Phyre^{2}

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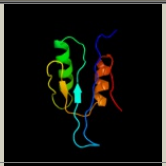
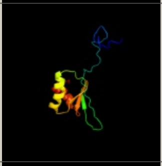
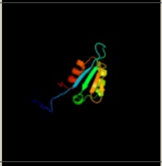
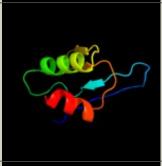
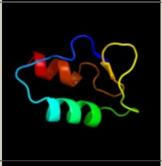
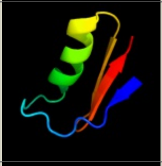
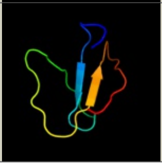
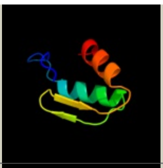
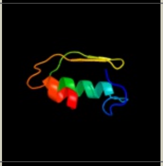
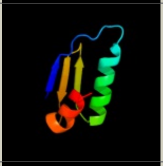
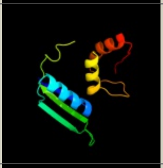
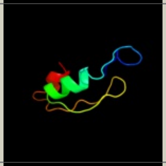
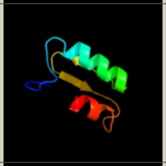
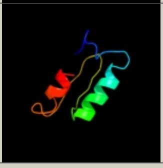
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1d1ra_	Alignment		99.9	100	**Fold:**eIF1-like **Superfamily:**eIF1-like **Family:**eIF1-like
2	c1d1rA_	Alignment		99.9	100	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical 11.4 kd protein ycih in pyrf-osmb **PDBTitle:** nmr solution structure of the product of the e. coli ycih2 gene.
3	c2xznF_	Alignment		99.9	22	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**eif1; **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
4	d2if1a_	Alignment		99.9	26	**Fold:**eIF1-like **Superfamily:**eIF1-like **Family:**eIF1-like
5	c2oghA_	Alignment		99.8	21	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor eif-1; **PDBTitle:** solution structure of yeast eif1
6	c2e9hA_	Alignment		86.2	12	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 5; **PDBTitle:** solution structure of the eif-5_eif-2b domain from human2 eukaryotic translation initiation factor 5
7	c2dcuB_	Alignment		81.9	18	**PDB header:**translation **Chain:** B: **PDB Molecule:**translation initiation factor 2 beta subunit; **PDBTitle:** crystal structure of translation initiation factor aif2betagamma2 heterodimer with gdp
8	d1neea1	Alignment		75.1	19	**Fold:**Ribosome binding domain-like **Superfamily:**Translation initiation factor 2 beta, aIF2beta, N-terminal domain **Family:**Translation initiation factor 2 beta, aIF2beta, N-terminal domain
9	c1neeA_	Alignment		69.8	21	**PDB header:**translation **Chain:** A: **PDB Molecule:**probable translation initiation factor 2 beta **PDBTitle:** structure of archaeal translation factor aif2beta from2 methanobacterium thermoautrophicum
10	d1k8ba_	Alignment		65.3	21	**Fold:**Ribosome binding domain-like **Superfamily:**Translation initiation factor 2 beta, aIF2beta, N-terminal domain **Family:**Translation initiation factor 2 beta, aIF2beta, N-terminal domain
11	d1qbaa1	Alignment		57.2	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes

12	d1gxua_	Alignment		56.2	18	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
13	c3br8A_	Alignment		43.3	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable acylphosphatase; **PDBTitle:** crystal structure of acylphosphatase from bacillus subtilis
14	c2gv1A_	Alignment		39.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable acylphosphatase; **PDBTitle:** nmr solution structure of the acylphosphatase from2 eschaerichia coli
15	d1ulra_	Alignment		37.9	19	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
16	c2bjeA_	Alignment		32.6	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acylphosphatase; **PDBTitle:** acylphosphatase from sulfolobus solfataricus. monclinic p212 space group
17	c3hyjD_	Alignment		29.4	13	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**protein duf199/whia; **PDBTitle:** crystal structure of the n-terminal laglidadg domain of duf199/whia
18	d1apsa_	Alignment		29.0	23	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
19	d1w2ia_	Alignment		26.4	21	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
20	d1urra_	Alignment		19.8	17	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
21	d2acya_	Alignment	not modelled	16.5	25	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
22	c1qbaA_	Alignment	not modelled	13.6	22	**PDB header:**glycosyl hydrolase **Chain:** A: **PDB Molecule:**chitobiase; **PDBTitle:** bacterial chitobiase, glycosyl hydrolase family 20
23	d1ka9f_	Alignment	not modelled	12.9	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
24	d1zhva2	Alignment	not modelled	12.8	10	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Atu0741-like
25	c3eubJ_	Alignment	not modelled	12.7	17	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of desulfo-xanthine oxidase with xanthine
26	d1thfd_	Alignment	not modelled	12.6	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
27	c2kyzA_	Alignment	not modelled	12.4	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**heavy metal binding protein; **PDBTitle:** nmr structure of heavy metal binding protein tm0320 from thermotoga2 maritima
28	d1in0a2	Alignment	not modelled	11.7	18	**Fold:**Ferredoxin-like **Superfamily:**YajQ-like **Family:**YajQ-like
29	d2a2pa1	Alignment	not modelled	11.6	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like

						Family: Selenoprotein W-related
30	c3ofgA_	Alignment	not modelled	10.8	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**boca/mesd chaperone for ywtd beta-propeller-egf protein 1; **PDBTitle:** structured domain of caenorhabditis elegans bmy-1
31	d2qswa1	Alignment	not modelled	10.2	16	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
32	c3b9jI_	Alignment	not modelled	9.7	17	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**xanthine oxidase; **PDBTitle:** structure of xanthine oxidase with 2-hydroxy-6-methylpurine
33	c3h7hA_	Alignment	not modelled	9.4	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt4; **PDBTitle:** crystal structure of the human transcription elongation factor dsif,2 hspt4/hspt5 (176-273)
34	c2kgsA_	Alignment	not modelled	9.3	32	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**uncharacterized protein rv0899/mt0922; **PDBTitle:** solution structure of the amino-terminal domain of ompatb, a pore2 forming protein from mycobacterium tuberculosis
35	d2f06a2	Alignment	not modelled	9.0	17	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
36	c1rm6F_	Alignment	not modelled	8.8	32	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**4-hydroxybenzoyl-coa reductase gamma subunit; **PDBTitle:** structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
37	d2aqea1	Alignment	not modelled	8.6	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**SWIRM domain
38	d1oqya1	Alignment	not modelled	8.4	12	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
39	c1n60D_	Alignment	not modelled	8.1	24	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**carbon monoxide dehydrogenase small chain; **PDBTitle:** crystal structure of the cu,mo-co dehydrogenase (codh); cyanide-2 inactivated form
40	d1whza_	Alignment	not modelled	8.1	20	**Fold:**dsRBD-like **Superfamily:**YcfA/nrd intein domain **Family:**YcfA-like
41	d1jrma_	Alignment	not modelled	7.9	26	**Fold:**YggU-like **Superfamily:**YggU-like **Family:**YggU-like
42	c3cw2M_	Alignment	not modelled	7.8	29	**PDB header:**translation **Chain:** M: **PDB Molecule:**translation initiation factor 2 subunit beta; **PDBTitle:** crystal structure of the intact archaeal translation2 initiation factor 2 from sulfolobus solfataricus .
43	c2eljA_	Alignment	not modelled	7.5	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional adapter 2; **PDBTitle:** solution structure of the swirm domain of baker's yeast2 transcriptional adapter 2
44	c1zhvA_	Alignment	not modelled	7.2	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein atu0741; **PDBTitle:** x-ray crystal structure protein atu0741 from agobacterium tumefaciens.2 northeast structural genomics consortium target atr8.
45	c3fd2A_	Alignment	not modelled	7.2	19	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**dna endonuclease i-msoi, linker, dna endonuclease i-msoi; **PDBTitle:** crystal structure of mmsoi/dna complex with calcium
46	c3fzyA_	Alignment	not modelled	7.1	26	**PDB header:**toxin **Chain:** A: **PDB Molecule:**rtx toxin rtxa; **PDBTitle:** crystal structure of pre-cleavage form of cysteine protease domain2 from vibrio cholerae rtxa toxin
47	c2uwjE_	Alignment	not modelled	7.0	22	**PDB header:**chaperone **Chain:** E: **PDB Molecule:**type iii export protein psce; **PDBTitle:** structure of the heterotrimeric complex which regulates2 type iii secretion needle formation
48	c1ffuA_	Alignment	not modelled	7.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cuts, iron-sulfur protein of carbon monoxide **PDBTitle:** carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor
49	c3hrdH_	Alignment	not modelled	6.9	14	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**nicotinate dehydrogenase small fes subunit; **PDBTitle:** crystal structure of nicotinate dehydrogenase
50	c3aq3A_	Alignment	not modelled	6.9	25	**PDB header:**toxin **Chain:** A: **PDB Molecule:**6b protein; **PDBTitle:** molecular insights into plant cell proliferation disturbance by2 agrobacterium protein 6b
51	c1in0B_	Alignment	not modelled	6.5	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**yajq protein; **PDBTitle:** yajq protein (hi1034)
52	c1ou5A_	Alignment	not modelled	6.3	23	**PDB header:**translation, transferase **Chain:** A: **PDB Molecule:**trna cca-adding enzyme; **PDBTitle:** crystal structure of human cca-adding enzyme
53	d1zata2	Alignment	not modelled	6.3	19	**Fold:**L,D-transpeptidase pre-catalytic domain-like **Superfamily:**L,D-transpeptidase pre-catalytic domain-like **Family:**L,D-transpeptidase pre-catalytic domain-like
54	d1h5ya_	Alignment	not modelled	6.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel

						Family: Histidine biosynthesis enzymes
55	d1v93a_	Alignment	not modelled	6.1	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**FAD-linked oxidoreductase **Family:**Methylenetetrahydrofolate reductase
56	d1bgva1	Alignment	not modelled	6.1	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
57	d2cuja1	Alignment	not modelled	5.9	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**SWIRM domain
58	d1dd4c_	Alignment	not modelled	5.8	39	**Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Family:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain
59	c3hrlA_	Alignment	not modelled	5.8	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**endonuclease-like protein; **PDBTitle:** crystal structure of a putative endonuclease-like protein (ngo0050)2 from neisseria gonorrhoeae
60	c3ihtB_	Alignment	not modelled	5.7	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**s-adenosyl-l-methionine methyl transferase; **PDBTitle:** crystal structure of s-adenosyl-l-methionine methyl transferase2 (yp_165822.1) from silicibacter pomeroyi dss-3 at 1.80 a resolution
61	c1t3qD_	Alignment	not modelled	5.7	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**quinoline 2-oxidoreductase small subunit; **PDBTitle:** crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
62	d3dhxa1	Alignment	not modelled	5.5	24	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
63	c3hluA_	Alignment	not modelled	5.4	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein duf2179; **PDBTitle:** crystal structure of uncharacterized protein conserved in bacteria2 duf2179 from eubacterium ventriosum
64	d1zcha1	Alignment	not modelled	5.4	28	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
65	d1b5ta_	Alignment	not modelled	5.3	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**FAD-linked oxidoreductase **Family:**Methylenetetrahydrofolate reductase
66	c3jsyA_	Alignment	not modelled	5.3	21	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** n-terminal fragment of ribosomal protein l10 from methanococcus2 jannaschii
67	c2w3zA_	Alignment	not modelled	5.2	6	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deacetylase; **PDBTitle:** structure of a streptococcus mutans ce4 esterase
68	d1gmua2	Alignment	not modelled	5.1	21	**Fold:**Ferredoxin-like **Superfamily:**Urease metallochaperone UreE, C-terminal domain **Family:**Urease metallochaperone UreE, C-terminal domain