Phyre2

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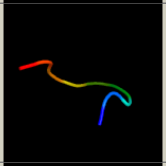
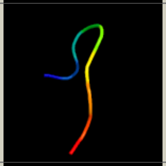
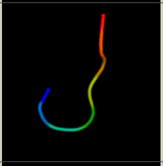
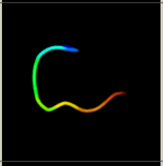
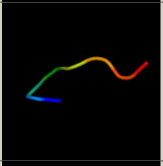
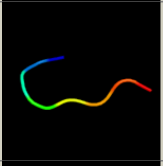
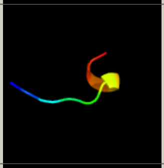
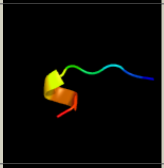
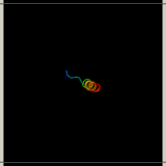
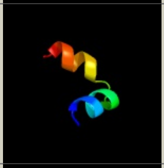
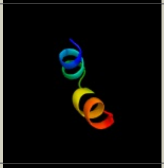
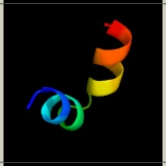
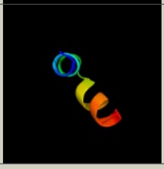
Description	RVBD2526_(-)_2851101_2851328
Date	Wed Aug 7 12:50:16 BST 2019
Unique Job ID	631aa338375603a9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6a7vU_	Alignment		95.7	41	**PDB header:**toxin/antitoxin **Chain:** U: **PDB Molecule:**antitoxin vapb11; **PDBTitle:** crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
2	d2b0aa1	Alignment		34.9	44	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Putative cyclase **Family:**Putative cyclase
3	c4cobA_	Alignment		29.7	56	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**kynurenine formamidase; **PDBTitle:** crystal structure kynurenine formamidase from pseudomonas aeruginosa
4	c4cogB_	Alignment		27.7	63	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**kynurenine formamidase; **PDBTitle:** crystal structure of kynurenine formamidase from burkholderia2 cenocepacia
5	c5nnaB_	Alignment		26.8	75	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**isatin hydrolase a; **PDBTitle:** isatin hydrolase a (iha) from labrenzia aggregata bound to benzyl2 benzoate
6	c4coaA_	Alignment		24.8	67	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**kynurenine formamidase; **PDBTitle:** crystal structure of kynurenine formamidase from bacillus2 anthracis complexed with 2-aminoacetophenone.
7	c3h6pD_	Alignment		24.5	67	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**esat-6-like protein esxr; **PDBTitle:** crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
8	c4j0nA_	Alignment		20.3	75	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**isatin hydrolase b; **PDBTitle:** crystal structure of a manganese dependent isatin hydrolase
9	c5nmpF_	Alignment		20.1	75	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**isatin hydrolase; **PDBTitle:** isatin hydrolase a (iha) from ralstonia solanacearum
10	d1r61a_	Alignment		19.8	75	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Putative cyclase **Family:**Putative cyclase
11	c3fmtF_	Alignment		19.8	36	**PDB header:**replication inhibitor/dna **Chain:** F: **PDB Molecule:**protein seqa; **PDBTitle:** crystal structure of seqa bound to dna

12	c1vw46_	Alignment		16.6	25	**PDB header:**ribosome **Chain:** 6: **PDB Molecule:**54s ribosomal protein l17, mitochondrial; **PDBTitle:** structure of the yeast mitochondrial large ribosomal subunit
13	c1xrxD_	Alignment		15.5	50	**PDB header:**replication inhibitor **Chain:** D: **PDB Molecule:**seqa protein; **PDBTitle:** crystal structure of a dna-binding protein
14	d1xrxa1	Alignment		15.5	50	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**SeqA N-terminal domain-like
15	d2b4va2	Alignment		12.4	38	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**RNA editing terminal uridyl transferase 2, RET2, catalytic domain
16	c4afjX_	Alignment		9.5	47	**PDB header:**transferase/peptide **Chain:** X: **PDB Molecule:**proto-oncogene frat1; **PDBTitle:** 5-aryl-4-carboxamide-1,3-oxazoles: potent and selective gsk-32 inhibitors
17	c4afjY_	Alignment		9.5	47	**PDB header:**transferase/peptide **Chain:** Y: **PDB Molecule:**proto-oncogene frat1; **PDBTitle:** 5-aryl-4-carboxamide-1,3-oxazoles: potent and selective gsk-32 inhibitors
18	c3zrkY_	Alignment		9.3	47	**PDB header:**transferase/peptide **Chain:** Y: **PDB Molecule:**proto-oncogene frat1; **PDBTitle:** identification of 2-(4-pyridyl)thienopyridinones as gsk-3beta2 inhibitors
19	c3zrlY_	Alignment		9.3	47	**PDB header:**transferase/peptide **Chain:** Y: **PDB Molecule:**proto-oncogene frat1; **PDBTitle:** identification of 2-(4-pyridyl)thienopyridinones as gsk-3beta2 inhibitors
20	c3zrmY_	Alignment		9.3	47	**PDB header:**transferase/peptide **Chain:** Y: **PDB Molecule:**proto-oncogene frat1; **PDBTitle:** identification of 2-(4-pyridyl)thienopyridinones as gsk-2 3beta inhibitors
21	c5oy4X_	Alignment	not modelled	9.2	47	**PDB header:**transferase **Chain:** X: **PDB Molecule:**proto-oncogene frat1; **PDBTitle:** gsk3beta complex with n-(6-(3,4-dihydroxyphenyl)-1h-pyrazolo[3,4-2 b]pyridin-3-yl)acetamide
22	c5ibzD_	Alignment	not modelled	8.8	38	**PDB header:**lyase **Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a novel cyclase (pfam04199).
23	d2o35a1	Alignment	not modelled	7.2	35	**Fold:**SMc04008-like **Superfamily:**SMc04008-like **Family:**SMc04008-like
24	c2o35A_	Alignment	not modelled	7.2	35	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein duf1244; **PDBTitle:** protein of unknown function (duf1244) from sinorhizobium meliloti