Phyre2

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Description	P0ADN6
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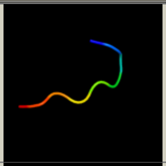
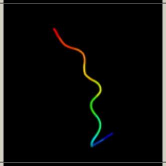
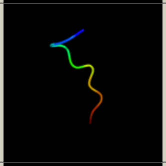
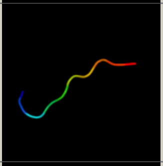
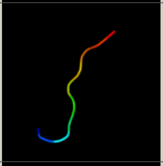
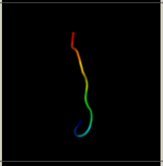
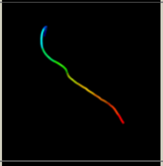
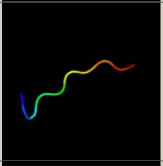
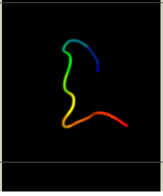
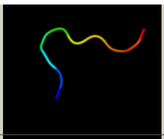
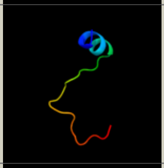
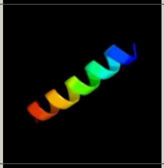
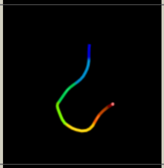
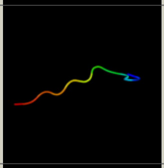
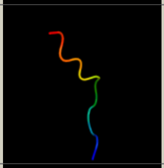
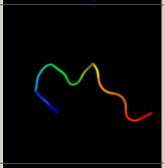
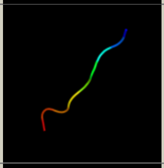
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2rfpA_	Alignment		30.4	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative ntp pyrophosphohydrolase; **PDBTitle:** crystal structure of putative ntp pyrophosphohydrolase2 (yp_001813558.1) from exiguobacterium sibiricum 255-15 at 1.74 a3 resolution
2	d1gpia_	Alignment		19.9	60	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Glycosyl hydrolase family 7 catalytic core
3	d2v3ia1	Alignment		19.3	70	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Glycosyl hydrolase family 7 catalytic core
4	d1q9ha_	Alignment		19.0	70	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Glycosyl hydrolase family 7 catalytic core
5	c2rfyB_	Alignment		17.8	50	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cellulose 1,4-beta-cellobiosidase; **PDBTitle:** crystal structure of cellobiohydrolase from melanocarpus2 albomyces complexed with cellobiose
6	d1ojja_	Alignment		16.5	40	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Glycosyl hydrolase family 7 catalytic core
7	d3ovwa_	Alignment		14.6	50	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Glycosyl hydrolase family 7 catalytic core
8	d1eg1a_	Alignment		14.0	50	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Glycosyl hydrolase family 7 catalytic core
9	d2j88h1	Alignment		13.8	67	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)
10	d1v54j_	Alignment		13.4	20	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIIa **Family:**Mitochondrial cytochrome c oxidase subunit VIIa
11	c2a7oA_	Alignment		11.8	36	**PDB header:**transcription **Chain:** A: **PDB Molecule:**huntingtin interacting protein b; **PDBTitle:** solution structure of the hset2/hypb sri domain

12	c2yf3F_	Alignment		11.7	30	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**mazg-like nucleoside triphosphate pyrophosphohydrolase; **PDBTitle:** crystal structure of dr2231, the mazg-like protein from2 deinococcus radiodurans, complex with manganese
13	c3cxbA_	Alignment		11.6	38	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein sifa; **PDBTitle:** crystal structure of sifa and skip
14	c2y69W_	Alignment		11.1	20	**PDB header:**electron transport **Chain:** W: **PDB Molecule:**cytochrome c oxidase polypeptide 7a1; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
15	d1j3ba1	Alignment		9.3	57	**Fold:**PEP carboxykinase-like **Superfamily:**PEP carboxykinase-like **Family:**PEP carboxykinase C-terminal domain
16	c2funB_	Alignment		8.6	33	**PDB header:**apoptosis/hydrolase **Chain:** B: **PDB Molecule:**caspase-8; **PDBTitle:** alternative p35-caspase-8 complex
17	c2h51B_	Alignment		8.0	25	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**caspase-1; **PDBTitle:** crystal structure of human caspase-1 (glu390->asp and arg286->lys) in2 complex with 3-[2-(2-benzyloxycarbonylamino-3-methyl-butyrylamino)-3 propionylamino]-4-oxo-pentanoic acid (z-vad-fmk)
18	c3o7vX_	Alignment		7.2	33	**PDB header:**rna binding protein/rna **Chain:** X: **PDB Molecule:**piwi-like protein 1; **PDBTitle:** crystal structure of human hiwi1 (v361m) paz domain (residues 277-399)2 in complex with 14-mer rna (12-bp + 2-nt overhang) containing 2'-och33 at its 3'-end
19	c3o7xC_	Alignment		7.1	33	**PDB header:**rna binding protein **Chain:** C: **PDB Molecule:**piwi-like protein 2; **PDBTitle:** crystal structure of human hili paz domain
20	c3ph0C_	Alignment		6.3	25	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**ascg; **PDBTitle:** crystal structure of the heteromolecular chaperone, asce-ascg, from2 the type iii secretion system in aeromonas hydrophila
21	c2p2cD_	Alignment	not modelled	5.6	38	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**caspase-2; **PDBTitle:** inhibition of caspase-2 by a designed ankyrin repeat2 protein (darpin)
22	c3lklB_	Alignment	not modelled	5.4	29	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**antisigma-factor antagonist stas; **PDBTitle:** crystal structure of the c-terminal domain of anti-sigma factor2 antagonist stas from rhodobacter sphaeroides
23	c3h0dB_	Alignment	not modelled	5.1	83	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**ctsr; **PDBTitle:** crystal structure of ctsr in complex with a 26bp dna duplex