Phyre^2

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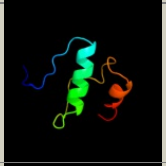
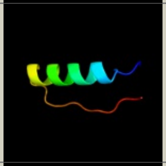
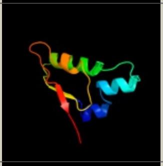
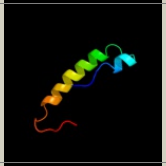
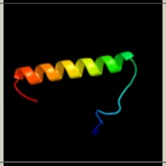
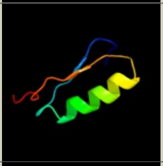
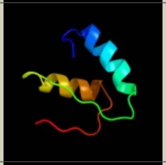
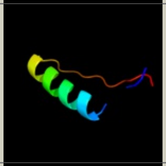
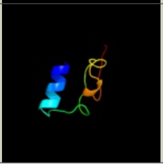
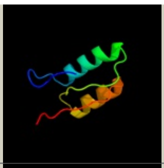
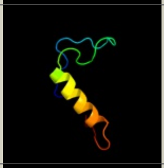
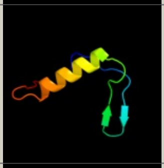
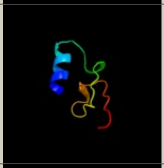
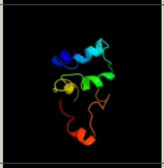
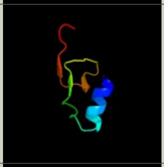
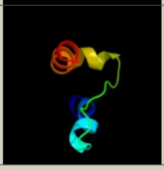
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2xsbA_	Alignment		65.2	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronoglucosaminidase; **PDBTitle:** ogoga pugnac complex
2	d2i4ra1	Alignment		44.1	11	**Fold:**AtpF-like **Superfamily:**AtpF-like **Family:**AtpF-like
3	d2cbia2	Alignment		35.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**alpha-D-glucuronidase/Hyaluronidase catalytic domain
4	c2cbjA_	Alignment		20.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronidase; **PDBTitle:** structure of the clostridium perfringens nagj family 842 glycoside hydrolase, a homologue of human o-glcnacase in3 complex with pugnac
5	c2k0mA_	Alignment		19.8	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of the uncharacterized protein from2 rhodospirillum rubrum gene locus rru_a0810. northeast3 structural genomics target rrr43
6	c3tp9B_	Alignment		19.5	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase and rhodanese domain protein; **PDBTitle:** crystal structure of alicyclobacillus acidocaldarius protein with2 beta-lactamase and rhodanese domains
7	d1lzia_	Alignment		19.2	19	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**alpha-1,3-galactosyltransferase-like
8	c1wv9B_	Alignment		18.9	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**rhodanese homolog tt1651; **PDBTitle:** crystal structure of rhodanese homolog tt1651 from an2 extremely thermophilic bacterium thermus thermophilus hb8
9	c3fq6A_	Alignment		16.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** the crystal structure of a methyltransferase domain from bacteroides2 thetaiotaomicron vpi
10	c2choA_	Alignment		13.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucosaminidase; **PDBTitle:** bacteroides thetaiotaomicron hexosaminidase with o-2 glcnacase activity
11	c2xe4A_	Alignment		12.4	28	**PDB header:**hydrolase/inhibitor **Chain:** A: **PDB Molecule:**oligopeptidase b; **PDBTitle:** structure of oligopeptidase b from leishmania major

12	d1jaka1	Alignment		10.6	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain
13	d1i0ea1	Alignment		10.5	22	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
14	c1ph4A_	Alignment		10.4	14	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**telomere-binding protein alpha subunit; **PDBTitle:** crystal structure of the oxytricha nova telomere end-binding protein2 complexed with noncognate ssdna ggggttttggcg
15	c1jb7A_	Alignment		10.4	14	**PDB header:**dna-binding protein/dna **Chain:** A: **PDB Molecule:**telomere-binding protein alpha subunit; **PDBTitle:** dna g-quartets in a 1.86 a resolution structure of an oxytricha nova2 telomeric protein-dna complex
16	c1qfmA_	Alignment		9.3	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (prolyl oligopeptidase); **PDBTitle:** prolyl oligopeptidase from porcine muscle
17	d1r8se_	Alignment		8.5	21	**Fold:**alpha-alpha superhelix **Superfamily:**Sec7 domain **Family:**Sec7 domain
18	d1bc9a_	Alignment		8.1	22	**Fold:**alpha-alpha superhelix **Superfamily:**Sec7 domain **Family:**Sec7 domain
19	c1yr2A_	Alignment		7.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**prolyl oligopeptidase; **PDBTitle:** structural and mechanistic analysis of two prolyl endopeptidases: role2 of inter-domain dynamics in catalysis and specificity
20	d1g0wa1	Alignment		6.9	15	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
21	c2dcqA_	Alignment	not modelled	6.8	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative protein at4g01050; **PDBTitle:** fully automated nmr structure determination of the2 rhodanese homology domain at4g01050(175-295) from3 arabidopsis thaliana
22	d1u6ra1	Alignment	not modelled	6.7	13	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
23	d1okta2	Alignment	not modelled	6.6	33	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
24	d2choa2	Alignment	not modelled	6.4	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**alpha-D-glucuronidase/Hyaluronidase catalytic domain
25	d1qh4a1	Alignment	not modelled	6.2	13	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
26	d1syxb1	Alignment	not modelled	6.2	21	**Fold:**GYF/BRK domain-like **Superfamily:**GYF domain **Family:**GYF domain
27	c1syxF_	Alignment	not modelled	6.2	21	**PDB header:**translation/immune system **Chain:** F: **PDB Molecule:**cd2 antigen cytoplasmic tail-binding protein 2; **PDBTitle:** the crystal structure of a binary u5 snrnp complex
28	d2r09a1	Alignment	not modelled	6.2	22	**Fold:**alpha-alpha superhelix **Superfamily:**Sec7 domain **Family:**Sec7 domain
						Fold: DeoB insert domain-like

29	d2i09a2	Alignment	not modelled	5.9	50	**Superfamily:**DeoB insert domain-like **Family:**DeoB insert domain-like
30	d1e7ua4	Alignment	not modelled	5.5	25	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Phoshoinositide 3-kinase (PI3K), catalytic domain
31	c3ktsA_	Alignment	not modelled	5.4	14	**PDB header:**transcriptional regulator **Chain:** A: **PDB Molecule:**glycerol uptake operon antiterminator regulatory protein; **PDBTitle:** crystal structure of glycerol uptake operon antiterminator regulatory2 protein from listeria monocytogenes str. 4b f2365
32	d1or7a2	Alignment	not modelled	5.3	14	**Fold:**Sigma2 domain of RNA polymerase sigma factors **Superfamily:**Sigma2 domain of RNA polymerase sigma factors **Family:**Sigma2 domain of RNA polymerase sigma factors
33	d2gjxa1	Alignment	not modelled	5.2	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain