Phyre^{2}

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Description	P76150
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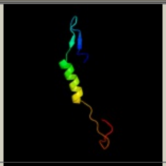
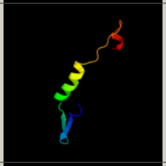
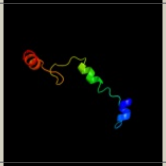
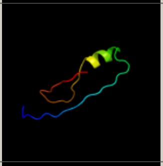
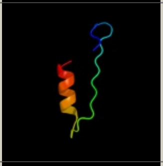
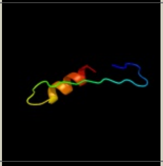
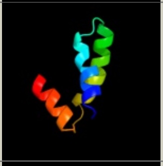
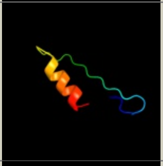
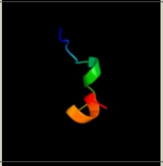
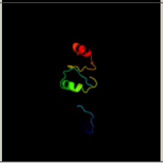
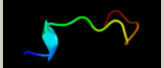
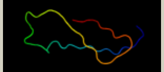
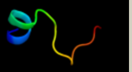
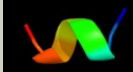
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2izpB_	Alignment		20.1	29	**PDB header:**toxin **Chain:** B: **PDB Molecule:**putative membrane antigen; **PDBTitle:** bipd - an invasion prtein associated with the type-iii2 secretion system of burkholderia pseudomallei.
2	d2izpa1	Alignment		17.2	29	**Fold:**IpaD-like **Superfamily:**IpaD-like **Family:**IpaD-like
3	c3hc7A_	Alignment		16.6	20	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**gene 12 protein; **PDBTitle:** crystal structure of lysin b from mycobacteriophage d29
4	d1oh4a_	Alignment		14.8	28	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 27 carbohydrate binding module, CBM27
5	c1msvB_	Alignment		13.5	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**s-adenosylmethionine decarboxylase proenzyme; **PDBTitle:** the s68a s-adenosylmethionine decarboxylase proenzyme2 processing mutant.
6	c3ep3A_	Alignment		12.9	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**s-adenosylmethionine decarboxylase alpha chain; **PDBTitle:** human adometdc d174n mutant with no putrescine bound
7	d1upka_	Alignment		10.8	18	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**Mo25 protein
8	d1jl0a_	Alignment		10.8	19	**Fold:**S-adenosylmethionine decarboxylase **Superfamily:**S-adenosylmethionine decarboxylase **Family:**S-adenosylmethionine decarboxylase
9	d1phpa_	Alignment		10.7	21	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
10	c3q2tC_	Alignment		9.5	32	**PDB header:**rna binding protein/rna **Chain:** C: **PDB Molecule:**cleavage and polyadenylation specificity factor subunit 6; **PDBTitle:** crystal structure of cfim68 rrm/cfim25/rna complex
11	c2hh9A_	Alignment		9.3	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiamin pyrophosphokinase; **PDBTitle:** thiamin pyrophosphokinase from candida albicans

12	d1ejia_	Alignment		9.2	38	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
13	d1pmhx_	Alignment		8.6	26	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 27 carbohydrate binding module, CBM27
14	c2k6rA_	Alignment		8.3	75	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**full sequence design 1 synthetic superstable; **PDBTitle:** protein folding on a highly rugged landscape: experimental2 observation of glassy dynamics and structural frustration
15	c2hjqA_	Alignment		8.2	47	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical protein yqbf; **PDBTitle:** nmr structure of bacillus subtilis protein yqbf, northeast2 structural genomics target sr449
16	c1fmeA_	Alignment		8.1	75	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**fsd-ey peptide; **PDBTitle:** solution structure of fsd-ey, a novel peptide assuming a2 beta-beta-alpha fold
17	c1fsvA_	Alignment		7.9	75	**PDB header:**beta beta alpha motif **Chain:** A: **PDB Molecule:**full sequence design 1 of beta beta alpha motif; **PDBTitle:** full sequence design 1 (fsd-1) of beta beta alpha motif,2 nmr, minimized average structure
18	c1fsdA_	Alignment		7.9	75	**PDB header:**novel sequence **Chain:** A: **PDB Molecule:**full sequence design 1 of beta beta alpha motif; **PDBTitle:** full sequence design 1 (fsd-1) of beta beta alpha motif,2 nmr, 41 structures
19	c3da7G_	Alignment		7.8	41	**PDB header:**protein binding **Chain:** G: **PDB Molecule:**barnase circular permutant; **PDBTitle:** a conformationally strained, circular permutant of barnase
20	c2l5gB_	Alignment		7.6	50	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative uncharacterized protein ncor2; **PDBTitle:** co-ordinates and 1h, 13c and 15n chemical shift assignments for the2 complex of gps2 53-90 and smrt 167-207
21	c2hvzA_	Alignment	not modelled	7.6	24	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**splicing factor, arginine/serine-rich 7; **PDBTitle:** solution structure of the rrm domain of sr rich factor 9g8
22	c1zmrA_	Alignment	not modelled	7.3	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of the e. coli phosphoglycerate kinase
23	c3cvzA_	Alignment	not modelled	7.3	25	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**s-layer protein; **PDBTitle:** structural insights into the molecular organization of the2 s-layer from clostridium difficile
24	c2rhqA_	Alignment	not modelled	7.1	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylalanyl-trna synthetase alpha chain; **PDBTitle:** phers from staphylococcus haemolyticus- rational protein2 engineering and inhibitor studies
25	d2arha1	Alignment	not modelled	7.0	35	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**Aq 1966-like
26	d1fiua_	Alignment	not modelled	7.0	54	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease NgoIV
27	d2hjqa2	Alignment	not modelled	6.9	27	**Fold:**GINS/PriA/YqbF domain **Superfamily:**PriA/YqbF domain **Family:**YqbF N-terminal domain-like
28	d1z1za1	Alignment	not modelled	6.7	25	**Fold:**Phage tail protein-like **Superfamily:**Phage tail protein-like **Family:**Lambda phage gpU-like
						Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins)

29	d1pgsa1	Alignment	not modelled	6.6	53	**Superfamily:**PHM/PNGase F **Family:**Glycosyl-asparaginase
30	c2o8kA_	Alignment	not modelled	6.6	47	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** nmr structure of the sigma-54 rpon domain bound to the-242 promoter element
31	c2ytuA_	Alignment	not modelled	6.6	38	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**friend leukemia integration 1 transcription **PDBTitle:** solution structure of the sam_pnt-domain of the human2 friend leukemiaintegration 1 transcription factor
32	c3hlzA_	Alignment	not modelled	6.6	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bt_1490; **PDBTitle:** crystal structure of bt_1490 (np_810393.1) from bacteroides2 thetaiotaomicron vpi-5482 at 1.50 a resolution
33	d1hd0a_	Alignment	not modelled	6.5	28	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
34	c1v0sA_	Alignment	not modelled	6.3	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phospholipase d; **PDBTitle:** uninhibited form of phospholipase d from streptomyces sp.2 strain pmf
35	d1z3xa1	Alignment	not modelled	6.2	25	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**GUN4-associated domain
36	d1mn4a_	Alignment	not modelled	6.2	23	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**DNA-binding domain from NDT80
37	d1k3ea_	Alignment	not modelled	6.2	16	**Fold:**Secretion chaperone-like **Superfamily:**Type III secretory system chaperone-like **Family:**Type III secretory system chaperone
38	c2c4bB_	Alignment	not modelled	6.2	41	**PDB header:**fusion protein **Chain:** B: **PDB Molecule:**barnase mcoeeti fusion; **PDBTitle:** inhibitor cystine knot protein mcoeeti fused to the2 catalytically inactive barnase mutant h102a
39	d2bida_	Alignment	not modelled	5.9	21	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
40	c2e5iA_	Alignment	not modelled	5.8	24	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**heterogeneous nuclear ribonucleoprotein l-like; **PDBTitle:** solution structure of rna binding domain 2 in heterogeneous2 nuclear ribonucleoprotein l-like
41	c2dkxA_	Alignment	not modelled	5.7	38	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sam pointed domain-containing ets transcription **PDBTitle:** solution structure of the sam_pnt-domain of ets2 transcription factor pdef (prostate ets)
42	d1jyoa_	Alignment	not modelled	5.4	13	**Fold:**Secretion chaperone-like **Superfamily:**Type III secretory system chaperone-like **Family:**Type III secretory system chaperone
43	c3md1B_	Alignment	not modelled	5.4	35	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**nuclear and cytoplasmic polyadenylated rna-binding protein **PDBTitle:** crystal structure of the second rrm domain of yeast poly(u)-binding2 protein (pub1)
44	d1x9ba_	Alignment	not modelled	5.4	44	**Fold:**Protozoan pheromone-like **Superfamily:**Hypothetical membrane protein Ta0354, soluble domain **Family:**Hypothetical membrane protein Ta0354, soluble domain
45	c3lgbB_	Alignment	not modelled	5.4	36	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna primase large subunit; **PDBTitle:** crystal structure of the fe-s domain of the yeast dna primase
46	c3if8A_	Alignment	not modelled	5.2	20	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**protein zwilch homolog; **PDBTitle:** crystal structure of zwilch, a member of the rzz kinetochore complex
47	d1erpa_	Alignment	not modelled	5.0	47	**Fold:**Protozoan pheromone-like **Superfamily:**Protozoan pheromone proteins **Family:**Protozoan pheromone proteins