Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1056_(-)_1177633_1178397
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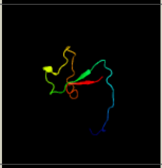
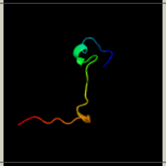
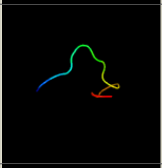
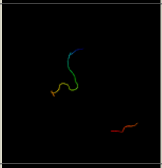
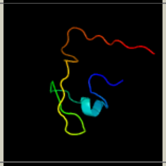
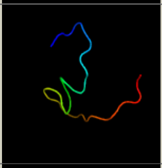
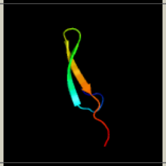
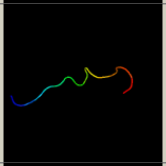
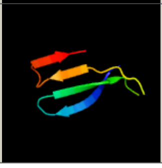
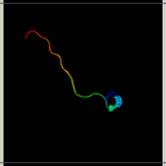
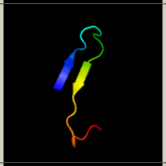
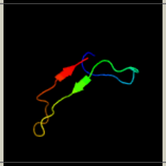
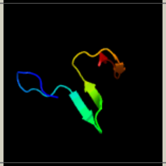
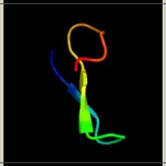
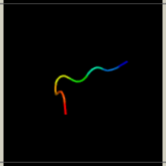
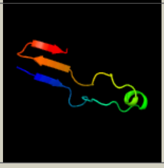
Unique Job ID	7730311afb9f08f6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3djmA_	Alignment		100.0	25	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein duf427; **PDBTitle:** crystal structure of a protein of unknown function from duf427 family2 (rsph17029_0682) from rhodobacter sphaeroides 2.4.1 at 2.51 a3 resolution
2	d1w66a1	Alignment		29.9	13	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**LplA-like
3	c5hj0C_	Alignment		22.1	18	**PDB header:**ligase **Chain:** C: **PDB Molecule:**kinetochore protein mis18; **PDBTitle:** crystal structure of mis18 'yippee-like' domain
4	c4b1qP_	Alignment		21.0	41	**PDB header:**toxin **Chain:** P: **PDB Molecule:**conotoxin cctx; **PDBTitle:** nmr structure of the glycosylated conotoxin cctx from conus consors
5	c4l0zA_	Alignment		20.4	42	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**runt-related transcription factor 1; **PDBTitle:** crystal structure of runx1 and ets1 bound to tcr alpha promoter2 (crystal form 2)
6	c2mjcA_	Alignment		14.1	67	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 3 subunit g; **PDBTitle:** zn-binding domain of eukaryotic translation initiation factor 3,2 subunit g
7	c3icoA_	Alignment		12.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of 6-phosphogluconolactonase from mycobacterium2 tuberculosis
8	d1w9sa_	Alignment		12.0	31	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 6 carbohydrate binding module, CBM6
9	c5o60X_	Alignment		11.7	33	**PDB header:**ribosome **Chain:** X: **PDB Molecule:**50s ribosomal protein l27; **PDBTitle:** structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
10	c1z8rA_	Alignment		11.7	44	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**coxsackievirus b4 polyprotein; **PDBTitle:** 2a cysteine proteinase from human coxsackievirus b4 (strain2 jvb / benschoten / new york / 51)
11	c4lmgD_	Alignment		10.1	33	**PDB header:**transcription activator/dna **Chain:** D: **PDB Molecule:**iron-regulated transcriptional activator aft2; **PDBTitle:** crystal structure of aft2 in complex with dna

12	c4azzB_	Alignment		10.1	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**levanase; **PDBTitle:** carbohydrate binding module cbm66 from bacillus subtilis
13	c4e6nB_	Alignment		9.7	19	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**methyltransferase type 12; **PDBTitle:** crystal structure of bacterial pnkp-c/hen1-n heterodimer
14	c6oswA_	Alignment		9.3	13	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**forkhead box m1; **PDBTitle:** an order-to-disorder structural switch activates the foxm12 transcription factor
15	c4cawA_	Alignment		9.1	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycylpeptide n-tetradecanoyltransferase; **PDBTitle:** crystal structure of aspergillus fumigatus n-myristoyl2 transferase in complex with myristoyl coa and a pyrazole3 sulphonamide ligand
16	c5c17A_	Alignment		8.9	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**merb2; **PDBTitle:** crystal structure of the mercury-bound form of merb2
17	c2kd2A_	Alignment		8.9	16	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**fas apoptotic inhibitory molecule 1; **PDBTitle:** nmr structure of faim-ctd
18	d1txna_	Alignment		7.9	40	**Fold:**Coproporphyrinogen III oxidase **Superfamily:**Coproporphyrinogen III oxidase **Family:**Coproporphyrinogen III oxidase
19	d1ne7a_	Alignment		7.8	16	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**NagB-like
20	d1m7ja2	Alignment		7.8	26	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**D-aminoacylase
21	c3oc6A_	Alignment	not modelled	7.7	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of 6-phosphogluconolactonase from mycobacterium2 smegmatis, apo form
22	d1iica2	Alignment	not modelled	7.3	22	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-myristoyl transferase, NMT
23	c6ch0I_	Alignment	not modelled	7.2	15	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**beta-lactamase; **PDBTitle:** structure of the quorum quenching lactonase from alicyclobacillus2 acidoterrestris bound to a glycerol molecule
24	d1vr3a1	Alignment	not modelled	7.1	21	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acireductone dioxygenase
25	d1rxta2	Alignment	not modelled	6.8	13	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-myristoyl transferase, NMT
26	c2pcjB_	Alignment	not modelled	6.8	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lipoprotein-releasing system atp-binding protein lold; **PDBTitle:** crystal structure of abc transporter (aq_297) from aquifex aeolicus2 vf5
27	d1wh2a_	Alignment	not modelled	6.7	18	**Fold:**GYF/BRK domain-like **Superfamily:**GYF domain **Family:**GYF domain
28	d2cu2a1	Alignment	not modelled	6.7	13	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Guanosine diphospho-D-mannose pyrophosphorylase/mannose-6-phosphate isomerase linker domain **Family:**Guanosine diphospho-D-mannose pyrophosphorylase/mannose-6-phosphate isomerase linker domain

29	d2a1fa1	Alignment	not modelled	6.6	17	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
30	d1z9da1	Alignment	not modelled	6.5	22	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
31	d1iyka2	Alignment	not modelled	6.2	12	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-myristoyl transferase, NMT
32	c2kl4A_	Alignment	not modelled	6.2	4	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**bh2032 protein; **PDBTitle:** nmr structure of the protein nb7804a
33	c2j0eA_	Alignment	not modelled	6.1	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** three dimensional structure and catalytic mechanism of 6-2 phosphogluconolactonase from trypanosoma brucei
34	d1tkla_	Alignment	not modelled	6.1	40	**Fold:**Coproporphyrinogen III oxidase **Superfamily:**Coproporphyrinogen III oxidase **Family:**Coproporphyrinogen III oxidase
35	c5eo6A_	Alignment	not modelled	6.1	40	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**coproporphyrinogen oxidase; **PDBTitle:** coproporphyrinogen iii oxidase (hemf) from acinetobacter baumannii
36	d1boba_	Alignment	not modelled	6.0	27	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
37	c3zf7t_	Alignment	not modelled	5.9	27	**PDB header:**ribosome **Chain:** T: **PDB Molecule:**60s ribosomal protein l19, putative; **PDBTitle:** high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
38	d2j44a2	Alignment	not modelled	5.9	9	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**PUD-like
39	c3cjsA_	Alignment	not modelled	5.8	37	**PDB header:**transferase/ribosomal protein **Chain:** A: **PDB Molecule:**ribosomal protein l11 methyltransferase; **PDBTitle:** minimal recognition complex between prma and ribosomal protein l11
40	c3m9bK_	Alignment	not modelled	5.7	21	**PDB header:**chaperone **Chain:** K: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
41	c2aexA_	Alignment	not modelled	5.6	40	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**coproporphyrinogen iii oxidase, mitochondrial; **PDBTitle:** the 1.58a crystal structure of human coproporphyrinogen oxidase2 reveals the structural basis of hereditary coproporphyria
42	c5xyiL_	Alignment	not modelled	5.6	44	**PDB header:**ribosome **Chain:** L: **PDB Molecule:**uncharacterized protein; **PDBTitle:** small subunit of trichomonas vaginalis ribosome
43	c6fhtB_	Alignment	not modelled	5.5	27	**PDB header:**lyase **Chain:** B: **PDB Molecule:**bacteriophytochrome,adenylate cyclase; **PDBTitle:** crystal structure of an artificial phytochrome regulated2 adenylate/guanylate cyclase in its dark adapted pr form
44	d1tsfa_	Alignment	not modelled	5.5	25	**Fold:**Rof/RNase P subunit-like **Superfamily:**Rof/RNase P subunit-like **Family:**RNase P subunit p29-like
45	c3zr6A_	Alignment	not modelled	5.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**galactocerebrosidase; **PDBTitle:** structure of galactocerebrosidase from mouse in complex with galactose
46	c3nmbA_	Alignment	not modelled	5.4	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative sugar hydrolase; **PDBTitle:** crystal structure of a putative sugar hydrolase (bacova_03189) from2 bacteroides ovatus at 2.40 a resolution
47	c3mhxB_	Alignment	not modelled	5.2	8	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**putative ferrous iron transport protein a; **PDBTitle:** crystal structure of stenotrophomonas maltophilia feoa complexed with2 zinc: a unique procaryotic sh3 domain protein possibly acting as a3 bacterial ferrous iron transport activating factor
48	c2c26A_	Alignment	not modelled	5.2	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** structural basis for the promiscuous specificity of the2 carbohydrate-binding modules from the beta-sandwich super3 family
49	d2k49a1	Alignment	not modelled	5.2	11	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
50	d1lnga_	Alignment	not modelled	5.1	28	**Fold:**SRP19 **Superfamily:**SRP19 **Family:**SRP19
51	c2xhaB_	Alignment	not modelled	5.1	20	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** crystal structure of domain 2 of thermotoga maritima n-utilization2 substance g (nusg)