


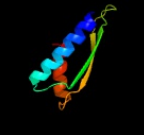















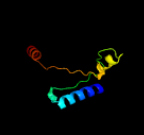




Phyre2

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 Description RVBD3623_(lpqG)_4062706_4063428
 Date Fri Aug 9 18:20:31 BST 2019
 Unique Job ID 63e3a1d8033a4514

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4hvxA_	 Alignment		100.0	27	PDB header: membrane protein Chain: A: PDB Molecule: 26 kda periplasmic immunogenic protein; PDBTitle: crystal structure of brucella abortus immunogenic bp26 protein
2	d1nyed_	 Alignment		50.2	17	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
3	c3k1dA_	 Alignment		27.7	17	PDB header: transferase Chain: A: PDB Molecule: 1,4-alpha-glucan-branching enzyme; PDBTitle: crystal structure of glycogen branching enzyme synonym: 1,4-alpha-d-2 glucan:1,4-alpha-d-glucan 6-glucosyl-transferase from mycobacterium3 tuberculosis h37rv
4	c2kxhB_	 Alignment		21.3	48	PDB header: protein binding Chain: B: PDB Molecule: peptide of far upstream element-binding protein 1; PDBTitle: solution structure of the first two rrm domains of fir in the complex2 with fbp nbx peptide
5	d1k7ka_	 Alignment		20.8	15	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: ITPase (Ham1)
6	c1m7xC_	 Alignment		19.3	11	PDB header: transferase Chain: C: PDB Molecule: 1,4-alpha-glucan branching enzyme; PDBTitle: the x-ray crystallographic structure of branching enzyme
7	d2onfa1	 Alignment		18.8	14	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
8	c2lfpA_	 Alignment		18.7	15	PDB header: viral protein Chain: A: PDB Molecule: bacteriophage spp1 complete nucleotide sequence; PDBTitle: structure of bacteriophage spp1 gp17 protein
9	c3am1A_	 Alignment		18.5	18	PDB header: transferase Chain: A: PDB Molecule: os06g0726400 protein; PDBTitle: structure of the starch branching enzyme i (bei) from oryza sativa l
10	c3s0yA_	 Alignment		18.2	8	PDB header: motor protein Chain: A: PDB Molecule: motility protein b; PDBTitle: the crystal structure of the periplasmic domain of motb (residues 64-2 256).
11	c3s0wB_	 Alignment		17.1	11	PDB header: motor protein Chain: B: PDB Molecule: motility protein b; PDBTitle: the crystal structure of the periplasmic domain of helicobacter pylori2 motb (residues 78-256).

12	c2rrlA_	Alignment		16.0	10	PDB header: protein transport Chain: A: PDB Molecule: flagellar hook-length control protein; PDBTitle: solution structure of the c-terminal domain of the flik
13	d2c8ma1	Alignment		15.9	27	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: LpIA-like
14	d1ukka_	Alignment		15.7	20	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
15	c2zf8A_	Alignment		14.5	17	PDB header: structural protein Chain: A: PDB Molecule: component of sodium-driven polar flagellar motor; PDBTitle: crystal structure of moty
16	d1m7xa3	Alignment		14.1	11	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
17	c5gquA_	Alignment		13.6	11	PDB header: transferase Chain: A: PDB Molecule: 1,4-alpha-glucan branching enzyme glgb; PDBTitle: crystal structure of branching enzyme from cyanothecce sp. atcc 51142
18	c4bzyC_	Alignment		13.3	14	PDB header: transferase Chain: C: PDB Molecule: 1,4-alpha-glucan-branching enzyme; PDBTitle: crystal structure of human glycogen branching enzyme (gbe1)
19	c2x48B_	Alignment		12.1	25	PDB header: viral protein Chain: B: PDB Molecule: cag38821; PDBTitle: orf 55 from sulfolobus islandicus rudivirus 1
20	c5yrxA_	Alignment		11.8	24	PDB header: dna binding protein Chain: A: PDB Molecule: nucleoid-associated protein rv3716c; PDBTitle: crystal structure of a hypothetical protein rv3716c from mycobacterium2 tuberculosis
21	d1u07a_	Alignment	not modelled	11.4	17	Fold: TolA/TonB C-terminal domain Superfamily: TolA/TonB C-terminal domain Family: TonB
22	c3amkA_	Alignment	not modelled	11.4	18	PDB header: transferase Chain: A: PDB Molecule: os06g0726400 protein; PDBTitle: structure of the starch branching enzyme i (bei) from oryza sativa l
23	c2dgaA_	Alignment	not modelled	11.3	17	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase; PDBTitle: crystal structure of hexameric beta-glucosidase in wheat
24	c6d9nA_	Alignment	not modelled	11.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: organic hydroperoxide resistance protein; PDBTitle: crystal structure of an organic hydroperoxide resistance protein from2 elizabethkingia anophelis with crystallant-derived thiocyanate bound
25	c2wskA_	Alignment	not modelled	10.9	14	PDB header: hydrolase Chain: A: PDB Molecule: glycogen debranching enzyme; PDBTitle: crystal structure of glycogen debranching enzyme glgx from2 escherichia coli k-12
26	c3mgjA_	Alignment	not modelled	10.9	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein mj1480; PDBTitle: crystal structure of the saccharop_dh_n domain of mj1480 protein from2 methanococcus jannaschii. northeast structural genomics consortium3 target mjr83a.
27	c5wtlB_	Alignment	not modelled	10.8	18	PDB header: membrane protein Chain: B: PDB Molecule: ompa family protein; PDBTitle: crystal structure of the periplasmic portion of outer membrane protein2 a (ompa) from capnocytophaga gingivalis
28	c4jhoA_	Alignment	not modelled	10.6	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-mannosidase/beta-glucosidase; PDBTitle: structural analysis and insights into glycon specificity of

						the rice2 gh1 os7bglu26 beta-d-mannosidase
29	c6mjnC_	Alignment	not modelled	10.5	17	PDB header: oxidoreductase Chain: C: PDB Molecule: organic hydroperoxide resistance protein; PDBTitle: crystal structure of an organic hydroperoxide resistance protein osmc,2 predicted redox protein, regulator of sulfide bond formation from3 legionella pneumophila
30	c2o0i1_	Alignment	not modelled	10.2	10	PDB header: surface active protein Chain: 1: PDB Molecule: c protein alpha-antigen; PDBTitle: crystal structure of the r185a mutant of the n-terminal domain of the2 group b streptococcus alpha c protein
31	c1mg1A_	Alignment	not modelled	10.1	27	PDB header: viral protein Chain: A: PDB Molecule: protein (htlv-1 gp21 ectodomain/maltose-binding protein PDBTitle: htlv-1 gp21 ectodomain/maltose-binding protein chimera
32	d1jcb4	Alignment	not modelled	9.8	12	Fold: Ferredoxin-like Superfamily: Anticodon-binding domain of PheRS Family: Anticodon-binding domain of PheRS
33	d2opla1	Alignment	not modelled	9.7	13	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
34	c3cyqM_	Alignment	not modelled	8.8	8	PDB header: membrane protein Chain: M: PDB Molecule: chemotaxis protein motb; PDBTitle: the crystal structure of the complex of the c-terminal domain of2 helicobacter pylori motb (residues 125-256) with n-acetylmuramic acid
35	c1zb8B_	Alignment	not modelled	8.7	14	PDB header: oxidoreductase Chain: B: PDB Molecule: organic hydroperoxide resistance protein; PDBTitle: crystal structure of xylella fastidiosa organic peroxide resistance2 protein
36	c2ql8A_	Alignment	not modelled	8.4	11	PDB header: oxidoreductase Chain: A: PDB Molecule: putative redox protein; PDBTitle: crystal structure of a putative redox protein (lsei_0423) from2 lactobacillus casei atcc 334 at 1.50 a resolution
37	c1qlE_	Alignment	not modelled	8.1	12	PDB header: unknown function Chain: E: PDB Molecule: osmotic inducible protein c like family; PDBTitle: crystal structure of osmc like protein from mycoplasma2 pneumoniae
38	d1qla_	Alignment	not modelled	8.1	12	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
39	c6izhE_	Alignment	not modelled	7.7	18	PDB header: hydrolase Chain: E: PDB Molecule: 2-aminomuconate deaminase; PDBTitle: crystal structure of deaminase amne from pseudomonas sp. ap-3
40	c2grxC_	Alignment	not modelled	7.7	17	PDB header: metal transport Chain: C: PDB Molecule: protein tonb; PDBTitle: crystal structure of tonb in complex with fhua, e. coli2 outer membrane receptor for ferrichrome
41	c2b99A_	Alignment	not modelled	7.6	17	PDB header: transferase Chain: A: PDB Molecule: riboflavin synthase; PDBTitle: crystal structure of an archaeal pentameric riboflavin2 synthase complex with a substrate analog inhibitor
42	c4y7jE_	Alignment	not modelled	7.6	17	PDB header: membrane protein,transport protein Chain: E: PDB Molecule: large conductance mechanosensitive channel protein, PDBTitle: structure of an archaeal mechanosensitive channel in expanded state
43	c1bf2A_	Alignment	not modelled	7.2	17	PDB header: hydrolase Chain: A: PDB Molecule: isoamylase; PDBTitle: structure of pseudomonas isoamylase
44	d2aizp1	Alignment	not modelled	7.2	20	Fold: Bacillus chorismate mutase-like Superfamily: OmpA-like Family: OmpA-like
45	c1qhoA_	Alignment	not modelled	7.1	19	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
46	c4f7dA_	Alignment	not modelled	6.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of ferredoxin-nadp reductase from burkholderia2 thailandensis e264
47	c2mb1A_	Alignment	not modelled	6.7	12	PDB header: de novo protein Chain: A: PDB Molecule: top7 fold protein top7m13; PDBTitle: solution nmr structure of de novo designed top7 fold protein top7m13,2 northeast structural genomics consortium (nesg) target or33
48	d1e4mm_	Alignment	not modelled	6.6	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Family 1 of glycosyl hydrolase
49	c1xx3A_	Alignment	not modelled	6.4	17	PDB header: transport protein Chain: A: PDB Molecule: tonb protein; PDBTitle: solution structure of escherichia coli tonb-ctd
50	c3m07A_	Alignment	not modelled	6.4	15	PDB header: unknown function Chain: A: PDB Molecule: putative alpha amylase; PDBTitle: 1.4 angstrom resolution crystal structure of putative alpha amylase2 from salmonella typhimurium.
51	c5zu0B_	Alignment	not modelled	6.2	15	PDB header: transferase Chain: B: PDB Molecule: protein arginine methyltransferase ndufaf7 homolog, PDBTitle: proteobacterial origin of protein arginine methylation and regulation2 of complex i assembly by mida
52	c2by0A_	Alignment	not modelled	6.2	15	PDB header: hydrolase Chain: A: PDB Molecule: malto oligosyltrehalose trehalohydrolase; PDBTitle: is radiation damage dependent on the dose-rate used during2 macromolecular crystallography data collection
53	d2hqsc1	Alignment	not modelled	6.1	18	Fold: Bacillus chorismate mutase-like Superfamily: OmpA-like Family: OmpA-like

54	c2l26A_	Alignment	not modelled	6.0	27	PDB header: membrane protein Chain: A: PDB Molecule: uncharacterized protein rv0899/mt0922; PDBTitle: rv0899 from mycobacterium tuberculosis contains two separated domains
55	c3mhyC_	Alignment	not modelled	5.9	10	PDB header: signaling protein Chain: C: PDB Molecule: pii-like protein pz; PDBTitle: a new pii protein structure
56	d1qwia_	Alignment	not modelled	5.6	17	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
57	d1uoka2	Alignment	not modelled	5.6	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
58	c2x7jA_	Alignment	not modelled	5.6	13	PDB header: transferase Chain: A: PDB Molecule: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene PDBTitle: structure of the menaquinone biosynthesis protein mend from2 bacillus subtilis
59	c3bmwA_	Alignment	not modelled	5.6	17	PDB header: transferase Chain: A: PDB Molecule: cyclomaltodextrin glucanotransferase; PDBTitle: cyclodextrin glycosyl transferase from thermoanaerobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor
60	c1nvmB_	Alignment	not modelled	5.3	21	PDB header: lyase/oxidoreductase Chain: B: PDB Molecule: acetaldehyde dehydrogenase (acylating); PDBTitle: crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
61	d1n2fa_	Alignment	not modelled	5.2	11	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
62	c3czkA_	Alignment	not modelled	5.2	12	PDB header: hydrolase Chain: A: PDB Molecule: sucrose hydrolase; PDBTitle: crystal structure analysis of sucrose hydrolase(suh) e322q-sucrose2 complex