Phyre^2

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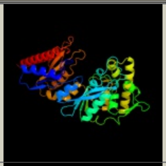
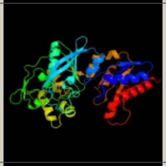
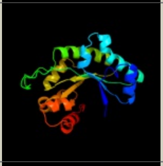
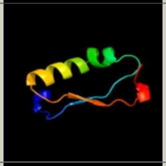
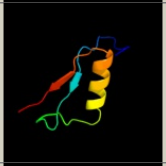
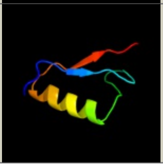
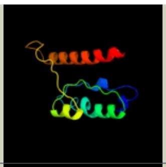
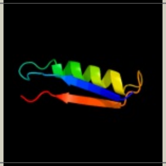
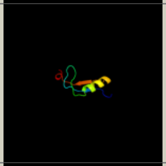
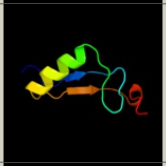
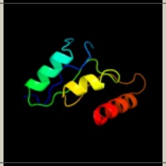
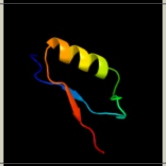
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cwcB_	Alignment		100.0	67	**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	38	**Fold:**Glycerate kinase I **Superfamily:**Glycerate kinase I **Family:**Glycerate kinase I
3	d1e0ta2	Alignment		95.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
4	d1liua2	Alignment		93.8	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
5	d1pkla2	Alignment		93.4	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
6	d1a3xa2	Alignment		90.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
7	d1vb5a_	Alignment		88.8	14	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
8	d1pswa_	Alignment		88.8	18	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**ADP-heptose LPS heptosyltransferase II
9	d2g50a2	Alignment		86.6	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
10	c1w2wJ_	Alignment		84.1	13	**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		83.8	27	**PDB header:**translation **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b subunit **PDBTitle:** crystal structure of human eif2b alpha

12	c1w5fA_	Alignment		83.1	17	**PDB header:**cell division **Chain:** A: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** ftsz, t7 mutated, domain swapped (t. maritima)
13	d1ydga_	Alignment		83.0	21	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
14	c3a11D_	Alignment		82.1	17	**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
15	d1t5oa_	Alignment		81.7	29	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
16	d1xi3a_	Alignment		80.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
17	c1a3wB_	Alignment		79.1	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** pyruvate kinase from saccharomyces cerevisiae complexed with fbp, pg,2 mn2+ and k+
18	c2h1fB_	Alignment		77.2	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**lipopolysaccharide heptosyltransferase-1; **PDBTitle:** e. coli heptosyltransferase waac with adp
19	c2yvkA_	Alignment		75.0	23	**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
20	c1aqfB_	Alignment		74.4	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** pyruvate kinase from rabbit muscle with mg, k, and l-2 phospholactate
21	c3eoeC_	Alignment	not modelled	74.3	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from toxoplasma gondii, 55.m00007
22	d1t9ka_	Alignment	not modelled	74.0	21	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
23	c1t5aB_	Alignment	not modelled	73.7	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase, m2 isozyme; **PDBTitle:** human pyruvate kinase m2
24	c3e0vB_	Alignment	not modelled	73.2	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from leishmania mexicana in2 complex with sulphate ions
25	c2vgbB_	Alignment	not modelled	73.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase isozymes r/l; **PDBTitle:** human erythrocyte pyruvate kinase
26	d2a0ua1	Alignment	not modelled	72.6	22	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
27	c1w59B_	Alignment	not modelled	72.5	18	**PDB header:**cell division **Chain:** B: **PDB Molecule:**cell division protein ftsz homolog 1; **PDBTitle:** ftsz dimer, empty (m. jannaschii)
28	d1rq2a1	Alignment	not modelled	71.9	20	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
29	c2q1vB	Alignment	not modelled	70.9	20	**PDB header:**cell cycle, signaling protein **Chain:** B: **PDB Molecule:**cell division protein ftsz;

29	c2q1yB_	Alignment	not modelled	70.9	20	**PDBTitle:** crystal structure of cell division protein ftsz from mycobacterium2 tuberculosis in complex with gtp-gamma-s
30	c3trjC_	Alignment	not modelled	70.6	12	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphoheptose isomerase; **PDBTitle:** structure of a phosphoheptose isomerase from francisella tularensis
31	d2vapa1	Alignment	not modelled	69.7	19	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
32	c3ma8A_	Alignment	not modelled	69.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of cgd1_2040, a pyruvate kinase from cryptosporidium2 parvum
33	c1pklB_	Alignment	not modelled	68.8	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyruvate kinase); **PDBTitle:** the structure of leishmania pyruvate kinase
34	c3t07D_	Alignment	not modelled	67.4	23	**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
35	c2e28A_	Alignment	not modelled	67.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure analysis of pyruvate kinase from bacillus2 stearothermophilus
36	c1e0tD_	Alignment	not modelled	66.2	17	**PDB header:**phosphotransferase **Chain:** D: **PDB Molecule:**pyruvate kinase; **PDBTitle:** r292d mutant of e. coli pyruvate kinase
37	c2ppvA_	Alignment	not modelled	65.7	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
38	c3khdC_	Alignment	not modelled	65.2	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pff1300w.
39	c2hjgA_	Alignment	not modelled	65.2	14	**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
40	c3na3A_	Alignment	not modelled	64.7	23	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**dna mismatch repair protein mlh1; **PDBTitle:** mutl protein homolog 1 isoform 1 from homo sapiens
41	c2p0yA_	Alignment	not modelled	64.0	11	**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	c2rhoB_	Alignment	not modelled	63.0	18	**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
43	c2f9iD_	Alignment	not modelled	62.5	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl **PDBTitle:** crystal structure of the carboxyltransferase subunit of acc2 from staphylococcus aureus
44	d2f9yb1	Alignment	not modelled	61.7	17	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
45	c2f9yB_	Alignment	not modelled	61.7	17	**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	c2v82A_	Alignment	not modelled	61.4	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxy-6-phosphogalactonate aldolase; **PDBTitle:** kdpgal complexed to kdpgal
47	c3o63B_	Alignment	not modelled	60.2	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable thiamine-phosphate pyrophosphorylase; **PDBTitle:** crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
48	d1ofua1	Alignment	not modelled	59.1	20	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
49	d2hzba1	Alignment	not modelled	56.9	16	**Fold:**CofD-like **Superfamily:**CofD-like **Family:**CofD-like
50	c2vxyA_	Alignment	not modelled	56.1	19	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** the structure of ftsz from bacillus subtilis at 1.7a2 resolution
51	c3hbmA_	Alignment	not modelled	55.2	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**udp-sugar hydrolase; **PDBTitle:** crystal structure of pseg from campylobacter jejuni
52	d1tk9a_	Alignment	not modelled	55.1	13	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
53	c2ze3A_	Alignment	not modelled	54.8	8	**PDB header:**isomerase **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
54	d1diha1	Alignment	not modelled	54.3	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain

55	d1j0aa_	Alignment	not modelled	53.8	26	**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
56	d1f8ya_	Alignment	not modelled	53.7	10	**Fold:**Flavodoxin-like **Superfamily:**N-(deoxy)ribosyltransferase-like **Family:**N-deoxyribosyltransferase
57	d1izca_	Alignment	not modelled	53.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
58	c1izcA_	Alignment	not modelled	53.6	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**macrophomate synthase intermolecular diels-alderase; **PDBTitle:** crystal structure analysis of macrophomate synthase
59	c1drwA_	Alignment	not modelled	53.2	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** escherichia coli dhpr/nhdh complex
60	c3qz6A_	Alignment	not modelled	52.6	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hpch/hpai aldolase; **PDBTitle:** the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
61	c1ofuB_	Alignment	not modelled	52.3	21	**PDB header:**bacterial cell division inhibitor **Chain:** B: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** crystal structure of sula:ftsz from pseudomonas aeruginosa
62	c1pixB_	Alignment	not modelled	52.3	14	**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
63	d1pjqa1	Alignment	not modelled	52.1	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Siroheme synthase N-terminal domain-like
64	d1pixa2	Alignment	not modelled	51.4	20	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
65	d1vrga1	Alignment	not modelled	48.7	35	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
66	d1vm6a3	Alignment	not modelled	48.6	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
67	d1j6ua1	Alignment	not modelled	48.2	15	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
68	c2vawA_	Alignment	not modelled	47.2	19	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** ftsz pseudomonas aeruginosa gdp
69	c1yadD_	Alignment	not modelled	46.7	20	**PDB header:**transcription **Chain:** D: **PDB Molecule:**regulatory protein teni; **PDBTitle:** structure of teni from bacillus subtilis
70	d1q7ra_	Alignment	not modelled	46.5	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
71	d1wv2a_	Alignment	not modelled	46.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
72	c3ct7E_	Alignment	not modelled	45.8	11	**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
73	c2bf9A_	Alignment	not modelled	45.1	22	**PDB header:**hormone **Chain:** A: **PDB Molecule:**pancreatic hormone; **PDBTitle:** anisotropic refinement of avian (turkey) pancreatic2 polypeptide at 0.99 angstroms resolution.
74	d1ycga1	Alignment	not modelled	44.5	29	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
75	d1on3a1	Alignment	not modelled	44.4	16	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
76	c1bknA_	Alignment	not modelled	44.3	38	**PDB header:**dna repair **Chain:** A: **PDB Molecule:**mutl; **PDBTitle:** crystal structure of an n-terminal 40kd fragment of e. coli2 dna mismatch repair protein mutl
77	d1x92a_	Alignment	not modelled	44.0	12	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
78	c1d4fD_	Alignment	not modelled	44.0	21	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**s-adenosylhomocysteine hydrolase; **PDBTitle:** crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
79	c2yvaB_	Alignment	not modelled	43.7	9	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dnaa initiator-associating protein diaa; **PDBTitle:** crystal structure of escherichia coli diaa
80	c1ronA_	Alignment	not modelled	42.7	22	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**neuropeptide y; **PDBTitle:** nmr solution structure of human neuropeptide y
81	c2x3vA	Alignment	not modelled	42.3	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphoheptose isomerase;

81	c2x5yA_	Alignment	not modelled	42.5	12	**PDBTitle:** crystal structure of gmha from burkholderia pseudomallei
82	c1tz5A_	Alignment	not modelled	42.1	15	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**chimera of pancreatic hormone and neuropeptide y; **PDBTitle:** [pnpy19-23]-hpp bound to dpc micelles
83	c3hgmD_	Alignment	not modelled	42.1	22	**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
84	d1nmpa_	Alignment	not modelled	42.0	17	**Fold:**NIF3 (NGG1p interacting factor 3)-like **Superfamily:**NIF3 (NGG1p interacting factor 3)-like **Family:**NIF3 (NGG1p interacting factor 3)-like
85	c1x0uB_	Alignment	not modelled	42.0	25	**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	c1xnwD_	Alignment	not modelled	41.5	29	**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
87	c3glmD_	Alignment	not modelled	41.5	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
88	d1w5fa1	Alignment	not modelled	41.4	18	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
89	c2yybA_	Alignment	not modelled	41.2	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha1606; **PDBTitle:** crystal structure of ttha1606 from thermus thermophilus hb8
90	c3h4lB_	Alignment	not modelled	41.1	25	**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
91	d1vima_	Alignment	not modelled	40.8	13	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
92	d1s2da_	Alignment	not modelled	40.5	21	**Fold:**Flavodoxin-like **Superfamily:**N-(deoxy)ribosyltransferase-like **Family:**N-deoxyribosyltransferase
93	d1w41a1	Alignment	not modelled	40.4	13	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
94	c3ijpA_	Alignment	not modelled	40.2	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** crystal structure of dihydrodipicolinate reductase from2 bartonella henselae at 2.0a resolution
95	c3tovB_	Alignment	not modelled	40.1	22	**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
96	c1on3E_	Alignment	not modelled	40.1	19	**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)
97	c3kv1A_	Alignment	not modelled	39.7	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional repressor; **PDBTitle:** crystal structure of putative sugar-binding domain of transcriptional2 repressor from vibrio fischeri
98	d1e0ta3	Alignment	not modelled	39.7	13	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
99	c3n6rF_	Alignment	not modelled	39.6	29	**PDB header:**ligase **Chain:** F: **PDB Molecule:**propionyl-coa carboxylase, beta subunit; **PDBTitle:** crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
100	c2dezA_	Alignment	not modelled	39.3	22	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**peptide yy; **PDBTitle:** structure of human pyy
101	c2q7xA_	Alignment	not modelled	39.2	10	**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
102	d1p3da1	Alignment	not modelled	38.3	16	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
103	c1vrgE_	Alignment	not modelled	38.2	33	**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
104	d2a7sa1	Alignment	not modelled	38.0	31	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
105	c3iz6A_	Alignment	not modelled	37.3	23	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**40s ribosomal protein sa (s2p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
106	c2zwmA_	Alignment	not modelled	37.0	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf; **PDBTitle:** crystal structure of yycf receiver domain from bacillus2

						subtilis
107	d1dxea_	Alignment	not modelled	36.9	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
108	c3bzrA_	Alignment	not modelled	36.7	22	**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
109	d3bzra1	Alignment	not modelled	36.7	22	**Fold:**EscU C-terminal domain-like **Superfamily:**EscU C-terminal domain-like **Family:**EscU C-terminal domain-like
110	c3pqeD_	Alignment	not modelled	36.5	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** crystal structure of l-lactate dehydrogenase from bacillus subtilis2 with h171c mutation
111	d1xnya1	Alignment	not modelled	36.4	29	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
112	c1ea6A_	Alignment	not modelled	36.3	34	**PDB header:**dna repair **Chain:** A: **PDB Molecule:**pms1 protein homolog 2; **PDBTitle:** n-terminal 40kda fragment of nhpms2 complexed with adp
113	c2decA_	Alignment	not modelled	35.9	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**325aa long hypothetical protein; **PDBTitle:** crystal structure of the ph0510 protein from pyrococcus horikoshii ot3
114	c2yxbA_	Alignment	not modelled	35.9	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase; **PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
115	d2ffea1	Alignment	not modelled	35.2	17	**Fold:**CofD-like **Superfamily:**CofD-like **Family:**CofD-like
116	c1zosE_	Alignment	not modelled	35.0	22	**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
117	d1efvb_	Alignment	not modelled	34.8	20	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
118	d1t0kb_	Alignment	not modelled	34.8	15	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
119	c2xhzC_	Alignment	not modelled	34.7	23	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**arabinose 5-phosphate isomerase; **PDBTitle:** probing the active site of the sugar isomerase domain from e. coli2 arabinose-5-phosphate isomerase via x-ray crystallography
120	c3oirA_	Alignment	not modelled	34.7	12	**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