







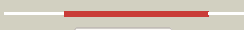















Phyre2

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Description	RVBD2613c (-) _2940619_2941206
Date	Wed Aug 7 12:50:25 BST 2019
Unique Job ID	d744c2e85243a163

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3anoA_	 Alignment		100.0	100	PDB header: transferase Chain: A; PDB Molecule: ap-4-a phosphorylase; PDBTitle: crystal structure of a novel diadenosine 5',5'''-p1,p4-tetraphosphate2 phosphorylase from mycobacterium tuberculosis h37rv
2	c3ksvA_	 Alignment		100.0	21	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: hypothetical protein from leishmania major
3	c3l7xA_	 Alignment		100.0	23	PDB header: cell cycle Chain: A; PDB Molecule: putative hit-like protein involved in cell-cycle PDBTitle: the crystal structure of smu.412c from streptococcus mutans ua159
4	c3imiB_	 Alignment		100.0	23	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: hit family protein; PDBTitle: 2.01 angstrom resolution crystal structure of a hit family protein2 from bacillus anthracis str. 'ames ancestor'
5	d1y23a_	 Alignment		100.0	25	Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins
6	c2eo4A_	 Alignment		100.0	24	PDB header: hydrolase Chain: A; PDB Molecule: 150aa long hypothetical histidine triad nucleotide-binding PDBTitle: crystal structure of hypothetical histidine triad nucleotide-binding2 protein st2152 from sulfolobus tokodaii strain7
7	c6iq1A_	 Alignment		100.0	19	PDB header: hydrolase Chain: A; PDB Molecule: adenosine 5'-monophosphoramidase; PDBTitle: crystal structure of histidine triad nucleotide-binding protein from2 candida albicans
8	c3lb5B_	 Alignment		100.0	21	PDB header: cell cycle Chain: B; PDB Molecule: hit-like protein involved in cell-cycle regulation; PDBTitle: crystal structure of hit-like protein involved in cell-cycle2 regulation from bartonella henselae with unknown ligand
9	c5cs2A_	 Alignment		100.0	20	PDB header: hydrolase Chain: A; PDB Molecule: histidine triad protein; PDBTitle: crystal structure of plasmodium falciparum diadenosine triphosphate2 hydrolase in complex with cyclomarin a
10	c1emsB_	 Alignment		100.0	24	PDB header: antitumor protein Chain: B; PDB Molecule: nit-fragile histidine triad fusion protein; PDBTitle: crystal structure of the c. elegans nitfhit protein
11	c3o0mB_	 Alignment		100.0	24	PDB header: hydrolase Chain: B; PDB Molecule: hit family protein; PDBTitle: crystal structure of a zn-bound histidine triad family protein from2 mycobacterium smegmatis

12	c1zwiA_	Alignment		100.0	13	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: putative galactose-1-phosphate uridylyl transferase; PDBTitle: x-ray structure of galt-like protein from arabidopsis thaliana2 at5g18200
13	c1gupC_	Alignment		100.0	16	PDB header: nucleotidyltransferase Chain: C; PDB Molecule: galactose-1-phosphate uridylyltransferase; PDBTitle: structure of nucleotidyltransferase complexed with udp-2 galactose
14	c3p0tB_	Alignment		100.0	25	PDB header: unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an hit-like protein from mycobacterium2 paratuberculosis
15	c5in3A_	Alignment		100.0	15	PDB header: transferase Chain: A; PDB Molecule: galactose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of glucose-1-phosphate bound nucleotidylated human2 galactose-1-phosphate uridylyltransferase
16	d1emsa1	Alignment		100.0	24	Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins
17	d1z84a2	Alignment		100.0	14	Fold: HIT-like Superfamily: HIT-like Family: Hexose-1-phosphate uridylyltransferase
18	d1guqa2	Alignment		100.0	16	Fold: HIT-like Superfamily: HIT-like Family: Hexose-1-phosphate uridylyltransferase
19	d1fita_	Alignment		100.0	30	Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins
20	d2oika1	Alignment		100.0	25	Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins
21	c3r6fA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: hit family protein; PDBTitle: crystal structure of a zinc-containing hit family protein from2 encephalitozoon cuniculi
22	d1rzya_	Alignment	not modelled	100.0	18	Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins
23	d1kpfa_	Alignment	not modelled	100.0	19	Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins
24	c3n1tE_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: E; PDB Molecule: hit-like protein hint; PDBTitle: crystal structure of the h101a mutant echint gmp complex
25	c4eguA_	Alignment	not modelled	99.9	25	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: histidine triad (hit) protein; PDBTitle: 0.95a resolution structure of a histidine triad protein from2 clostridium difficile
26	d1xqua_	Alignment	not modelled	99.9	19	Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins
27	c1xquA_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A; PDB Molecule: hit family hydrolase; PDBTitle: hit family hydrolase from clostridium thermocellum cth-393
28	c6d6jB_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: B; PDB Molecule: hit family hydrolase; PDBTitle: crystal structure of hit family hydrolase from legionella pneumophila2 philadelphia 1 PDB header: metal binding protein

29	c3qj7A_	Alignment	not modelled	99.9	25	Chain: A: PDB Molecule: putative histidine triad family protein; PDBTitle: crystal structure of a histidine triad family protein from entamoeba2 histolytica, bound to sulfate
30	c3i24B_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: B: PDB Molecule: hit family hydrolase; PDBTitle: crystal structure of a hit family hydrolase protein from vibrio2 fischeri. northeast structural genomics consortium target id vfr176
31	c4q61J_	Alignment	not modelled	99.9	19	PDB header: cell cycle Chain: J: PDB Molecule: uncharacterized hit-like protein hp_0404; PDBTitle: hit like protein from helicobacter pylori 26695
32	c3oheA_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: histidine triad (hit) protein; PDBTitle: crystal structure of a histidine triad protein (maqu_1709) from2 marinobacter aquaeolei vt8 at 1.20 a resolution
33	c4incA_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: histidine triad nucleotide-binding protein 2, PDBTitle: human histidine triad nucleotide binding protein 2
34	c3nrdB_	Alignment	not modelled	99.9	27	PDB header: nucleotide binding protein Chain: B: PDB Molecule: histidine triad (hit) protein; PDBTitle: crystal structure of a histidine triad (hit) protein (smc02904) from2 sinorhizobium meliloti 1021 at 2.06 a resolution
35	c3i4sB_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: B: PDB Molecule: histidine triad protein; PDBTitle: crystal structure of histidine triad protein blr8122 from2 bradyrhizobium japonicum
36	d1z84a1	Alignment	not modelled	99.8	22	Fold: HIT-like Superfamily: HIT-like Family: Hexose-1-phosphate uridylyltransferase
37	c4ndgB_	Alignment	not modelled	99.7	22	PDB header: dna binding protein/rna/dna Chain: B: PDB Molecule: aprataxin; PDBTitle: human aprataxin (aptx) bound to rna-dna and zn - adenosine vanadate2 transition state mimic complex
38	c3splC_	Alignment	not modelled	99.5	15	PDB header: hydrolase/dna Chain: C: PDB Molecule: aprataxin-like protein; PDBTitle: crystal structure of aprataxin ortholog hnt3 in complex with dna and2 amp
39	c3jb9c_	Alignment	not modelled	99.5	14	PDB header: rna binding protein/rna Chain: C: PDB Molecule: u5 snrna; PDBTitle: cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
40	c4i5wA_	Alignment	not modelled	99.5	23	PDB header: transferase Chain: A: PDB Molecule: 5',5'''-p-1,p-4-tetraphosphate phosphorylase 2; PDBTitle: crystal structure of yeast ap4a phosphorylase apa2 in complex with amp
41	c4qvua_	Alignment	not modelled	99.4	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf4931 family protein (bce0241) from bacillus2 cereus atcc 10987 at 2.65 a resolution
42	c6id1U_	Alignment	not modelled	99.1	18	PDB header: splicing Chain: U: PDB Molecule: cwf19-like protein 2; PDBTitle: cryo-em structure of a human intron lariat spliceosome after prp432 loaded (ils2 complex) at 2.9 angstrom resolution
43	d3bl9a1	Alignment	not modelled	98.9	25	Fold: HIT-like Superfamily: HIT-like Family: mRNA decapping enzyme Dcp5 C-terminal domain
44	c3bl9B_	Alignment	not modelled	98.7	25	PDB header: hydrolase Chain: B: PDB Molecule: scavenger mrna-decapping enzyme dcps; PDBTitle: synthetic gene encoded dcps bound to inhibitor dg157493
45	d1vlra1	Alignment	not modelled	98.6	23	Fold: HIT-like Superfamily: HIT-like Family: mRNA decapping enzyme Dcp5 C-terminal domain
46	d1guqa1	Alignment	not modelled	98.5	13	Fold: HIT-like Superfamily: HIT-like Family: Hexose-1-phosphate uridylyltransferase
47	c1xmlA_	Alignment	not modelled	98.5	22	PDB header: chaperone Chain: A: PDB Molecule: heat shock-like protein 1; PDBTitle: structure of human dcps
48	c5bv3C_	Alignment	not modelled	98.4	17	PDB header: hydrolase Chain: C: PDB Molecule: m7gpppx diphosphatase; PDBTitle: yeast scavenger decapping enzyme in complex with m7gdp
49	c6gbsB_	Alignment	not modelled	98.3	24	PDB header: hydrolase Chain: B: PDB Molecule: putative mrna decapping protein; PDBTitle: crystal structure of the c. thermophilum scavenger decapping enzyme2 dcps apo form
50	c4lvjA_	Alignment	not modelled	92.6	17	PDB header: dna binding protein/dna Chain: A: PDB Molecule: plasmid recombination enzyme; PDBTitle: mobm relaxase domain (mobv; mob_pre) bound to plasmid pmv158 orit dna2 (22nt). mn-bound crystal structure at ph 5.5
51	d2pofa1	Alignment	not modelled	90.2	12	Fold: HIT-like Superfamily: HIT-like Family: CDH-like
52	d1mg4a_	Alignment	not modelled	49.8	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: Doublecortin (DC) Family: Doublecortin (DC)
53	c5kcia_	Alignment	not modelled	49.8	26	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein ypl067c; PDBTitle: crystal structure of htc1
54	d1uf0a_	Alignment	not modelled	47.3	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: Doublecortin (DC) Family: Doublecortin (DC) PDB header: hydrolase

55	c4atuL	Alignment	not modelled	38.4	22	Chain: I: PDB Molecule: neuronal migration protein doublecortin; PDBTitle: human doublecortin n-dc repeat plus linker, and tubulin (2xrp) docked2 into an 8a cryo-em map of doublecortin-stabilised microtubules3 reconstructed in absence of kinesin
56	d1mjda	Alignment	not modelled	30.1	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: Doublecortin (DC) Family: Doublecortin (DC)
57	c2dnfA	Alignment	not modelled	27.1	11	PDB header: protein binding Chain: A: PDB Molecule: doublecortin domain-containing protein 2; PDBTitle: solution structure of rsgi ruh-062, a dcx domain from human
58	c1vr7A	Alignment	not modelled	26.6	15	PDB header: lyase Chain: A: PDB Molecule: s-adenosylmethionine decarboxylase proenzyme; PDBTitle: crystal structure of s-adenosylmethionine decarboxylase proenzyme2 (tm0655) from thermotoga maritima at 1.2 a resolution
59	c5ip4E	Alignment	not modelled	26.4	12	PDB header: transferase Chain: E: PDB Molecule: neuronal migration protein doublecortin; PDBTitle: x-ray structure of the c-terminal domain of human doublecortin
60	d1vr7a1	Alignment	not modelled	25.5	15	Fold: S-adenosylmethionine decarboxylase Superfamily: S-adenosylmethionine decarboxylase Family: Bacterial S-adenosylmethionine decarboxylase
61	c2v4xA	Alignment	not modelled	23.8	15	PDB header: viral protein Chain: A: PDB Molecule: capsid protein p27; PDBTitle: crystal structure of jaagsiekte sheep retrovirus capsid n-2 terminal domain
62	c6f21B	Alignment	not modelled	23.8	24	PDB header: toxin Chain: B: PDB Molecule: dendroaspis polylepsis mt9; PDBTitle: crystal structure of toxin mt9 from mamba venom
63	c1ayeA	Alignment	not modelled	22.3	19	PDB header: serine protease Chain: A: PDB Molecule: procarboxypeptidase a2; PDBTitle: human procarboxypeptidase a2
64	d1tfsa	Alignment	not modelled	21.4	25	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Snake venom toxins
65	d1ntxa	Alignment	not modelled	20.9	25	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Snake venom toxins
66	d1v76a	Alignment	not modelled	20.7	17	Fold: Rof/RNase P subunit-like Superfamily: Rof/RNase P subunit-like Family: RNase P subunit p29-like
67	c5mm2A	Alignment	not modelled	19.4	30	PDB header: virus Chain: A: PDB Molecule: capsid protein vp4c; PDBTitle: nora virus structure
68	c2zaeC	Alignment	not modelled	18.8	17	PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease p protein component 1; PDBTitle: crystal structure of protein ph1601p in complex with protein ph1771p2 of archaeal ribonuclease p from pyrococcus horikoshii ot3
69	c5lxjA	Alignment	not modelled	18.3	29	PDB header: viral protein Chain: A: PDB Molecule: phosphoprotein; PDBTitle: solution nmr structure of the x domain of peste des petits ruminants2 phosphoprotein
70	d1oqka	Alignment	not modelled	17.6	16	Fold: Rof/RNase P subunit-like Superfamily: Rof/RNase P subunit-like Family: RNase P subunit p29-like
71	c5j1mD	Alignment	not modelled	17.3	40	PDB header: hydrolase Chain: D: PDB Molecule: toxR-activated gene (tage); PDBTitle: crystal structure of csd1-csd2 dimer ii
72	c2qwwB	Alignment	not modelled	17.1	32	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of multiple antibiotic-resistance repressor (marr)2 (yp_013417.1) from listeria monocytogenes 4b f2365 at 2.07 a3 resolution
73	d1iq9a	Alignment	not modelled	17.0	29	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Snake venom toxins
74	c6k0aF	Alignment	not modelled	16.6	22	PDB header: rna binding protein/rna Chain: F: PDB Molecule: ribonuclease p protein component 1; PDBTitle: cryo-em structure of an archaeal ribonuclease p
75	d1tsfa	Alignment	not modelled	16.3	20	Fold: Rof/RNase P subunit-like Superfamily: Rof/RNase P subunit-like Family: RNase P subunit p29-like
76	d1b77a2	Alignment	not modelled	16.2	13	Fold: DNA clamp Superfamily: DNA clamp Family: DNA polymerase processivity factor
77	d3ebxa	Alignment	not modelled	15.9	29	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Snake venom toxins
78	c6ahrD	Alignment	not modelled	14.7	14	PDB header: hydrolase/rna Chain: D: PDB Molecule: ribonuclease p protein subunit p29; PDBTitle: cryo-em structure of human ribonuclease p
79	c3csqC	Alignment	not modelled	14.4	20	PDB header: hydrolase Chain: C: PDB Molecule: morphogenesis protein 1; PDBTitle: crystal and cryoem structural studies of a cell wall2 degrading enzyme in the bacteriophage phi29 tail
80	c3txxD	Alignment	not modelled	13.4	28	PDB header: transferase Chain: D: PDB Molecule: putrescine carbamoyltransferase; PDBTitle: crystal structure of putrescine transcarbamylase from enterococcus2 faecalis
						Fold: Snake toxin-like

81	d1qm7a_	Alignment	not modelled	13.3	23	Superfamily: Snake toxin-like Family: Snake venom toxins
82	c3bdeA_	Alignment	not modelled	13.1	10	PDB header: unknown function Chain: A: PDB Molecule: mll5499 protein; PDBTitle: crystal structure of a dabb family protein with a ferredoxin-like fold2 (mll5499) from mesorhizobium loti maff303099 at 1.79 a resolution
83	c5b0hB_	Alignment	not modelled	12.6	24	PDB header: metal binding protein Chain: B: PDB Molecule: leukocyte cell-derived chemotaxin-2; PDBTitle: crystal structure of human leukocyte cell-derived chemotaxin 2
84	d1vb0a_	Alignment	not modelled	12.5	42	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Snake venom toxins
85	d1vlva1	Alignment	not modelled	12.2	17	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
86	d1jb3a_	Alignment	not modelled	12.2	30	Fold: OB-fold Superfamily: TIMP-like Family: The laminin-binding domain of agrin
87	c2aydA_	Alignment	not modelled	11.8	21	PDB header: transcription Chain: A: PDB Molecule: wrky transcription factor 1; PDBTitle: crystal structure of the c-terminal wrky domain of atwrky1, an sa-2 induced and partially npr1-dependent transcription factor
88	c4agrB_	Alignment	not modelled	11.7	26	PDB header: sugar binding protein Chain: B: PDB Molecule: galectin; PDBTitle: structure of a tetrameric galectin from cinachyrella sp. (ball2 sponge)
89	c6b4aB_	Alignment	not modelled	11.4	18	PDB header: structural protein Chain: B: PDB Molecule: doublecortin; PDBTitle: crystal structure of the c-terminal domain of doublecortin (tgdcx)2 from toxoplasma gondii me49
90	d1g6ma_	Alignment	not modelled	11.2	23	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Snake venom toxins
91	d1pc0a_	Alignment	not modelled	10.7	20	Fold: Rof/RNase P subunit-like Superfamily: Rof/RNase P subunit-like Family: RNase P subunit p29-like
92	d1v6pa_	Alignment	not modelled	10.6	23	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Snake venom toxins
93	c3fmbA_	Alignment	not modelled	10.5	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dimeric protein of unknown function and ferredoxin-like PDBTitle: crystal structure of dimeric protein of unknown function and 2 ferredoxin-like fold (yp_212648.1) from bacteroides fragilis nctc3 9343 at 1.85 a resolution
94	d1dxha1	Alignment	not modelled	10.5	17	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
95	d1wiia_	Alignment	not modelled	10.4	17	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Putative zinc binding domain
96	c6q8iK_	Alignment	not modelled	10.2	50	PDB header: splicing Chain: K: PDB Molecule: protein red; PDBTitle: nterminal domain of human smu1 in complex with human redmid
97	c2yv9B_	Alignment	not modelled	10.2	12	PDB header: metal transport Chain: B: PDB Molecule: chloride intracellular channel exc-4; PDBTitle: crystal structure of the clic homologue exc-4 from c.2 elegans
98	d1ml4a1	Alignment	not modelled	10.1	20	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
99	c5op0B_	Alignment	not modelled	9.9	21	PDB header: transferase Chain: B: PDB Molecule: dna polymerase ligd, polymerase domain; PDBTitle: structure of prim-polc from mycobacterium smegmatis