Phyre^2

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Description	C0Z3Y0
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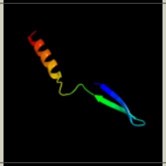
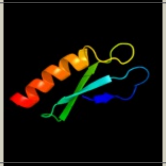
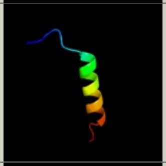
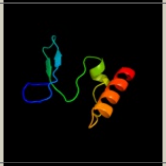
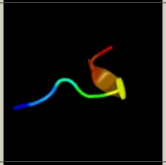
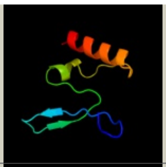
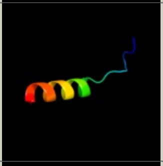
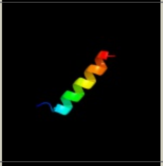
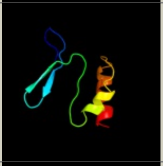
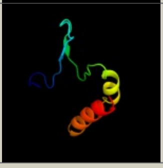
Unique Job ID	da141fae6baaea74

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ju0A_	Alignment		99.9	29	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** structure of the arm-type binding domain of hai7 integrase
2	c3jtzA_	Alignment		99.9	39	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** structure of the arm-type binding domain of hpi integrase
3	c1z1bA_	Alignment		97.9	21	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of a lambda integrase dimer bound to a2 coc' core site
4	c3igmA_	Alignment		66.6	8	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**pf14_0633 protein; **PDBTitle:** a 2.2a crystal structure of the ap2 domain of pf14_0633 from p.2 falciparum, bound as a domain-swapped dimer to its cognate dna
5	c1kjkA_	Alignment		49.4	30	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** solution structure of the lambda integrase amino-terminal2 domain
6	d1z1ba1	Alignment		49.4	30	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**lambda integrase N-terminal domain
7	d1j6xa_	Alignment		20.6	13	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
8	c2zcyM_	Alignment		19.9	14	**PDB header:**hydrolase **Chain:** M: **PDB Molecule:**proteasome component pre4; **PDBTitle:** yeast 20s proteasome:syringolin a-complex
9	c3pcqM_	Alignment		17.2	50	**PDB header:**photosynthesis **Chain:** M: **PDB Molecule:**photosystem i reaction center subunit xii; **PDBTitle:** femtosecond x-ray protein nanocrystallography
10	c1jb0M_	Alignment		17.0	50	**PDB header:**photosynthesis **Chain:** M: **PDB Molecule:**photosystem 1 reaction centre subunit xii; **PDBTitle:** crystal structure of photosystem i: a photosynthetic reaction center2 and core antenna system from cyanobacteria
11	d1jb0m_	Alignment		17.0	50	**Fold:**Single transmembrane helix **Superfamily:**Subunit XII of photosystem I reaction centre, PsaM **Family:**Subunit XII of photosystem I reaction centre, PsaM

12	d1ryp2_	Alignment		17.0	14	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
13	d1gcca_	Alignment		15.6	24	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**GCC-box binding domain
14	d1vjea_	Alignment		15.4	33	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
15	d1j6wa_	Alignment		14.9	33	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
16	d3bypa1	Alignment		13.9	10	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Cation efflux protein cytoplasmic domain-like **Family:**Cation efflux protein cytoplasmic domain-like
17	c3h4pj_	Alignment		12.2	12	**PDB header:**hydrolase **Chain:** J: **PDB Molecule:**proteasome subunit alpha; **PDBTitle:** proteasome 20s core particle from methanocaldococcus2 jannaschii
18	d1j98a_	Alignment		11.3	14	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
19	d1yarh1	Alignment		10.9	11	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
20	d1rypl_	Alignment		10.3	14	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
21	d1irui_	Alignment	not modelled	9.7	15	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
22	c3n3fB_	Alignment	not modelled	9.4	14	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**collagen alpha-1(xv) chain; **PDBTitle:** crystal structure of the human collagen xv trimerization domain: a2 potent trimerizing unit common to multiplexin collagens
23	c2zztA_	Alignment	not modelled	8.4	33	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the cytosolic domain of the cation2 diffusion facilitator family protein
24	d2outa2	Alignment	not modelled	8.1	25	**Fold:**GINS/PriA/YqbF domain **Superfamily:**PriA/YqbF domain **Family:**YqbF N-terminal domain-like
25	c3hshA_	Alignment	not modelled	8.0	24	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**collagen alpha-1(xviii) chain; **PDBTitle:** crystal structure of human collagen xviii trimerization domain2 (tetragonal crystal form)
26	c3imoC_	Alignment	not modelled	7.5	15	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**integron cassette protein; **PDBTitle:** structure from the mobile metagenome of vibrio cholerae.2 integron cassette protein vch_cass14
27	c3ol0C_	Alignment	not modelled	7.3	36	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**de novo designed monomer trefoil-fold sub-domain which **PDBTitle:** crystal structure of monofoil-4p homo-trimer: de novo designed monomer2 trefoil-fold sub-domain which forms homo-trimer assembly
28	d1vkza1	Alignment	not modelled	7.3	19	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif

						Family:BC C-terminal domain-like
29	d1iruh_	Alignment	not modelled	7.0	16	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
30	d1x48a1	Alignment	not modelled	6.0	15	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
31	d2fmla1	Alignment	not modelled	5.9	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Nudix-associated domain
32	c2outA_	Alignment	not modelled	5.5	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**mu-like prophage flumu protein gp35, protein **PDBTitle:** solution structure of hi1506, a novel two domain protein2 from haemophilus influenzae
33	d1ryp1_	Alignment	not modelled	5.4	21	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
34	c3g5oA_	Alignment	not modelled	5.1	13	**PDB header:**toxin/antitoxin **Chain:** A: **PDB Molecule:**uncharacterized protein rv2865; **PDBTitle:** the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis