Phyre^{2}

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Description	P0AA04
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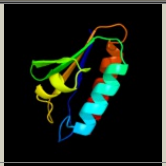
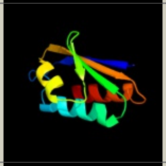
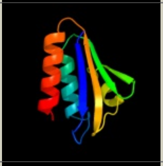
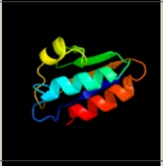
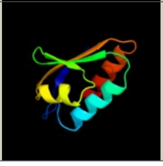
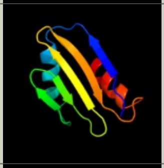
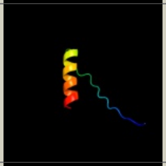
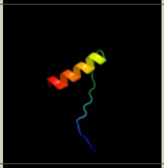
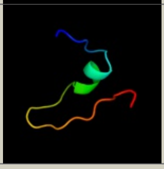
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1cm3a_	Alignment		100.0	98	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
2	d1ka5a_	Alignment		100.0	33	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
3	c3ihsB_	Alignment		100.0	37	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**phosphocarrier protein hpr; **PDBTitle:** crystal structure of a phosphocarrier protein hpr from2 bacillus anthracis str. ames
4	d1mo1a_	Alignment		100.0	46	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
5	d1ptfa_	Alignment		100.0	35	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
6	d1qr5a_	Alignment		100.0	35	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
7	c3le1B_	Alignment		100.0	43	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphotransferase system, hpr-related proteins; **PDBTitle:** crystal structure of apohpr monomer from thermoanaerobacter2 tengcongensis
8	d1pcha_	Alignment		100.0	34	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
9	d2hpra_	Alignment		100.0	36	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
10	d1zvvj1	Alignment		100.0	45	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
11	d2nzul1	Alignment		100.0	40	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like

12	d1vq3a_	Alignment		63.6	32	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
13	c2dgbA_	Alignment		60.6	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein purs; **PDBTitle:** structure of thermus thermophilus purs in the p21 form
14	c2jpiA_	Alignment		58.0	14	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** chemical shift assignments of pa4090 from pseudomonas2 aeruginosa
15	d1gtda_	Alignment		50.4	10	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
16	c2zw2B_	Alignment		42.4	23	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein sts178; **PDBTitle:** crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stpurs)
17	c3goeA_	Alignment		42.1	13	**PDB header:**recombination, replication **Chain:** A: **PDB Molecule:**dna repair protein rad60; **PDBTitle:** molecular mimicry of sumo promotes dna repair
18	c2ekeC_	Alignment		18.4	13	**PDB header:**ligase/protein binding **Chain:** C: **PDB Molecule:**ubiquitin-like protein smt3; **PDBTitle:** structure of a sumo-binding-motif mimic bound to smt3p-2 ubc9p: conservation of a noncovalent ubiquitin-like3 protein-e2 complex as a platform for selective4 interactions within a sumo pathway
19	d2etna2	Alignment		14.9	21	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
20	c2etnA_	Alignment		13.4	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**anti-cleavage anti-grea transcription factor **PDBTitle:** crystal structure of thermus aquaticus gfh1
21	d1t4aa_	Alignment	not modelled	13.2	13	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
22	d1yema_	Alignment	not modelled	12.8	21	**Fold:**CYTH-like phosphatases **Superfamily:**CYTH-like phosphatases **Family:**CYTH domain
23	d1srva_	Alignment	not modelled	12.6	19	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
24	d1r11a3	Alignment	not modelled	12.3	17	**Fold:**MutS N-terminal domain-like **Superfamily:**tRNA-intron endonuclease N-terminal domain-like **Family:**tRNA-intron endonuclease N-terminal domain-like
25	c2e6gI_	Alignment	not modelled	12.2	20	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**5'-nucleotidase sure; **PDBTitle:** crystal structure of the stationary phase survival protein sure from2 thermus thermophilus hb8 in complex with phosphate
26	c2dc4A_	Alignment	not modelled	11.2	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**165aa long hypothetical protein; **PDBTitle:** structure of ph1012 protein from pyrococcus horikoshii ot3
27	d1dk7a_	Alignment	not modelled	11.2	19	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
28	d2vbua1	Alignment	not modelled	10.9	31	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin kinase-like **Family:**CTP-dependent riboflavin kinase-like
						PDB header:ligand binding protein **Chain:** B: **PDB Molecule:**putative ligand binding protein;

29	c3k6qB_	Alignment	not modelled	10.1	29	**PDBTitle:** crystal structure of an antitoxin part of a putative toxin/antitoxin2 system (swol_0700) from syntrophomonas wolfei subsp. wolfei at 1.80 a3 resolution
30	d2f23a2	Alignment	not modelled	10.0	23	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
31	c3bmbB_	Alignment	not modelled	10.0	20	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**regulator of nucleoside diphosphate kinase; **PDBTitle:** crystal structure of a new rna polymerase interacting2 protein
32	d1we3a2	Alignment	not modelled	9.5	20	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
33	d1l5xa_	Alignment	not modelled	9.1	17	**Fold:**SurE-like **Superfamily:**SurE-like **Family:**SurE-like
34	c2pn0D_	Alignment	not modelled	8.7	26	**PDB header:**transcription **Chain:** D: **PDB Molecule:**prokaryotic transcription elongation factor **PDBTitle:** prokaryotic transcription elongation factor grea/greb from2 nitrosomonas europaea
35	d1euvb_	Alignment	not modelled	8.6	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
36	d1aopa2	Alignment	not modelled	8.6	24	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
37	d1sjpa2	Alignment	not modelled	8.6	23	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
38	c3m6cA_	Alignment	not modelled	8.1	23	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**60 kda chaperonin 1; **PDBTitle:** crystal structure of mycobacterium tuberculosis groel1 apical domain
39	c2p4vA_	Alignment	not modelled	8.1	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor greb; **PDBTitle:** crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
40	d1w96c1	Alignment	not modelled	7.8	38	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
41	c2l66B_	Alignment	not modelled	7.8	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, abrb family; **PDBTitle:** the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea.
42	c2v4oB_	Alignment	not modelled	7.6	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**multifunctional protein sur e; **PDBTitle:** crystal structure of salmonella typhimurium sure at 2.752 angstrom resolution in monoclinic form
43	d1grja2	Alignment	not modelled	7.6	26	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
44	c2jxxA_	Alignment	not modelled	7.4	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**nfatc2-interacting protein; **PDBTitle:** nmr solution structure of ubiquitin-like domain of2 nfatc2ip. northeast structural genomics consortium target3 hr5627
45	d2fy9a1	Alignment	not modelled	7.4	12	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**AbrB N-terminal domain-like
46	c1ztgD_	Alignment	not modelled	7.3	7	**PDB header:**dna, rna binding protein/dna **Chain:** D: **PDB Molecule:**poly(rc)-binding protein 1; **PDBTitle:** human alpha polyc binding protein kh1
47	d1yfba1	Alignment	not modelled	7.1	29	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**AbrB N-terminal domain-like
48	d1kida_	Alignment	not modelled	6.9	20	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
49	d1b5sa_	Alignment	not modelled	6.8	33	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**CAT-like
50	d1ulza1	Alignment	not modelled	6.8	13	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
51	d2uyzb1	Alignment	not modelled	6.6	11	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
52	c1ibaA_	Alignment	not modelled	6.5	12	**PDB header:**phoshphotransferase **Chain:** A: **PDB Molecule:**glucose permease; **PDBTitle:** glucose permease (domain iib), nmr, 11 structures
53	d2io3b1	Alignment	not modelled	6.3	7	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
54	c2ro5B_	Alignment	not modelled	6.2	22	**PDB header:**transcription **Chain:** B: **PDB Molecule:**stage v sporulation protein t; **PDBTitle:** rdc-refined solution structure of the n-terminal dna2 recognition domain of the bacillus subtilis transition-3 state regulator spovt
						PDB header:transferase **Chain:** C: **PDB Molecule:**lipoamide acyltransferase component of

55	c2ii4C_	Alignment	not modelled	6.2	5	branched-chain **PDBTitle:** crystal structure of a cubic core of the dihydrolipoamide2 acyltransferase (e2b) component in the branched-chain alpha-ketoacid3 dehydrogenase complex (bckdc), coenzyme a-bound form
56	d1dpba_	Alignment	not modelled	6.2	19	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**CAT-like
57	c2yx5A_	Alignment	not modelled	6.1	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0062 protein mj1593; **PDBTitle:** crystal structure of methanocaldococcus jannaschii purs, one of the2 subunits of formylglycinamide ribonucleotide amidotransferase in the3 purine biosynthetic pathway
58	d2j9ga1	Alignment	not modelled	6.1	22	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
59	d1q2ha_	Alignment	not modelled	6.1	50	**Fold:**Dimerisation interlock **Superfamily:**Phenylalanine zipper **Family:**Adapter protein APS, dimerisation domain
60	c2w1tB_	Alignment	not modelled	6.0	24	**PDB header:**transcription **Chain:** B: **PDB Molecule:**stage v sporulation protein t; **PDBTitle:** crystal structure of b. subtilis spovt
61	d2bfdb2	Alignment	not modelled	5.8	21	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
62	c3gebC_	Alignment	not modelled	5.6	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**eyes absent homolog 2; **PDBTitle:** crystal structure of edeya2
63	c2hjwA_	Alignment	not modelled	5.4	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** crystal structure of the bc domain of acc2
64	d1j9ja_	Alignment	not modelled	5.3	13	**Fold:**SurE-like **Superfamily:**SurE-like **Family:**SurE-like
65	c2k8hA_	Alignment	not modelled	5.3	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**small ubiquitin protein; **PDBTitle:** solution structure of sumo from trypanosoma brucei
66	d1w96a1	Alignment	not modelled	5.1	38	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
67	d1oela2	Alignment	not modelled	5.1	18	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain