












Phyre2

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Description	RVBD2513 (-) _2830171_2830593
Date	Wed Aug 7 12:50:14 BST 2019
Unique Job ID	93d074a6af54a711

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4n2gA_	Alignment		21.4	35	PDB header: hydrolase Chain: A: PDB Molecule: protein-arginine deiminase type-2; PDBTitle: crystal structure of protein arginine deiminase 2 (d169a, 10 mm ca2+)
2	d1qkia2	Alignment		15.2	53	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Glucose 6-phosphate dehydrogenase-like
3	c5hp5A_	Alignment		13.5	33	PDB header: hydrolase Chain: A: PDB Molecule: protein-arginine deiminase type-1; PDBTitle: srtructure of human peptidylarginine deiminase type i (pad1)
4	d1p9pa_	Alignment		13.3	30	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: tRNA(m1G37)-methyltransferase TrmD
5	c2dexX_	Alignment		11.2	33	PDB header: hydrolase Chain: X: PDB Molecule: protein-arginine deiminase type iv; PDBTitle: crystal structure of human peptidylarginine deiminase 4 in complex2 with histone h3 n-terminal peptide including arg17
6	c3iwpK_	Alignment		10.9	28	PDB header: metal binding protein Chain: K: PDB Molecule: copper homeostasis protein cutc homolog; PDBTitle: crystal structure of human copper homeostasis protein cutc
7	c4r9xB_	Alignment		10.6	25	PDB header: metal transport Chain: B: PDB Molecule: copper homeostasis protein cutc; PDBTitle: crystal structure of putative copper homeostasis protein cutc from2 bacillus anthracis
8	c3imoC_	Alignment		10.0	22	PDB header: unknown function Chain: C: PDB Molecule: integron cassette protein; PDBTitle: structure from the mobile metagenome of vibrio cholerae. integron2 cassette protein vch_cass14
9	d1oy5a_	Alignment		10.0	31	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: tRNA(m1G37)-methyltransferase TrmD
10	c4e9iB_	Alignment		9.9	53	PDB header: oxidoreductase Chain: B: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: glucose-6-p dehydrogenase (apo form) from trypanosoma cruzi
11	c4lqvA_	Alignment		9.7	47	PDB header: oxidoreductase Chain: A: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: x-ray crystal structure of glucose-6-phosphate 1-dehydrogenase from2 mycobacterium avium

12	c3ujjP	Alignment		9.7	64	PDB header: immune system Chain: P: PDB Molecule: gp120; PDBTitle: crystal structure of anti-hiv-1 v3 fab 4025 in complex with con a2 peptide
13	c1oy5B	Alignment		9.3	31	PDB header: transferase Chain: B: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure of trna (m1g37) methyltransferase from aquifex2 aeolicus
14	c5hi8B	Alignment		8.7	15	PDB header: lyase Chain: B: PDB Molecule: antenna protein; PDBTitle: structure of t-type phycobiliprotein lyase cpet from prochlorococcus2 phage p-hm1
15	d2dexx3	Alignment		8.3	31	Fold: Pentein, beta/alpha-propeller Superfamily: Pentein Family: Peptidylarginine deiminase Pad4, catalytic C-terminal domain
16	c3ffrA	Alignment		8.1	13	PDB header: transferase Chain: A: PDB Molecule: phosphoserine aminotransferase serc; PDBTitle: crystal structure of a phosphoserine aminotransferase serc (chu_0995)2 from cytophaga hutchinsonii atcc 33406 at 1.75 a resolution
17	c3gb3B	Alignment		7.6	20	PDB header: fluorescent protein Chain: B: PDB Molecule: killerred; PDBTitle: x-ray structure of genetically encoded photosensitizer killerred in2 native form
18	c6hegA	Alignment		7.5	41	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase hrpb; PDBTitle: crystal structure of escherichia coli deah/rna helicase hrpb
19	c5dkuB	Alignment		7.1	25	PDB header: transferase Chain: B: PDB Molecule: prex dna polymerase; PDBTitle: c-terminal his tagged appol exonuclease mutant
20	c3ky7A	Alignment		6.9	30	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
21	c5o60U	Alignment	not modelled	6.9	13	PDB header: ribosome Chain: U: PDB Molecule: 50s ribosomal protein l23; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
22	c3a0mF	Alignment	not modelled	6.2	73	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
23	c4k1cB	Alignment	not modelled	5.9	32	PDB header: membrane protein/metal transport Chain: B: PDB Molecule: vacuolar calcium ion transporter; PDBTitle: vcx1 calcium/proton exchanger
24	c1ynuA	Alignment	not modelled	5.9	25	PDB header: lyase Chain: A: PDB Molecule: 1-aminocyclopropane-1-carboxylate synthase; PDBTitle: crystal structure of apple acc synthase in complex with l-vinylglycine
25	c2rv9A	Alignment	not modelled	5.6	26	PDB header: hydrolase Chain: A: PDB Molecule: glucanase; PDBTitle: solution structure of chitosan-binding module 1 derived from2 chitosanase/glucanase from paenibacillus sp. ik-5
26	d1h9aa2	Alignment	not modelled	5.5	24	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Glucose 6-phosphate dehydrogenase-like
27	c4kppA	Alignment	not modelled	5.5	24	PDB header: membrane protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of h+/ca2+ exchanger cax
28	d1cm3a	Alignment	not modelled	5.4	27	Fold: HPr-like Superfamily: HPr-like Family: HPr-like

29	c3le1B_	 Alignment	not modelled	5.3	20	PDB header: transferase Chain: B: PDB Molecule: phosphotransferase system, hpr-related proteins; PDBTitle: crystal structure of apohpr monomer from thermoanaerobacter2 tengcongensis Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Alr1493-like
30	d2ga1a1	 Alignment	not modelled	5.3	65	