Phyre2

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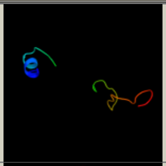
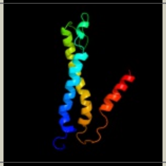
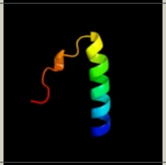
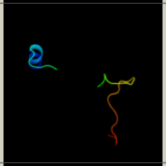
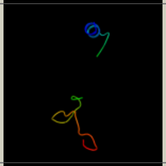
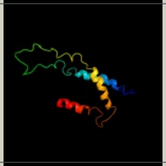
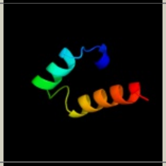
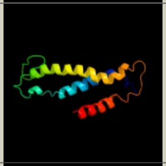
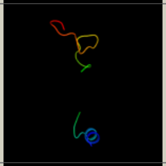
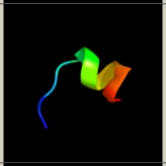
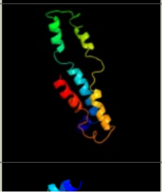
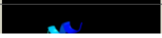
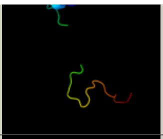
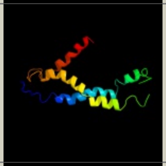
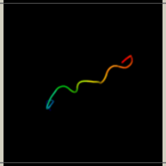
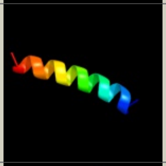
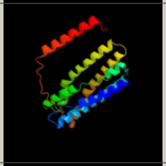
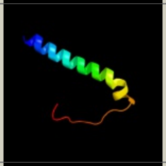
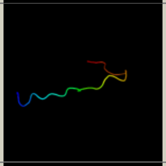
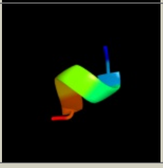
Description	P0A6W3
Date	Thu Jan 5 11:04:03 GMT 2012
Unique Job ID	a7b26f2152cebb70

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3quvB_	Alignment		12.8	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of a trna-guanine-n1-methyltransferase from2 mycobacterium abscessus
2	c3dl8H_	Alignment		12.5	12	**PDB header:**protein transport **Chain:** H: **PDB Molecule:**preprotein translocase subunit secy; **PDBTitle:** structure of the complex of aquifex aeolicus secyeg and2 bacillus subtilis seca
3	c2jxpA_	Alignment		11.8	14	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**putative lipoprotein b; **PDBTitle:** solution nmr structure of uncharacterized lipoprotein b2 from nitrosomonas europaea. northeast structural genomics3 target ner45a
4	d1p9pa_	Alignment		11.3	18	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**tRNA(m1G37)-methyltransferase TrmD
5	d1uala_	Alignment		10.7	21	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**tRNA(m1G37)-methyltransferase TrmD
6	c2akiY_	Alignment		10.6	13	**PDB header:**protein transport **Chain:** Y: **PDB Molecule:**preprotein translocase secy subunit; **PDBTitle:** normal mode-based flexible fitted coordinates of a2 translocating secyeg protein-conducting channel into the3 cryo-em map of a secyeg-nascent chain-70s ribosome complex4 from e. coli
7	d1o5ha_	Alignment		10.3	11	**Fold:**Methenyltetrahydrofolate cyclohydrolase-like **Superfamily:**Methenyltetrahydrofolate cyclohydrolase-like **Family:**Methenyltetrahydrofolate cyclohydrolase-like
8	c3dinF_	Alignment		10.1	14	**PDB header:**membrane protein, protein transport **Chain:** F: **PDB Molecule:**preprotein translocase subunit secy; **PDBTitle:** crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
9	c3knuD_	Alignment		7.5	25	**PDB header:**transferase **Chain:** D: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of trna (guanine-n1)-methyltransferase from2 anaplasma phagocytophilum
10	d2c42a2	Alignment		7.5	31	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**PFOR PP module
11	c2zqpY_	Alignment		7.3	13	**PDB header:**protein transport **Chain:** Y: **PDB Molecule:**preprotein translocase secy subunit; **PDBTitle:** crystal structure of secye translocon from thermus2 thermophilus
						

12	c3ky7A_	Alignment		6.8	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** 2.35 angstrom resolution crystal structure of a putative trna2 (guanine-7-)-methyltransferase (trmd) from staphylococcus aureus3 subsp. aureus mrsa252
13	c3j01A_	Alignment		6.0	13	**PDB header:**ribosome/ribosomal protein **Chain:** A: **PDB Molecule:**preprotein translocase secy subunit; **PDBTitle:** structure of the ribosome-secye complex in the membrane environment
14	c2vznA_	Alignment		5.9	36	**PDB header:**allergen **Chain:** A: **PDB Molecule:**venom allergen 3; **PDBTitle:** crystal structure of the major allergen from fire ant2 venom, sol i 3
15	d1xrda1	Alignment		5.9	26	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
16	c3aqpB_	Alignment		5.8	15	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**probable secdf protein-export membrane protein; **PDBTitle:** crystal structure of secdf, a translocon-associated membrane protein,2 from thermus thrmophilus
17	d2cbia2	Alignment		5.6	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**alpha-D-glucuronidase/Hyaluronidase catalytic domain
18	d3dtub2	Alignment		5.6	12	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
19	c3b9eA_	Alignment		5.5	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase a; **PDBTitle:** crystal structure of inactive mutant e315m chitinase a from2 vibrio harveyi
20	d1bh9b_	Alignment		5.4	43	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
21	c3o7oB_	Alignment	not modelled	5.3	50	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endoglucanase; **PDBTitle:** use of synthetic symmetrization in the crystallization and structure2 determination of cela from thermotoga maritima
22	d1x7fa2	Alignment	not modelled	5.3	50	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Outer surface protein, N-terminal domain
23	d2choa2	Alignment	not modelled	5.2	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**alpha-D-glucuronidase/Hyaluronidase catalytic domain
24	c3rkoF_	Alignment	not modelled	5.1	12	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**nadh-quinone oxidoreductase subunit j; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution