Phyre2

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Description	P76193
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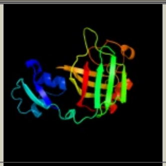
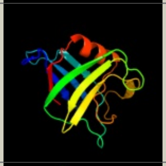
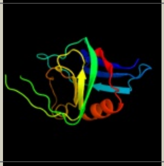
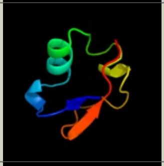
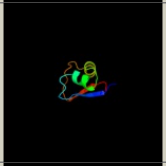
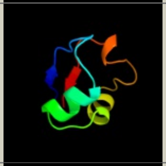
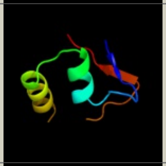
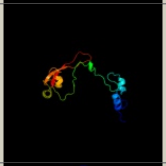
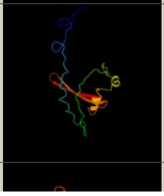
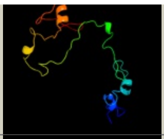
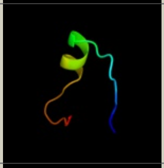
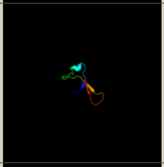
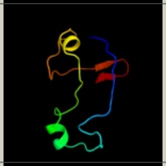
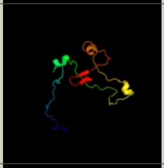
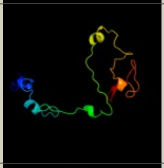
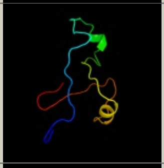
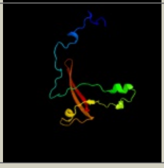
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1y7mB_	Alignment		100.0	38	**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	39	**Fold:**L,D-transpeptidase catalytic domain-like **Superfamily:**L,D-transpeptidase catalytic domain-like **Family:**L,D-transpeptidase catalytic domain-like
3	c2hklB_	Alignment		100.0	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**l,d-transpeptidase; **PDBTitle:** crystal structure of enterococcus faecium l,d-2 transpeptidase c442s mutant
4	d1zata1	Alignment		100.0	30	**Fold:**L,D-transpeptidase catalytic domain-like **Superfamily:**L,D-transpeptidase catalytic domain-like **Family:**L,D-transpeptidase catalytic domain-like
5	d1y7ma2	Alignment		98.1	36	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
6	c2l9yA_	Alignment		98.0	39	**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)
7	d1e0ga_	Alignment		97.6	31	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
8	c2djpA_	Alignment		97.6	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
9	c2gu1A_	Alignment		91.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc peptidase; **PDBTitle:** crystal structure of a zinc containing peptidase from2 vibrio cholerae
10	c1h5nC_	Alignment		87.9	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dmso reductase; **PDBTitle:** dmso reductase modified by the presence of dms and air
11	c1y5iA_	Alignment		86.3	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**respiratory nitrate reductase 1 alpha chain; **PDBTitle:** the crystal structure of the narghi mutant nari-k86a

12	c1eu1A_	Alignment		49.9	16	**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.
13	c3mcaB_	Alignment		44.8	29	**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
14	d1wjja_	Alignment		43.1	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
15	d1y5ia1	Alignment		39.9	18	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
16	c1kqgA_	Alignment		37.7	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**formate dehydrogenase, nitrate-inducible, major subunit; **PDBTitle:** formate dehydrogenase n from e. coli
17	c2e7zA_	Alignment		34.7	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**acetylene hydratase ahy; **PDBTitle:** acetylene hydratase from pelobacter acetylenicus
18	c1tmoA_	Alignment		31.9	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**trimethylamine n-oxide reductase; **PDBTitle:** trimethylamine n-oxide reductase from shewanella massilia
19	d1eu1a1	Alignment		27.0	14	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
20	c2iv2X_	Alignment		26.3	22	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**formate dehydrogenase h; **PDBTitle:** reinterpretation of reduced form of formate dehydrogenase h2 from e. coli
21	c1bmv2_	Alignment	not modelled	20.8	17	**PDB header:**virus/rna **Chain:** 2: **PDB Molecule:**protein (icosahedral virus - b and c domain); **PDBTitle:** protein-rna interactions in an icosahedral virus at 3.02 angstroms resolution
22	c2kkeA_	Alignment	not modelled	16.9	37	**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
23	d1ogya1	Alignment	not modelled	16.4	20	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
24	d2jioa1	Alignment	not modelled	16.4	15	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
25	c1vlfQ_	Alignment	not modelled	15.1	13	**PDB header:**oxidoreductase **Chain:** Q: **PDB Molecule:**pyrogallol hydroxytransferase large subunit; **PDBTitle:** crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici complexed3 with inhibitor 1,2,4,5-tetrahydroxy-benzene
26	c2k50A_	Alignment	not modelled	13.9	11	**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.
27	d2hthb1	Alignment	not modelled	13.0	16	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**VPS36 N-terminal domain-like
						Fold: Double psi beta-barrel

28	d1kqfa1	Alignment	not modelled	13.0	12	**Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
29	c2ivfA_	Alignment	not modelled	11.4	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ethylbenzene dehydrogenase alpha-subunit; **PDBTitle:** ethylbenzene dehydrogenase from aromatoleum aromaticum
30	d2c42a3	Alignment	not modelled	11.0	11	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Pyruvate-ferredoxin oxidoreductase, PFOR, domain II
31	d2vgna1	Alignment	not modelled	10.3	12	**Fold:**Sm-like fold **Superfamily:**Dom34/Pelota N-terminal domain-like **Family:**Dom34/Pelota N-terminal domain-like
32	d1h0ha1	Alignment	not modelled	10.3	11	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
33	d1g8ka1	Alignment	not modelled	8.4	25	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
34	d1k78a1	Alignment	not modelled	8.1	71	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
35	c3pjvD_	Alignment	not modelled	7.9	12	**PDB header:**lyase **Chain:** D: **PDB Molecule:**cyclic dimeric gmp binding protein; **PDBTitle:** structure of pseudomonas fluorescence lapd periplasmic domain
36	d1vlfm1	Alignment	not modelled	7.8	15	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
37	d2qi2a1	Alignment	not modelled	7.5	16	**Fold:**Sm-like fold **Superfamily:**Dom34/Pelota N-terminal domain-like **Family:**Dom34/Pelota N-terminal domain-like
38	d6paxa1	Alignment	not modelled	6.8	57	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
39	d1qvpa_	Alignment	not modelled	6.7	21	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**FeoA-like
40	d1qvca_	Alignment	not modelled	6.7	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
41	d1t3la1	Alignment	not modelled	6.1	17	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
42	c2vw9B_	Alignment	not modelled	5.9	13	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**single-stranded dna binding protein; **PDBTitle:** single stranded dna binding protein complex from2 helicobacter pylori
43	c2iheA_	Alignment	not modelled	5.4	13	**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
44	c2bfuL_	Alignment	not modelled	5.2	33	**PDB header:**virus **Chain:** L: **PDB Molecule:**cowpea mosaic virus, large (l) subunit; **PDBTitle:** x-ray structure of cpmv top component
45	c2inpE_	Alignment	not modelled	5.2	9	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**phenol hydroxylase component pho; **PDBTitle:** structure of the phenol hydroxylase-regulatory protein2 complex
46	d1e0ta1	Alignment	not modelled	5.2	36	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
47	c3rf1B_	Alignment	not modelled	5.1	21	**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