2 substitution
99	d1jyea_	Alignment	not modelled	25.0	15	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
100	c1xdwA_	Alignment	not modelled	24.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad+-dependent (r)-2-hydroxyglutarate **PDBTitle:** nad+-dependent (r)-2-hydroxyglutarate dehydrogenase from2 acidaminococcus fermentans
101	c1lc3A_	Alignment	not modelled	24.7	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**biliverdin reductase a; **PDBTitle:** crystal structure of a biliverdin reductase enzyme-cofactor2 complex
102	d1otha2	Alignment	not modelled	24.7	18	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
103	d2glka1	Alignment	not modelled	24.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
						PDB header:structural genomics, unknown function

104	c3pf6C_	Alignment	not modelled	24.5	39	**Chain:** C: **PDB Molecule:**hypothetical protein pp-luz7_gp033; **PDBTitle:** the structure of uncharacterized protein pp-luz7_gp033 from2 pseudomonas phage luz7.
105	c3gv0A_	Alignment	not modelled	24.3	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of laci family transcription regulator from2 agrobacterium tumefaciens
106	c3ip3D_	Alignment	not modelled	24.3	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, putative; **PDBTitle:** structure of putative oxidoreductase (tm_0425) from2 thermotoga maritima
107	c1kmhA_	Alignment	not modelled	24.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atpase alpha subunit; **PDBTitle:** crystal structure of spinach chloroplast f1-atpase2 complexed with tentoxin
108	c2ixaA_	Alignment	not modelled	23.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-n-acetylgalactosaminidase; **PDBTitle:** a-zyme, n-acetylgalactosaminidase
109	c2zkqj_	Alignment	not modelled	23.9	18	**PDB header:**ribosomal protein/rna **Chain:** J: **PDB Molecule:** **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
110	c3db2C_	Alignment	not modelled	23.8	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative nadph-dependent oxidoreductase; **PDBTitle:** crystal structure of a putative nadph-dependent oxidoreductase2 (dhaf_2064) from desulfitobacterium hafniense dcb-2 at 1.70 a3 resolution
111	d2a9da2	Alignment	not modelled	23.7	20	**Fold:**Oxidoreductase molybdopterin-binding domain **Superfamily:**Oxidoreductase molybdopterin-binding domain **Family:**Oxidoreductase molybdopterin-binding domain
112	c2ehhE_	Alignment	not modelled	23.3	13	**PDB header:**lyase **Chain:** E: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
113	d1y81a1	Alignment	not modelled	23.0	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
114	d1uc2a_	Alignment	not modelled	22.8	26	**Fold:**Hypothetical protein PH1602 **Superfamily:**Hypothetical protein PH1602 **Family:**Hypothetical protein PH1602
115	d1ryda1	Alignment	not modelled	22.7	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
116	c2o48X_	Alignment	not modelled	22.6	18	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**dimeric dihydrodiol dehydrogenase; **PDBTitle:** crystal structure of mammalian dimeric dihydrodiol dehydrogenase
117	c3bi8A_	Alignment	not modelled	22.3	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of dihydrodipicolinate synthase from clostridium2 botulinum
118	c3eb2A_	Alignment	not modelled	22.2	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
119	d1jx6a_	Alignment	not modelled	22.2	10	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
120	c2qvcC_	Alignment	not modelled	22.1	12	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**sugar abc transporter, periplasmic sugar-binding **PDBTitle:** crystal structure of a periplasmic sugar abc transporter2 from thermotoga maritima