







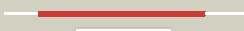






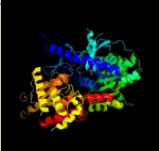



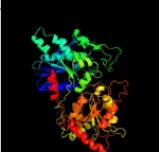




Phyre2

Email	mdejesus@rockefeller.edu
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Date	Wed Jul 31 22:05:42 BST 2019
Unique Job ID	6184a714b242517f


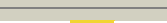
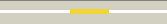



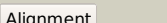
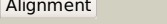








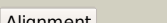
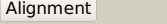
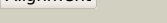






Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ygpa_	 Alignment		100.0	22	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Oligosaccharide phosphorylase
2	d2atia1	 Alignment		100.0	26	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Oligosaccharide phosphorylase
3	d1l5wa_	 Alignment		100.0	24	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Oligosaccharide phosphorylase
4	c5lrbB_	 Alignment		100.0	23	PDB header: transferase Chain: B: PDB Molecule: alpha-1,4 glucan phosphorylase; PDBTitle: plastidial phosphorylase from barley in complex with acarbose
5	c3ddsB_	 Alignment		100.0	25	PDB header: transferase Chain: B: PDB Molecule: glycogen phosphorylase, liver form; PDBTitle: crystal structure of glycogen phosphorylase complexed with an2 anthranilimide based inhibitor gsk261
6	c2c4mA_	 Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: glycogen phosphorylase; PDBTitle: starch phosphorylase: structural studies explain oxanion-dependent2 kinetic stability and regulatory control.
7	c4l22A_	 Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: phosphorylase; PDBTitle: crystal structure of putative glycogen phosphorylase from2 streptococcus mutans
8	d2gj4a1	 Alignment		100.0	24	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Oligosaccharide phosphorylase
9	c4bqeA_	 Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: alpha-glucan phosphorylase 2,4-glucan phosphorylase; PDBTitle: arabidopsis thaliana cytosolic alpha-1,4-glucan phosphorylase (phs2)
10	c6ngngB_	 Alignment		99.8	15	PDB header: transferase Chain: B: PDB Molecule: granule-bound starch synthase; PDBTitle: granule bound starch synthase i from cyanophora paradoxa bound to2 acarbose and adp
11	c4hlnA_	 Alignment		99.8	16	PDB header: transferase Chain: A: PDB Molecule: starch synthase i; PDBTitle: structure of barley starch synthase i in complex with2 maltooligosaccharide

12	c6gnfC_	Alignment		99.7	18	PDB header: transferase Chain: C: PDB Molecule: glycogen synthase; PDBTitle: granule bound starch synthase from cyanobacterium sp. c6gnfC_ bound to 2 acarbose and adp
13	c6gneB_	Alignment		99.7	15	PDB header: transferase Chain: B: PDB Molecule: probable starch synthase 4, chloroplastic/amyloplastic; PDBTitle: catalytic domain of starch synthase iv from Arabidopsis thaliana bound to 2 adp and acarbose
14	c3nb0A_	Alignment		99.6	17	PDB header: transferase Chain: A: PDB Molecule: glycogen [starch] synthase isoform 2; PDBTitle: glucose-6-phosphate activated form of yeast glycogen synthase
15	c3vufA_	Alignment		99.6	19	PDB header: transferase Chain: A: PDB Molecule: granule-bound starch synthase 1, PDBTitle: crystal structure of rice granule bound starch synthase i catalytic2 domain in complex with adp
16	c3o3cD_	Alignment		99.5	15	PDB header: transferase Chain: D: PDB Molecule: glycogen [starch] synthase isoform 2; PDBTitle: glycogen synthase basal state udp complex
17	c4qlbD_	Alignment		99.3	18	PDB header: transferase Chain: D: PDB Molecule: probable glycogen [starch] synthase; PDBTitle: structural basis for the recruitment of glycogen synthase by 2 glycogenin
18	d1rzua_	Alignment		99.2	19	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
19	c2r60A_	Alignment		99.2	16	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase, group 1; PDBTitle: structure of apo sucrose phosphate synthase (sps) of 2 Halothermothrix orenii
20	c2x6rA_	Alignment		99.1	17	PDB header: isomerase Chain: A: PDB Molecule: trehalose-synthase tret; PDBTitle: crystal structure of trehalose synthase tret from P. horikoshii produced by soaking in trehalose
21	c2qzsA_	Alignment	not modelled	99.0	18	PDB header: transferase Chain: A: PDB Molecule: glycogen synthase; PDBTitle: crystal structure of wild-type E. coli GS in complex with adp and 2 glucose (wtgsb)
22	c5jijA_	Alignment	not modelled	99.0	16	PDB header: transferase Chain: A: PDB Molecule: alpha,alpha-trehalose-phosphate synthase; PDBTitle: structure of Mycobacterium thermoresistibile trehalose-6-phosphate2 synthase (apo form). PDB header: sugar binding protein
23	c2xmpB_	Alignment	not modelled	98.9	16	Chain: B: PDB Molecule: trehalose-synthase tret; PDBTitle: crystal structure of trehalose synthase tret mutant e326a2 from P. horikoshii in complex with UDP
24	d2bisa1	Alignment	not modelled	98.9	19	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
25	d1uqta_	Alignment	not modelled	98.8	14	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Trehalose-6-phosphate synthase, OtsA
26	c5v0tB_	Alignment	not modelled	98.5	15	PDB header: transferase Chain: B: PDB Molecule: alpha,alpha-trehalose-phosphate synthase (udp-forming); PDBTitle: crystal structure of an alpha,alpha-trehalose-phosphate synthase (udp-2 forming) from Burkholderia xenovorans in complex with glucose-6-3 phosphate
27	c3s29C_	Alignment	not modelled	98.5	18	PDB header: transferase Chain: C: PDB Molecule: sucrose synthase 1; PDBTitle: the crystal structure of sucrose synthase-1 from Arabidopsis thaliana2 and its functional implications.
						PDB header: transferase

28	c4x7pB_	Alignment	not modelled	98.5	13	Chain: B: PDB Molecule: tarm; PDBTitle: crystal structure of apo s. aureus tarm
29	c5hutB_	Alignment	not modelled	98.5	13	PDB header: transferase Chain: B: PDB Molecule: alpha,alpha-trehalose-phosphate synthase [udp-forming]; PDBTitle: structure of candida albicans trehalose-6-phosphate synthase in2 complex with udp-glucose
30	c1uquB_	Alignment	not modelled	98.4	12	PDB header: synthase Chain: B: PDB Molecule: alpha, alpha-trehalose-phosphate synthase; PDBTitle: trehalose-6-phosphate from e. coli bound with udp-glucose.
31	c5hxaA_	Alignment	not modelled	98.4	12	PDB header: protein binding Chain: A: PDB Molecule: alpha,alpha-trehalose-phosphate synthase (udp-forming); PDBTitle: crystal structure of an udp-forming alpha, alpha-terhalose-phosphate2 synthase from burkholderia xenovorans
32	c6fj3A_	Alignment	not modelled	98.4	18	PDB header: membrane protein Chain: A: PDB Molecule: parathyroid hormone/parathyroid hormone-related peptide PDBTitle: high resolution crystal structure of parathyroid hormone 1 receptor in2 complex with a peptide agonist.
33	c3oy2A_	Alignment	not modelled	98.4	15	PDB header: viral protein,transferase Chain: A: PDB Molecule: glycosyltransferase b7361; PDBTitle: crystal structure of a putative glycosyltransferase from paramecium2 bursaria chlorella virus ny2a
34	c4pqgB_	Alignment	not modelled	98.2	15	PDB header: transferase Chain: B: PDB Molecule: glycosyltransferase gtf1; PDBTitle: crystal structure of the pneumococcal o-glcnac transferase gtfA in2 complex with udp and glcnac
35	c5lqdB_	Alignment	not modelled	98.0	21	PDB header: transferase Chain: B: PDB Molecule: alpha,alpha-trehalose-phosphate synthase; PDBTitle: trehalose-6-phosphate synthase, gdp-glucose-dependent otsa
36	c3c4vB_	Alignment	not modelled	98.0	20	PDB header: transferase Chain: B: PDB Molecule: predicted glycosyltransferases; PDBTitle: structure of the retaining glycosyltransferase msha:the2 first step in mycothiol biosynthesis. organism:3 corynebacterium glutamicum : complex with udp and 1l-ins-1-4 p.
37	c5hvoD_	Alignment	not modelled	98.0	15	PDB header: transferase Chain: D: PDB Molecule: alpha,alpha-trehalose-phosphate synthase (udp-forming); PDBTitle: structure of aspergillus fumigatus trehalose-6-phosphate synthase b in2 complex with udp and validoxylamine a
38	c5d00A_	Alignment	not modelled	98.0	16	PDB header: transferase Chain: A: PDB Molecule: n-acetyl-alpha-d-glucosaminyl l-malate synthase; PDBTitle: crystal structure of bsha from b. subtilis complexed with n-2 acetylglucosaminyl-malate and ump
39	c5e9tA_	Alignment	not modelled	97.9	17	PDB header: transferase/chaperone Chain: A: PDB Molecule: glycosyltransferase gtf1; PDBTitle: crystal structure of gtfA/b complex
40	c5vafD_	Alignment	not modelled	97.7	13	PDB header: cell adhesion Chain: D: PDB Molecule: accessory sec system protein asp1; PDBTitle: crystal structure of accessory secretion protein 1
41	c2gejA_	Alignment	not modelled	97.6	20	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol mannosyltransferase (pima); PDBTitle: crystal structure of phosphatidylinositol mannosyltransferase (pima)2 from mycobacterium smegmatis in complex with gdp-man
42	c2jjmH_	Alignment	not modelled	97.5	16	PDB header: transferase Chain: H: PDB Molecule: glycosyl transferase, group 1 family protein; PDBTitle: crystal structure of a family gt4 glycosyltransferase from bacillus2 anthracis orf ba1558.
43	c4xsuB_	Alignment	not modelled	97.5	17	PDB header: transferase Chain: B: PDB Molecule: alr3699 protein; PDBTitle: crystal structure of anabaena alr3699/hepe in complex with udp and2 glucose
44	c3okaA_	Alignment	not modelled	97.5	14	PDB header: transferase Chain: A: PDB Molecule: gdp-mannose-dependent alpha-(1-6)-phosphatidylinositol PDBTitle: crystal structure of corynebacterium glutamicum pimb' in complex with2 gdp-man (triclinic crystal form)
45	c6d9tA_	Alignment	not modelled	97.4	15	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase; PDBTitle: bsha from staphylococcus aureus complexed with udp
46	c4rbnD_	Alignment	not modelled	97.3	18	PDB header: transferase Chain: D: PDB Molecule: sucrose synthase:glycosyl transferases group 1; PDBTitle: the crystal structure of nitrosomonas europaea sucrose synthase:2 insights into the evolutionary origin of sucrose metabolism in3 prokaryotes
47	c6ejjA_	Alignment	not modelled	97.3	16	PDB header: transferase Chain: A: PDB Molecule: wlac protein; PDBTitle: structure of a glycosyltransferase
48	c2x0dA_	Alignment	not modelled	97.3	11	PDB header: transferase Chain: A: PDB Molecule: wsaf; PDBTitle: apo structure of wsaf
49	d2f9fa1	Alignment	not modelled	97.2	19	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
50	d2bfwa1	Alignment	not modelled	97.0	14	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1

51	c3t5tA_	Alignment	not modelled	96.8	15	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase; PDBTitle: vall from streptomyces hygroscopicus in apo form
52	c4xywA_	Alignment	not modelled	96.8	18	PDB header: transferase Chain: A: PDB Molecule: o-antigen biosynthesis glycosyltransferase wbnh; PDBTitle: glycosyltransferases wbnh
53	c3ot5D_	Alignment	not modelled	96.7	12	PDB header: isomerase Chain: D: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: 2.2 angstrom resolution crystal structure of putative udp-n-2 acetylglucosamine 2-epimerase from listeria monocytogenes
54	d2iw1a1	Alignment	not modelled	96.3	14	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
55	c5i45A_	Alignment	not modelled	96.3	17	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferases group 1 family protein; PDBTitle: 1.35 angstrom crystal structure of c-terminal domain of glycosyl2 transferase group 1 family protein (lppc) from francisella3 tularensis.
56	c4u33F_	Alignment	not modelled	96.1	20	PDB header: transferase Chain: F: PDB Molecule: alpha-1,4-glucan:maltose-1-phosphate maltosyltransferase; PDBTitle: structure of mtb glge bound to maltose
57	c3beoA_	Alignment	not modelled	96.0	15	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: a structural basis for the allosteric regulation of non-2 hydrolyzing udp-glcna2 2-epimerases
58	c3zt5D_	Alignment	not modelled	95.9	23	PDB header: hydrolase Chain: D: PDB Molecule: putative glucanohydrolase pep1a; PDBTitle: glge isoform 1 from streptomyces coelicolor with maltose2 bound
59	c5zesA_	Alignment	not modelled	95.7	14	PDB header: transferase Chain: A: PDB Molecule: udp-glucose:tetrahydrobiopterin glycosyltransferase; PDBTitle: udp glucose alpha tetrahydrobiopterin glycosyltransferase from2 synechococcus species pcc 7942 - udp complex
60	d1f6da_	Alignment	not modelled	95.6	12	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
61	c5enzA_	Alignment	not modelled	95.6	13	PDB header: isomerase Chain: A: PDB Molecule: udp-glcna2 2-epimerase; PDBTitle: s. aureus mnaa-udp co-structure
62	c5dldA_	Alignment	not modelled	95.2	11	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: crystal structure of a udp-n-acetylglucosamine 2-epimerase from2 burkholderia vietnamiensis complexed with udp-glcna2 and udp
63	c3rhzB_	Alignment	not modelled	95.1	11	PDB header: transferase Chain: B: PDB Molecule: nucleotide sugar synthetase-like protein; PDBTitle: structure and functional analysis of a new subfamily of2 glycosyltransferases required for glycosylation of serine-rich3 streptococcal adhesions
64	c3dzcA_	Alignment	not modelled	94.7	13	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: 2.35 angstrom resolution structure of webc (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae.
65	c2vsnB_	Alignment	not modelled	94.6	13	PDB header: transferase Chain: B: PDB Molecule: xcogt; PDBTitle: structure and topological arrangement of an o-glcna2 transferase homolog: insight into molecular control of3 intracellular glycosylation
66	c5dxfA_	Alignment	not modelled	94.3	8	PDB header: hydrolase Chain: A: PDB Molecule: trehalose-6-phosphate phosphatase; PDBTitle: structure of candida albicans trehalose-6-phosphate phosphatase n-2 terminal domain
67	c4w6qC_	Alignment	not modelled	92.4	14	PDB header: transferase Chain: C: PDB Molecule: glucosyltransferase; PDBTitle: glycosyltransferase c from streptococcus agalactiae
68	c5n80A_	Alignment	not modelled	92.2	11	PDB header: transferase Chain: A: PDB Molecule: lipopolysaccharide 1,6-galactosyltransferase; PDBTitle: glycosyltransferase lps biosynthesis in complex with udp
69	c5djsA_	Alignment	not modelled	92.0	14	PDB header: transferase Chain: A: PDB Molecule: tetratricopeptide tpr_2 repeat protein; PDBTitle: thermobaculum terrenum o-glcna2 transferase mutant - k341m
70	c4nesA_	Alignment	not modelled	90.7	13	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: crystal structure of methanocaldococcus jannaschii udp-glcna2 2-2 epimerase in complex with udp-glcna2 and udp
71	c3s2uA_	Alignment	not modelled	90.2	12	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine--n-acetylmuramyl-(pentapeptide) PDBTitle: crystal structure of the pseudomonas aeruginosa murg:udp-glcna2 substrate complex
72	c4bfcA_	Alignment	not modelled	88.3	11	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-d-manno-octulosonic-acid transferase; PDBTitle: crystal structure of the c-terminal cmp-kdo binding domain of waaa2 from acinetobacter baumannii
73	d1v4va_	Alignment	not modelled	82.4	10	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
74	c4x1tA_	Alignment	not modelled	80.9	13	PDB header: transferase Chain: A: PDB Molecule: monogalactosyldiacylglycerol synthase 1, chloroplastic; PDBTitle: the crystal structure of arabidopsis thaliana galactolipid synthase2 mgd1 in complex with udp

75	c3qhpB	 Alignment	not modelled	79.0	10	PDB header: transferase Chain: B: PDB Molecule: type 1 capsular polysaccharide biosynthesis protein j PDBTitle: crystal structure of the catalytic domain of cholesterol-alpha-2 glucosyltransferase from helicobacter pylori
76	c4hwgA	 Alignment	not modelled	78.7	14	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: structure of udp-n-acetylglucosamine 2-epimerase from rickettsia2 bellii
77	c2q6vA	 Alignment	not modelled	74.4	9	PDB header: transferase Chain: A: PDB Molecule: glucuronosyltransferase gumk; PDBTitle: crystal structure of gumk in complex with udp
78	c2iv3B	 Alignment	not modelled	72.3	14	PDB header: transferase Chain: B: PDB Molecule: glycosyltransferase; PDBTitle: crystal structure of avigt4, a glycosyltransferase involved2 in avilamycin a biosynthesis
79	c5xvsA	 Alignment	not modelled	69.9	8	PDB header: hydrolase Chain: A: PDB Molecule: gdp/udp-n,n'-diacetylbacillosamine 2-epimerase PDBTitle: crystal structure of udp-glcna2 2-epimerase neuc complexed with udp
80	c5e9uB	 Alignment	not modelled	64.1	16	PDB header: transferase/chaperone Chain: B: PDB Molecule: glycosyltransferase-stabilizing protein gtf2; PDBTitle: crystal structure of gtfA/b complex bound to udp and glcna2
81	d2d7pa1	 Alignment	not modelled	64.1	10	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
82	d1phpa	 Alignment	not modelled	63.3	18	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
83	d1vpea	 Alignment	not modelled	60.4	16	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
84	c3pe3D	 Alignment	not modelled	60.3	15	PDB header: transferase Chain: D: PDB Molecule: udp-n-acetylglucosamine--peptide n- PDBTitle: structure of human o-glcna2 transferase and its complex with a peptide2 substrate
85	c2kutA	 Alignment	not modelled	58.1	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of gmr58a from geobacter metallireducens.2 northeast structural genomics consortium target gmr58a
86	d1w36c1	 Alignment	not modelled	56.9	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
87	c2brqB	 Alignment	not modelled	56.5	23	PDB header: structural protein Chain: B: PDB Molecule: filamin a; PDBTitle: crystal structure of the filamin a repeat 21 complexed with2 the integrin beta7 cytoplasmic tail peptide
88	c2kl6A	 Alignment	not modelled	48.3	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of the cardb domain of pf1109 from2 pyrococcus furiosus. northeast structural genomics3 consortium target pfr193a
89	c5vhvB	 Alignment	not modelled	48.3	14	PDB header: hydrolase/dna Chain: B: PDB Molecule: alkylpurine dna glycosylase alkC; PDBTitle: pseudomonas fluorescens alkylpurine dna glycosylase alkC bound to dna2 containing an oxocarbenium-intermediate analog
90	c4b7lB	 Alignment	not modelled	48.3	16	PDB header: structural protein Chain: B: PDB Molecule: filamin-b; PDBTitle: crystal structure of human filamin b actin binding domain2 with 1st filamin repeat
91	c6dgvA	 Alignment	not modelled	47.3	21	PDB header: fluorescent protein Chain: A: PDB Molecule: fluorescent gaba sensor precursor; PDBTitle: igabasnfr fluorescent gaba sensor precursor
92	d2w0pa1	 Alignment	not modelled	44.6	23	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
93	d2d7na1	 Alignment	not modelled	42.1	10	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
94	c3iswB	 Alignment	not modelled	42.1	23	PDB header: structural protein Chain: B: PDB Molecule: filamin-a; PDBTitle: crystal structure of filamin-a immunoglobulin-like repeat 21 bound to2 an n-terminal peptide of cfr
95	c2w0pB	 Alignment	not modelled	42.1	23	PDB header: cell adhesion Chain: B: PDB Molecule: filamin-a; PDBTitle: crystal structure of the filamin a repeat 21 complexed with2 the migfilin peptide
96	c2brqA	 Alignment	not modelled	42.1	23	PDB header: structural protein Chain: A: PDB Molecule: filamin a; PDBTitle: crystal structure of the filamin a repeat 21 complexed with2 the integrin beta7 cytoplasmic tail peptide
97	d2bp3a1	 Alignment	not modelled	40.7	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
98	d1v6sa	 Alignment	not modelled	39.5	33	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
99	c2uva1	 Alignment	not modelled	36.5	14	PDB header: transferase Chain: I: PDB Molecule: fatty acid synthase beta subunits; PDBTitle: crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the beta subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid

						synthase and is described in remark 400
100	d1y2ta_	Alignment	not modelled	35.0	44	Fold: Cytolysin/lectin Superfamily: Cytolysin/lectin Family: Fungal fruit body lectin
101	d1x99a_	Alignment	not modelled	34.6	44	Fold: Cytolysin/lectin Superfamily: Cytolysin/lectin Family: Fungal fruit body lectin
102	c6hxqB_	Alignment	not modelled	33.5	6	PDB header: lyase Chain: B: PDB Molecule: citryl-coa synthetase large subunit; PDBTitle: structure of citryl-coa synthetase from hydrogenobacter thermophilus
103	c3tcyA_	Alignment	not modelled	32.9	20	PDB header: oxidoreductase Chain: A: PDB Molecule: phenylalanine-4-hydroxylase; PDBTitle: crystallographic structure of phenylalanine hydroxylase from <i>Chromobacterium violaceum</i> (cpah) bound to phenylalanine in a site3 distal to the active site
104	d2e9ia1	Alignment	not modelled	32.2	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
105	d1xjta_	Alignment	not modelled	31.7	8	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Phage lysozyme
106	c6mgcA_	Alignment	not modelled	31.5	22	PDB header: transferase Chain: A: PDB Molecule: capsule polysaccharide export protein kpsc; PDBTitle: escherichia coli kpsc, n-terminal domain
107	d1ltkA_	Alignment	not modelled	31.3	26	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
108	c2vkzH_	Alignment	not modelled	30.5	16	PDB header: transferase Chain: H: PDB Molecule: fatty acid synthase subunit beta; PDBTitle: structure of the cerulenin-inhibited fungal fatty acid synthase type i2 multienzyme complex
109	d16pka_	Alignment	not modelled	30.4	30	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
110	c3iswA_	Alignment	not modelled	29.6	16	PDB header: structural protein Chain: A: PDB Molecule: filamin-a; PDBTitle: crystal structure of filamin-a immunoglobulin-like repeat 21 bound to 2 an n-terminal peptide of cfr
111	c4dg5A_	Alignment	not modelled	29.5	22	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of staphylococcal phosphoglycerate kinase
112	d1vjda_	Alignment	not modelled	29.4	26	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
113	d2dica1	Alignment	not modelled	29.0	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
114	c2ofeA_	Alignment	not modelled	28.9	44	PDB header: sugar binding protein Chain: A: PDB Molecule: sclerotium rolfsii lectin; PDBTitle: the crystal structure of sclerotium rolfsii lectin in complex with n-2 acetyl-d-glucosamine
115	d1fw8a_	Alignment	not modelled	28.7	22	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
116	d2csua3	Alignment	not modelled	28.4	32	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
117	d2dj4a1	Alignment	not modelled	28.4	23	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
118	c5bt8D_	Alignment	not modelled	28.2	30	PDB header: transferase Chain: D: PDB Molecule: phosphoglycerate kinase; PDBTitle: x-ray crystal structure of phosphoglycerate kinase from acinetobacter2 baumannii
119	c1zmrA_	Alignment	not modelled	28.1	33	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of the e. coli phosphoglycerate kinase
120	c2g3oB_	Alignment	not modelled	27.6	19	PDB header: luminescent protein Chain: B: PDB Molecule: green fluorescent protein 2; PDBTitle: the 2.1a crystal structure of copgfp