Phyre2

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Description	P0AD19
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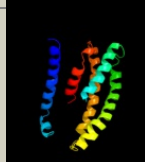
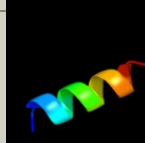
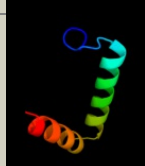
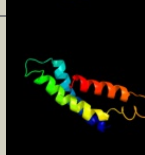
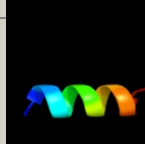
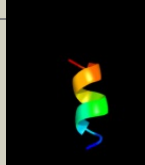
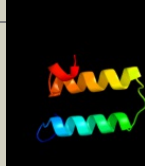
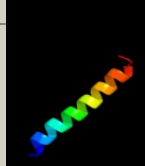
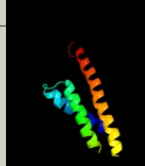
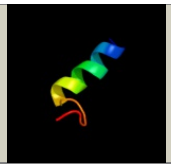
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2yvxD_	Alignment		89.6	17	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
2	d2yvxa3	Alignment		44.9	17	**Fold:**MgtE membrane domain-like **Superfamily:**MgtE membrane domain-like **Family:**MgtE membrane domain-like
3	d1l7va_	Alignment		16.2	16	**Fold:**ABC transporter involved in vitamin B12 uptake, BtuC **Superfamily:**ABC transporter involved in vitamin B12 uptake, BtuC **Family:**ABC transporter involved in vitamin B12 uptake, BtuC
4	d1z0kb1	Alignment		13.7	36	**Fold:**Long alpha-hairpin **Superfamily:**Rabenosyn-5 Rab-binding domain-like **Family:**Rabenosyn-5 Rab-binding domain-like
5	c3zv0A_	Alignment		13.3	19	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**protein shq1; **PDBTitle:** structure of the shq1p-cbf5p complex
6	c3rfuC_	Alignment		13.1	17	**PDB header:**hydrolase, membrane protein **Chain:** C: **PDB Molecule:**copper efflux atpase; **PDBTitle:** crystal structure of a copper-transporting pib-type atpase
7	d1yzma1	Alignment		12.8	36	**Fold:**Long alpha-hairpin **Superfamily:**Rabenosyn-5 Rab-binding domain-like **Family:**Rabenosyn-5 Rab-binding domain-like
8	c1ckxA_	Alignment		11.8	45	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cystic fibrosis transmembrane conductance **PDBTitle:** cystic fibrosis transmembrane conductance regulator:2 solution structures of peptides based on the phe508 region,3 the most common site of disease-causing delta-f508 mutation
9	c1ciiA_	Alignment		9.6	15	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
10	c2ks1B_	Alignment		8.6	30	**PDB header:**transferase **Chain:** B: **PDB Molecule:**epidermal growth factor receptor; **PDBTitle:** heterodimeric association of transmembrane domains of erbb1 and erbb22 receptors enabling kinase activation
11	c3p5nA_	Alignment		8.1	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**riboflavin uptake protein; **PDBTitle:** structure and mechanism of the s component of a bacterial ecf2 transporter

12	d2akza2	Alignment		8.0	25	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
13	c1ckwA_	Alignment		7.2	50	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**protein (cystic fibrosis transmembrane **PDBTitle:** cystic fibrosis transmembrane conductance regulator:2 solution structures of peptides based on the phe508 region,3 the most common site of disease-causing delta-f508 mutation
14	c1unyA_	Alignment		6.6	28	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles

15	c2ju0B_	Alignment		5.3	26	**PDB header:**metal binding protein/signaling protein **Chain:** B: **PDB Molecule:**phosphatidylinositol 4-kinase pik1; **PDBTitle:** structure of yeast frequenin bound to pdtins 4-kinase