Phyre^2

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Description	P0AE63
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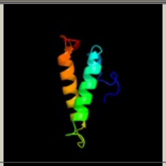
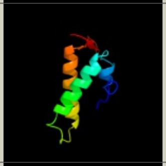
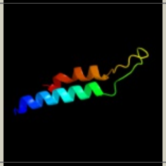
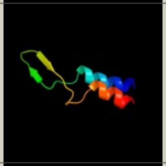
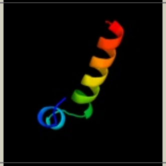
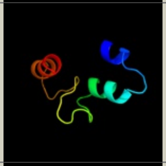
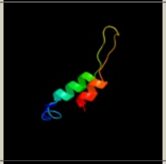
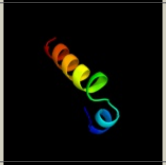
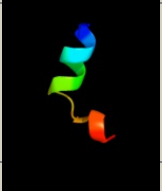
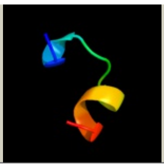
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1sg7A_	Alignment		100.0	100	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative cation transport regulator chab; **PDBTitle:** nmr solution structure of the putative cation transport2 regulator chab
2	d1sg7a1	Alignment		100.0	100	**Fold:**ChaB-like **Superfamily:**ChaB-like **Family:**ChaB-like
3	d1k32a4	Alignment		30.6	22	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Tail specific protease, catalytic domain
4	d1fc6a4	Alignment		28.1	32	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Tail specific protease, catalytic domain
5	c2q9qC_	Alignment		22.7	11	**PDB header:**replication **Chain:** C: **PDB Molecule:**dna replication complex gins protein psf1; **PDBTitle:** the crystal structure of full length human gins complex
6	d1knca_	Alignment		18.5	26	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**AhpD
7	c1bpoA_	Alignment		17.5	31	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**protein (clathrin); **PDBTitle:** clathrin heavy-chain terminal domain and linker
8	d1bpoa1	Alignment		16.4	26	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**Clathrin heavy-chain linker domain
9	d2e9xa1	Alignment		15.8	11	**Fold:**GINS helical bundle-like **Superfamily:**GINS helical bundle-like **Family:**PSF1 N-terminal domain-like
10	c3mopM_	Alignment		11.0	33	**PDB header:**signaling protein, immune system **Chain:** M: **PDB Molecule:**interleukin-1 receptor-associated kinase-like 2; **PDBTitle:** the ternary death domain complex of myd88, irak4, and irak2
11	c1o8tA_	Alignment		8.8	33	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**apolipoprotein c-ii; **PDBTitle:** global structure and dynamics of human apolipoprotein cii2 in complex with micelles: evidence for increased mobility3 of the helix involvved in the activation of lipoprotein4 lipase.

12	c1trlB_	Alignment		8.2	35	**PDB header:**hydrolase (metalloprotease) **Chain:** B: **PDB Molecule:**thermolysin fragment 255 - 316; **PDBTitle:** nmr solution structure of the c-terminal fragment 255-3162 of thermolysin: a dimer formed by subunits having the3 native structure
13	d2qfka1	Alignment		6.4	29	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
14	c1fc9A_	Alignment		5.7	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**photosystem ii d1 protease; **PDBTitle:** photosystem ii d1 c-terminal processing protease
15	d2ddza1	Alignment		5.7	21	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**PH0223-like
16	c2kwuA_	Alignment		5.5	45	**PDB header:**protein binding/signaling protein **Chain:** A: **PDB Molecule:**dna polymerase iota; **PDBTitle:** solution structure of ubm2 of murine polymerase iota in complex with2 ubiquitin
17	d1tnsa_	Alignment		5.3	33	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like

18	d1qpma_	Alignment		5.2	8	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like