Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0A7M2
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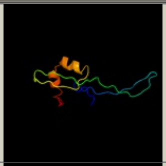
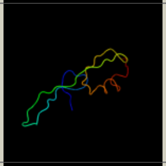
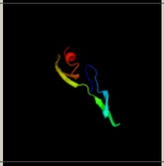
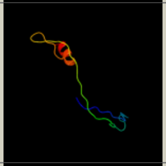
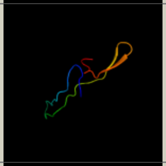
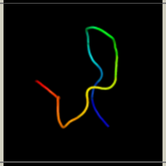
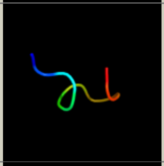
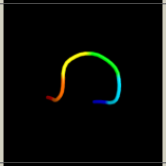
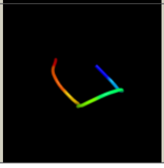
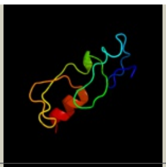
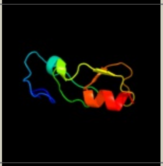
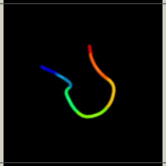
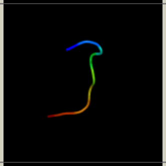
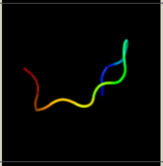
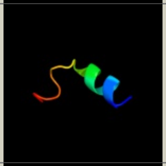
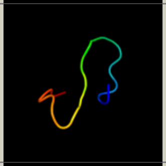
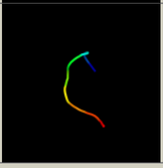
Unique Job ID	7c9aeb5c317bc664

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2qamz1	Alignment		100.0	100	**Fold:**L28p-like **Superfamily:**L28p-like **Family:**Ribosomal protein L28
2	c3bboY_	Alignment		100.0	39	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**ribosomal protein l28; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
3	d2jz6a1	Alignment		99.9	31	**Fold:**L28p-like **Superfamily:**L28p-like **Family:**Ribosomal protein L28
4	c2jl81_	Alignment		99.8	33	**PDB header:**ribosome **Chain:** 1: **PDB Molecule:**50s ribosomal protein l28; **PDBTitle:** insights into translational termination from the structure2 of rf2 bound to the ribosome (part 4 of 4).3 this file contains the 50s subunit.
5	d2zjru1	Alignment		99.2	25	**Fold:**L28p-like **Superfamily:**L28p-like **Family:**Ribosomal protein L28
6	d2j0111	Alignment		97.7	36	**Fold:**L28p-like **Superfamily:**L28p-like **Family:**Ribosomal protein L28
7	d2cu8a1	Alignment		44.6	21	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
8	c2k5cA_	Alignment		34.9	33	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein pf0385; **PDBTitle:** nmr structure for pf0385
9	c2uz0B_	Alignment		22.4	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**tributyrin esterase; **PDBTitle:** the crystal crystal structure of the esta protein, a2 virulence factor esta protein from streptococcus pneumonia
10	d2yt9a2	Alignment		14.7	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
11	c2elrA_	Alignment		14.6	43	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 406; **PDBTitle:** solution structure of the 15th c2h2 zinc finger of human2 zinc finger protein 406

12	c1dvpA_	Alignment		14.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine **PDBTitle:** crystal structure of the vhs and fyve tandem domains of hrs,2 a protein involved in membrane trafficking and signal3 transduction
13	c3zyqA_	Alignment		10.2	14	**PDB header:**signaling **Chain:** A: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine kinase **PDBTitle:** crystal structure of the tandem vhs and fyve domains of hepatocyte2 growth factor-regulated tyrosine kinase substrate (hgs-hrs) at 1.483 a resolution
14	d2dmda2	Alignment		9.4	57	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
15	c2c4iA_	Alignment		9.1	56	**PDB header:**glycoprotein **Chain:** A: **PDB Molecule:**avidin; **PDBTitle:** crystal structure of engineered avidin
16	d1ibia2	Alignment		8.6	23	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
17	c2oz5A_	Alignment		7.4	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phosphotyrosine protein phosphatase ptpb; **PDBTitle:** crystal structure of mycobacterium tuberculosis protein tyrosine2 phosphatase ptpb in complex with the specific inhibitor omts
18	c2jtgA_	Alignment		7.4	20	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**thap domain-containing protein 1; **PDBTitle:** solution structure of the thap-zinc finger of thap1
19	c3jyvN_	Alignment		7.3	40	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**40s ribosomal protein s29(a); **PDBTitle:** structure of the 40s rrna and proteins and p/e trna for eukaryotic2 ribosome based on cryo-em map of thermomyces lanuginosus ribosome at3 8.9a resolution
20	c1wbiD_	Alignment		7.3	44	**PDB header:**avidin-related protein **Chain:** D: **PDB Molecule:**avidin-related protein 2; **PDBTitle:** avr2
21	c3iufA_	Alignment	not modelled	7.0	43	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**zinc finger protein ubi-d4; **PDBTitle:** crystal structure of the c2h2-type zinc finger domain of2 human ubi-d4
22	c2xznN_	Alignment	not modelled	6.7	50	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**rps29e; **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
23	d1dxga_	Alignment	not modelled	6.7	33	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Desulforedoxin
24	d2fkza1	Alignment	not modelled	6.6	28	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
25	d1zfoa_	Alignment	not modelled	6.5	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LASP-1
26	d1ywfa1	Alignment	not modelled	6.5	18	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Mycobacterial PtpB-like
27	c2zkqn_	Alignment	not modelled	6.1	50	**PDB header:**ribosomal protein/rna **Chain:** N: **PDB Molecule:** **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
28	d2htna1	Alignment	not modelled	6.0	19	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin

29	d2csha2	Alignment	not modelled	5.8	30	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
30	d2b8ta2	Alignment	not modelled	5.7	11	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Type II thymidine kinase zinc finger
31	c2qm0B_	Alignment	not modelled	5.6	9	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**bes; **PDBTitle:** crystal structure of bes protein from bacillus cereus
32	d2d8ya1	Alignment	not modelled	5.5	17	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
33	d2cota2	Alignment	not modelled	5.3	38	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
34	c1ardA_	Alignment	not modelled	5.3	38	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**yeast transcription factor adr1; **PDBTitle:** structures of dna-binding mutant zinc finger domains:2 implications for dna binding
35	d2adra1	Alignment	not modelled	5.2	38	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
36	c3hi2C_	Alignment	not modelled	5.2	25	**PDB header:**dna binding protein/toxin **Chain:** C: **PDB Molecule:**hth-type transcriptional regulator mqsa(ygit); **PDBTitle:** structure of the n-terminal domain of the e. coli antitoxin mqsa2 (ygit/b3021) in complex with the e. coli toxin mqsr (ygiu/b3022)
37	d1llmc2	Alignment	not modelled	5.1	25	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
38	d1dvpa2	Alignment	not modelled	5.0	15	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**FYVE, a phosphatidylinositol-3-phosphate binding domain