Phyre2

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Description	P56579
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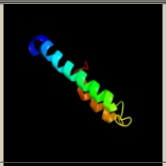
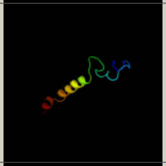
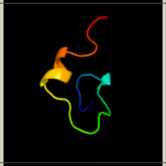
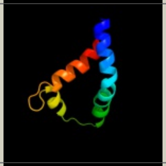
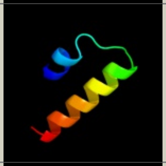
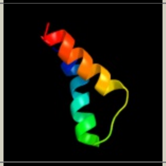
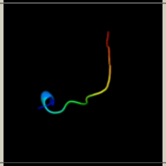
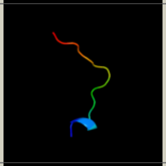
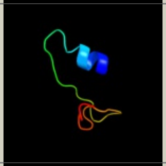
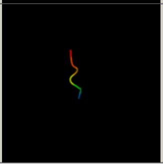
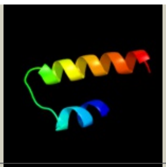
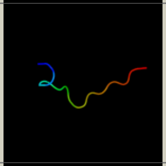
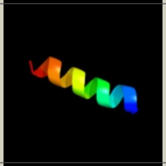
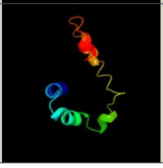
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2g3vC_	Alignment		16.7	21	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**cag pathogenicity island protein 13; **PDBTitle:** crystal structure of cags (hp0534, cag13) from helicobacter2 pylori
2	c2zshB_	Alignment		11.9	50	**PDB header:**hormone receptor **Chain:** B: **PDB Molecule:**della protein gai; **PDBTitle:** structural basis of gibberellin(ga3)-induced della2 recognition by the gibberellin receptor
3	d1wpga4	Alignment		11.8	23	**Fold:**Calcium ATPase, transmembrane domain M **Superfamily:**Calcium ATPase, transmembrane domain M **Family:**Calcium ATPase, transmembrane domain M
4	d2incb1	Alignment		10.5	22	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like
5	d1kf6d_	Alignment		10.1	35	**Fold:**Heme-binding four-helical bundle **Superfamily:**Fumarate reductase respiratory complex transmembrane subunits **Family:**Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
6	d3e9va1	Alignment		8.0	13	**Fold:**BTG domain-like **Superfamily:**BTG domain-like **Family:**BTG domain-like
7	c1p58C_	Alignment		7.4	37	**PDB header:**virus **Chain:** C: **PDB Molecule:**major envelope protein e; **PDBTitle:** complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
8	d1w2za3	Alignment		6.4	7	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
9	d1w6ga3	Alignment		5.9	27	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
10	c2o01D_	Alignment		5.7	28	**PDB header:**photosynthesis **Chain:** D: **PDB Molecule:**photosystem i reaction center subunit ii, **PDBTitle:** the structure of a plant photosystem i supercomplex at 3.42 angstrom resolution
11	c2a3zC_	Alignment		5.6	50	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**wiskott-aldrich syndrome protein; **PDBTitle:** ternary complex of the wh2 domain of wasp with actin-dnase i

12	d2z15a1	Alignment		5.6	20	**Fold:**BTG domain-like **Superfamily:**BTG domain-like **Family:**BTG domain-like
13	d1d6za3	Alignment		5.4	20	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
14	d2p7tc1	Alignment		5.4	29	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
15	d1hlma_	Alignment		5.1	8	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins

16	c2wseD_	Alignment		5.1	34	**PDB header:**photosynthesis **Chain:** D: **PDB Molecule:**photosystem i reaction center subunit ii, **PDBTitle:** improved model of plant photosystem i