Phyre^2

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Description	RVBD3755c_(-)_4201467_4202066
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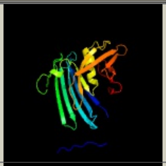
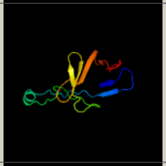
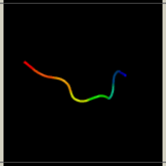
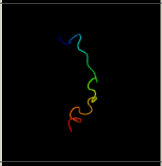
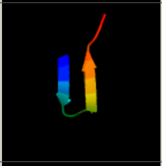
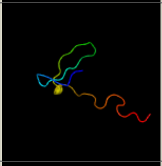
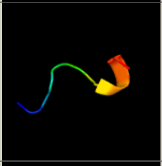
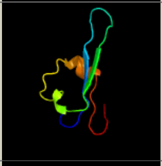
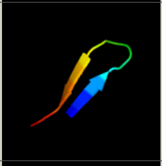
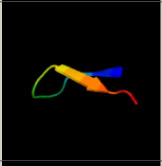
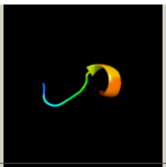
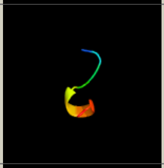
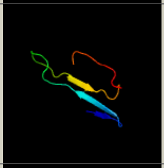
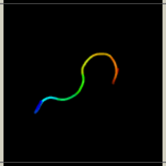
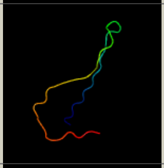
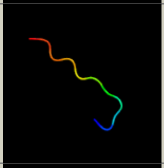
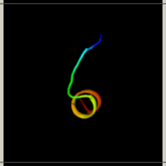
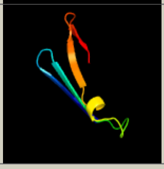
Unique Job ID	b39b46940847cdbe

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2h1ta1	 Alignment		100.0	27	**Fold:**Spiral beta-roll **Superfamily:**PA1994-like **Family:**PA1994-like
2	d1jiwi_	 Alignment		45.3	14	**Fold:**Streptavidin-like **Superfamily:**beta-Barrel protease inhibitors **Family:**Metalloprotease inhibitor
3	c5aj1A_	 Alignment		19.9	50	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**swi/snf-related matrix-associated actin-dependent regulator **PDBTitle:** solution structure of the smarc domain
4	c2k7mA_	 Alignment		14.1	28	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**gap junction alpha-5 protein; **PDBTitle:** structure of the connexin40 carboxyl terminal domain
5	c4d77A_	 Alignment		12.0	29	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**gliomedin; **PDBTitle:** high-resolution structure of the extracellular olfactomedin2 domain from gliomedin
6	c2gtjA_	 Alignment		12.0	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**fyn-binding protein; **PDBTitle:** reduced form of adap hsh3-n-domain
7	c6homD_	 Alignment		10.8	50	**PDB header:**gene regulation **Chain:** D: **PDB Molecule:**ccr4-not transcription complex subunit 4, isoform l; **PDBTitle:** drosophila not4 cbm peptide bound to human caf40
8	c5tvzA_	 Alignment		10.7	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nucleoporin pom152; **PDBTitle:** solution nmr structure of saccharomyces cerevisiae pom152 ig-like2 repeat, residues 718-820
9	c5amoA_	 Alignment		10.6	29	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**noelin; **PDBTitle:** structure of a mouse olfactomedin-1 disulfide-linked dimer of the2 olfactomedin domain and part of the coiled coil
10	c4wxuA_	 Alignment		10.1	36	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**myocilin; **PDBTitle:** crystal structure of the selenomthionine incorporated myocilin2 olfactomedin domain e396d variant.
11	c3m4wH_	 Alignment		9.9	63	**PDB header:**signaling protein/signaling protein **Chain:** H: **PDB Molecule:**sigma-e factor negative regulatory protein; **PDBTitle:** structural basis for the negative regulation of bacterial stress2 response by rseb

12	c6homB_	Alignment		9.3	50	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**ccr4-not transcription complex subunit 4, isoform l; **PDBTitle:** drosophila not4 cbm peptide bound to human caf40
13	c6honD_	Alignment		9.3	50	**PDB header:**gene regulation **Chain:** D: **PDB Molecule:**ccr4-not transcription complex subunit 4, isoform l; **PDBTitle:** drosophila not4 cbm peptide bound to human caf40
14	c2w56B_	Alignment		9.2	22	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**vc0508; **PDBTitle:** structure of the hypothetical protein vc0508 from vibrio cholerae2 vsp-ii pathogenicity island
15	c6honB_	Alignment		9.1	50	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**ccr4-not transcription complex subunit 4, isoform l; **PDBTitle:** drosophila not4 cbm peptide bound to human caf40
16	c6eluJ_	Alignment		8.9	27	**PDB header:**antitoxin **Chain:** J: **PDB Molecule:**serum resistance associated; vsg protein; **PDBTitle:** structure of serum resistance associated protein from t. b.2 rhodesiense
17	d1jz8a4	Alignment		8.8	18	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**beta-Galactosidase, domain 5
18	d2d81a1	Alignment		8.7	36	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**PHB depolymerase-like
19	d1o1za_	Alignment		8.0	36	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Glycerophosphoryl diester phosphodiesterase
20	d3bb9a1	Alignment		7.9	9	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SO0125-like
21	c6nk6G_	Alignment	not modelled	7.9	16	**PDB header:**virus like particle/signaling protein **Chain:** G: **PDB Molecule:**e2 glycoprotein; **PDBTitle:** electron cryo-microscopy of chikungunya vlp in complex with mouse2 mxra8 receptor
22	c1wx4B_	Alignment	not modelled	7.9	25	**PDB header:**oxidoreductase/metal transport **Chain:** B: **PDB Molecule:**melc; **PDBTitle:** crystal structure of the oxy-form of the copper-bound streptomyces2 castaneoglobisporus tyrosinase complexed with a caddie protein3 prepared by the addition of dithiothreitol
23	c5afbA_	Alignment	not modelled	7.8	36	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**latrophilin-3; **PDBTitle:** crystal structure of the latrophilin3 lectin and2 olfactomedin domains
24	c2mpvA_	Alignment	not modelled	7.3	27	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**major fimbrial subunit of aggregative adherence fimbria ii **PDBTitle:** structural insight into host recognition and biofilm formation by2 aggregative adherence fimbriae of enteroaggregative escherichia coli
25	d1l5aa2	Alignment	not modelled	7.2	33	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**NRPS condensation domain (amide synthase)
26	c3rlgA_	Alignment	not modelled	7.0	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sphingomyelin phosphodiesterase d lisictox-alphaia1a; **PDBTitle:** crystal structure of loxosceles intermedia phospholipase d isoform 12 h12a mutant
27	d2q07a3	Alignment	not modelled	6.6	57	**Fold:**Cystatin-like **Superfamily:**Pre-PUA domain **Family:**AF0587 pre C-terminal domain-like
						PDB header:virus

28	c3j0cH_	Alignment	not modelled	6.5	15	**Chain:** H: **PDB Molecule:**e2 envelope glycoprotein; **PDBTitle:** models of e1, e2 and cp of venezuelan equine encephalitis virus tc-832 strain restrained by a near atomic resolution cryo-em map
29	c3n43B_	Alignment	not modelled	6.3	15	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**e2 envelope glycoprotein; **PDBTitle:** crystal structures of the mature envelope glycoprotein complex2 (trypsin cleavage) of chikungunya virus.
30	c5u9oD_	Alignment	not modelled	6.3	14	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**plastid division protein cdp1, chloroplastic,plastid **PDBTitle:** cocrystal structure of the intermembrane space region of the plastid2 division proteins parc6 and pdv1
31	c2xfbl_	Alignment	not modelled	6.2	15	**PDB header:**virus **Chain:** I: **PDB Molecule:**e2 envelope glycoprotein; **PDBTitle:** the chikungunya e1 e2 envelope glycoprotein complex fit into2 the sindbis virus cryo-em map
32	c6g1cV_	Alignment	not modelled	5.9	20	**PDB header:**antitoxin **Chain:** V: **PDB Molecule:**antitoxin hicb; **PDBTitle:** crystal structure of the n-terminal domain of burkholderia2 pseudomallei antitoxin hicb
33	c2r9qD_	Alignment	not modelled	5.9	35	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**2'-deoxycytidine 5'-triphosphate deaminase; **PDBTitle:** crystal structure of 2'-deoxycytidine 5'-triphosphate deaminase from2 agrobacterium tumefaciens
34	c4q6xA_	Alignment	not modelled	5.8	29	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phospholipase d stsictox-betaic1; **PDBTitle:** structure of phospholipase d beta1b1i from sicarius terrosus venom at2 2.14 a resolution
35	c2f9rC_	Alignment	not modelled	5.7	29	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**sphingomyelinase d 1; **PDBTitle:** crystal structure of the inactive state of the smase i, a2 sphingomyelinase d from loxosceles laeta venom
36	d1yb3a1	Alignment	not modelled	5.4	12	**Fold:**YktB/PF0168-like **Superfamily:**YktB/PF0168-like **Family:**PF0168-like
37	c4hvmC_	Alignment	not modelled	5.4	11	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**tlmii; **PDBTitle:** crystal structure of tallysomycin biosynthesis protein tlmii
38	c3fzeA_	Alignment	not modelled	5.3	36	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein ste5; **PDBTitle:** structure of the 'minimal scaffold' (ms) domain of ste5 that2 cocatalyzes fus3 phosphorylation by ste7
39	d1vd6a1	Alignment	not modelled	5.2	36	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Glycerophosphoryl diester phosphodiesterase