Phyre^2

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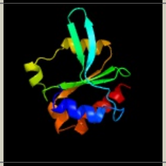
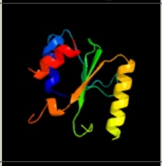
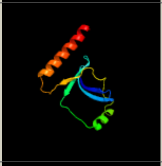
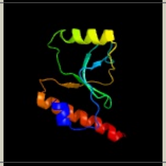
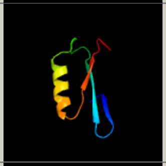
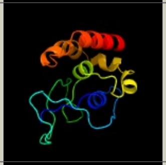
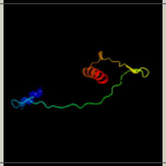
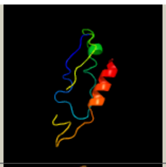
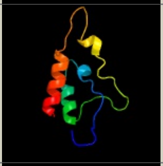
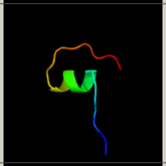
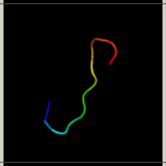
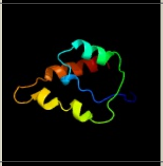
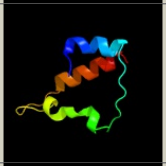
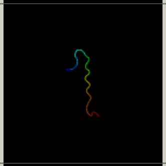
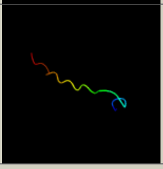
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3r3pB_	Alignment		99.7	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mobile intron protein; **PDBTitle:** homing endonuclease i-bth0305i catalytic domain
2	c3hrlA_	Alignment		99.5	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**endonuclease-like protein; **PDBTitle:** crystal structure of a putative endonuclease-like protein (ngo0050)2 from neisseria gonorrhoeae
3	d1cw0a_	Alignment		99.4	22	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Very short patch repair (VSR) endonuclease
4	d1vsra_	Alignment		97.9	22	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Very short patch repair (VSR) endonuclease
5	c4parC_	Alignment		97.4	13	**PDB header:**dna binding protein/dna **Chain:** C: **PDB Molecule:**uncharacterized protein abasi; **PDBTitle:** the 5-hydroxymethylcytosine-specific restriction enzyme abasi in a2 complex with product-like dna
6	c4oq2A_	Alignment		97.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**restriction endonuclease pvurts1 i; **PDBTitle:** 5hmc specific restriction endonuclease pvurts1i
7	c6rdu2_	Alignment		95.2	6	**PDB header:**proton transport **Chain:** 2: **PDB Molecule:**asa-2: polytomella f-atp synthase associated subunit 2; **PDBTitle:** cryo-em structure of polytomella f-atp synthase, rotary substate 1e,2 monomer-masked refinement
8	c1zelA_	Alignment		87.8	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rv2827c; **PDBTitle:** crystal structure of rv2827c protein from mycobacterium tuberculosis
9	d1zela2	Alignment		73.8	22	**Fold:**Rv2827c C-terminal domain-like **Superfamily:**Rv2827c C-terminal domain-like **Family:**Rv2827c C-terminal domain-like
10	d1m0da_	Alignment		55.5	16	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Endonuclease I (Holliday junction resolvase)
11	c6mp2B_	Alignment		35.4	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**blman5b; **PDBTitle:** crystal structure of blman5b solved by siras

12	c6gvbC_	Alignment		33.6	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**exo-beta-1,4-mannosidase; **PDBTitle:** crystal structure of cutibacterium acnes exo-beta-1,4-mannosidase
13	c3ttsD_	Alignment		31.9	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of beta-galactosidase from bacillus circulans sp.2 alkalophilus
14	d2fcla1	Alignment		26.2	24	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**TM1012-like
15	c4ytkA_	Alignment		21.1	36	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt5; **PDBTitle:** structure of the kow1-linker1 domain of transcription elongation2 factor spt5
16	c5e9aB_	Alignment		13.2	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure analysis of the cold-adamped beta-galactosidase from2 rahnella sp. r3
17	d1kwga2	Alignment		11.4	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
18	c3otbB_	Alignment		11.0	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna(his) guanylyltransferase; **PDBTitle:** crystal structure of human trnahis guanylyltransferase (thg1) - dgtp2 complex
19	c3wbzD_	Alignment		10.8	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**likely histidyl trna-specific guanylyltransferase; **PDBTitle:** crystal structure of c. albicans trna(his) guanylyltransferase (thg1)2 with atp
20	c5xoxD_	Alignment		10.6	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**trna(his) guanylyltransferase; **PDBTitle:** crystal structure of trna(his) guanylyltranserase from saccharomyces2 cerevisiae
21	c4uzsB_	Alignment	not modelled	9.3	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of bifidobacterium bifidum beta-galactosidase
22	d1texa_	Alignment	not modelled	8.9	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
23	c4uozC_	Alignment	not modelled	8.6	20	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**beta-galactosidase; **PDBTitle:** beta-(1,6)-galactosidase from bifidobacterium animalis subsp. lactis2 bl-04 nucleophile mutant e324a in complex with galactose
24	c4kgkB_	Alignment	not modelled	6.6	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thg1-like uncharacterized protein; **PDBTitle:** bacterial trna(his) guanylyltransferase (thg1)-like protein in complex2 with gtp
25	d1a7ia1	Alignment	not modelled	6.6	9	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
26	d1ju3a2	Alignment	not modelled	6.6	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**PepX catalytic domain-like
27	d2od0a1	Alignment	not modelled	6.3	17	**Fold:**Secretion chaperone-like **Superfamily:**YgaC/TfoX-N like **Family:**TfoX N-terminal domain-like
28	c2ovfA_	Alignment	not modelled	5.7	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**stal; **PDBTitle:** crystal structure of stal-pap complex
						PDB header:transferase

29	c2hw2A_	Alignment	not modelled	5.4	14	**Chain:** A: **PDB Molecule:**rifampin adp-ribosyl transferase; **PDBTitle:** crystal structure of rifampin adp-ribosyl transferase in complex with2 rifampin
30	c3rnlA_	 Alignment	not modelled	5.4	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfotransferase; **PDBTitle:** crystal structure of sulfotransferase from alicyclobacillus2 acidocaldarius