Phyre^2

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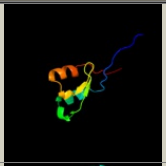
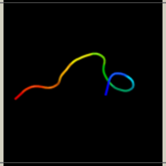
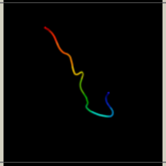
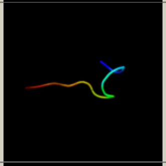
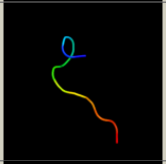
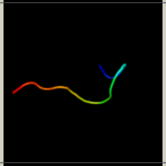
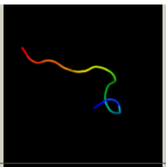
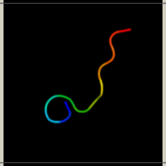
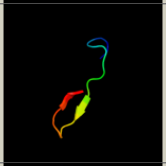
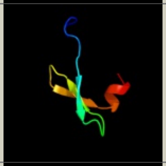
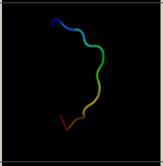
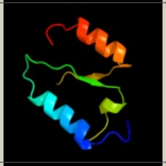
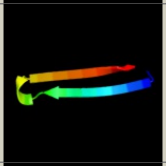
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1h16a_	Alignment		100.0	79	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
2	c2y8nC_	Alignment		100.0	29	**PDB header:**lyase **Chain:** C: **PDB Molecule:**4-hydroxyphenylacetate decarboxylase large subunit; **PDBTitle:** crystal structure of glycyl radical enzyme
3	d1r9da_	Alignment		100.0	31	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
4	c2f3oB_	Alignment		100.0	27	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**pyruvate formate-lyase 2; **PDBTitle:** crystal structure of a glycyl radical enzyme from archaeoglobus2 fulgidus
5	d1aisa1	Alignment		26.3	27	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
6	d1nh2a1	Alignment		25.1	15	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
7	d1qnaa1	Alignment		25.0	17	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
8	d1nh2a2	Alignment		24.8	42	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
9	d1mp9a1	Alignment		23.8	33	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
10	d1aisa2	Alignment		23.5	42	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
11	d1qnaa2	Alignment		22.9	42	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain

12	d1cdwa2	Alignment		22.3	42	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
13	d1mp9a2	Alignment		21.5	42	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
14	d1cdwa1	Alignment		19.4	11	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
15	d1pg5b2	Alignment		18.9	17	**Fold:**Rubredoxin-like **Superfamily:**Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain **Family:**Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain
16	c1wd6B_	Alignment		18.8	25	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein ydhr; **PDBTitle:** crystal structure of jw1657 from escherichia coli
17	c3iz5P_	Alignment		16.9	25	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**60s ribosomal protein l15 (l15e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
18	c2z1dA_	Alignment		16.3	10	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hydrogenase expression/formation protein hypd; **PDBTitle:** crystal structure of [nife] hydrogenase maturation protein, hypd from2 thermococcus kodakaraensis
19	d2hiqa1	Alignment		15.7	25	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Hypothetical protein YdhR
20	c1vraB_	Alignment		14.0	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**arginine biosynthesis bifunctional protein argj; **PDBTitle:** crystal structure of arginine biosynthesis bifunctional protein argj2 (10175521) from bacillus halodurans at 2.00 a resolution
21	c1yo8A_	Alignment	not modelled	12.8	17	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**thrombospondin-2; **PDBTitle:** structure of the c-terminal domain of human thrombospondin-2
22	c3h0mE_	Alignment	not modelled	12.1	21	**PDB header:**ligase **Chain:** E: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase **PDBTitle:** structure of trna-dependent amidotransferase gatcab from2 aquifex aeolicus
23	d1xlya_	Alignment	not modelled	11.8	33	**Fold:**RNA-binding protein She2p **Superfamily:**RNA-binding protein She2p **Family:**RNA-binding protein She2p
24	d2fzcb2	Alignment	not modelled	11.4	15	**Fold:**Rubredoxin-like **Superfamily:**Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain **Family:**Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain
25	d1vqom1	Alignment	not modelled	10.4	24	**Fold:**Ribosomal proteins S24e, L23 and L15e **Superfamily:**Ribosomal proteins S24e, L23 and L15e **Family:**L15e
26	c4a1cL_	Alignment	not modelled	10.3	25	**PDB header:**ribosome **Chain:** L: **PDB Molecule:**ribosomal protein l15; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
27	d1jj2l_	Alignment	not modelled	10.2	24	**Fold:**Ribosomal proteins S24e, L23 and L15e **Superfamily:**Ribosomal proteins S24e, L23 and L15e **Family:**L15e
28	c2kwuA_	Alignment	not modelled	9.9	36	**PDB header:**protein binding/signaling protein **Chain:** A: **PDB Molecule:**dna polymerase iota;

28	c2kwdA_	Alignment	not modelled	9.9	30	**PDBTitle:** solution structure of ubm2 of murine polymerase iota in complex with2 ubiquitin
29	d1v82a_	Alignment	not modelled	9.8	20	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**1,3-glucuronyltransferase
30	c2vzkD_	Alignment	not modelled	9.8	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glutamate n-acetyltransferase 2 beta chain; **PDBTitle:** structure of the acyl-enzyme complex of an n-terminal2 nucleophile (ntn) hydrolase, oat2
31	c2z8uQ_	Alignment	not modelled	9.5	32	**PDB header:**transcription **Chain:** Q: **PDB Molecule:**tata-box-binding protein; **PDBTitle:** methanococcus jannaschii tbp
32	c2q82A_	Alignment	not modelled	9.4	43	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**core protein p7; **PDBTitle:** crystal structure of core protein p7 from pseudomonas phage2 phi12. northeast structural genomics target oc1
33	c1eysH_	Alignment	not modelled	8.7	11	**PDB header:**electron transport **Chain:** H: **PDB Molecule:**photosynthetic reaction center; **PDBTitle:** crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
34	d8ruci_	Alignment	not modelled	8.6	25	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
35	d1gk8i_	Alignment	not modelled	8.5	17	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
36	c2hx6A_	Alignment	not modelled	8.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease; **PDBTitle:** solution structure analysis of the phage t42 endoribonuclease regb
37	d1cmwa2	Alignment	not modelled	8.4	28	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
38	d1ej7s_	Alignment	not modelled	8.3	29	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
39	d1tfra2	Alignment	not modelled	8.3	18	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
40	d1wdds_	Alignment	not modelled	7.7	21	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
41	d1ffki_	Alignment	not modelled	7.6	31	**Fold:**Ribosomal proteins S24e, L23 and L15e **Superfamily:**Ribosomal proteins S24e, L23 and L15e **Family:**L15e
42	c3al0B_	Alignment	not modelled	7.4	20	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; **PDBTitle:** crystal structure of the glutamine transamidosome from thermotoga2 maritima in the glutamylation state.
43	c1d3uA_	Alignment	not modelled	7.4	42	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**tata-binding protein; **PDBTitle:** tata-binding protein/transcription factor (ii)b/bre+tata-2 box complex from pyrococcus woesei
44	c2j6pF_	Alignment	not modelled	7.3	16	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**sb(v)-as(v) reductase; **PDBTitle:** structure of as-sb reductase from leishmania major
45	c3eikB_	Alignment	not modelled	7.3	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**tata-box-binding protein; **PDBTitle:** double stranded dna binding protein
46	d2v6ai1	Alignment	not modelled	7.2	17	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
47	c1mp9B_	Alignment	not modelled	7.0	33	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**tata-binding protein; **PDBTitle:** tbp from a mesothermophilic archaeon, sulfolobus2 acidocaldarius
48	c3gqjA_	Alignment	not modelled	6.9	25	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cell inhibiting factor (cif); **PDBTitle:** crystal structure of cell inhibiting factor (cif) from photorhabdus2 luminescens
49	d2f2ab2	Alignment	not modelled	6.9	14	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**GatB/GatE catalytic domain-like
50	c3f3hA_	Alignment	not modelled	6.5	27	**PDB header:**antitumor protein **Chain:** A: **PDB Molecule:**immunomodulatory protein ling zhi-8; **PDBTitle:** crystal structure and anti-tumor activity of lz-8 from the fungus2 ganoderma lucidium
51	d1uzdc1	Alignment	not modelled	6.5	17	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
52	c3ol0C_	Alignment	not modelled	6.3	50	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**de novo designed monomer trefoil-fold sub-domain which **PDBTitle:** crystal structure of monofoil-4p homo-trimer: de novo designed monomer2 trefoil-fold sub-domain which forms homo-trimer assembly
53	d1v5ra1	Alignment	not modelled	6.3	33	**Fold:**N domain of copper amine oxidase-like **Superfamily:**GAS2 domain-like **Family:**GAS2 domain
						PDB header:ribosome **Chain:** L: **PDB Molecule:**60s ribosomal protein l15-a;

54	c1s1iL_	Alignment	not modelled	6.1	35	**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, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
55	c3q3jA_	Alignment	not modelled	6.1	22	**PDB header:**membrane protein/protein binding **Chain:** A: **PDB Molecule:**plexin-a2; **PDBTitle:** crystal structure of plexin a2 rbd in complex with rnd1
56	c3su8X_	Alignment	not modelled	6.1	29	**PDB header:**apoptosis/signaling protein **Chain:** X: **PDB Molecule:**plexin-b1; **PDBTitle:** crystal structure of a truncated intracellular domain of plexin-b1 in2 complex with rac1
57	d2nlua1	Alignment	not modelled	5.9	39	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**PWWP domain
58	d1eysh1	Alignment	not modelled	5.8	11	**Fold:**PRC-barrel domain **Superfamily:**PRC-barrel domain **Family:**Photosynthetic reaction centre, H-chain, cytoplasmic domain
59	c3ajfA_	Alignment	not modelled	5.6	43	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** structural insigths into dsrna binding and rna silencing suppression2 by ns3 protein of rice hoja blanca tenuivirus
60	c1ux6A_	Alignment	not modelled	5.5	19	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**thrombospondin-1; **PDBTitle:** structure of a thrombospondin c-terminal fragment reveals a2 novel calcium core in the type 3 repeats
61	d1xo1a2	Alignment	not modelled	5.4	22	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
62	c1zswA_	Alignment	not modelled	5.1	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**glyoxalase family protein; **PDBTitle:** crystal structure of bacillus cereus metallo protein from glyoxalase2 family
63	d1v54b1	Alignment	not modelled	5.1	11	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Periplasmic domain of cytochrome c oxidase subunit II
64	c3bl9B_	Alignment	not modelled	5.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**scavenger mrna-decapping enzyme dcps; **PDBTitle:** synthetic gene encoded dcps bound to inhibitor dg157493
65	c3gr1A_	Alignment	not modelled	5.0	22	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**protein prgh; **PDBTitle:** periplamic domain of the t3ss inner membrane protein prgh2 from s.typhimurium (fragment 170-392)