Phyre^2

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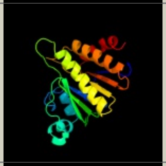
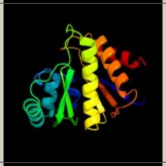
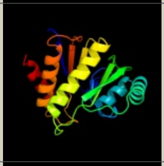
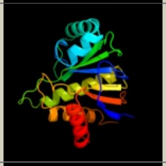
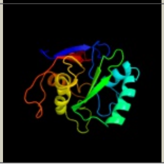
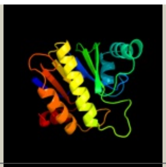
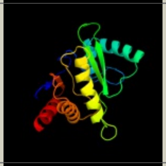
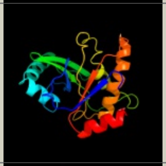
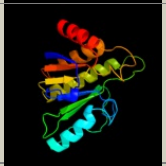
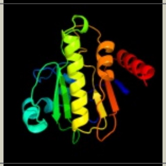
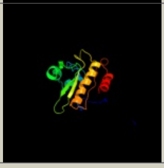
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1spva_	Alignment		100.0	99	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
2	c2x47A_	Alignment		100.0	47	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**macro domain-containing protein 1; **PDBTitle:** crystal structure of human macrod1
3	c1zr5B_	Alignment		100.0	27	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**h2afy protein; **PDBTitle:** crystal structure of the macro-domain of human core histone variant2 macroh2a1.2
4	d1zr5a1	Alignment		100.0	27	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
5	c2xd7B_	Alignment		100.0	24	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**core histone macro-h2a.2; **PDBTitle:** crystal structure of the macro domain of human core histone2 h2a
6	d1yd9a1	Alignment		100.0	29	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
7	c3q6zA_	Alignment		100.0	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 14; **PDBTitle:** human parp14 (artd8)-macro domain 1 in complex with adenosine-5-2 diphosphoribose
8	c3q71A_	Alignment		100.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 14; **PDBTitle:** human parp14 (artd8) - macro domain 2 in complex with adenosine-5-2 diphosphoribose
9	d1vhua_	Alignment		100.0	32	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
10	c3kh6A_	Alignment		100.0	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 15; **PDBTitle:** human poly(adp-ribose) polymerase 15, macro domain 2 in2 complex with adenosine-5-diphosphoribose
11	d2acfa1	Alignment		100.0	34	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain

12	c2dx6B_	Alignment		100.0	37	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ttha0132; **PDBTitle:** crystal structure of conserved hypothetical protein, ttha0132 from2 thermus thermophilus hb8
13	c2vriA_	Alignment		100.0	26	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** structure of the nsp3 x-domain of human coronavirus nl63
14	c3ew5B_	Alignment		100.0	27	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**macro domain of non-structural protein 3; **PDBTitle:** structure of the tetragonal crystal form of x (adrp) domain2 from fcov
15	c3ejfA_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** crystal structure of ibv x-domain at ph 8.5
16	c3ejgA_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** crystal structure of hcov-229e x-domain
17	c3gqeA_	Alignment		100.0	28	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** crystal structure of macro domain of venezuelan equine encephalitis2 virus
18	c3ewqA_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** hcov-229e nsp3 adrp domain
19	c3gpqA_	Alignment		100.0	27	**PDB header:**viral protein/rna **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** crystal structure of macro domain of chikungunya virus in complex with2 rna
20	c2eeeA_	Alignment		100.0	14	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**uncharacterized protein c6orf130; **PDBTitle:** solution structure of the a1pp domain from human protein2 c6orf130
21	d1njra_	Alignment	not modelled	99.9	17	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
22	d2fg1a1	Alignment	not modelled	99.9	18	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
23	c3siiA_	Alignment	not modelled	98.5	17	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**poly(adp-ribose) glycohydrolase; **PDBTitle:** the x-ray crystal structure of poly(adp-ribose) glycohydrolase bound2 to the inhibitor adp-hpd from thermomonospora curvata
24	d1gyta1	Alignment	not modelled	97.3	10	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Leucine aminopeptidase (Aminopeptidase A), N-terminal domain
25	c1gytG_	Alignment	not modelled	76.4	10	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** e. coli aminopeptidase a (pepa)
26	c3jruB_	Alignment	not modelled	35.4	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable cytosol aminopeptidase; **PDBTitle:** crystal structure of leucyl aminopeptidase (pepa) from xoo0834,2 xanthomonas oryzae pv. oryzae kacc10331
27	c3h8gC_	Alignment	not modelled	30.5	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** bestatin complex structure of leucine aminopeptidase from pseudomonas2 putida
28	d2amxa1	Alignment	not modelled	29.4	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenosine/AMP deaminase

29	c2vg2C_	Alignment	not modelled	29.0	8	**PDB header:**transferase **Chain:** C: **PDB Molecule:**undecaprenyl pyrophosphate synthetase; **PDBTitle:** rv2361 with ipp
30	c2zf8A_	Alignment	not modelled	18.5	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**component of sodium-driven polar flagellar motor; **PDBTitle:** crystal structure of moty
31	c3g5rA_	Alignment	not modelled	14.2	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methylenetetrahydrofolate--trna-(uracil-5-)- **PDBTitle:** crystal structure of thermus thermophilus trmfo in complex with2 tetrahydrofolate
32	c2yztA_	Alignment	not modelled	13.5	5	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha1756; **PDBTitle:** crystal structure of uncharacterized conserved protein from thermus2 thermophilus hb8
33	d1mlda1	Alignment	not modelled	12.0	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
34	c2vfwB_	Alignment	not modelled	9.5	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**short-chain z-isoprenyl diphosphate synthetase; **PDBTitle:** rv1086 native
35	c3ugsB_	Alignment	not modelled	9.4	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** crystal structure of a probable undecaprenyl diphosphate synthase2 (upps) from campylobacter jejuni
36	d2o5aa1	Alignment	not modelled	8.3	16	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Iojap/YbeB-like
37	c3krbB_	Alignment	not modelled	5.9	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldose reductase; **PDBTitle:** structure of aldose reductase from giardia lamblia at 1.75a resolution
38	c3k6qB_	Alignment	not modelled	5.7	8	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**putative ligand binding protein; **PDBTitle:** crystal structure of an antitoxin part of a putative toxin/antitoxin2 system (swol_0700) from syntrophomonas wolfei subsp. wolfei at 1.80 a3 resolution
39	d1ueha_	Alignment	not modelled	5.6	10	**Fold:**Undecaprenyl diphosphate synthase **Superfamily:**Undecaprenyl diphosphate synthase **Family:**Undecaprenyl diphosphate synthase