Phyre^2

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Description	Q6BF87
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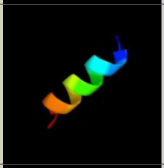
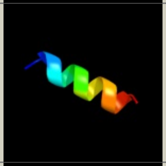
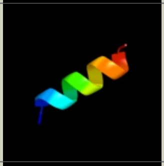
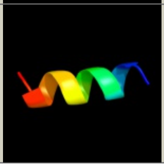
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2hg5D_	Alignment		10.4	17	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**kcsa channel; **PDBTitle:** cs+ complex of a k channel with an amide to ester substitution in the2 selectivity filter
2	c3t41B_	Alignment		6.4	36	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**epidermin leader peptide processing serine protease epip; **PDBTitle:** 1.95 angstrom resolution crystal structure of epidermin leader peptide2 processing serine protease (epip) s393a mutant from staphylococcus3 aureus
3	d1r0re_	Alignment		6.3	29	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases
4	c3lpcA_	Alignment		5.7	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aprb2; **PDBTitle:** crystal structure of a subtilisin-like protease
5	c1s2nB_	Alignment		5.6	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**extracellular subtilisin-like serine proteinase; **PDBTitle:** crystal strucure of a cold adapted subtilisin-like serine proteinase
6	c2b6nA_	Alignment		5.6	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**proteinase k; **PDBTitle:** the 1.8 a crystal structure of a proteinase k like enzyme from a2 psychrotroph serratia species
7	c1loiA_	Alignment		5.5	56	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cyclic 3',5'-amp specific phosphodiesterase rd1; **PDBTitle:** n-terminal splice region of rat c-amp phosphodiesterase,2 nmr, 7 structures
8	c2iy9A_	Alignment		5.3	31	**PDB header:**toxin **Chain:** A: **PDB Molecule:**suba; **PDBTitle:** crystal structure of the a-subunit of the ab5 toxin from e.2 coli

9	d1xx7a_	Alignment		5.3	30	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain