Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P64526
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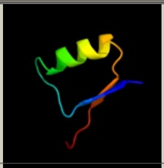
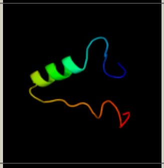
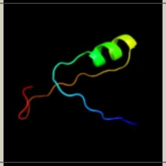
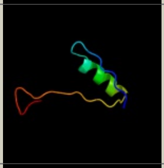
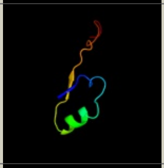
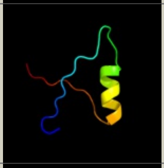
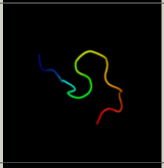
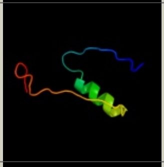
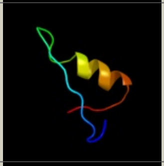
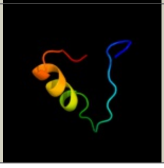
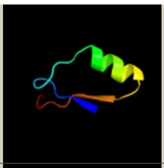
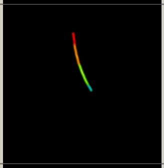
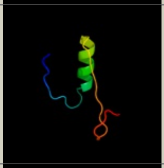
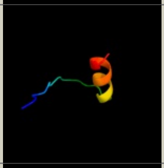
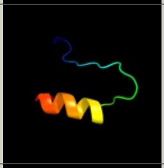
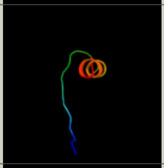
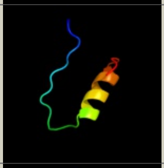
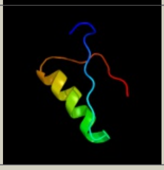
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1xpja_	Alignment		45.7	27	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein VC0232
2	d1p6ta2	Alignment		37.8	20	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
3	c1xtyD_	Alignment		24.1	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** crystal structure of sulfolobus solfataricus peptidyl-trna2 hydrolase
4	d1rlka_	Alignment		22.6	28	**Fold:**Peptidyl-tRNA hydrolase II **Superfamily:**Peptidyl-tRNA hydrolase II **Family:**Peptidyl-tRNA hydrolase II
5	d1ltqa1	Alignment		19.1	34	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**phosphatase domain of polynucleotide kinase
6	c2gcfA_	Alignment		16.7	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cation-transporting atpase pacs; **PDBTitle:** solution structure of the n-terminal domain of the coppper(i) atpase2 pacs in its apo form
7	c2zv3E_	Alignment		15.6	19	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** crystal structure of project mj0051 from methanocaldococcus2 jannaschii dsm 2661
8	c3hieA_	Alignment		15.2	16	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**exocyst complex component sec3; **PDBTitle:** structure of the membrane-binding domain of the sec3 subunit2 of the exocyst complex
9	c2d3kA_	Alignment		15.1	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** structural study on project id ph1539 from pyrococcus2 horikoshii ot3
10	c2ofhX_	Alignment		14.1	27	**PDB header:**hydrolase, membrane protein **Chain:** X: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** solution structure of the n-terminal domain of the zinc(ii) atpase2 ziaa in its apo form
11	c2ldiA_	Alignment		11.8	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** nmr solution structure of ziaan sub mutant

12	d2obba1	Alignment		11.3	26	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**BT0820-like
13	c3bwvB_	Alignment		10.8	44	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative 5'(3')-deoxyribonucleotidase; **PDBTitle:** crystal structure of deoxyribonucleotidase-like protein (np_764060.1)2 from staphylococcus epidermidis atcc 12228 at 1.55 a resolution
14	d1q7sa_	Alignment		9.9	20	**Fold:**Peptidyl-tRNA hydrolase II **Superfamily:**Peptidyl-tRNA hydrolase II **Family:**Peptidyl-tRNA hydrolase II
15	d1lnga_	Alignment		9.7	27	**Fold:**SRP19 **Superfamily:**SRP19 **Family:**SRP19
16	c2k2pA_	Alignment		9.5	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1203; **PDBTitle:** solution nmr structure of protein atu1203 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att10, ontario center for structural proteomics target atc1183
17	c3dluA_	Alignment		9.5	17	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**signal recognition particle 19 kda protein; **PDBTitle:** structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
18	d2qifa1	Alignment		9.4	24	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
19	c3dxsX_	Alignment		9.0	13	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**copper-transporting atpase ran1; **PDBTitle:** crystal structure of a copper binding domain from hma7, a p-2 type atpase
20	c2kyzA_	Alignment		8.5	19	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**heavy metal binding protein; **PDBTitle:** nmr structure of heavy metal binding protein tm0320 from thermotoga2 maritima
21	c2ejbA_	Alignment	not modelled	8.4	30	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable aromatic acid decarboxylase; **PDBTitle:** crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
22	d3erja1	Alignment	not modelled	8.1	20	**Fold:**Peptidyl-tRNA hydrolase II **Superfamily:**Peptidyl-tRNA hydrolase II **Family:**Peptidyl-tRNA hydrolase II
23	c3s88I_	Alignment	not modelled	8.0	33	**PDB header:**immune system/viral protein **Chain:** I: **PDB Molecule:**envelope glycoprotein; **PDBTitle:** crystal structure of sudan ebolavirus glycoprotein (strain gulu) bound2 to 16f6
24	d1dosa_	Alignment	not modelled	7.8	30	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
25	c2l3mA_	Alignment	not modelled	7.5	15	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**copper-ion-binding protein; **PDBTitle:** solution structure of the putative copper-ion-binding protein from2 bacillus anthracis str. ames
26	d2f06a2	Alignment	not modelled	7.5	21	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
27	d1l3ac_	Alignment	not modelled	7.2	23	**Fold:**ssDNA-binding transcriptional regulator domain **Superfamily:**ssDNA-binding transcriptional regulator domain **Family:**Plant transcriptional regulator PBF-2
28	d1wija_	Alignment	not modelled	7.1	29	**Fold:**LEM/SAP HeH motif **Superfamily:**DNA-binding domain of EIN3-like **Family:**DNA-binding domain of EIN3-like
29	c3g87B	Alignment	not modelled	7.1	22	**PDB header:**transferase activator/transferase **Chain:** B: **PDB Molecule:**n6 adenine specific dna methylase;

29	c3q87B_	Alignment	not modelled	7.1	22	**PDBTitle:** structure of eukaryotic translation termination complex2 methyltransferase mtq2-trm112
30	c3csyK_	Alignment	not modelled	6.9	38	**PDB header:**immune system/viral protein **Chain:** K: **PDB Molecule:**envelope glycoprotein gp1; **PDBTitle:** crystal structure of the trimeric prefusion ebola virus glycoprotein2 in complex with a neutralizing antibody from a human survivor
31	d2aw0a_	Alignment	not modelled	6.8	18	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
32	c1y3kA_	Alignment	not modelled	6.3	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the apo form of the fifth domain of2 menkes protein
33	d2ggpb1	Alignment	not modelled	6.2	17	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
34	c3q94B_	Alignment	not modelled	6.2	41	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase, class ii; **PDBTitle:** the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
35	c3a58A_	Alignment	not modelled	6.0	16	**PDB header:**protein transport/exocytosis **Chain:** A: **PDB Molecule:**exocyst complex component sec3; **PDBTitle:** crystal structure of sec3p - rho1p complex from2 saccharomyces cerevisiae
36	c2r39A_	Alignment	not modelled	5.9	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**fixg-related protein; **PDBTitle:** crystal structure of fixg-related protein from vibrio parahaemolyticus
37	c2i7dB_	Alignment	not modelled	5.7	56	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**5'(3')-deoxyribonucleotidase, cytosolic type; **PDBTitle:** structure of human cytosolic deoxyribonucleotidase in2 complex with deoxyuridine, alf4 and mg2+
38	d1p6ta1	Alignment	not modelled	5.6	17	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
39	c2kt2A_	Alignment	not modelled	5.3	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mercuric reductase; **PDBTitle:** structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
40	c3n1hA_	Alignment	not modelled	5.3	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**stwhy2; **PDBTitle:** crystal structure of stwhy2
41	c3cqrB_	Alignment	not modelled	5.3	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**violaxanthin de-epoxidase, chloroplast; **PDBTitle:** crystal structure of the lipocalin domain of violaxanthin2 de-epoxidase (vde) at ph5
42	c3fwaA_	Alignment	not modelled	5.1	15	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**reticuline oxidase; **PDBTitle:** structure of berberine bridge enzyme, c166a variant in complex with2 (s)-reticuline