

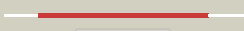






























Phyre2

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Description	RVBD0539 (-) _631746_632378
Date	Fri Jul 26 01:50:09 BST 2019
Unique Job ID	b29a23a9bb71311f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5mm1A_	 Alignment		99.9	21	PDB header: membrane protein Chain: A: PDB Molecule: dolichol monophosphate mannose synthase; PDBTitle: dolichyl phosphate mannose synthase in complex with gdp and dolichyl2 phosphate mannose
2	c2ffuA_	 Alignment		99.9	19	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 2; PDBTitle: crystal structure of human ppgalnact-2 complexed with udp and ea2
3	c5tz8C_	 Alignment		99.9	16	PDB header: transferase Chain: C: PDB Molecule: glycosyl transferase; PDBTitle: crystal structure of s. aureus tars
4	c6e4rB_	 Alignment		99.9	17	PDB header: transferase Chain: B: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 9; PDBTitle: crystal structure of the drosophila melanogaster polypeptide n-2 acetylgalactosaminyl transferase pgant9b
5	c3f1yC_	 Alignment		99.9	21	PDB header: transferase Chain: C: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus
6	c2d7iA_	 Alignment		99.9	17	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 10; PDBTitle: crystal structure of pp-galnac-t10 with udp, galnac and mn2+
7	c5nqaA_	 Alignment		99.9	17	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 4; PDBTitle: crystal structure of galnac-t4 in complex with the monoglycopeptide 3
8	c6iwqE_	 Alignment		99.9	20	PDB header: transferase Chain: E: PDB Molecule: n-acetylgalactosaminyltransferase 7; PDBTitle: crystal structure of galnac-t7 with mn2+
9	c6h4mA_	 Alignment		99.9	10	PDB header: transferase Chain: A: PDB Molecule: probable ss-1,3-n-acetylglucosaminyltransferase; PDBTitle: tarp-udp-glcnac-3rbop
10	d1xhba2	 Alignment		99.9	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
11	c1xhbA_	 Alignment		99.9	20	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 1; PDBTitle: the crystal structure of udp-galnac: polypeptide alpha-n-2 acetylgalactosaminyltransferase-t1

12	c2z86D	Alignment		99.9	14	PDB header: transferase Chain: D: PDB Molecule: chondroitin synthase; PDBTitle: crystal structure of chondroitin polymerase from escherichia coli2 strain k4 (k4cp) complexed with udp-glcua and udp
13	c5heaA	Alignment		99.9	14	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase (galt1); PDBTitle: cgt structure in hexamer
14	c3ckvA	Alignment		99.9	26	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a mycobacterial protein
15	c5ekeB	Alignment		99.9	21	PDB header: transferase Chain: B: PDB Molecule: uncharacterized glycosyltransferase sll0501; PDBTitle: structure of the polyisoprenyl-phosphate glycosyltransferase gtrb2 (f215a mutant)
16	c4hg6A	Alignment		99.9	18	PDB header: transferase Chain: A: PDB Molecule: cellulose synthase subunit a; PDBTitle: structure of a cellulose synthase - cellulose translocation2 intermediate
17	c3bcvA	Alignment		99.9	18	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase protein; PDBTitle: crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
18	c4fixA	Alignment		99.9	16	PDB header: transferase Chain: A: PDB Molecule: udp-galactofuranosyl transferase glft2; PDBTitle: crystal structure of glft2
19	d1qg8a	Alignment		99.8	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Spore coat polysaccharide biosynthesis protein SpsA
20	d1omza	Alignment		99.8	9	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Exostosin
21	c1omxB	Alignment	not modelled	99.8	10	PDB header: transferase Chain: B: PDB Molecule: alpha-1,4-n-acetylhexosaminyltransferase extl2; PDBTitle: crystal structure of mouse alpha-1,4-n-acetylhexosaminyltransferase2 (extl2)
22	c2qgiA	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: atp synthase subunits region orf 6; PDBTitle: the udp complex structure of the sixth gene product of the f1-atpase2 operon of rhodobacter blasticus
23	c6p61D	Alignment	not modelled	99.7	17	PDB header: transferase Chain: D: PDB Molecule: glycosyltransferase; PDBTitle: structure of a glycosyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
24	c3zf8A	Alignment	not modelled	99.7	10	PDB header: transferase Chain: A: PDB Molecule: mannan polymerase complexes subunit mnn9; PDBTitle: crystal structure of saccharomyces cerevisiae mnn9 in2 complex with gdp and mn.
25	c5z8bB	Alignment	not modelled	99.7	10	PDB header: transferase Chain: B: PDB Molecule: kfia protein; PDBTitle: truncated n-acetylglucosaminyl transferase kfia from e. coli k5 strain2 apo form
26	d2bo4a1	Alignment	not modelled	99.4	20	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: MGS-like
27	c5ggfC	Alignment	not modelled	99.3	16	PDB header: transferase, sugar binding protein Chain: C: PDB Molecule: protein o-linked-mannose beta-1,2-n- PDBTitle: crystal structure of human protein o-mannose beta-1,2-n-2 acetylglucosaminyltransferase form ii PDB header: transferase Chain: B: PDB Molecule: beta-1,4-galactosyltransferase 7;

28	c4irqB_	Alignment	not modelled	98.6	15	PDBTitle: crystal structure of catalytic domain of human beta1,2 4galactosyltransferase 7 in closed conformation in complex with3 manganese and udp
29	d1fo8a_	Alignment	not modelled	97.5	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: N-acetylglucosaminyltransferase I
30	d1pzta_	Alignment	not modelled	97.5	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: beta 1,4 galactosyltransferase (b4GalT1)
31	c2wvmA_	Alignment	not modelled	95.7	21	PDB header: transferase Chain: A: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: h309a mutant of mannosyl-3-phosphoglycerate synthase from2 thermus thermophilus hb27 in complex with3 gdp-alpha-d-mannose and mg(ii)
32	c3lw6A_	Alignment	not modelled	95.4	18	PDB header: transferase Chain: A: PDB Molecule: beta-4-galactosyltransferase 7; PDBTitle: crystal structure of drosophila beta1,4-galactosyltransferase-7
33	c5vcmA_	Alignment	not modelled	91.6	17	PDB header: transferase Chain: A: PDB Molecule: alpha-1,6-mannosyl-glycoprotein 2-beta-n- PDBTitle: alpha-1,6-mannosyl-glycoprotein 2-beta-n-acetylglucosaminyltransferase2 with bound udp and manganese
34	c2zu8A_	Alignment	not modelled	90.5	17	PDB header: transferase Chain: A: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: crystal structure of mannosyl-3-phosphoglycerate synthase2 from pyrococcus horikoshii
35	c6fxyA_	Alignment	not modelled	75.8	12	PDB header: transferase Chain: A: PDB Molecule: procollagen-lysine,2-oxoglutarate 5-dioxygenase 3; PDBTitle: crystal structure of full-length human lysyl hydroxylase lh3 -2 cocrystal with fe2+, mn2+, udp-gal - structure from long-wavelength3 s-sad
36	c2d0jD_	Alignment	not modelled	75.0	15	PDB header: transferase Chain: D: PDB Molecule: galactosylgalactosylxyloylprotein 3-beta- PDBTitle: crystal structure of human gcat-s apo form
37	d1v82a_	Alignment	not modelled	70.9	20	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: 1,3-glucuronyltransferase
38	d3cu0a1	Alignment	not modelled	68.6	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: 1,3-glucuronyltransferase
39	c2gamA_	Alignment	not modelled	57.8	13	PDB header: transferase Chain: A: PDB Molecule: beta-1,6-n-acetylglucosaminyltransferase; PDBTitle: x-ray crystal structure of murine leukocyte-type core 2 b1,6-n-2 acetylglucosaminyltransferase (c2gnt-I) in complex with galb1,3galnac
40	d1vh3a_	Alignment	not modelled	57.2	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylytransferase
41	d1lk5a1	Alignment	not modelled	47.7	11	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain
42	d1uj4a1	Alignment	not modelled	41.4	10	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain
43	d2nqra3	Alignment	not modelled	28.8	13	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
44	d1zbsa2	Alignment	not modelled	24.5	44	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
45	c6cgaA_	Alignment	not modelled	17.2	16	PDB header: hydrolase Chain: A: PDB Molecule: effector protein lem4 (lpg1101); PDBTitle: structure of the had domain of effector protein lem4 (lpg1101) from2 legionella pneumophila
46	d2ftsa3	Alignment	not modelled	15.0	13	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
47	c3ssmB_	Alignment	not modelled	14.7	24	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: myce methyltransferase from the mycinamycin biosynthetic pathway in2 complex with mg and sah, crystal form 1
48	c5yh1A_	Alignment	not modelled	13.7	21	PDB header: ribosomal protein Chain: A: PDB Molecule: member of s1p family of ribosomal proteins; PDBTitle: member of s1p family of ribosomal proteins pf0399 dhh domain
49	d1ffki_	Alignment	not modelled	13.5	12	Fold: Ribosomal proteins S24e, L23 and L15e Superfamily: Ribosomal proteins S24e, L23 and L15e Family: L15e
50	c2wawA_	Alignment	not modelled	13.3	20	PDB header: unknown function Chain: A: PDB Molecule: moba relate protein; PDBTitle: crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1
51	d1m0sa1	Alignment	not modelled	13.1	13	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain
52	c6nonB_	Alignment	not modelled	12.8	15	PDB header: dna binding protein Chain: B: PDB Molecule: coobyric acid ac-diamide synthase; PDBTitle: structure of cyanthece apo mcda
53	d1jj2l_	Alignment	not modelled	12.7	6	Fold: Ribosomal proteins S24e, L23 and L15e Superfamily: Ribosomal proteins S24e, L23 and L15e Family: L15e

54	c4ehxA	Alignment	not modelled	12.3	11	PDB header: transferase Chain: A: PDB Molecule: tetraacyldisaccharide 4'-kinase; PDBTitle: crystal structure of lpkx from aquifex aeolicus at 1.9 angstrom2 resolution
55	d1vqom1	Alignment	not modelled	11.1	12	Fold: Ribosomal proteins S24e, L23 and L15e Superfamily: Ribosomal proteins S24e, L23 and L15e Family: L15e
56	c5vcsB	Alignment	not modelled	11.1	15	PDB header: transferase Chain: B: PDB Molecule: alpha-1,6-mannosyl-glycoprotein 2-beta-n-acetylglucosaminyltransferase2 with bound acceptor
57	c4a1cL	Alignment	not modelled	10.9	15	PDB header: ribosome Chain: L: PDB Molecule: ribosomal protein l15; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
58	c3iz5P	Alignment	not modelled	10.9	12	PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein l15 (l15e); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
59	c1uz5A	Alignment	not modelled	10.7	28	PDB header: molybdopterin biosynthesis Chain: A: PDB Molecule: 402aa long hypothetical molybdopterin PDBTitle: the crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikosii
60	c2fq1A	Alignment	not modelled	10.7	8	PDB header: hydrolase Chain: A: PDB Molecule: isochorismatase; PDBTitle: crystal structure of the two-domain non-ribosomal peptide synthetase2 entb containing isochorismate lyase and aryl-carrier protein domains
61	c3zf7Q	Alignment	not modelled	10.5	23	PDB header: ribosome Chain: Q: PDB Molecule: ribosomal protein l15; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
62	c3brcA	Alignment	not modelled	10.2	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein of unknown function; PDBTitle: crystal structure of a conserved protein of unknown function from2 methanobacterium thermoautotrophicum
63	c3j21M	Alignment	not modelled	9.9	12	PDB header: ribosome Chain: M: PDB Molecule: 50s ribosomal protein l15e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
64	c3ktsA	Alignment	not modelled	9.7	8	PDB header: transcriptional regulator Chain: A: PDB Molecule: glycerol uptake operon antiterminator regulatory protein; PDBTitle: crystal structure of glycerol uptake operon antiterminator regulatory2 protein from listeria monocytogenes str. 4b f2365
65	c3nyiA	Alignment	not modelled	9.6	10	PDB header: lipid binding protein Chain: A: PDB Molecule: fat acid-binding protein; PDBTitle: the crystal structure of a fat acid (stearic acid)-binding protein2 from eubacterium ventriosum atcc 27560.
66	d1zxaa1	Alignment	not modelled	9.5	50	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
67	c2g4rB	Alignment	not modelled	9.3	16	PDB header: biosynthetic protein Chain: B: PDB Molecule: molybdopterin biosynthesis mog protein; PDBTitle: anomalous substructure of moga
68	c3j39N	Alignment	not modelled	9.1	12	PDB header: ribosome Chain: N: PDB Molecule: 60s ribosomal protein l15; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
69	d1pzxa	Alignment	not modelled	8.9	10	Fold: DAK1/DegV-like Superfamily: DAK1/DegV-like Family: DegV-like
70	c3kf8C	Alignment	not modelled	8.6	25	PDB header: structural protein Chain: C: PDB Molecule: protein stn1; PDBTitle: crystal structure of c. tropicalis stn1-ten1 complex
71	c4ytgA	Alignment	not modelled	8.1	18	PDB header: hydrolase Chain: A: PDB Molecule: peptidylarginine deiminase; PDBTitle: crystal structure of porphyromonas gingivalis peptidylarginine2 deiminase (ppad) mutant c351a in complex with dipeptide met-arg.
72	c1s1iL	Alignment	not modelled	8.1	12	PDB header: ribosome Chain: L: PDB Molecule: 60s ribosomal protein l15-a; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.
73	c5i1aA	Alignment	not modelled	8.0	27	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein lpg2271 from legionella2 pneumophila
74	c2iqIA	Alignment	not modelled	7.7	25	PDB header: cell cycle Chain: A: PDB Molecule: dna damage response protein kinase dun1; PDBTitle: nmr structure of the yeast dun1 fha domain in complex with2 a doubly phosphorylated (pt) peptide derived from rad533 scd1
75	d1ta0a	Alignment	not modelled	7.6	9	Fold: HAD-like Superfamily: HAD-like Family: NLI interacting factor-like phosphatase
76	c2j0bA	Alignment	not modelled	7.6	13	PDB header: transferase Chain: A: PDB Molecule: beta-1,3-n-acetylglucosaminyltransferase manic fringe; PDBTitle: structure of the catalytic domain of mouse manic fringe in2 complex with udp and manganese
77	d1w55a1	Alignment	not modelled	7.4	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylytransferase

78	c2nqqA_	Alignment	not modelled	7.3	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin biosynthesis protein moea; PDBTitle: moea r137q
79	c3fdjA_	Alignment	not modelled	7.2	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: degv family protein; PDBTitle: the structure of a degv family protein from eubacterium eligens.
80	c4lhbC_	Alignment	not modelled	7.1	25	PDB header: transferase Chain: C: PDB Molecule: molybdopterin adenylyltransferase; PDBTitle: crystal structure of tungsten cofactor synthesizing protein moab from2 pyrococcus furiosus
81	c3agrB_	Alignment	not modelled	7.1	33	PDB header: hydrolase Chain: B: PDB Molecule: nucleoside triphosphate hydrolase; PDBTitle: crystal structure of nucleoside triphosphate hydrolases from neospora2 caninum
82	c4xpuA_	Alignment	not modelled	6.9	19	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease v; PDBTitle: the crystal structure of endov from e.coli
83	d1wd5a_	Alignment	not modelled	6.9	23	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
84	c4oxxA_	Alignment	not modelled	6.9	23	PDB header: electron transport Chain: A: PDB Molecule: cinodoxin; PDBTitle: crystal structure of cinodoxin, surface entropy reduction mutant
85	c3gnnA_	Alignment	not modelled	6.8	17	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide pyrophosphorylase from2 burkholderi pseudomallei
86	c5y4bA_	Alignment	not modelled	6.7	15	PDB header: electron transport Chain: A: PDB Molecule: bola-like protein 2; PDBTitle: solution structure of yeast fra2
87	d1uz5a3	Alignment	not modelled	6.7	26	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
88	c5d5pC_	Alignment	not modelled	6.7	26	PDB header: transferase Chain: C: PDB Molecule: hcgB; PDBTitle: hcgB from methanococcus maripaludis
89	d1qapa1	Alignment	not modelled	6.4	20	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
90	c2w36B_	Alignment	not modelled	6.4	11	PDB header: hydrolase Chain: B: PDB Molecule: endonuclease v; PDBTitle: structures of endonuclease v with dna reveal initiation of2 deaminated adenine repair
91	c5gvvF_	Alignment	not modelled	6.3	6	PDB header: transferase Chain: F: PDB Molecule: glycosyl transferase family 8; PDBTitle: crystal structure of the glycosyltransferase glye in streptococcus2 pneumoniae tigr4
92	d1x9aa_	Alignment	not modelled	6.1	8	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrH-like
93	c3igfB_	Alignment	not modelled	6.0	23	PDB header: atp binding protein Chain: B: PDB Molecule: all4481 protein; PDBTitle: crystal structure of the all4481 protein from nostoc sp. pcc 7120,2 northeast structural genomics consortium target nsr300
94	d2d1pc1	Alignment	not modelled	5.8	20	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrH-like
95	c5kxbB_	Alignment	not modelled	5.8	7	PDB header: signaling protein Chain: B: PDB Molecule: osmolarity two-component system protein ssk1; PDBTitle: co-crystal structure of the saccharomyces cerevisiae histidine2 phosphotransfer signaling protein ypd1 and the receiver domain of its3 downstream response regulator ssk1
96	c5xyiM_	Alignment	not modelled	5.8	15	PDB header: ribosome Chain: M: PDB Molecule: ribosomal protein l7ae, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
97	d1gq2a2	Alignment	not modelled	5.7	14	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Malic enzyme N-domain
98	c3j3aM_	Alignment	not modelled	5.7	7	PDB header: ribosome Chain: M: PDB Molecule: 40s ribosomal protein s12; PDBTitle: structure of the human 40s ribosomal proteins
99	c3ga2A_	Alignment	not modelled	5.7	11	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease v; PDBTitle: crystal structure of the endonuclease_v (bsu36170) from bacillus2 subtilis, northeast structural genomics consortium target sr624