Phyre2

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Description	P45763
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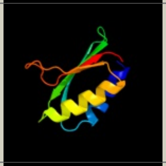
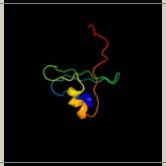
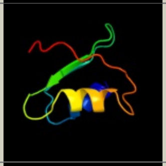
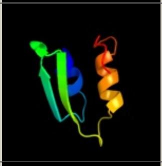
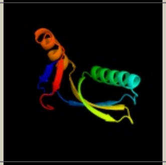
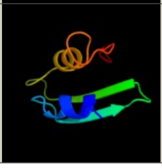
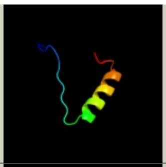
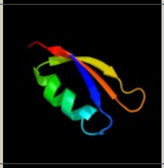
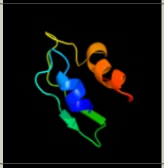
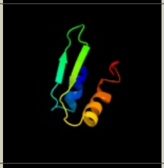
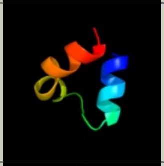
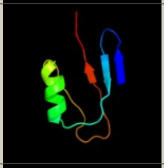
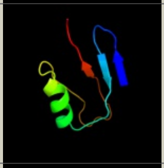
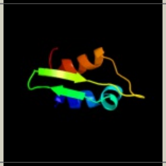
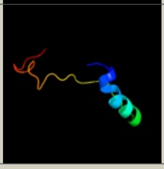
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1yf5L_	Alignment		100.0	22	**PDB header:**transport protein **Chain:** L: **PDB Molecule:**general secretion pathway protein l; **PDBTitle:** cyto-epsl: the cytoplasmic domain of epsl, an inner membrane component2 of the type ii secretion system of vibrio cholerae
2	d2bh1a2	Alignment		100.0	24	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Cyto-EpsL domain
3	c2w7vB_	Alignment		99.8	11	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**general secretion pathway protein l; **PDBTitle:** periplasmic domain of epsl from vibrio parahaemolyticus
4	d2bh1a1	Alignment		99.7	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Cyto-EpsL domain
5	c2ychA_	Alignment		98.0	16	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**competence protein pilm; **PDBTitle:** pilm-piln type iv pilus biogenesis complex
6	d1p6ta2	Alignment		27.1	11	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
7	d1s6ua_	Alignment		25.7	5	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
8	c2l3mA_	Alignment		21.0	8	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**copper-ion-binding protein; **PDBTitle:** solution structure of the putative copper-ion-binding protein from2 bacillus anthracis str. ames
9	d1e4ft1	Alignment		19.7	6	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
10	d2qifa1	Alignment		16.9	10	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
11	d2aw0a_	Alignment		16.7	4	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain

12	d2dyna_	Alignment		12.9	16	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
13	d1dcja_	Alignment		12.9	19	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
14	d1cpza_	Alignment		10.8	4	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
15	d1sb6a_	Alignment		10.4	6	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
16	c2ky4A_	Alignment		9.4	3	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**phycobilisome linker polypeptide; **PDBTitle:** solution nmr structure of the pbs linker domain of phycobilisome2 linker polypeptide from anabaena sp. northeast structural genomics3 consortium target nsr123e
17	d1uv7a_	Alignment		8.8	6	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**General secretion pathway protein M, EpsM **Family:**General secretion pathway protein M, EpsM
18	c1uv7A_	Alignment		8.8	6	**PDB header:**transport **Chain:** A: **PDB Molecule:**general secretion pathway protein m; **PDBTitle:** periplasmic domain of epsm from vibrio cholerae
19	d1p6ta1	Alignment		8.6	12	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
20	c3p14C_	Alignment		7.8	16	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**l-rhamnose isomerase; **PDBTitle:** crystal structure of l-rhamnose isomerase with a novel high thermo-2 stability from bacillus halodurans
21	c2x29A_	Alignment	not modelled	7.7	30	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**tumor necrosis factor ligand superfamily member **PDBTitle:** crystal structure of human4-1bb ligand ectodomain
22	c3dxsX_	Alignment	not modelled	7.7	11	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**copper-transporting atpase ran1; **PDBTitle:** crystal structure of a copper binding domain from hma7, a p-2 type atpase
23	d1d8wa_	Alignment	not modelled	7.3	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**L-rhamnose isomerase
24	c2jpiA_	Alignment	not modelled	7.2	6	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** chemical shift assignments of pa4090 from pseudomonas2 aeruginosa
25	c2yciX_	Alignment	not modelled	7.1	19	**PDB header:**transferase **Chain:** X: **PDB Molecule:**5-methyltetrahydrofolate corrinoid/iron sulfur protein **PDBTitle:** methyltransferase native
26	d1f44a1	Alignment	not modelled	7.1	4	**Fold:**SAM domain-like **Superfamily:**lambda integrase-like, N-terminal domain **Family:**lambda integrase-like, N-terminal domain
27	c2k2pA_	Alignment	not modelled	7.0	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1203; **PDBTitle:** solution nmr structure of protein atu1203 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att10, ontario center for structural proteomics target atc1183
28	d1q8la_	Alignment	not modelled	7.0	5	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain

29	c2dhiA_	Alignment	not modelled	7.0	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**pleckstrin homology domain-containing family b **PDBTitle:** solution structure of the ph domain of evectin-2 from mouse
30	c2kkhA_	Alignment	not modelled	6.6	10	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**putative heavy metal transporter; **PDBTitle:** structure of the zinc binding domain of the atpase hma4
31	c1y3kA_	Alignment	not modelled	5.9	5	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the apo form of the fifth domain of2 menkes protein
32	d1afia_	Alignment	not modelled	5.6	7	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
33	c2rloA_	Alignment	not modelled	5.6	6	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**centaurin-gamma 1; **PDBTitle:** split ph domain of pi3-kinase enhancer
34	c3lstB_	Alignment	not modelled	5.4	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**calo1 methyltransferase; **PDBTitle:** crystal structure of calo1, methyltransferase in calicheamicin2 biosynthesis, sah bound form
35	d1f6ya_	Alignment	not modelled	5.3	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Methyltetrahydrofolate-utiluzing methyltransferases