Phyre2

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Description	P0A9M5
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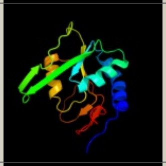
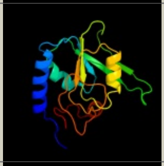
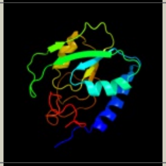
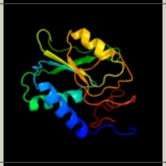
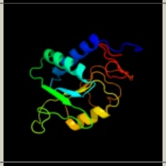
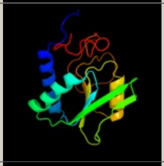
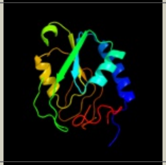
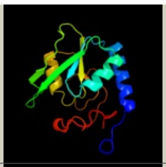
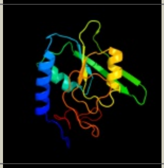
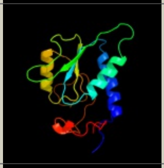
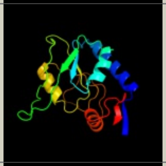
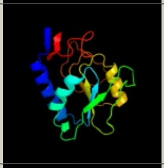
Unique Job ID	66cc4d7caf5f2975

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1nula_	Alignment		100.0	99	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
2	c2jkzB_	Alignment		100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** saccharomyces cerevisiae hypoxanthine-guanine2 phosphoribosyltransferase in complex with gmp (guanosine 5'3 -monophosphate) (orthorhombic crystal form)
3	d1vdma1	Alignment		100.0	26	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
4	c3kb8A_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxanthine phosphoribosyltransferase; **PDBTitle:** 2.09 angstrom resolution structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-1) from bacillus anthracis str. 'ames3 ancestor' in complex with gmp
5	d1fsga_	Alignment		100.0	21	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
6	d1p17b_	Alignment		100.0	24	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
7	d1pzma_	Alignment		100.0	21	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
8	d1tc1a_	Alignment		100.0	23	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
9	d1cjba_	Alignment		100.0	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
10	d1g9sa_	Alignment		99.9	19	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
11	c1yfzA_	Alignment		99.9	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** novel imp binding in feedback inhibition of hypoxanthine-guanine2 phosphoribosyltransferase from thermoanaerobacter tengcongensis

12	d1yfza1	Alignment		99.9	23	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
13	d1hgxa_	Alignment		99.9	21	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
14	d1z7ga1	Alignment		99.9	16	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
15	c3o7mD_	Alignment		99.9	24	**PDB header:**transferase **Chain:** D: **PDB Molecule:**hypoxanthine phosphoribosyltransferase; **PDBTitle:** 1.98 angstrom resolution crystal structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-2) from bacillus anthracis str. 'ames3 ancestor'
16	c1pzmB_	Alignment		99.9	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** crystal structure of hgprt-ase from leishmania tarentolae in complex2 with gmp
17	d1j7ja_	Alignment		99.9	15	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
18	c2jbhA_	Alignment		99.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosyltransferase domain-containing protein 1; **PDBTitle:** human phosphoribosyl transferase domain containing 1
19	c2ywtA_	Alignment		99.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** crystal structure of hypoxanthine-guanine2 phosphoribosyltransferase with gmp from thermus3 thermophilus hb8
20	d2igba1	Alignment		99.9	15	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
21	d1dqna_	Alignment	not modelled	99.9	20	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
22	d1a3ca_	Alignment	not modelled	99.9	16	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
23	d1w30a_	Alignment	not modelled	99.9	11	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
24	d1ufra_	Alignment	not modelled	99.9	12	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
25	d1ecfa1	Alignment	not modelled	99.7	21	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
26	d1gph11	Alignment	not modelled	99.7	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
27	c1ecjB_	Alignment	not modelled	99.7	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutamine phosphoribosylpyrophosphate **PDBTitle:** escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
28	d1g2qa_	Alignment	not modelled	99.6	21	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
						PDB header:transferase(glutamine amidotransferase)

29	c1gph1_	Alignment	not modelled	99.6	17	**Chain:** 1: **PDB Molecule:**glutamine phosphoribosyl-pyrophosphate amidotransferase; **PDBTitle:** structure of the allosteric regulatory enzyme of purine biosynthesis
30	d1wd5a_	Alignment	not modelled	99.6	21	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
31	d1zn7a1	Alignment	not modelled	99.6	26	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
32	c2dy0A_	Alignment	not modelled	99.6	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenine phosphoribosyltransferase; **PDBTitle:** crystal structure of project jw0458 from escherichia coli
33	d1o57a2	Alignment	not modelled	99.5	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
34	c2wnsB_	Alignment	not modelled	99.5	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** human orotate phosphoribosyltransferase (oprtase) domain of2 uridine 5'-monophosphate synthase (umps) in complex with3 its substrate orotidine 5'-monophosphate (omp)
35	d1y0ba1	Alignment	not modelled	99.5	19	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
36	c1o57A_	Alignment	not modelled	99.5	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**pur operon repressor; **PDBTitle:** crystal structure of the purine operon repressor of2 bacillus subtilis
37	c3mjdA_	Alignment	not modelled	99.5	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 1.9 angstrom crystal structure of orotate2 phosphoribosyltransferase (pyre) francisella tularensis.
38	d1vcha1	Alignment	not modelled	99.5	19	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
39	d1l1qa_	Alignment	not modelled	99.5	22	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
40	d1mzva_	Alignment	not modelled	99.5	22	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
41	c3n2lA_	Alignment	not modelled	99.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 2.1 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase (pyre) from vibrio cholerae o1 biovar eltor3 str. n16961
42	d1lh0a_	Alignment	not modelled	99.5	13	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
43	c2przB_	Alignment	not modelled	99.5	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**orotate phosphoribosyltransferase 1; **PDBTitle:** s. cerevisiae orotate phosphoribosyltransferase complexed2 with omp
44	c2p1zA_	Alignment	not modelled	99.4	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosyltransferase; **PDBTitle:** crystal structure of phosphoribosyltransferase from corynebacterium2 diphtheriae
45	d1qb7a_	Alignment	not modelled	99.4	22	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
46	d2aeea1	Alignment	not modelled	99.4	13	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
47	c3dezA_	Alignment	not modelled	99.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** crystal structure of orotate phosphoribosyltransferase from2 streptococcus mutans
48	c2yzkC_	Alignment	not modelled	99.4	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** crystal structure of orotate phosphoribosyltransferase from2 aeropyrum pernix
49	c3lpnB_	Alignment	not modelled	99.3	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** crystal structure of the phosphoribosylpyrophosphate (prpp) synthetase2 from thermoplasma volcanium in complex with an atp analog (ampcpp).
50	c3m3hA_	Alignment	not modelled	99.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 1.75 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase from bacillus anthracis str. 'ames3 ancestor'
51	c3qw4B_	Alignment	not modelled	99.1	16	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**ump synthase; **PDBTitle:** structure of leishmania donovani ump synthase
52	c3efhB_	Alignment	not modelled	99.1	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase 1; **PDBTitle:** crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
53	c1dkrB_	Alignment	not modelled	99.1	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase; **PDBTitle:** crystal structures of bacillus subtilis phosphoribosylpyrophosphate2 synthetase: molecular basis of allosteric inhibition and activation.
						PDB header:regulatory protein

54	c2c4kD_	Alignment	not modelled	99.0	17	**Chain:** D: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase- **PDBTitle:** crystal structure of human phosphoribosylpyrophosphate2 synthetase-associated protein 39 (pap39)
55	c1u9yD_	Alignment	not modelled	99.0	19	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** crystal structure of phosphoribosyl diphosphate synthase2 from methanocaldococcus jannaschii
56	d1dkua2	Alignment	not modelled	99.0	22	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
57	d2c4ka2	Alignment	not modelled	99.0	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
58	d1u9ya2	Alignment	not modelled	98.9	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
59	c3dahB_	Alignment	not modelled	98.8	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** 2.3 a crystal structure of ribose-phosphate pyrophosphokinase from2 burkholderia pseudomallei
60	c2e55D_	Alignment	not modelled	98.7	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**uracil phosphoribosyltransferase; **PDBTitle:** structure of aq2163 protein from aquifex aeolicus
61	c2ehjA_	Alignment	not modelled	98.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uracil phosphoribosyltransferase; **PDBTitle:** structure of uracil phosphoribosyl transferase
62	d1o5oa_	Alignment	not modelled	98.6	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
63	d1i5ea_	Alignment	not modelled	98.6	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
64	c3dmpD_	Alignment	not modelled	98.4	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**uracil phosphoribosyltransferase; **PDBTitle:** 2.6 a crystal structure of uracil phosphoribosyltransferase2 from burkholderia pseudomallei
65	d1bd3a_	Alignment	not modelled	98.2	13	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
66	d1xtta1	Alignment	not modelled	98.2	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
67	d1v9sa1	Alignment	not modelled	98.0	16	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
68	d1u9ya1	Alignment	not modelled	78.1	14	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
69	d2c4ka1	Alignment	not modelled	63.6	14	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
70	d1dkua1	Alignment	not modelled	61.9	14	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
71	d1u0sy_	Alignment	not modelled	55.4	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
72	d1dcfa_	Alignment	not modelled	55.0	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**Receiver domain of the ethylene receptor
73	c3h5iA_	Alignment	not modelled	47.3	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator/sensory box protein/ggdef **PDBTitle:** crystal structure of the n-terminal domain of a response2 regulator/sensory box/ggdef 3-domain protein from3 carboxydothermus hydrogenoformans
74	c3mmnA_	Alignment	not modelled	46.4	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histidine kinase homolog; **PDBTitle:** crystal structure of the receiver domain of the histidine kinase cki12 from arabidopsis thaliana complexed with mg2+
75	c2v5iA_	Alignment	not modelled	43.5	16	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**salmonella typhimurium db7155 bacteriophage det7 **PDBTitle:** structure of the receptor-binding protein of bacteriophage2 det7: a podoviral tailspike in a myovirus
76	d1h3da1	Alignment	not modelled	42.9	50	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
77	c3gl9B_	Alignment	not modelled	41.1	17	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** the structure of a histidine kinase-response regulator2 complex sheds light into two-component signaling and3 reveals a novel cis autophosphorylation mechanism
78	d1qo0d_	Alignment	not modelled	39.1	7	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**Positive regulator of the amidase operon AmiR
79	d1nvta1	Alignment	not modelled	39.1	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain

80	c2vd3B_	Alignment	not modelled	36.7	36	**PDB header:**transferase **Chain:** B: **PDB Molecule:**atp phosphoribosyltransferase; **PDBTitle:** the structure of histidine inhibited hisg from2 methanobacterium thermoautotrophicum
81	d1d2na_	Alignment	not modelled	35.2	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
82	c3a0rB_	Alignment	not modelled	34.8	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
83	c3eodA_	Alignment	not modelled	34.0	7	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein hnr; **PDBTitle:** crystal structure of n-terminal domain of e. coli rssb
84	c3lufB_	Alignment	not modelled	31.4	5	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**two-component system response regulator/ggdef **PDBTitle:** structure of probable two-component system response2 regulator/ggdef domain protein
85	d1uf1a_	Alignment	not modelled	31.3	10	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
86	d1k68a_	Alignment	not modelled	31.0	4	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
87	c2zayA_	Alignment	not modelled	31.0	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans
88	c1z9vA_	Alignment	not modelled	30.2	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein mth0776; **PDBTitle:** solution structure of mth0776 from methanobacterium2 thermoautotrophicum (strain h)
89	d1ve4a1	Alignment	not modelled	30.0	55	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
90	d1o63a_	Alignment	not modelled	29.9	36	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
91	d1nh8a1	Alignment	not modelled	27.8	36	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
92	c3lteH_	Alignment	not modelled	27.7	16	**PDB header:**transcription **Chain:** H: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
93	c2nt3A_	Alignment	not modelled	27.1	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator homolog; **PDBTitle:** receiver domain from myxococcus xanthus social motility protein frzs2 (y102a mutant)
94	c2ayxA_	Alignment	not modelled	27.1	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor kinase protein rcsc; **PDBTitle:** solution structure of the e.coli rcsc c-terminus (residues2 700-949) containing linker region and phosphoreceiver3 domain
95	d1z7me1	Alignment	not modelled	26.9	55	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
96	c2ekdD_	Alignment	not modelled	26.6	30	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein ph0250; **PDBTitle:** structural study of project id ph0250 from pyrococcus horikoshii ot3
97	c3k1rA_	Alignment	not modelled	25.6	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**harmonin; **PDBTitle:** structure of harmonin npdz1 in complex with the sam-pbm of2 sans
98	d1vmea1	Alignment	not modelled	25.0	8	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
99	d1p77a1	Alignment	not modelled	24.0	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
100	d1peya_	Alignment	not modelled	23.9	21	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
101	c1q1kA_	Alignment	not modelled	23.8	64	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp phosphoribosyltransferase; **PDBTitle:** structure of atp-phosphoribosyltransferase from e. coli complexed with2 pr-atp
102	c3khtA_	Alignment	not modelled	23.7	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator from hahella chejuensis
103	c1sy7B_	Alignment	not modelled	23.6	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**catalase 1; **PDBTitle:** crystal structure of the catalase-1 from neurospora crassa, native2 structure at 1.75a resolution.
104	d1dbwa_	Alignment	not modelled	23.1	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
105	c2rjnA_	Alignment	not modelled	23.1	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**response regulator receiver:metal-dependent **PDBTitle:** crystal structure of an uncharacterized protein q2bku2

						from2 neptuniibacter caesariensis
106	c1nh7A_	Alignment	not modelled	22.8	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp phosphoribosyltransferase; **PDBTitle:** atp phosphoribosyltransferase (atp-prtase) from mycobacterium2 tuberculosis
107	d2ayxa1	Alignment	not modelled	22.6	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
108	c3tqrA_	Alignment	not modelled	22.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii
109	d1mb3a_	Alignment	not modelled	22.4	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
110	c3hjbA_	Alignment	not modelled	22.3	9	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** 1.5 angstrom crystal structure of glucose-6-phosphate isomerase from2 vibrio cholerae.
111	d1gm5a3	Alignment	not modelled	22.2	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
112	c3o82B_	Alignment	not modelled	21.9	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**peptide arylation enzyme; **PDBTitle:** structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine
113	c3rqiA_	Alignment	not modelled	21.8	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator protein; **PDBTitle:** crystal structure of a response regulator protein from burkholderia2 pseudomallei with a phosphorylated aspartic acid, calcium ion and3 citrate
114	c3g7sA_	Alignment	not modelled	21.7	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**long-chain-fatty-acid--coa ligase (fadd-1); **PDBTitle:** crystal structure of a long-chain-fatty-acid-coa ligase2 (fadd1) from archaeoglobus fulgidus
115	d1zesa1	Alignment	not modelled	21.6	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
116	d1w25a2	Alignment	not modelled	20.9	21	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
117	c3luaA_	Alignment	not modelled	20.9	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of a signal receiver domain of two component signal2 transduction (histidine kinase) from clostridium thermocellum
118	c3cg0A_	Alignment	not modelled	20.8	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**response regulator receiver modulated diguanylate cyclase **PDBTitle:** crystal structure of signal receiver domain of modulated diguanylate2 cyclase from desulfovibrio desulfuricans g20, an example of alternate3 folding
119	c3ilhA_	Alignment	not modelled	20.7	20	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**two component response regulator; **PDBTitle:** crystal structure of two component response regulator from cytophaga2 hutchinsonii
120	d2a9pa1	Alignment	not modelled	20.1	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related