Phyre2

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Description	P0AB03
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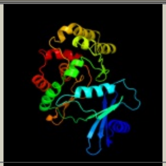
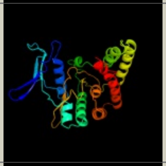
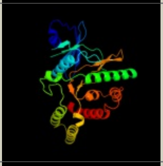
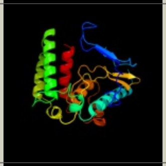
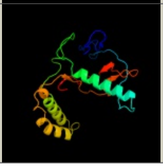
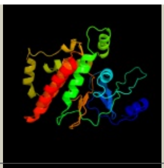
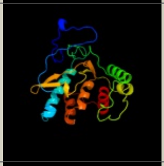
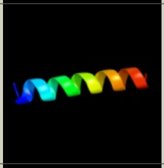
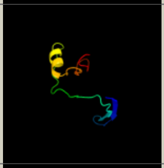
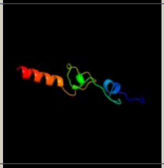
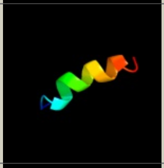
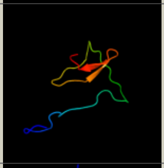
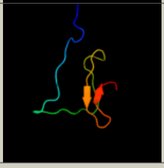
Unique Job ID	82ecc2b3de4e7e37

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3f7wA_	Alignment		98.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative fructosamine-3-kinase; **PDBTitle:** crystal structure of putative fructosamine-3-kinase (yp_290396.1) from2 thermobifida fusca yx-er1 at 1.85 a resolution
2	c3csvA_	Alignment		97.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminoglycoside phosphotransferase; **PDBTitle:** crystal structure of a putative aminoglycoside phosphotransferase2 (yp_614837.1) from silicibacter sp. tm1040 at 2.15 a resolution
3	d1j7la_	Alignment		97.4	18	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**APH phosphotransferases
4	c3lzhA_	Alignment		97.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aph(2")-id/aph(2")-iva; **PDBTitle:** crystal structure of aminoglycoside phosphotransferase aph(2")-2 id/aph(2")-iva
5	c3ovcA_	Alignment		97.0	14	**PDB header:**transferase/antibiotic **Chain:** A: **PDB Molecule:**hygromycin-b 4-o-kinase; **PDBTitle:** crystal structure of aminoglycoside phosphotransferase aph(4)-ia
6	c3jr1A_	Alignment		97.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative fructosamine-3-kinase; **PDBTitle:** crystal structure of putative fructosamine-3-kinase2 (yp_719053.1) from haemophilus somnus 129pt at 2.32 a3 resolution
7	d1nd4a_	Alignment		96.9	18	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**APH phosphotransferases
8	c3hamA_	Alignment		96.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminoglycoside phosphotransferase; **PDBTitle:** structure of the gentamicin-aph(2")-iia complex
9	c3i0oA_	Alignment		95.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**spectinomycin phosphotransferase; **PDBTitle:** crystal structure of spectinomycin phosphotransferase,2 aph(9)-ia, in complex with adp and spectinomcyin
10	c3attA_	Alignment		94.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of rv3168 with atp
11	c3dxpA_	Alignment		94.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acyl-coa dehydrogenase; **PDBTitle:** crystal structure of a putative aminoglycoside phosphotransferase2 (reut_a1007) from ralstonia eutropha jmp134 at 2.32 a resolution

12	d2pula1	Alignment		85.2	12	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**APH phosphotransferases
13	c3r78B_	Alignment		65.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminoglycoside 3'-phosphotransferase apha1-iab; **PDBTitle:** crystal structure of the aminoglycoside phosphotransferase aph(3')-ia,2 atp-bound
14	c2plyB_	Alignment		57.1	23	**PDB header:**translation/rna **Chain:** B: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** structure of the mrna binding fragment of elongation factor2 selb in complex with secis rna.
15	d2v9va2	Alignment		49.9	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal fragment of elongation factor SelB
16	c2xznH_	Alignment		36.3	19	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**ribosomal protein s8 containing protein; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
17	d1oy0a_	Alignment		27.9	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
18	c2fs1A_	Alignment		22.6	50	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**psd-1; **PDBTitle:** solution structure of psd-1
19	c1s1hH_	Alignment		22.1	18	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**40s ribosomal protein s22; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
20	d2gy9h1	Alignment		19.9	26	**Fold:**Ribosomal protein S8 **Superfamily:**Ribosomal protein S8 **Family:**Ribosomal protein S8
21	d1gjsa_	Alignment	not modelled	19.5	44	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**GA module, an albumin-binding domain
22	c1nyqA_	Alignment	not modelled	18.2	32	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase 1; **PDBTitle:** structure of staphylococcus aureus threonyl-trna synthetase2 complexed with an analogue of threonyl adenylate
23	d1i94h_	Alignment	not modelled	17.7	24	**Fold:**Ribosomal protein S8 **Superfamily:**Ribosomal protein S8 **Family:**Ribosomal protein S8
24	d1an7a_	Alignment	not modelled	16.7	24	**Fold:**Ribosomal protein S8 **Superfamily:**Ribosomal protein S8 **Family:**Ribosomal protein S8
25	d1seia_	Alignment	not modelled	16.1	20	**Fold:**Ribosomal protein S8 **Superfamily:**Ribosomal protein S8 **Family:**Ribosomal protein S8
26	d1na6a2	Alignment	not modelled	14.7	25	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Type II restriction endonuclease catalytic domain
27	c2v9vA_	Alignment	not modelled	14.4	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** crystal structure of moorella thermoacetica selb(377-511)
28	c2pywA_	Alignment	not modelled	13.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** structure of a. thaliana 5-methylthioribose kinase in complex with adp2 and mtr
						PDB header:transferase

29	c2q83A_	Alignment	not modelled	13.0	13	**Chain:** A: **PDB Molecule:**ytaa protein; **PDBTitle:** crystal structure of ytaa (2635576) from bacillus subtilis at 2.50 a2 resolution
30	c1qf6A_	Alignment	not modelled	12.7	20	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**threonyl-trna synthetase; **PDBTitle:** structure of e. coli threonyl-trna synthetase complexed with its2 cognate trna
31	c3bbnH_	Alignment	not modelled	12.2	22	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**ribosomal protein s8; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
32	c3ez4B_	Alignment	not modelled	12.1	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-methyl-2-oxobutanoate hydroxymethyltransferase; **PDBTitle:** crystal structure of 3-methyl-2-oxobutanoate2 hydroxymethyltransferase from burkholderia pseudomallei
33	d1m9fd_	Alignment	not modelled	11.8	19	**Fold:**Retrovirus capsid protein, N-terminal core domain **Superfamily:**Retrovirus capsid protein, N-terminal core domain **Family:**Retrovirus capsid protein, N-terminal core domain
34	d1zyla1	Alignment	not modelled	11.0	13	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**APH phosphotransferases
35	d1ve2a1	Alignment	not modelled	10.9	23	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
36	c2pqrD_	Alignment	not modelled	10.8	88	**PDB header:**apoptosis **Chain:** D: **PDB Molecule:**wd repeat protein ykr036c; **PDBTitle:** crystal structure of yeast fis1 complexed with a fragment of yeast2 caf4
37	d2ppqa1	Alignment	not modelled	10.8	14	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**APH phosphotransferases
38	c3dxqB_	Alignment	not modelled	10.7	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**choline/ethanolamine kinase family protein; **PDBTitle:** crystal structure of choline/ethanolamine kinase family protein2 (np_106042.1) from mesorhizobium loti at 2.55 a resolution
39	c2f3iA_	Alignment	not modelled	10.4	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii 17.1 **PDBTitle:** solution structure of a subunit of rna polymerase ii
40	d1m9dc_	Alignment	not modelled	10.2	19	**Fold:**Retrovirus capsid protein, N-terminal core domain **Superfamily:**Retrovirus capsid protein, N-terminal core domain **Family:**Retrovirus capsid protein, N-terminal core domain
41	c2kdnA_	Alignment	not modelled	9.6	36	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein pfe0790c; **PDBTitle:** solution structure of pfe0790c, a putative bola-like2 protein from the protozoan parasite plasmodium falciparum.
42	c2wlvA_	Alignment	not modelled	9.6	22	**PDB header:**virus protein **Chain:** A: **PDB Molecule:**gag polyprotein; **PDBTitle:** structure of the n-terminal capsid domain of hiv-2
43	d1w0ba_	Alignment	not modelled	9.0	43	**Fold:**Spectrin repeat-like **Superfamily:**Alpha-hemoglobin stabilizing protein AHSP **Family:**Alpha-hemoglobin stabilizing protein AHSP
44	d1nyra4	Alignment	not modelled	9.0	30	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
45	c3cf6E_	Alignment	not modelled	8.9	39	**PDB header:**signaling protein/gtp-binding protein **Chain:** E: **PDB Molecule:**rap guanine nucleotide exchange factor (gef) 4; **PDBTitle:** structure of epac2 in complex with cyclic-amp and rap
46	c3tr7A_	Alignment	not modelled	8.7	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** structure of a uracil-dna glycosylase (ung) from coxiella burnetii
47	d1upka_	Alignment	not modelled	8.6	21	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**Mo25 protein
48	c1na6B_	Alignment	not modelled	8.5	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**restriction endonuclease ecorii; **PDBTitle:** crystal structure of restriction endonuclease ecorii mutant2 r88a
49	d1m3ua_	Alignment	not modelled	7.9	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
50	d2cqqa1	Alignment	not modelled	7.6	40	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
51	c2f5xC_	Alignment	not modelled	7.4	21	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**bugd; **PDBTitle:** structure of periplasmic binding protein bugd
52	d1z8ua1	Alignment	not modelled	7.2	43	**Fold:**Spectrin repeat-like **Superfamily:**Alpha-hemoglobin stabilizing protein AHSP **Family:**Alpha-hemoglobin stabilizing protein AHSP
53	c3lyrA_	Alignment	not modelled	6.9	47	**PDB header:**transcription activator **Chain:** A: **PDB Molecule:**transcription factor coe1; **PDBTitle:** human early b-cell factor 1 (ebf1) dna-binding domain
54	c3cdxB_	Alignment	not modelled	6.4	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**succinylglutamatedesuccinylase/aspartoacylase; **PDBTitle:** crystal structure of2

						succinylglutamatedesuccinylase/aspartoacylase from3 rhodobacter sphaeroides
55	d1ouoa_	Alignment	not modelled	6.4	25	**Fold:**His-Me finger endonucleases **Superfamily:**His-Me finger endonucleases **Family:**Endonuclease I
56	d1l9bh2	Alignment	not modelled	5.6	100	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction centre subunit H, transmembrane region **Family:**Photosystem II reaction centre subunit H, transmembrane region
57	c2owrD_	Alignment	not modelled	5.2	6	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** crystal structure of vaccinia virus uracil-dna glycosylase
58	d2f1fa1	Alignment	not modelled	5.1	33	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
59	d2fgca2	Alignment	not modelled	5.1	28	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like