Phyre2

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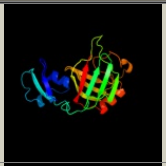
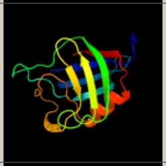
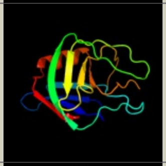
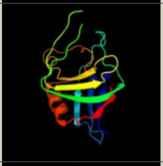
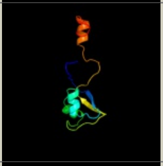
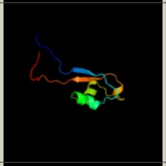
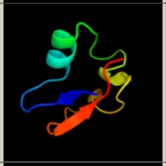
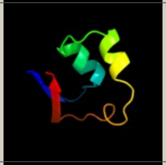
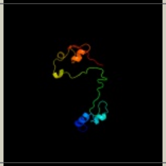
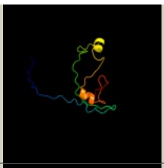
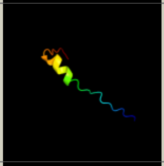
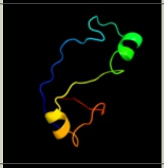
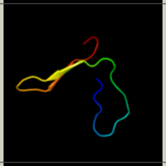
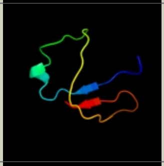
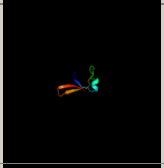
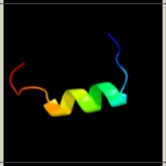
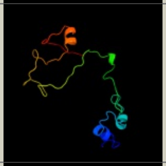
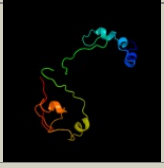
Description	P75954
Date	Wed Jan 25 15:21:04 GMT 2012
Unique Job ID	310acfc0b616e7d5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1y7mB_	Alignment		100.0	33	**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	35	**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	25	**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	26	**Fold:**L,D-transpeptidase catalytic domain-like **Superfamily:**L,D-transpeptidase catalytic domain-like **Family:**L,D-transpeptidase catalytic domain-like
5	c2l9yA_	Alignment		98.2	15	**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	c2djpA_	Alignment		98.0	25	**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
7	d1y7ma2	Alignment		97.7	34	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
8	d1e0ga_	Alignment		97.5	24	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
9	c2gu1A_	Alignment		93.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc peptidase; **PDBTitle:** crystal structure of a zinc containing peptidase from2 vibrio cholerae
10	c1h5nC_	Alignment		61.2	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dmso reductase; **PDBTitle:** dmso reductase modified by the presence of dms and air
11	c3mcaB_	Alignment		59.7	21	**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

12	c1y5iA_	Alignment		47.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**respiratory nitrate reductase 1 alpha chain; **PDBTitle:** the crystal structure of the narghi mutant nari-k86a
13	c2vdaB_	Alignment		26.9	36	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**maltoporin; **PDBTitle:** solution structure of the seca-signal peptide complex
14	d1y5ia1	Alignment		16.4	13	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
15	d2hthb1	Alignment		15.8	19	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**VPS36 N-terminal domain-like
16	c2k50A_	Alignment		14.5	14	**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	d1wjja_	Alignment		14.2	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
18	c2kkeA_	Alignment		13.5	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
19	c1eu1A_	Alignment		13.4	15	**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.
20	c1tmoA_	Alignment		13.2	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**trimethylamine n-oxide reductase; **PDBTitle:** trimethylamine n-oxide reductase from shewanella massilia
21	d2vgna1	Alignment	not modelled	7.4	17	**Fold:**Sm-like fold **Superfamily:**Dom34/Pelota N-terminal domain-like **Family:**Dom34/Pelota N-terminal domain-like
22	d1k78a1	Alignment	not modelled	7.2	71	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
23	d2qi2a1	Alignment	not modelled	7.1	26	**Fold:**Sm-like fold **Superfamily:**Dom34/Pelota N-terminal domain-like **Family:**Dom34/Pelota N-terminal domain-like
24	c3d12A_	Alignment	not modelled	6.9	38	**PDB header:**hydrolase/membrane protein **Chain:** A: **PDB Molecule:**hemagglutinin-neuraminidase; **PDBTitle:** crystal structures of nipah virus g attachment glycoprotein in complex2 with its receptor ephrin-b3
25	d1ogya1	Alignment	not modelled	6.9	15	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
26	c3obyB_	Alignment	not modelled	6.8	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of archaeoglobus fulgidus pelota reveals inter-2 domain structural plasticity
27	d1t3la1	Alignment	not modelled	6.7	30	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
28	d1eu1a1	Alignment	not modelled	6.3	12	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
						PDB header:ligase

29	c3rf1B_	Alignment	not modelled	6.1	21	**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
30	d6paxa1	Alignment	not modelled	6.1	57	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
31	c3nadB_	Alignment	not modelled	5.8	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**ferulate decarboxylase; **PDBTitle:** crystal structure of phenolic acid decarboxylase from bacillus pumilus2 ui-670
32	c3agjD_	Alignment	not modelled	5.6	28	**PDB header:**translation/hydrolase **Chain:** D: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
33	c3agjB_	Alignment	not modelled	5.6	28	**PDB header:**translation/hydrolase **Chain:** B: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
34	d1r1ga_	Alignment	not modelled	5.4	55	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Short-chain scorpion toxins
35	c1r1gA_	Alignment	not modelled	5.4	55	**PDB header:**toxin **Chain:** A: **PDB Molecule:**neurotoxin bmk37; **PDBTitle:** crystal structure of the scorpion toxin bmbkttx1
36	c1r1gB_	Alignment	not modelled	5.4	55	**PDB header:**toxin **Chain:** B: **PDB Molecule:**neurotoxin bmk37; **PDBTitle:** crystal structure of the scorpion toxin bmbkttx1
37	c2bfuL_	Alignment	not modelled	5.4	33	**PDB header:**virus **Chain:** L: **PDB Molecule:**cowpea mosaic virus, large (l) subunit; **PDBTitle:** x-ray structure of cpmv top component