






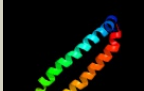
















Phyre2

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 Description RVBD3017c_(esxQ)_3376500_3376862
 Date Thu Aug 8 16:20:18 BST 2019
 Unique Job ID 2c0a6d58a358f717

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3q4hB_	 Alignment		100.0	52	PDB header: metal transport Chain: B; PDB Molecule: low molecular weight protein antigen 7; PDBTitle: crystal structure of the mycobacterium smegmatis esxgh complex2 (msmeg_0620-msmeg_0621)
2	c3h6pD_	 Alignment		100.0	65	PDB header: structural genomics, unknown function Chain: D; PDB Molecule: esat-6-like protein esxr; PDBTitle: crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
3	c2kg7B_	 Alignment		98.6	56	PDB header: unknown function Chain: B; PDB Molecule: esat-6-like protein eshx; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
4	d1wa8b1	 Alignment		98.4	18	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
5	c4lwsB_	 Alignment		97.5	12	PDB header: unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
6	c4lwsA_	 Alignment		97.1	15	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
7	d1wa8a1	 Alignment		95.6	13	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
8	c3gvmA_	 Alignment		95.4	9	PDB header: viral protein Chain: A; PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
9	c4iogD_	 Alignment		94.5	14	PDB header: unknown function Chain: D; PDB Molecule: secreted protein esxb; PDBTitle: the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. Sterne
10	c3zbhC_	 Alignment		90.4	9	PDB header: unknown function Chain: C; PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
11	c2vs0B_	 Alignment		90.0	11	PDB header: cell invasion Chain: B; PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa

12	c2do5A_	Alignment		29.6	45	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: splicing factor 3b subunit 2; PDBTitle: solution structure of the sap domain of human splicing2 factor 3b subunit 2
13	d1ju8a_	Alignment		26.3	35	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Albumin 1
14	c3wofB_	Alignment		25.9	60	PDB header: transferase/transcription Chain: B; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of p23-45 gp39 (6-132) bound to thermus thermophilus2 rna polymerase beta-flap domain
15	c3wodG_	Alignment		23.2	60	PDB header: transferase/transcription Chain: G; PDB Molecule: putative uncharacterized protein; PDBTitle: rna polymerase-gp39 complex
16	c5tc1M_	Alignment		21.4	46	PDB header: viral protein/rna Chain: M; PDB Molecule: maturation protein; PDBTitle: in situ structures of the genome and genome-delivery apparatus in2 ssrna bacteriophage ms2
17	c3qbzA_	Alignment		21.2	33	PDB header: cell cycle Chain: A; PDB Molecule: ddk kinase regulatory subunit dbf4; PDBTitle: crystal structure of the rad53-recognition domain of saccharomyces2 cerevisiae dbf4
18	c5t2sA_	Alignment		20.0	25	PDB header: cell cycle Chain: A; PDB Molecule: ddk kinase regulatory subunit dbf4,serine/threonine-protein PDBTitle: structure of the fha1 domain of rad53 bound simultaneously to the brct2 domain of dbf4 and a phosphopeptide.
19	d1p8ba_	Alignment		19.8	35	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Albumin 1
20	d3cr3a1	Alignment		19.6	23	Fold: DhaL-like Superfamily: DhaL-like Family: DhaL-like
21	c2ru8A_	Alignment	not modelled	16.3	35	PDB header: replication Chain: A; PDB Molecule: primosomal protein 1; PDBTitle: dnat c-terminal domain
22	c6d8tA_	Alignment	not modelled	14.6	35	PDB header: toxin Chain: A; PDB Molecule: potassium channel toxin alpha-ktx 5.4; PDBTitle: nmr solution structure of tamapin, mutant e25k/k27e
23	d1scya_	Alignment	not modelled	14.5	33	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Short-chain scorpion toxins
24	c1scya_	Alignment	not modelled	14.5	33	PDB header: neurotoxin Chain: A; PDB Molecule: scyllatoxin; PDBTitle: determination of the three-dimensional structure of scyllatoxin by 1h2 nuclear magnetic resonance
25	c5is0E_	Alignment	not modelled	14.2	21	PDB header: transport protein Chain: E; PDB Molecule: transient receptor potential cation channel subfamily v PDBTitle: structure of trpv1 in complex with capsazepine, determined in lipid2 nanodisc
26	c2izpB_	Alignment	not modelled	13.6	7	PDB header: toxin Chain: B; PDB Molecule: putative membrane antigen; PDBTitle: bipd - an invasion prtein associated with the type-iii2 secretion system of burkholderia pseudomallei.
27	c2ky3A_	Alignment	not modelled	13.1	35	PDB header: toxin Chain: A; PDB Molecule: potassium channel toxin alpha-ktx 5.4; PDBTitle: solution structure of gs-alpha-ktx5.4 synthetic scorpion like
28	c6d93A_	Alignment	not modelled	13.0	35	PDB header: toxin Chain: A; PDB Molecule: potassium channel toxin alpha-ktx 5.4; PDBTitle: nmr solution structure of tamapin, mutant y31a

29	d1un8a1	Alignment	not modelled	12.8	17	Fold: DhaL-like Superfamily: DhaL-like Family: DhaL-like
30	c4c0lA	Alignment	not modelled	12.5	17	PDB header: hydrolase Chain: A: PDB Molecule: mitochondrial rho gtpase; PDBTitle: crystal structure of drosophila miro ef hand and cgtase domains2 bound to one magnesium ion and mg:gdp (mggdp-miros)
31	c6d8rA	Alignment	not modelled	12.5	35	PDB header: toxin Chain: A: PDB Molecule: potassium channel toxin alpha-ktx 5.4; PDBTitle: nmr solution structure of tamapin, mutant e25k
32	c6d8yA	Alignment	not modelled	12.3	35	PDB header: toxin Chain: A: PDB Molecule: potassium channel toxin alpha-ktx 5.4; PDBTitle: nmr solution structure of tamapin, mutant y31h
33	d2izpa1	Alignment	not modelled	11.3	7	Fold: lpaD-like Superfamily: lpaD-like Family: lpaD-like
34	c4bjjB	Alignment	not modelled	11.3	54	PDB header: transcription Chain: B: PDB Molecule: transcription factor tau subunit sfc7; PDBTitle: sfc1-sfc7 dimerization module
35	c6d8qA	Alignment	not modelled	11.0	35	PDB header: toxin Chain: A: PDB Molecule: potassium channel toxin alpha-ktx 5.4; PDBTitle: nmr solution structure of tamapin, mutant dp30/y31+n
36	c4o8uE	Alignment	not modelled	10.9	53	PDB header: unknown function Chain: E: PDB Molecule: uncharacterized protein pf2046; PDBTitle: structure of pf2046
37	c6d3tA	Alignment	not modelled	10.8	35	PDB header: toxin Chain: A: PDB Molecule: potassium channel toxin alpha-ktx 5.4; PDBTitle: nmr solution structure of tamapin, mutant dp30
38	d1pnha	Alignment	not modelled	10.8	33	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Short-chain scorpion toxins
39	c1pnhA	Alignment	not modelled	10.8	33	PDB header: toxin Chain: A: PDB Molecule: scorpion toxin; PDBTitle: solution structure of po5-nh2, a scorpion toxin analog with high2 affinity for the apamin-sensitive potassium channel
40	c3zqbB	Alignment	not modelled	10.7	25	PDB header: cell invasion Chain: B: PDB Molecule: protein prgi, cell invasion protein sipd; PDBTitle: prgi-sipd from salmonella typhimurium
41	c6d9oA	Alignment	not modelled	10.6	35	PDB header: toxin Chain: A: PDB Molecule: potassium channel toxin alpha-ktx 5.4; PDBTitle: nmr solution structure of tamapin, mutant e25a
42	c6d8sA	Alignment	not modelled	10.2	35	PDB header: toxin Chain: A: PDB Molecule: potassium channel toxin alpha-ktx 5.4; PDBTitle: nmr solution structure of tamapin, mutant k27e
43	c2p7nA	Alignment	not modelled	9.6	31	PDB header: cell invasion Chain: A: PDB Molecule: pathogenicity island 1 effector protein; PDBTitle: crystal structure of the pathogenicity island 1 effector protein from2 chromobacterium violaceum. northeast structural genomics consortium3 (nesgc) target cvr69.
44	c6d9pA	Alignment	not modelled	9.6	35	PDB header: toxin Chain: A: PDB Molecule: potassium channel toxin alpha-ktx 5.4; PDBTitle: nmr solution structure of tamapin, mutant k27a
45	c2iunD	Alignment	not modelled	9.0	67	PDB header: viral protein Chain: D: PDB Molecule: avian adenovirus celo long fibre; PDBTitle: structure of the c-terminal head domain of the avian adenovirus celo2 long fibre (p21 crystal form)
46	c6d8uA	Alignment	not modelled	8.7	35	PDB header: toxin Chain: A: PDB Molecule: potassium channel toxin alpha-ktx 5.4; PDBTitle: nmr solution structure of tamapin, mutant k20e
47	d1e6va1	Alignment	not modelled	8.7	38	Fold: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain Superfamily: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain Family: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain
48	c4hdeA	Alignment	not modelled	8.0	16	PDB header: lipid binding protein Chain: A: PDB Molecule: sco1/senc family lipoprotein; PDBTitle: the crystal structure of a sco1/senc family lipoprotein from bacillus2 anthracis str. ames
49	c3nzzA	Alignment	not modelled	7.9	25	PDB header: cell invasion Chain: A: PDB Molecule: cell invasion protein sipd; PDBTitle: crystal structure of the salmonella type iii secretion system tip2 protein sipd
50	c4b2gB	Alignment	not modelled	7.0	34	PDB header: signaling protein Chain: B: PDB Molecule: gh3-1 auxin conjugating enzyme; PDBTitle: crystal structure of an indole-3-acetic acid amido synthase from vitis2 vinifera involved in auxin homeostasis
51	d1aisa1	Alignment	not modelled	6.8	30	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
52	d1f15a	Alignment	not modelled	6.7	42	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Bromoviridae-like VP
53	d1r5ta	Alignment	not modelled	6.7	23	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Cytidine deaminase
54	c3dktD	Alignment	not modelled	6.6	18	PDB header: structural protein/virus like particle Chain: D: PDB Molecule: maritimacin; PDBTitle: crystal structure of thermotoga maritima encapsulin
						PDB header: viral protein

55	c6c3rB_	Alignment	not modelled	6.6	46	Chain: B: PDB Molecule: cricket paralysis virus 1a protein; PDBTitle: cricket paralysis virus rna1 suppressor protein crpv-1a
56	c3fybA_	Alignment	not modelled	6.4	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein of unknown function (duf1244); PDBTitle: crystal structure of a protein of unknown function (duf1244) from2 alcanivorax borkumensis
57	c6avhA_	Alignment	not modelled	6.1	24	PDB header: ligase, plant protein Chain: A: PDB Molecule: gh3.15 acyl acid amido synthetase; PDBTitle: gh3.15 acyl acid amido synthetase
58	c5n1qD_	Alignment	not modelled	6.0	45	PDB header: transferase Chain: D: PDB Molecule: methyl-coenzyme m reductase iii from methanothermococcus PDBTitle: methyl-coenzyme m reductase iii from methanothermococcus2 thermolithotrophicus at 1.9 a resolution
59	c1mtpB_	Alignment	not modelled	6.0	50	PDB header: structural genomics Chain: B: PDB Molecule: serine proteinase inhibitor (serpin), chain b; PDBTitle: the x-ray crystal structure of a serpin from a thermophilic prokaryote
60	d1laja_	Alignment	not modelled	6.0	24	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Bromoviridae-like VP
61	c1lajA_	Alignment	not modelled	6.0	24	PDB header: virus/rna Chain: A: PDB Molecule: capsid protein; PDBTitle: the structure of tomato aspermy virus by x-ray2 crystallography
62	d2o35a1	Alignment	not modelled	5.9	22	Fold: SMc04008-like Superfamily: SMc04008-like Family: SMc04008-like
63	c2o35A_	Alignment	not modelled	5.9	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein duf1244; PDBTitle: protein of unknown function (duf1244) from sinorhizobium meliloti
64	d2akab1	Alignment	not modelled	5.8	35	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
65	c3jcuO_	Alignment	not modelled	5.8	44	PDB header: membrane protein Chain: O: PDB Molecule: oxygen-evolving enhancer protein 1, chloroplastic; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
66	c2jorA_	Alignment	not modelled	5.7	38	PDB header: blood clotting Chain: A: PDB Molecule: fibrinogen alpha chain; PDBTitle: nmr solution structure, stability, and interaction of the2 recombinant bovine fibrinogen alphac-domain fragment
67	d1hbna1	Alignment	not modelled	5.7	40	Fold: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain Superfamily: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain Family: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain
68	d1vi7a1	Alignment	not modelled	5.5	35	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: YigZ N-terminal domain-like
69	d1e6ya1	Alignment	not modelled	5.5	45	Fold: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain Superfamily: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain Family: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain
70	d2axto1	Alignment	not modelled	5.4	40	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: PsbO-like
71	c3q8aF_	Alignment	not modelled	5.4	14	PDB header: transferase Chain: F: PDB Molecule: ribosomal rna small subunit methyltransferase g; PDBTitle: t. thermophilus 16s rrna g527 methyltransferase in complex with adohcy2 in space group p61
72	c5lnkm_	Alignment	not modelled	5.3	38	PDB header: oxidoreductase Chain: M: PDB Molecule: mitochondrial complex i, nd4 subunit; PDBTitle: entire ovine respiratory complex i