

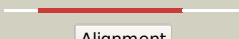

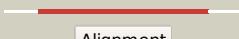











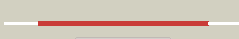













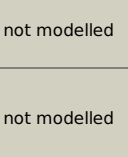


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1518_(-)_1709650_1710609
Date	Fri Aug 2 13:30:10 BST 2019
Unique Job ID	a7202160c5ba6141

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2z86D_	 Alignment		100.0	22	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
2	d1xhba2	 Alignment		100.0	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
3	c2ffuA_	 Alignment		100.0	15	PDB header: transferase Chain: A; PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 2; PDBTitle: crystal structure of human ppgalnact-2 complexed with udp and ea2
4	c5tz8C_	 Alignment		100.0	18	PDB header: transferase Chain: C; PDB Molecule: glycosyl transferase; PDBTitle: crystal structure of s. aureus tars
5	c1xhba_	 Alignment		100.0	17	PDB header: transferase Chain: A; PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 1; PDBTitle: the crystal structure of udp-galnac: polypeptide alpha-n-2 acetylgalactosaminyltransferase-t1
6	c6e4rB_	 Alignment		100.0	13	PDB header: transferase Chain: B; PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 9; PDBTitle: crystal structure of the drosophila melanogaster polypeptide n-2 acetylgalactosaminyl transferase pgant9b
7	c6h4mA_	 Alignment		100.0	16	PDB header: transferase Chain: A; PDB Molecule: probable ss-1,3-n-acetylglucosaminyltransferase; PDBTitle: tarp-udp-glcnac-3rbop
8	c2d7iA_	 Alignment		100.0	20	PDB header: transferase Chain: A; PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 10; PDBTitle: crystal structure of pp-galnac-t10 with udp, galnac and mn2+
9	c6iwaE_	 Alignment		100.0	14	PDB header: transferase Chain: E; PDB Molecule: n-acetylgalactosaminyltransferase 7; PDBTitle: crystal structure of galnac-t7 with mn2+
10	c5nqaA_	 Alignment		100.0	16	PDB header: transferase Chain: A; PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 4; PDBTitle: crystal structure of galnac-t4 in complex with the monoglycopeptide 3
11	c5heaA_	 Alignment		100.0	18	PDB header: transferase Chain: A; PDB Molecule: putative glycosyltransferase (galt1); PDBTitle: cgt structure in hexamer

12	c4fixA_	Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: udp-galactofuranosyl transferase glft2; PDBTitle: crystal structure of glft2
13	d1qg8a_	Alignment		100.0	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Spore coat polysaccharide biosynthesis protein SpsA
14	c5mm1A_	Alignment		100.0	17	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
15	c4hg6A_	Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: cellulose synthase subunit a; PDBTitle: structure of a cellulose synthase - cellulose translocation2 intermediate
16	c3bcvA_	Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase protein; PDBTitle: crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
17	c6p61D_	Alignment		100.0	22	PDB header: transferase Chain: D: PDB Molecule: glycosyltransferase; PDBTitle: structure of a glycosyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
18	c3flvC_	Alignment		100.0	18	PDB header: transferase Chain: C: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus
19	c1omxB_	Alignment		100.0	13	PDB header: transferase Chain: B: PDB Molecule: alpha-1,4-n-acetylhexosaminyltransferase extl2; PDBTitle: crystal structure of mouse alpha-1,4-n-acetylhexosaminyltransferase2 (extl2)
20	d1omza_	Alignment		100.0	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Exostosin
21	c3ckvA_	Alignment	not modelled	100.0	20	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a mycobacterial protein
22	c5ekeB_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: B: PDB Molecule: uncharacterized glycosyltransferase sll0501; PDBTitle: structure of the polyisoprenyl-phosphate glycosyltransferase gtrb2 (f215a mutant)
23	c3zf8A_	Alignment	not modelled	99.9	12	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.
24	c5z8bB_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: B: PDB Molecule: kfia protein; PDBTitle: truncated n-acetylglucosaminyl transferase kfia from e. coli k5 strain2 apo form
25	c2qgiA_	Alignment	not modelled	99.9	12	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
26	c5ggfC_	Alignment	not modelled	99.8	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
27	c4irqB_	Alignment	not modelled	99.3	17	PDB header: transferase Chain: B: PDB Molecule: beta-1,4-galactosyltransferase 7; PDBTitle: crystal structure of catalytic domain of human beta1,2 4galactosyltransferase 7 in closed conformation in complex with3 manganese and udp
						Fold: Nucleotide-diphospho-sugar transferases

28	d2bo4a1	Alignment	not modelled	99.0	13	Superfamily: Nucleotide-diphospho-sugar transferases Family: MGS-like
29	d1fo8a	Alignment	not modelled	98.9	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: N-acetylglucosaminyltransferase I
30	d1pzta	Alignment	not modelled	98.7	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: beta 1,4 galactosyltransferase (b4GalT1)
31	c6fxyA	Alignment	not modelled	98.5	11	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
32	c5vcmA	Alignment	not modelled	98.3	14	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
33	c3lw6A	Alignment	not modelled	98.0	16	PDB header: transferase Chain: A: PDB Molecule: beta-4-galactosyltransferase 7; PDBTitle: crystal structure of drosophila beta1,4-galactosyltransferase-7
34	c2d0jD	Alignment	not modelled	96.9	24	PDB header: transferase Chain: D: PDB Molecule: galactosylgalactosylxylosylprotein 3-beta- PDBTitle: crystal structure of human gcat-s apo form
35	d1v82a	Alignment	not modelled	96.6	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: 1,3-glucuronyltransferase
36	c2wvmA	Alignment	not modelled	95.8	19	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)
37	d3cu0a1	Alignment	not modelled	95.6	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: 1,3-glucuronyltransferase
38	d1vh1a	Alignment	not modelled	94.8	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
39	c4kt7A	Alignment	not modelled	94.5	12	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; PDBTitle: the crystal structure of 4-diphosphocytidyl-2c-methyl-d-2 erythritolsynthase from anaerococcus prevotii dsm 20548
40	c2zu8A	Alignment	not modelled	94.1	16	PDB header: transferase Chain: A: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: crystal structure of mannosyl-3-phosphoglycerate synthase2 from pyrococcus horikoshii
41	d1iina	Alignment	not modelled	94.0	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidylyltransferase
42	c4ys8B	Alignment	not modelled	93.4	17	PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; PDBTitle: crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidylyltransferase (ispd) from burkholderia thailandensis
43	d1h5ra	Alignment	not modelled	93.3	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidylyltransferase
44	c5vcsB	Alignment	not modelled	93.0	18	PDB header: transferase Chain: B: PDB Molecule: alpha-1,6-mannosyl-glycoprotein 2-beta-n- PDBTitle: alpha-1,6-mannosyl-glycoprotein 2-beta-n- acetylglucosaminyltransferase2 with bound acceptor
45	c2wawA	Alignment	not modelled	92.6	7	PDB header: unknown function Chain: A: PDB Molecule: moba relate protein; PDBTitle: crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1
46	c5ddtA	Alignment	not modelled	92.0	10	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; PDBTitle: crystal structure of ispd from bacillus subtilis at 1.80 angstroms2 resolution, crystal form i
47	c2px7A	Alignment	not modelled	91.8	15	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; PDBTitle: crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidylyltransferase from thermus thermophilus hb8
48	d1lwva	Alignment	not modelled	91.7	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidylyltransferase
49	d1vh3a	Alignment	not modelled	91.5	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
50	d1fxoa	Alignment	not modelled	90.6	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidylyltransferase
51	c5xhwA	Alignment	not modelled	88.6	13	PDB header: transferase Chain: A: PDB Molecule: putative 6-deoxy-d-mannoheptose pathway protein; PDBTitle: crystal structure of hddc from yersinia pseudotuberculosis
52	d1vica	Alignment	not modelled	88.2	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase PDB header: transferase

53	c4jisB_	Alignment	not modelled	87.9	13	Chain: B: PDB Molecule: ribitol-5-phosphate cytidyltransferase; PDBTitle: crystal structure of ribitol 5-phosphate cytidyltransferase (tari)2 from bacillus subtilis
54	d1w77a1	Alignment	not modelled	87.4	9	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
55	c3f1cB_	Alignment	not modelled	86.3	6	PDB header: transferase Chain: B: PDB Molecule: putative 2-c-methyl-d-erythritol 4-phosphate PDBTitle: crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase from listeria monocytogenes
56	c3polA_	Alignment	not modelled	85.6	15	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: 2.3 angstrom crystal structure of 3-deoxy-manno-octulosonate2 cytidyltransferase (kdsb) from acinetobacter baumannii.
57	c6b5kA_	Alignment	not modelled	84.0	17	PDB header: transferase Chain: A: PDB Molecule: glucose-1-phosphate thymidyltransferase; PDBTitle: mycobacterium tuberculosis rmla in complex with mg/dttp
58	c2xmhB_	Alignment	not modelled	83.3	17	PDB header: transferase Chain: B: PDB Molecule: ctp-inositol-1-phosphate cytidyltransferase; PDBTitle: the x-ray structure of ctp:inositol-1-phosphate cytidyltransferase2 from archaeoglobus fulgidus
59	c3okrC_	Alignment	not modelled	83.2	15	PDB header: transferase Chain: C: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
60	c2xwIB_	Alignment	not modelled	83.1	6	PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: crystal structure of ispd from mycobacterium smegmatis in complex with2 ctp and mg
61	c5gvvF_	Alignment	not modelled	83.1	9	PDB header: transferase Chain: F: PDB Molecule: glycosyl transferase family 8; PDBTitle: crystal structure of the glycosyltransferase glye in streptococcus2 pneumoniae tigr4
62	c6cglA_	Alignment	not modelled	82.3	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
63	c4mybA_	Alignment	not modelled	82.2	8	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: crystal structure of francisella tularensis 2-c-methyl-d-erythritol 4-2 phosphate cytidyltransferase (ispd)
64	d1mc3a_	Alignment	not modelled	80.6	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
65	c3tztB_	Alignment	not modelled	77.8	14	PDB header: transferase Chain: B: PDB Molecule: glycosyl transferase family 8; PDBTitle: the structure of a protein in glycosyl transferase family 8 from2 anaerococcus prevotii.
66	c4jd0A_	Alignment	not modelled	77.5	16	PDB header: transferase Chain: A: PDB Molecule: nucleotidyl transferase; PDBTitle: structure of the inositol-1-phosphate ctp transferase from t.2 maritima.
67	c4xwiA_	Alignment	not modelled	76.5	10	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: x-ray crystal structure of cmp-kdo synthase from pseudomonas2 aeruginosa
68	d2oi6a2	Alignment	not modelled	73.9	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
69	c3okrA_	Alignment	not modelled	72.4	13	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
70	d1i52a_	Alignment	not modelled	71.1	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
71	d1w55a1	Alignment	not modelled	70.9	8	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
72	c2pa4B_	Alignment	not modelled	69.7	10	PDB header: transferase Chain: B: PDB Molecule: utp-glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of udp-glucose pyrophosphorylase from corynebacteria2 glutamicum in complex with magnesium and udp-glucose
73	c6oewB_	Alignment	not modelled	69.5	13	PDB header: transferase Chain: B: PDB Molecule: cytidyltransferase; PDBTitle: structure of a cytidyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
74	d1vgwa_	Alignment	not modelled	68.8	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
75	c3tqdA_	Alignment	not modelled	67.6	19	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: structure of the 3-deoxy-d-manno-octulosonate cytidyltransferase2 (kdsb) from coxiella burnetii PDB header: transferase

76	c2e3dB_	Alignment	not modelled	67.5	16	Chain: B: PDB Molecule: utp--glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of e. coli glucose-1-phosphate2 uridylyltransferase
77	c6aokA_	Alignment	not modelled	66.4	24	PDB header: hydrolase Chain: A: PDB Molecule: ceg4; PDBTitle: crystal structure of legionella pneumophila effector ceg4 with n-2 terminal tev protease cleavage sequence
78	d1qwja_	Alignment	not modelled	65.7	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
79	c3d8vA_	Alignment	not modelled	63.6	16	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of glmu from mycobacterium tuberculosis2 in complex with uridine-diphosphate-n-acetylglucosamine
80	c3foqA_	Alignment	not modelled	61.6	16	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of n-acetylglucosamine-1-phosphate2 uridylyltransferase (glmu) from mycobacterium tuberculosis in3 a cubic space group.
81	c2we9A_	Alignment	not modelled	60.4	9	PDB header: unknown function Chain: A: PDB Molecule: moba-related protein; PDBTitle: crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv
82	c3d5nB_	Alignment	not modelled	59.4	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: q97w15_sulso; PDBTitle: crystal structure of the q97w15_sulso protein from sulfobolus2 solfataricus. nesg target ssr125.
83	c3hl3A_	Alignment	not modelled	59.0	11	PDB header: transferase Chain: A: PDB Molecule: glucose-1-phosphate thymidylyltransferase; PDBTitle: 2.76 angstrom crystal structure of a putative glucose-1-phosphate2 thymidylyltransferase from bacillus anthracis in complex with a3 sucrose.
84	c4mndA_	Alignment	not modelled	57.3	16	PDB header: transferase Chain: A: PDB Molecule: ctp l-myo-inositol-1-phosphate cytidylyltransferase/cdp-l- PDBTitle: crystal structure of archaeoglobus fulgidus ipct-dipps bifunctional2 membrane protein
85	c3oamD_	Alignment	not modelled	50.2	16	PDB header: transferase Chain: D: PDB Molecule: 3-deoxy-manno-octulosonate cytidylyltransferase; PDBTitle: crystal structure of cytidylyltransferase from vibrio cholerae
86	c5l6sF_	Alignment	not modelled	49.7	9	PDB header: transferase Chain: F: PDB Molecule: glucose-1-phosphate adenylyltransferase; PDBTitle: crystal structure of e. coli adp-glucose pyrophosphorylase (agpase) in2 complex with a positive allosteric regulator beta-fructose-1,6-3 diphosphate (fbp) - agpase*fbp
87	c1w57A_	Alignment	not modelled	46.3	7	PDB header: transferase Chain: A: PDB Molecule: ispd/ispf bifunctional enzyme; PDBTitle: structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
88	c2ux8G_	Alignment	not modelled	46.1	14	PDB header: transferase Chain: G: PDB Molecule: glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of sphingomonas elodea atcc 31461 glucose-2 1-phosphate uridylyltransferase in complex with glucose-3 1-phosphate.
89	c2j0bA_	Alignment	not modelled	43.8	24	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
90	d1vkpa_	Alignment	not modelled	43.3	8	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
91	d1h7ea_	Alignment	not modelled	42.6	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
92	d1vpaa_	Alignment	not modelled	42.5	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
93	c1jyIC_	Alignment	not modelled	42.1	13	PDB header: transferase Chain: C: PDB Molecule: ctp:phosphocholine cytidylyltransferase; PDBTitle: catalytic mechanism of ctp:phosphocholine2 cytidylyltransferase from streptococcus pneumoniae (licc)
94	c3ngwA_	Alignment	not modelled	41.6	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis protein a PDBTitle: crystal structure of molybdopterin-guanine dinucleotide biosynthesis2 protein a from archaeoglobus fulgidus, northeast structural genomics3 consortium target gr189
95	c2e8bA_	Alignment	not modelled	40.7	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: probable molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of the putative protein (aq1419) from aquifex2 aeolicus vf5
96	c4rxuA_	Alignment	not modelled	40.1	11	PDB header: transport protein Chain: A: PDB Molecule: periplasmic sugar-binding protein; PDBTitle: crystal structure of carbohydrate transporter solute binding protein2 caur_1924 from chloroflexus aurantiacus, target efi-511158, in3 complex with d-glucose
97	c5dteD_	Alignment	not modelled	39.7	11	PDB header: transport protein Chain: D: PDB Molecule: monosaccharide-transporting atpase; PDBTitle: crystal structure of an abc transporter periplasmic solute binding2 protein (ipr025997) from actinobacillus succinogenes 130z(asuc_0081,3 target efi-511065) with bound d-allose
98	c1zcvA_	Alignment	not modelled	38.6	9	PDB header: transferase Chain: A: PDB Molecule: glycogenin-1;

98	c1zcyA	Alignment	not modelled	38.8	9	PDBTitle: apo form of a mutant of glycogenin in which asp159 is replaced by ser
99	d2jera1	Alignment	not modelled	36.9	22	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
100	d1yp2a2	Alignment	not modelled	35.3	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
101	c2f59B	Alignment	not modelled	35.1	14	PDB header: transferase Chain: B: PDB Molecule: 6,7-dimethyl-8-ribityllumazine synthase 1; PDBTitle: lumazine synthase ribh1 from brucella abortus (gene bruab1_0785,2 swiss-prot entry q57dy1) complexed with inhibitor 5-nitro-6-(d-3 ribitylamino)-2,4(1h,3h) pyrimidinedione
102	c3rsbB	Alignment	not modelled	34.9	8	PDB header: transferase Chain: B: PDB Molecule: adenosylcobinamide-phosphate guanylyltransferase; PDBTitle: structure of the archaeal gtp:adocbi-p guanylyltransferase (coby) from2 methanocaldococcus jannaschii
103	c2jerG	Alignment	not modelled	34.9	22	PDB header: hydrolase Chain: G: PDB Molecule: agmatine deiminase; PDBTitle: agmatine deiminase of enterococcus faecalis catalyzing its2 reaction.
104	c2vshB	Alignment	not modelled	34.8	10	PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate PDBTitle: synthesis of cdp-activated ribitol for teichoic acid2 precursors in streptococcus pneumoniae
105	c4ytgA	Alignment	not modelled	32.4	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.
106	c5d5pC	Alignment	not modelled	32.3	13	PDB header: transferase Chain: C: PDB Molecule: hcg; PDBTitle: hcgb from methanococcus maripaludis
107	c2qh5B	Alignment	not modelled	32.1	9	PDB header: isomerase Chain: B: PDB Molecule: mannose-6-phosphate isomerase; PDBTitle: crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori
108	c1rp1A	Alignment	not modelled	31.4	20	PDB header: hydrolase Chain: A: PDB Molecule: pancreatic lipase related protein 1; PDBTitle: dog pancreatic lipase related protein 1
109	c3brcA	Alignment	not modelled	31.0	16	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
110	c6bwhB	Alignment	not modelled	30.7	18	PDB header: transferase Chain: B: PDB Molecule: 2-phospho-l-lactate guanylyltransferase; PDBTitle: crystal structure of mycobacterium tuberculosis rv2983 in complex2 with pep
111	c3bzbA	Alignment	not modelled	30.1	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein cmq451c from the2 primitive red alga cyanidioschyzon merolae
112	d1xkna	Alignment	not modelled	29.9	28	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
113	d1ga8a	Alignment	not modelled	29.7	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Galactosyltransferase LgtC
114	c1ga8A	Alignment	not modelled	29.7	19	PDB header: transferase Chain: A: PDB Molecule: galactosyl transferase lgtc; PDBTitle: crystal structure of galactosyltransferase lgtc in complex2 with donor and acceptor sugar analogs.
115	d1ejba	Alignment	not modelled	28.3	14	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
116	c3jukA	Alignment	not modelled	28.2	13	PDB header: transferase Chain: A: PDB Molecule: udp-glucose pyrophosphorylase (galu); PDBTitle: the crystal structure of udp-glucose pyrophosphorylase complexed with2 udp-glucose
117	d2ewoa1	Alignment	not modelled	28.1	13	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
118	c5i1fA	Alignment	not modelled	27.5	15	PDB header: transferase Chain: A: PDB Molecule: utp--glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of utp-glucose-1-phosphate uridylyltransferase from2 burkholderia vietnamiensis in complex with uridine-5'-diphosphate-3 glucose
119	d1zbra1	Alignment	not modelled	25.8	19	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
120	d1e5ka	Alignment	not modelled	25.5	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Molybdenum cofactor biosynthesis protein MobA