Phyre^2

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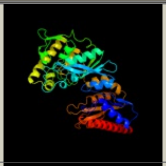
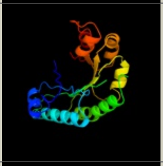
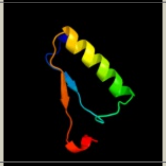
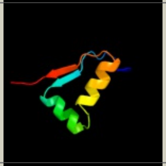
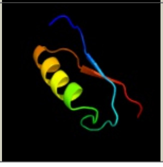
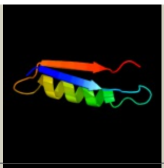
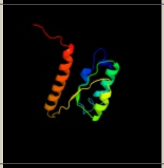
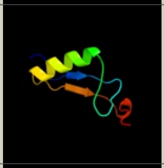
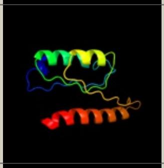
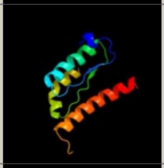
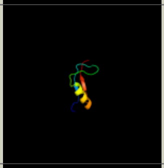
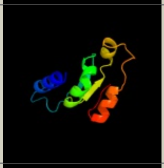
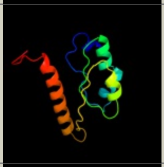
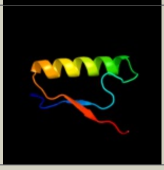
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cwcB_	Alignment		100.0	56	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative glycerate kinase 2; **PDBTitle:** crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2
2	d1to6a_	Alignment		100.0	39	**Fold:**Glycerate kinase I **Superfamily:**Glycerate kinase I **Family:**Glycerate kinase I
3	d1e0ta2	Alignment		95.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
4	d1liua2	Alignment		94.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
5	d1pkla2	Alignment		93.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
6	d1a3xa2	Alignment		89.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
7	d1vb5a_	Alignment		88.7	16	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
8	d1pswa_	Alignment		87.3	15	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**ADP-heptose LPS heptosyltransferase II
9	d2g50a2	Alignment		87.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
10	c1w2wJ_	Alignment		84.6	22	**PDB header:**isomerase **Chain:** J: **PDB Molecule:**5-methylthioribose-1-phosphate isomerase; **PDBTitle:** crystal structure of yeast ypr118w, a methylthioribose-1-2 phosphate isomerase related to regulatory eif2b subunits
11	c3ecsD_	Alignment		84.2	24	**PDB header:**translation **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b subunit **PDBTitle:** crystal structure of human eif2b alpha

12	d1ydga_	Alignment		83.9	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
13	c1w5fA_	Alignment		83.5	20	**PDB header:**cell division **Chain:** A: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** ftsz, t7 mutated, domain swapped (t. maritima)
14	d1t5oa_	Alignment		82.7	29	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
15	d2vapa1	Alignment		82.6	22	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
16	d1rq2a1	Alignment		82.1	24	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
17	c3a11D_	Alignment		81.6	18	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b, delta **PDBTitle:** crystal structure of ribose-1,5-bisphosphate isomerase from2 thermococcus kodakaraensis kod1
18	c1a3wB_	Alignment		80.5	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** pyruvate kinase from saccharomyces cerevisiae complexed with fbp, pg,2 mn2+ and k+
19	c1w59B_	Alignment		78.7	21	**PDB header:**cell division **Chain:** B: **PDB Molecule:**cell division protein ftsz homolog 1; **PDBTitle:** ftsz dimer, empty (m. jannaschii)
20	c2yvkA_	Alignment		75.8	30	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**methylthioribose-1-phosphate isomerase; **PDBTitle:** crystal structure of 5-methylthioribose 1-phosphate2 isomerase product complex from bacillus subtilis
21	d1t9ka_	Alignment	not modelled	75.7	30	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
22	c2h1fB_	Alignment	not modelled	74.2	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**lipopolysaccharide heptosyltransferase-1; **PDBTitle:** e. coli heptosyltransferase waac with adp
23	d2a0ua1	Alignment	not modelled	73.9	21	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
24	c1aqfB_	Alignment	not modelled	73.4	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** pyruvate kinase from rabbit muscle with mg, k, and l-2 phospholactate
25	c1t5aB_	Alignment	not modelled	71.7	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase, m2 isozyme; **PDBTitle:** human pyruvate kinase m2
26	c2vgbB_	Alignment	not modelled	71.6	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase isozymes r/l; **PDBTitle:** human erythrocyte pyruvate kinase
27	d1xi3a_	Alignment	not modelled	71.1	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
28	d1izca_	Alignment	not modelled	69.2	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
29	c1izcA	Alignment	not modelled	69.2	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**macrophomate synthase intermolecular

29	c1izcA_	Alignment	not modelled	69.2	20	diels-alderase; **PDBTitle:** crystal structure analysis of macrophomate synthase
30	c3eoeC_	Alignment	not modelled	69.1	23	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from toxoplasma gondii, 55.m00007
31	c2q1yB_	Alignment	not modelled	68.5	22	**PDB header:**cell cycle, signaling protein **Chain:** B: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** crystal structure of cell division protein ftsz from mycobacterium2 tuberculosis in complex with gtp-gamma-s
32	c3e0vB_	Alignment	not modelled	68.4	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from leishmania mexicana in2 complex with sulphate ions
33	c2rhoB_	Alignment	not modelled	67.1	22	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** synthetic gene encoded bacillus subtilis ftsz ncs dimer with2 bound gdp and gtp-gamma-s
34	c1pklB_	Alignment	not modelled	65.6	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyruvate kinase); **PDBTitle:** the structure of leishmania pyruvate kinase
35	c3t07D_	Alignment	not modelled	65.5	18	**PDB header:**transferase/transferase inhibitor **Chain:** D: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of s. aureus pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid
36	d1wv2a_	Alignment	not modelled	65.4	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
37	d1ofua1	Alignment	not modelled	65.2	24	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
38	c1e0tD_	Alignment	not modelled	64.6	13	**PDB header:**phosphotransferase **Chain:** D: **PDB Molecule:**pyruvate kinase; **PDBTitle:** r292d mutant of e. coli pyruvate kinase
39	c2ppvA_	Alignment	not modelled	64.4	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein belonging to the upf0052 (se_0549) from2 staphylococcus epidermidis atcc 12228 at 2.00 a resolution
40	c3tovB_	Alignment	not modelled	63.4	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyl transferase family 9; **PDBTitle:** the crystal structure of the glycosyl transferase family 9 from2 veillonella parvula dsm 2008
41	c2p0yA_	Alignment	not modelled	63.0	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein lp_0780; **PDBTitle:** crystal structure of q88yi3_lacpl from lactobacillus2 plantarum. northeast structural genomics consortium target3 lpr6
42	c2f9iD_	Alignment	not modelled	62.7	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl **PDBTitle:** crystal structure of the carboxyltransferase subunit of acc2 from staphylococcus aureus
43	c1ofuB_	Alignment	not modelled	62.7	24	**PDB header:**bacterial cell division inhibitor **Chain:** B: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** crystal structure of sula:ftsz from pseudomonas aeruginosa
44	d2f9yb1	Alignment	not modelled	61.3	15	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
45	c2f9yB_	Alignment	not modelled	61.3	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl transferase subunit **PDBTitle:** the crystal structure of the carboxyltransferase subunit of acc from2 escherichia coli
46	d1ecfa1	Alignment	not modelled	59.7	12	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
47	c2hjgA_	Alignment	not modelled	59.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gtp-binding protein enga; **PDBTitle:** the crystal structure of the b. subtilis yphc gtpase in2 complex with gdp
48	c2vxyA_	Alignment	not modelled	58.4	25	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** the structure of ftsz from bacillus subtilis at 1.7a2 resolution
49	c3hbmA_	Alignment	not modelled	56.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**udp-sugar hydrolase; **PDBTitle:** crystal structure of pseg from campylobacter jejuni
50	c2e28A_	Alignment	not modelled	56.2	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure analysis of pyruvate kinase from bacillus2 stearothermophilus
51	d2hzba1	Alignment	not modelled	55.4	18	**Fold:**CofD-like **Superfamily:**CofD-like **Family:**CofD-like
52	d1vima_	Alignment	not modelled	55.3	13	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
53	c3ma8A_	Alignment	not modelled	55.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of cgd1_2040, a pyruvate kinase from cryptosporidium2 parvum
54	d2naca2	Alignment	not modelled	53.1	12	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
						PDB header:isomerase

55	c2ze3A_	Alignment	not modelled	53.0	14	**Chain:** A: **PDB Molecule:**dfa0005; **PDBTitle:** crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus
56	c2v82A_	Alignment	not modelled	52.9	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxy-6-phosphogalactonate aldolase; **PDBTitle:** kdpgal complexed to kdpgal
57	d1pjqa1	Alignment	not modelled	52.1	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Siroheme synthase N-terminal domain-like
58	c2vawA_	Alignment	not modelled	51.4	23	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** ftsz pseudomonas aeruginosa gdp
59	c1pixB_	Alignment	not modelled	51.1	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**glutaconyl-coa decarboxylase a subunit; **PDBTitle:** crystal structure of the carboxyltransferase subunit of the2 bacterial ion pump glutaconyl-coenzyme a decarboxylase
60	d1f8ya_	Alignment	not modelled	50.8	5	**Fold:**Flavodoxin-like **Superfamily:**N-(deoxy)ribosyltransferase-like **Family:**N-deoxyribosyltransferase
61	d1q7ra_	Alignment	not modelled	50.0	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
62	c2bf9A_	Alignment	not modelled	49.9	26	**PDB header:**hormone **Chain:** A: **PDB Molecule:**pancreatic hormone; **PDBTitle:** anisotropic refinement of avian (turkey) pancreatic2 polypeptide at 0.99 angstroms resolution.
63	c3trjC_	Alignment	not modelled	49.9	13	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphoheptose isomerase; **PDBTitle:** structure of a phosphoheptose isomerase from francisella tularensis
64	d1diha1	Alignment	not modelled	49.6	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
65	d1vrga1	Alignment	not modelled	49.6	31	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
66	d1w5fa1	Alignment	not modelled	49.6	19	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
67	d1j0aa_	Alignment	not modelled	49.2	14	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
68	c4a1dG_	Alignment	not modelled	49.0	15	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**rpl30; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of3 molecule 4.
69	c3na3A_	Alignment	not modelled	48.8	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**dna mismatch repair protein mlh1; **PDBTitle:** mutl protein homolog 1 isoform 1 from homo sapiens
70	c3ct7E_	Alignment	not modelled	48.1	12	**PDB header:**isomerase **Chain:** E: **PDB Molecule:**d-allulose-6-phosphate 3-epimerase; **PDBTitle:** crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12
71	d1pixa2	Alignment	not modelled	47.5	20	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
72	d1t0kb_	Alignment	not modelled	47.2	13	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
73	c1ronA_	Alignment	not modelled	47.2	22	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**neuropeptide y; **PDBTitle:** nmr solution structure of human neuropeptide y
74	c1tz5A_	Alignment	not modelled	46.8	30	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**chimera of pancreatic hormone and neuropeptide y; **PDBTitle:** [pnpy19-23]-hpp bound to dpc micelles
75	d1p3da1	Alignment	not modelled	45.3	15	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
76	d1w41a1	Alignment	not modelled	44.8	21	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
77	c3pqeD_	Alignment	not modelled	44.4	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** crystal structure of l-lactate dehydrogenase from bacillus subtilis2 with h171c mutation
78	d1on3a1	Alignment	not modelled	44.0	24	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
79	c3khdC_	Alignment	not modelled	43.9	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pff1300w.
80	c1drwA_	Alignment	not modelled	43.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** escherichia coli dhpr/nhdh complex

81	d1j6ua1	Alignment	not modelled	43.7	9	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
82	d1dxea_	Alignment	not modelled	42.7	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
83	c1xnwD_	Alignment	not modelled	42.3	27	**PDB header:**ligase **Chain:** D: **PDB Molecule:**propionyl-coa carboxylase complex b subunit; **PDBTitle:** acyl-coa carboxylase beta subunit from s. coelicolor (pccb),2 apo form #2, mutant d422i
84	c3o63B_	Alignment	not modelled	42.3	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable thiamine-phosphate pyrophosphorylase; **PDBTitle:** crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
85	c1x0uB_	Alignment	not modelled	42.2	29	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hypothetical methylmalonyl-coa decarboxylase alpha subunit; **PDBTitle:** crystal structure of the carboxyl transferase subunit of putative pcc2 of sulfolobus tokodaii
86	c3glmD_	Alignment	not modelled	41.4	23	**PDB header:**lyase **Chain:** D: **PDB Molecule:**glutaconyl-coa decarboxylase subunit a; **PDBTitle:** glutaconyl-coa decarboxylase a subunit from clostridium2 symbiosum co-crystallized with crotonyl-coa
87	c2dezA_	Alignment	not modelled	41.3	26	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**peptide yy; **PDBTitle:** structure of human pyy
88	c3bzrA_	Alignment	not modelled	41.3	15	**PDB header:**membrane protein, protein transport **Chain:** A: **PDB Molecule:**escu; **PDBTitle:** crystal structure of escu c-terminal domain with n262d mutation, space2 group p 41 21 2
89	d3bzra1	Alignment	not modelled	41.3	15	**Fold:**EscU C-terminal domain-like **Superfamily:**EscU C-terminal domain-like **Family:**EscU C-terminal domain-like
90	d1ycga1	Alignment	not modelled	40.3	32	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
91	d1k9vf_	Alignment	not modelled	40.2	13	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
92	c3qz6A_	Alignment	not modelled	40.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hpch/hpai aldolase; **PDBTitle:** the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
93	d2csua2	Alignment	not modelled	40.0	24	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
94	c3n6rF_	Alignment	not modelled	39.9	29	**PDB header:**ligase **Chain:** F: **PDB Molecule:**propionyl-coa carboxylase, beta subunit; **PDBTitle:** crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
95	c1zosE_	Alignment	not modelled	39.3	19	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**5'-methylthioadenosine / s-adenosylhomocysteine **PDBTitle:** structure of 5'-methylthionadenosine/s-adenosylhomocysteine2 nucleosidase from s. pneumoniae with a transition-state3 inhibitor mt-imma
96	c2yybA_	Alignment	not modelled	38.7	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha1606; **PDBTitle:** crystal structure of ttha1606 from thermus thermophilus hb8
97	c2r6r1_	Alignment	not modelled	38.5	20	**PDB header:**cell cycle **Chain:** 1: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** aquifex aeolicus ftsz
98	d2a7sa1	Alignment	not modelled	38.2	31	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
99	c1on3E_	Alignment	not modelled	38.0	24	**PDB header:**transferase **Chain:** E: **PDB Molecule:**methylmalonyl-coa carboxyltransferase 12s **PDBTitle:** transcarboxylase 12s crystal structure: hexamer assembly2 and substrate binding to a multienzyme core (with3 methylmalonyl-coenzyme a and methylmalonic acid bound)
100	d1xnya1	Alignment	not modelled	37.7	27	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
101	d1nmpa_	Alignment	not modelled	37.6	24	**Fold:**NIF3 (NGG1p interacting factor 3)-like **Superfamily:**NIF3 (NGG1p interacting factor 3)-like **Family:**NIF3 (NGG1p interacting factor 3)-like
102	c1vrgE_	Alignment	not modelled	37.6	35	**PDB header:**ligase **Chain:** E: **PDB Molecule:**propionyl-coa carboxylase, beta subunit; **PDBTitle:** crystal structure of propionyl-coa carboxylase, beta subunit (tm0716)2 from thermotoga maritima at 2.30 a resolution
103	c3t7yB_	Alignment	not modelled	37.5	18	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**yop proteins translocation protein u; **PDBTitle:** structure of an autocleavage-inactive mutant of the cytoplasmic domain2 of ct091, the yscu homologue of chlamydia trachomatis
104	d2nv0a1	Alignment	not modelled	37.5	9	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
105	d1jvna2	Alignment	not modelled	37.2	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)

106	c2yxbA_	Alignment	not modelled	36.9	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase; **PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
107	c2zkiH_	Alignment	not modelled	36.9	16	**PDB header:**transcription **Chain:** H: **PDB Molecule:**199aa long hypothetical trp repressor binding **PDBTitle:** crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
108	c2q7xA_	Alignment	not modelled	36.8	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**upf0052 protein sp_1565; **PDBTitle:** crystal structure of a putative phospho transferase (sp_1565) from2 streptococcus pneumoniae tigr4 at 2.00 a resolution
109	c3hgmD_	Alignment	not modelled	36.7	18	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**universal stress protein tead; **PDBTitle:** universal stress protein tead from the trap transporter2 teaabc of halomonas elongata
110	c3ceuA_	Alignment	not modelled	36.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiamine phosphate pyrophosphorylase; **PDBTitle:** crystal structure of thiamine phosphate pyrophosphorylase2 (bt_0647) from bacteroides thetaiotaomicron. northeast3 structural genomics consortium target btr268
111	c3oirA_	Alignment	not modelled	36.1	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sulfate transporter sulfate transporter family protein; **PDBTitle:** crystal structure of sulfate transporter family protein from wolinella2 succinogenes
112	d2ffea1	Alignment	not modelled	35.4	12	**Fold:**CofD-like **Superfamily:**CofD-like **Family:**CofD-like
113	c2zklA_	Alignment	not modelled	35.3	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**capsular polysaccharide synthesis enzyme cap5f; **PDBTitle:** crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
114	c2bg5C_	Alignment	not modelled	35.1	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**phosphoenolpyruvate-protein kinase; **PDBTitle:** crystal structure of the phosphoenolpyruvate-binding enzyme2 i-domain from the thermoanaerobacter tengcongensis pep:3 sugar phosphotransferase system (pts)
115	c3h4lB_	Alignment	not modelled	35.0	22	**PDB header:**dna binding protein, protein binding **Chain:** B: **PDB Molecule:**dna mismatch repair protein pms1; **PDBTitle:** crystal structure of n terminal domain of a dna repair protein
116	d2bo1a1	Alignment	not modelled	34.7	17	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
117	d1vhca_	Alignment	not modelled	34.2	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
118	c2hwgA_	Alignment	not modelled	33.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** structure of phosphorylated enzyme i of the2 phosphoenolpyruvate:sugar phosphotransferase system
119	c2v5jB_	Alignment	not modelled	33.4	7	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; **PDBTitle:** apo class ii aldolase hpch
120	c3f6sI_	Alignment	not modelled	33.4	21	**PDB header:**electron transport **Chain:** I: **PDB Molecule:**flavodoxin; **PDBTitle:** desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers