Phyre^2

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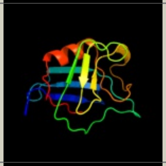
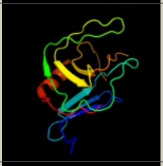
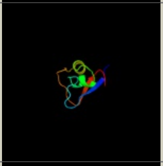
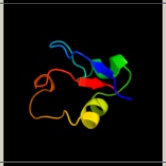
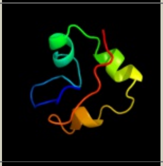
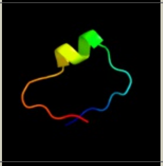
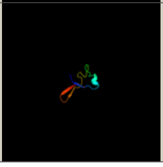
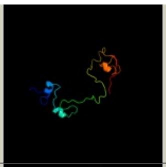
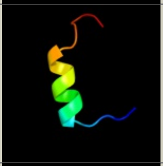
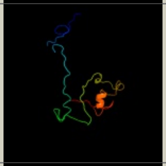
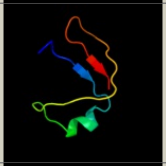
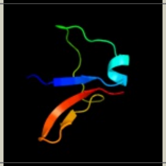
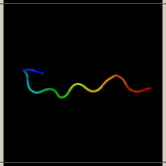
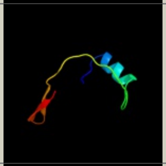
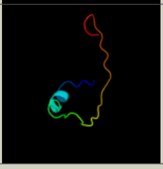
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1y7mB_	Alignment		100.0	32	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein bsu14040; **PDBTitle:** crystal structure of the b. subtilis ykud protein at 2 a2 resolution
2	d1y7ma1	Alignment		100.0	36	**Fold:**L,D-transpeptidase catalytic domain-like **Superfamily:**L,D-transpeptidase catalytic domain-like **Family:**L,D-transpeptidase catalytic domain-like
3	d1zata1	Alignment		100.0	29	**Fold:**L,D-transpeptidase catalytic domain-like **Superfamily:**L,D-transpeptidase catalytic domain-like **Family:**L,D-transpeptidase catalytic domain-like
4	c2hklB_	Alignment		100.0	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**l,d-transpeptidase; **PDBTitle:** crystal structure of enterococcus faecium l,d-2 transpeptidase c442s mutant
5	c2l9yA_	Alignment		98.3	24	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**cvnh-lysm lectin; **PDBTitle:** solution structure of the mocvnh-lysm module from the rice blast2 fungus magnaporthe oryzae protein (mgg_03307)
6	d1y7ma2	Alignment		98.0	29	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
7	c2djpA_	Alignment		97.9	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein sb145; **PDBTitle:** the solution structure of the lysm domain of human2 hypothetical protein sb145
8	d1e0ga_	Alignment		97.8	20	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
9	c2gu1A_	Alignment		95.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc peptidase; **PDBTitle:** crystal structure of a zinc containing peptidase from2 vibrio cholerae
10	c3mcaB_	Alignment		51.1	25	**PDB header:**translation regulation/hydrolase **Chain:** B: **PDB Molecule:**protein dom34; **PDBTitle:** structure of the dom34-hbs1 complex and implications for its role in2 no-go decay
11	d1wjja_	Alignment		46.7	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB

12	c1h5nC_	Alignment		41.6	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dmso reductase; **PDBTitle:** dmso reductase modified by the presence of dms and air
13	c2kkeA_	Alignment		26.0	42	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of a dimeric protein of unknown2 function from methanobacterium thermoautotrophicum,3 northeast structural genomics consortium target tr5
14	c1y5iA_	Alignment		17.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**respiratory nitrate reductase 1 alpha chain; **PDBTitle:** the crystal structure of the narghi mutant nari-k86a
15	d1ogya1	Alignment		14.4	15	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
16	c2k50A_	Alignment		10.2	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**replication factor a related protein; **PDBTitle:** solution nmr structure of the replication factor a related2 protein from methanobacterium thermoautotrophicum.3 northeast structural genomics target tr91a.
17	c2kenA_	Alignment		9.6	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein; **PDBTitle:** solution nmr structure of the ob domain (residues 67-166)2 of mm0293 from methanosarcina mazei. northeast structural3 genomics consortium target mar214a.
18	c3rf1B_	Alignment		9.3	29	**PDB header:**ligase **Chain:** B: **PDB Molecule:**glycyl-trna synthetase alpha subunit; **PDBTitle:** the crystal structure of glycyl-trna synthetase subunit alpha from2 campylobacter jejuni subsp. jejuni nctc 11168
19	c2vw9B_	Alignment		9.0	14	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**single-stranded dna binding protein; **PDBTitle:** single stranded dna binding protein complex from2 helicobacter pylori
20	c2iheA_	Alignment		8.9	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** crystal structure of wild-type single-stranded dna binding protein2 from thermus aquaticus
21	d2hthb1	Alignment	not modelled	7.3	27	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**VPS36 N-terminal domain-like
22	c1r1gA_	Alignment	not modelled	7.2	36	**PDB header:**toxin **Chain:** A: **PDB Molecule:**neurotoxin bmk37; **PDBTitle:** crystal structure of the scorpion toxin bmbkttx1
23	d1r1ga_	Alignment	not modelled	7.2	36	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Short-chain scorpion toxins
24	c1eqqD_	Alignment	not modelled	7.2	15	**PDB header:**replication/rna **Chain:** D: **PDB Molecule:**single stranded dna binding protein; **PDBTitle:** single stranded dna binding protein and ssdna complex
25	c1r1gB_	Alignment	not modelled	6.9	36	**PDB header:**toxin **Chain:** B: **PDB Molecule:**neurotoxin bmk37; **PDBTitle:** crystal structure of the scorpion toxin bmbkttx1
26	d1y0pa3	Alignment	not modelled	6.4	17	**Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
27	d2c42a3	Alignment	not modelled	6.1	25	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Pyruvate-ferredoxin oxidoreductase, PFOR, domain II
28	d2hh8a1	Alignment	not modelled	5.6	33	**Fold:**YdfO-like **Superfamily:**YdfO-like **Family:**YdfO-like

29	c1eu1A_	Alignment	not modelled	5.5	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dimethyl sulfoxide reductase; **PDBTitle:** the crystal structure of rhodobacter sphaeroides dimethylsulfoxide2 reductase reveals two distinct molybdenum coordination environments.