

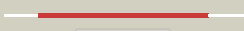
















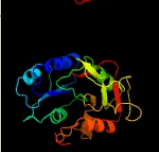

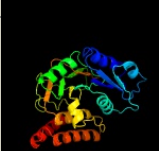











Phyre2

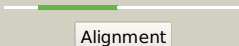
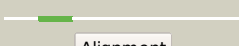
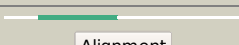
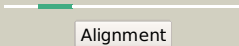
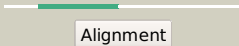
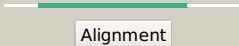
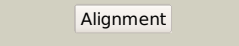
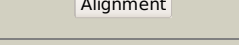
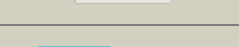
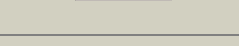
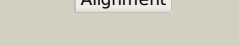
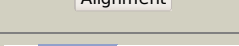

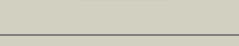



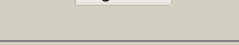
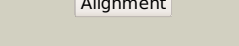


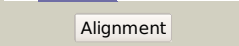
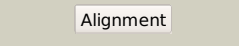

Email mdejesus@rockefeller.edu
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 Date Thu Aug 8 16:20:47 BST 2019
 Unique Job ID 01e69083480203e5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ffuA_	 Alignment		100.0	12	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 2; PDBTitle: crystal structure of human ppgalnact-2 complexed with udp and ea2
2	c1xhbA_	 Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 1; PDBTitle: the crystal structure of udp-galnac: polypeptide alpha-n-2 acetylgalactosaminyltransferase-t1
3	c6e4rB_	 Alignment		100.0	15	PDB header: transferase Chain: B: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 9; PDBTitle: crystal structure of the drosophila melanogaster polypeptide n-2 acetylgalactosaminyl transferase pgant9b
4	d1xhba2	 Alignment		100.0	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
5	c5nqaA_	 Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 4; PDBTitle: crystal structure of galnac-t4 in complex with the monoglycopeptide 3
6	c2d7iA_	 Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 10; PDBTitle: crystal structure of pp-galnac-t10 with udp, galnac and mn2+
7	c6iwqE_	 Alignment		100.0	13	PDB header: transferase Chain: E: PDB Molecule: n-acetylgalactosaminyltransferase 7; PDBTitle: crystal structure of galnac-t7 with mn2+
8	c2z86D_	 Alignment		100.0	16	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
9	c4fixA_	 Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: udp-galactofuranosyl transferase glft2; PDBTitle: crystal structure of glft2
10	c5tz8C_	 Alignment		100.0	13	PDB header: transferase Chain: C: PDB Molecule: glycosyl transferase; PDBTitle: crystal structure of s. aureus tars
11	c6h4mA_	 Alignment		100.0	10	PDB header: transferase Chain: A: PDB Molecule: probable ss-1,3-n-acetylglucosaminyltransferase; PDBTitle: tarp-udp-glnac-3rbop

12	c5mm1A_	Alignment		100.0	16	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
13	c4hg6A_	Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: cellulose synthase subunit a; PDBTitle: structure of a cellulose synthase - cellulose translocation2 intermediate
14	c5heaA_	Alignment		100.0	11	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase (galt1); PDBTitle: cgt structure in hexamer
15	d1qg8a_	Alignment		100.0	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Spore coat polysaccharide biosynthesis protein SpsA
16	d1omza_	Alignment		99.9	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Exostosin
17	c3flyC_	Alignment		99.9	14	PDB header: transferase Chain: C: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus
18	c1omxB_	Alignment		99.9	8	PDB header: transferase Chain: B: PDB Molecule: alpha-1,4-n-acetylhexosaminyltransferase extl2; PDBTitle: crystal structure of mouse alpha-1,4-n-acetylhexosaminyltransferase2 (extl2)
19	c3zf8A_	Alignment		99.9	13	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.
20	c3bcvA_	Alignment		99.9	14	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase protein; PDBTitle: crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
21	c3ckvA_	Alignment	not modelled	99.9	18	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	14	PDB header: transferase Chain: B: PDB Molecule: uncharacterized glycosyltransferase sli0501; PDBTitle: structure of the polyisoprenyl-phosphate glycosyltransferase gtrb2 (f215a mutant)
23	c6p61D_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: D: PDB Molecule: glycosyltransferase; PDBTitle: structure of a glycosyltransferase from leptospira borgpetersenii2 serovar hardjo-bovis (strain jb197)
24	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
25	c5z8bB_	Alignment	not modelled	99.9	11	PDB header: transferase Chain: B: PDB Molecule: kfia protein; PDBTitle: truncated n-acetylglucosaminyl transferase kfia from e. coli k5 strain2 apo form
26	c5ggfC_	Alignment	not modelled	99.7	13	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	99.1	16	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
28	d2bo4a1	Alignment	not modelled	98.9	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: MGS-like

29	d1fo8a_	Alignment	not modelled	98.8	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: N-acetylglucosaminyltransferase I
30	c5vcmA_	Alignment	not modelled	98.5	15	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
31	d1pzta_	Alignment	not modelled	98.3	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: beta 1,4 galactosyltransferase (b4GalT1)
32	c6fxyA_	Alignment	not modelled	97.5	15	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
33	c3lw6A_	Alignment	not modelled	97.4	20	PDB header: transferase Chain: A: PDB Molecule: beta-4-galactosyltransferase 7; PDBTitle: crystal structure of drosophila beta1,4-galactosyltransferase-7
34	d1v82a_	Alignment	not modelled	94.9	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: 1,3-glucuronyltransferase
35	d1vh3a_	Alignment	not modelled	94.6	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
36	c2wvmA_	Alignment	not modelled	94.2	15	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	93.4	20	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: 1,3-glucuronyltransferase
38	c2d0jD_	Alignment	not modelled	92.9	12	PDB header: transferase Chain: D: PDB Molecule: galactosylgalactosylxylosylprotein 3-beta- PDBTitle: crystal structure of human gcat-s apo form
39	c4xwiA_	Alignment	not modelled	88.9	13	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: x-ray crystal structure of cmp-kdo synthase from pseudomonas2 aeruginosa
40	c5gvvF_	Alignment	not modelled	86.5	14	PDB header: transferase Chain: F: PDB Molecule: glycosyl transferase family 8; PDBTitle: crystal structure of the glycosyltransferase glye in streptococcus2 pneumoniae tigr4
41	c2zu8A_	Alignment	not modelled	85.7	11	PDB header: transferase Chain: A: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: crystal structure of mannosyl-3-phosphoglycerate synthase2 from pyrococcus horikoshii
42	c4uegB_	Alignment	not modelled	81.2	11	PDB header: transferase Chain: B: PDB Molecule: glycogenin-2; PDBTitle: crystal structure of human glycogenin-2 catalytic domain
43	c5vcsB_	Alignment	not modelled	80.9	14	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
44	c4kt7A_	Alignment	not modelled	70.3	13	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: the crystal structure of 4-diphosphocytidyl-2c-methyl-d-2 erythritolsynthase from anaerococcus prevotii dsm 20548
45	c2vshB_	Alignment	not modelled	68.9	12	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
46	c2wawA_	Alignment	not modelled	66.6	9	PDB header: unknown function Chain: A: PDB Molecule: moba relate protein; PDBTitle: crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1
47	d1ga8a_	Alignment	not modelled	64.8	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Galactosyltransferase LgtC
48	c1ga8A_	Alignment	not modelled	64.8	15	PDB header: transferase Chain: A: PDB Molecule: galactosyl transferase lgtc; PDBTitle: crystal structure of galactosyltransferase lgtc in complex2 with donor and acceptor sugar analogs.
49	c1zctB_	Alignment	not modelled	61.7	9	PDB header: transferase Chain: B: PDB Molecule: glycogenin-1; PDBTitle: structure of glycogenin truncated at residue 270 in a complex with udp
50	c6aokA_	Alignment	not modelled	58.5	27	PDB header: hydrolase Chain: A: PDB Molecule: ceg4; PDBTitle: crystal structure of legionella pneumophila effector ceg4 with n-2 terminal tev protease cleavage sequence
51	d1ll2a_	Alignment	not modelled	58.2	9	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Glycogenin
52	c1zcyA_	Alignment	not modelled	57.4	8	PDB header: transferase Chain: A: PDB Molecule: glycogenin-1; PDBTitle: apo form of a mutant of glycogenin in which asp159 is replaced by ser
53	c6b5kA_	Alignment	not modelled	55.6	13	PDB header: transferase Chain: A: PDB Molecule: glucose-1-phosphate thymidyltransferase; PDBTitle: mycobacterium tuberculosis rmla in complex with mg/dttp

54	c3f1cB	 Alignment	not modelled	51.8	11	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
55	c4ytgA	 Alignment	not modelled	50.1	14	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.
56	d1w77a1	 Alignment	not modelled	49.6	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
57	c6cglA	 Alignment	not modelled	48.0	9	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
58	c4ys8B	 Alignment	not modelled	47.5	17	PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd) from burkholderia thailandensis
59	d1vica	 Alignment	not modelled	46.7	9	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
60	d1fxoa	 Alignment	not modelled	45.0	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
61	d1vgwa	 Alignment	not modelled	35.3	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
62	c5d5pC	 Alignment	not modelled	33.0	21	PDB header: transferase Chain: C: PDB Molecule: hcgB; PDBTitle: hcgB from methanococcus maripaludis
63	c2xmhB	 Alignment	not modelled	30.7	13	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
64	c5ddtA	 Alignment	not modelled	30.6	12	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: crystal structure of ispd from bacillus subtilis at 1.80 angstroms2 resolution, crystal form i
65	d1lwva	 Alignment	not modelled	29.8	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
66	c4jd0A	 Alignment	not modelled	29.2	9	PDB header: transferase Chain: A: PDB Molecule: nucleotidyl transferase; PDBTitle: structure of the inositol-1-phosphate ctp transferase from t.2 maritima.
67	c2gamA	 Alignment	not modelled	28.8	11	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
68	c3brcA	 Alignment	not modelled	26.7	19	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
69	c3tztB	 Alignment	not modelled	26.0	11	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.
70	c5yh1A	 Alignment	not modelled	23.0	18	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
71	c3okrC	 Alignment	not modelled	22.8	13	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)
72	c6i3mF	 Alignment	not modelled	22.3	17	PDB header: translation Chain: F: PDB Molecule: translation initiation factor eif-2b subunit beta; PDBTitle: eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
73	c3polA	 Alignment	not modelled	21.6	10	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.
74	c1w57A	 Alignment	not modelled	21.5	14	PDB header: transferase Chain: A: PDB Molecule: ispd/ispf bifunctional enzyme; PDBTitle: structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
75	c4jisB	 Alignment	not modelled	19.6	10	PDB header: transferase Chain: B: PDB Molecule: ribitol-5-phosphate cytidyltransferase; PDBTitle: crystal structure of ribitol 5-phosphate cytidyltransferase (tari)2 from bacillus subtilis
76	c5n6nC	 Alignment	not modelled	18.5	23	PDB header: signaling protein Chain: C: PDB Molecule: neutral trehalase; PDBTitle: crystal structure of the 14-3-3:neutral trehalase nth1 complex
		 Alignment				PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate

77	c3okrA_	Alignment	not modelled	17.8	15	cytidyltransferase; PDBTitle: structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
78	c6qg0G_	Alignment	not modelled	17.7	18	PDB header: translation Chain: G: PDB Molecule: translation initiation factor eif-2b subunit delta; PDBTitle: structure of eif2b-eif2 (phosphorylated at ser51) complex (model 1)
79	c4mndA_	Alignment	not modelled	16.6	10	PDB header: transferase Chain: A: PDB Molecule: ctp l-myo-inositol-1-phosphate cytidyltransferase/cdp-l PDBTitle: crystal structure of archaeoglobus fulgidus ipct-dipps bifunctional2 membrane protein
80	d1rm4a1	Alignment	not modelled	16.5	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
81	d2pkqo1	Alignment	not modelled	16.0	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
82	d1h5ra_	Alignment	not modelled	15.8	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
83	c2px7A_	Alignment	not modelled	15.7	22	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase from thermus thermophilus hb8
84	d1uasa2	Alignment	not modelled	15.7	7	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
85	c3d5nB_	Alignment	not modelled	15.4	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: q97w15_sulso; PDBTitle: crystal structure of the q97w15_sulso protein from sulfobolus solfataricus. nesg target ssr125.
86	c6i3mD_	Alignment	not modelled	15.3	18	PDB header: translation Chain: D: PDB Molecule: translation initiation factor eif-2b subunit delta; PDBTitle: eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
87	c6ifdD_	Alignment	not modelled	15.3	8	PDB header: sugar binding protein Chain: D: PDB Molecule: cmp-n-acetylneuraminate synthetase; PDBTitle: crystal structure of cmp-n-acetylneuraminate synthetase from vibrio2 cholerae in complex with cdp and mg2+.
88	d1szna2	Alignment	not modelled	15.2	4	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
89	c1t0oA_	Alignment	not modelled	14.6	4	PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase; PDBTitle: the structure of alpha-galactosidase from trichoderma reesei complexed2 with beta-d-galactose
90	c2we9A_	Alignment	not modelled	14.5	15	PDB header: unknown function Chain: A: PDB Molecule: moba-related protein; PDBTitle: crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv
91	d1iina_	Alignment	not modelled	14.3	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
92	c3a5vA_	Alignment	not modelled	14.3	4	PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase; PDBTitle: crystal structure of alpha-galactosidase i from mortierella vinacea
93	c2l82A_	Alignment	not modelled	14.3	28	PDB header: de novo protein Chain: A: PDB Molecule: designed protein or32; PDBTitle: solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or32
94	d1j4aa2	Alignment	not modelled	14.0	22	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
95	c6i7tB_	Alignment	not modelled	13.5	5	PDB header: translation Chain: B: PDB Molecule: translation initiation factor eif-2b subunit alpha; PDBTitle: eif2b:eif2 complex
96	c3ecsD_	Alignment	not modelled	13.2	16	PDB header: translation Chain: D: PDB Molecule: translation initiation factor eif-2b subunit alpha; PDBTitle: crystal structure of human eif2b alpha
97	c4ehxA_	Alignment	not modelled	12.5	25	PDB header: transferase Chain: A: PDB Molecule: tetraacyldisaccharide 4'-kinase; PDBTitle: crystal structure of lpxk from aquifex aeolicus at 1.9 angstrom2 resolution
98	d1yp2a2	Alignment	not modelled	12.1	3	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
99	c1uasa_	Alignment	not modelled	11.8	7	PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase; PDBTitle: crystal structure of rice alpha-galactosidase