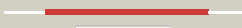























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0315 (-)_383602_384486
Date	Tue Jul 23 14:50:38 BST 2019
Unique Job ID	c15e020875598dde

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4wzfA_	 Alignment		100.0	100	PDB header: hydrolase activator Chain: A: PDB Molecule: 1,3-beta-glucanase; PDBTitle: crystal structural basis for rv0315, an immunostimulatory antigen and2 pseudo beta-1, 3-glucanase of mycobacterium tuberculosis
2	c3rq0A_	 Alignment		100.0	57	PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolases family protein 16; PDBTitle: the crystal structure of a glycosyl hydrolases (gh) family protein 162 from mycobacterium smegmatis str. mc2 155
3	c5dxdA_	 Alignment		100.0	67	PDB header: hydrolase Chain: A: PDB Molecule: putative beta-glucanase; PDBTitle: crystal structure of putative beta-glucanase (rv0315 ortholog) from2 mycobacterium abscessus
4	c4xdqA_	 Alignment		100.0	62	PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase family protein; PDBTitle: crystal structure of a glycoside hydrolase family protein (rv03152 ortholog) from mycobacterium thermorestrictibile
5	c1upsB_	 Alignment		100.0	21	PDB header: glycosyl hydrolase Chain: B: PDB Molecule: glcnac-alpha-1,4-gal-releasing endo-beta-galactosidase; PDBTitle: glcnac[alpha]1-4gal releasing endo-[beta]-galactosidase from2 clostridium perfringens
6	c4xxpA_	 Alignment		100.0	66	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein (rv0315 ortholog); PDBTitle: crystal structure of an uncharacterized protein (rv0315 ortholog) from2 mycobacterium paratuberculosis
7	c2vy0B_	 Alignment		100.0	28	PDB header: hydrolase Chain: B: PDB Molecule: endo-beta-1,3-glucanase; PDBTitle: the x-ray structure of endo-beta-1,3-glucanase from2 pyrococcus furiosus
8	c1o4zA_	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: beta-agarase b; PDBTitle: the three-dimensional structure of beta-agarase b from2 zobellia galactanivorans
9	d1o4za_	 Alignment		100.0	20	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Glycosyl hydrolases family 16
10	c5wutB_	 Alignment		100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: ulam111; PDBTitle: crystal structure of laminarinase from flavobacterium sp. umi-01
11	d1o4ya_	 Alignment		100.0	17	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Glycosyl hydrolases family 16

12	c4bowB_	Alignment		100.0	27	PDB header: hydrolase Chain: B; PDB Molecule: endo-1,3-beta-glucanase, family gh16; PDBTitle: crystal structure of lama_e269s from z. galactanivorans in complex2 with laminaritriose and laminaritetraose
13	c3ilnB_	Alignment		100.0	27	PDB header: hydrolase Chain: B; PDB Molecule: laminarinase; PDBTitle: x-ray structure of the laminarinase from rhodothermus marinus
14	c3dgtA_	Alignment		100.0	26	PDB header: hydrolase Chain: A; PDB Molecule: endo-1,3-beta-glucanase; PDBTitle: the 1.5 a crystal structure of endo-1,3-beta-glucanase from2 streptomyces sioyaensis
15	c2hykA_	Alignment		100.0	32	PDB header: hydrolase Chain: A; PDB Molecule: beta-1,3-glucanase; PDBTitle: the crystal structure of an endo-beta-1,3-glucanase from alkaliphilic2 nocardioopsis sp.strain f96
16	c3azyA_	Alignment		100.0	29	PDB header: hydrolase Chain: A; PDB Molecule: laminarinase; PDBTitle: crystal structure of the laminarinase catalytic domain from thermotoga2 maritima msb8
17	c3wz1A_	Alignment		100.0	21	PDB header: hydrolase Chain: A; PDB Molecule: agarase; PDBTitle: catalytic domain of beta-agarase from microbulbifer thermotolerans2 jamb-a94
18	c4awdB_	Alignment		100.0	23	PDB header: hydrolase Chain: B; PDB Molecule: beta-porphyrinase; PDBTitle: crystal structure of the beta-porphyrinase bpg16b (bacple_01689) from2 the human gut bacterium bacteroides plebeius
19	c6hy3A_	Alignment		100.0	20	PDB header: hydrolase Chain: A; PDB Molecule: beta-agarase c; PDBTitle: three-dimensional structure of agac from zobellia galactanivorans
20	c5nbpA_	Alignment		100.0	29	PDB header: hydrolase Chain: A; PDB Molecule: glycosyl hydrolase family 16; PDBTitle: bacteroides ovatus mixed linkage glucan pul (mlgul) gh16 in complex2 with g4g4g3g product
21	d1upsa1	Alignment	not modelled	100.0	22	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Glycosyl hydrolases family 16
22	c5ocrC_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: C; PDB Molecule: kappa-carrageenase; PDBTitle: crystal structure of the kappa-carrageenase zobellia_236 from zobellia2 galactanivorans
23	c5t9xC_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: C; PDB Molecule: glycoside hydrolase; PDBTitle: crystal structure of bugh16bwt
24	c3juuA_	Alignment	not modelled	100.0	23	PDB header: hydrolase/carbohydrate Chain: A; PDB Molecule: porphyranase b; PDBTitle: crystal structure of porphyranase b (porb) from zobellia2 galactanivorans
25	c2cl2A_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A; PDB Molecule: putative laminarinase; PDBTitle: endo-1,3(4)-beta-glucanase from phanerochaete chrysosporium, solved2 using native sulfur sad, exhibiting intact heptasaccharide3 glycosylation
26	c4cteB_	Alignment	not modelled	100.0	30	PDB header: hydrolase Chain: B; PDB Molecule: endo-1,3-beta-glucanase, family gh16; PDBTitle: crystal structure of the catalytic domain of the modular2 laminarinase zglamc mutant e142s in complex with a thio-3 oligosaccharide
27	c6jhjA_	Alignment	not modelled	100.0	29	PDB header: hydrolase Chain: A; PDB Molecule: lamcat; PDBTitle: structure of marine bacterial laminarinase mutant-e135a
28	d1dypa_	Alignment	not modelled	100.0	22	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Glycosyl hydrolases family 16

29	c4asmB_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: beta-agarase d; PDBTitle: crystal structure of the catalytic domain of beta-agarase d from <i>Zobellia galactanivorans</i>
30	c3wdvB_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: beta-1,3-1,4-glucanase; PDBTitle: the complex structure of pttic16a with cellotetraose
31	c3ilfA_	Alignment	not modelled	100.0	22	PDB header: hydrolase/carbohydrate Chain: A: PDB Molecule: porphyranase a; PDBTitle: crystal structure of porphyranase a (pora) in complex with neo-2 porphyrotetraose
32	c5jvvA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: beta-1,3-glucosyltransferase; PDBTitle: crystal structure and characterization an elongating gh family 162 beta-1,3-glucosyltransferase
33	c3o5sA_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucanase; PDBTitle: crystal structure of the endo-beta-1,3-1,4 glucanase from <i>Bacillus subtilis</i> (strain 168)
34	c5ndlA_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: crh-like protein; PDBTitle: crh5 transglycosylase complexed with nag4
35	c3wvjA_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucanase; PDBTitle: the crystal structure of native glycosidic hydrolase
36	d1gbga_	Alignment	not modelled	100.0	21	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Glycosyl hydrolases family 16
37	d2ayha_	Alignment	not modelled	100.0	20	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Glycosyl hydrolases family 16
38	c3i4iA_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: 1,3-1,4-beta-glucanase; PDBTitle: crystal structure of a prokaryotic beta-1,3-1,4-glucanase (lichenase)2 derived from a mouse hindgut metagenome
39	d1mvea_	Alignment	not modelled	100.0	20	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Glycosyl hydrolases family 16
40	d1cpma_	Alignment	not modelled	100.0	20	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Glycosyl hydrolases family 16
41	d1cpna_	Alignment	not modelled	100.0	20	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Glycosyl hydrolases family 16
42	c5dzfB_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: endo-glucanase; PDBTitle: crystal structure of the catalytic nucleophile mutant of vveg16 in2 complex with a mixed-linkage glucan octasaccharide
43	c1axkB_	Alignment	not modelled	100.0	20	PDB header: fusion protein Chain: B: PDB Molecule: gluxyn-1; PDBTitle: engineered bacillus bifunctional enzyme gluxyn-1
44	c2vh9A_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: cellulase; PDBTitle: crystal structure of ngx1-delta yniig in complex with xllg, a2 xyloglucan derived oligosaccharide
45	d1umza_	Alignment	not modelled	100.0	21	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Glycosyl hydrolases family 16
46	d1ajka_	Alignment	not modelled	100.0	20	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Glycosyl hydrolases family 16
47	d1ajoa_	Alignment	not modelled	99.8	19	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Glycosyl hydrolases family 16
48	c3hbKA_	Alignment	not modelled	97.4	14	PDB header: hydrolase Chain: A: PDB Molecule: putative glycosyl hydrolase; PDBTitle: crystal structure of putative glycosyl hydrolase, was domain of2 unknown function (duf1080) (yp_001302580.1) from <i>Parabacteroides distans</i> atcc 8503 at 2.36 a resolution
49	c3nmbA_	Alignment	not modelled	97.1	11	PDB header: hydrolase Chain: A: PDB Molecule: putative sugar hydrolase; PDBTitle: crystal structure of a putative sugar hydrolase (bacova_03189) from <i>Bacteroides ovatus</i> at 2.40 a resolution
50	c4jqtA_	Alignment	not modelled	96.7	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative glycosyl hydrolase; PDBTitle: crystal structure of a putative glycosyl hydrolase (bt3469) from <i>Bacteroides thetaiotaomicron</i> vpi-5482 at 2.49 a resolution
51	c3h3lB_	Alignment	not modelled	96.4	14	PDB header: hydrolase Chain: B: PDB Molecule: putative sugar hydrolase; PDBTitle: crystal structure of putative sugar hydrolase (yp_001304206.1) from <i>Parabacteroides distans</i> atcc 8503 at 1.59 a resolution
52	c4azzB_	Alignment	not modelled	95.8	13	PDB header: hydrolase Chain: B: PDB Molecule: levanase; PDBTitle: carbohydrate binding module cbm66 from <i>Bacillus subtilis</i>
53	c2v73B_	Alignment	not modelled	95.0	11	PDB header: sugar-binding protein Chain: B: PDB Molecule: putative exo-alpha-sialidase; PDBTitle: the structure of the family 40 cbm from <i>C. perfringens</i> nanj2 in complex with a sialic acid containing molecule
54	c2jkbA_	Alignment	not modelled	94.9	7	PDB header: lyase Chain: A: PDB Molecule: sialidase b; PDBTitle: crystal structure of streptococcus pneumoniae nanb in2 complex with 2,7-anhydro-neu5ac

55	d1n1ta1	Alignment	not modelled	93.7	11	Fold: Concanavalin A-like lectins/gluconases Superfamily: Concanavalin A-like lectins/gluconases Family: Trypanosoma sialidase, C-terminal domain
56	d2sliA1	Alignment	not modelled	93.4	10	Fold: Concanavalin A-like lectins/gluconases Superfamily: Concanavalin A-like lectins/gluconases Family: Leech intramolecular trans-sialidase, N-terminal domain
57	d1fnYA	Alignment	not modelled	93.2	18	Fold: Concanavalin A-like lectins/gluconases Superfamily: Concanavalin A-like lectins/gluconases Family: Legume lectins
58	c3zypA	Alignment	not modelled	92.7	15	PDB header: metal binding protein Chain: A: PDB Molecule: cip1; PDBTitle: cellulose induced protein, cip1
59	c3s5qA	Alignment	not modelled	92.6	11	PDB header: hydrolase Chain: A: PDB Molecule: putative glycosylhydrolase; PDBTitle: crystal structure of a putative glycosyl hydrolase (bdj_2473) from 2 parabacteroides distasonis atcc 8503 at 1.85 a resolution
60	c4qvsA	Alignment	not modelled	92.4	12	PDB header: unknown function Chain: A: PDB Molecule: s-layer domain-containing protein; PDBTitle: 2.1 angstrom resolution crystal structure of s-layer domain-containing 2 protein (residues 221-444) from clostridium thermocellum atcc 27405
61	d1w0pa1	Alignment	not modelled	92.1	19	Fold: Concanavalin A-like lectins/gluconases Superfamily: Concanavalin A-like lectins/gluconases Family: Vibrio cholerae sialidase, N-terminal and insertion domains
62	d1g9fa	Alignment	not modelled	91.6	18	Fold: Concanavalin A-like lectins/gluconases Superfamily: Concanavalin A-like lectins/gluconases Family: Legume lectins
63	c4c1wA	Alignment	not modelled	90.0	8	PDB header: sugar binding protein Chain: A: PDB Molecule: neuraminidase; PDBTitle: carbohydrate binding domain from streptococcus pneumoniae 2 nana sialidase complexed with 3'-sialyllactose
64	c1za4A	Alignment	not modelled	89.5	11	PDB header: cell adhesion Chain: A: PDB Molecule: thrombospondin 1; PDBTitle: crystal structure of the thrombospondin-1 n-terminal domain 2 in complex with arixtra
65	c2vu9A	Alignment	not modelled	89.3	14	PDB header: hydrolase Chain: A: PDB Molecule: botulinum neurotoxin a heavy chain; PDBTitle: crystal structure of botulinum neurotoxin serotype a2 binding domain in complex with gt1b
66	c6er3B	Alignment	not modelled	89.0	8	PDB header: sugar binding protein Chain: B: PDB Molecule: bnr/asp-box repeat protein; PDBTitle: ruminococcus gnavus it-sialidase cbm40 bound to alpha2,3 sialyllactose
67	d1lu1a	Alignment	not modelled	88.5	19	Fold: Concanavalin A-like lectins/gluconases Superfamily: Concanavalin A-like lectins/gluconases Family: Legume lectins
68	c2uurA	Alignment	not modelled	88.3	14	PDB header: structural protein Chain: A: PDB Molecule: collagen alpha-1(ix) chain; PDBTitle: n-terminal nc4 domain of collagen ix
69	c1z0hB	Alignment	not modelled	88.2	16	PDB header: hydrolase Chain: B: PDB Molecule: botulinum neurotoxin type b; PDBTitle: n-terminal helix reorients in recombinant c-fragment of 2 clostridium botulinum type b
70	d1g8wa	Alignment	not modelled	88.0	22	Fold: Concanavalin A-like lectins/gluconases Superfamily: Concanavalin A-like lectins/gluconases Family: Legume lectins
71	d1epwa1	Alignment	not modelled	87.6	15	Fold: Concanavalin A-like lectins/gluconases Superfamily: Concanavalin A-like lectins/gluconases Family: Clostridium neurotoxins, the second last domain
72	d2ah2a1	Alignment	not modelled	87.1	13	Fold: Concanavalin A-like lectins/gluconases Superfamily: Concanavalin A-like lectins/gluconases Family: Trypanosoma sialidase, C-terminal domain
73	c4yw5A	Alignment	not modelled	87.1	7	PDB header: hydrolase Chain: A: PDB Molecule: neuraminidase c; PDBTitle: crystal structure of streptococcus pneumoniae nanc, complex with 2 oseltamivir carboxylate
74	c2e76D	Alignment	not modelled	87.1	17	PDB header: photosynthesis Chain: D: PDB Molecule: cytochrome b6-f complex iron-sulfur subunit; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
75	d2erfa1	Alignment	not modelled	86.5	10	Fold: Concanavalin A-like lectins/gluconases Superfamily: Concanavalin A-like lectins/gluconases Family: Laminin G-like module
76	d1w0pa2	Alignment	not modelled	86.5	8	Fold: Concanavalin A-like lectins/gluconases Superfamily: Concanavalin A-like lectins/gluconases Family: Vibrio cholerae sialidase, N-terminal and insertion domains
77	c2sliA	Alignment	not modelled	86.3	11	PDB header: hydrolase Chain: A: PDB Molecule: intramolecular trans-sialidase; PDBTitle: leech intramolecular trans-sialidase complexed with 2,7-2 anhydro-neu5ac, the reaction product
78	d2d3sa1	Alignment	not modelled	86.3	18	Fold: Concanavalin A-like lectins/gluconases Superfamily: Concanavalin A-like lectins/gluconases Family: Legume lectins
79	c5kxcB	Alignment	not modelled	86.3	18	PDB header: sugar binding protein Chain: B: PDB Molecule: wisteria floribunda agglutinin; PDBTitle: wisteria floribunda lectin in complex with galnac(beta1-4)glcnac2 (lactinac) at ph 8.5.
80	c5jzB	Alignment	not modelled	85.5	16	PDB header: hydrolase Chain: B: PDB Molecule: non-reducing end alpha-l-arabinofuranosidase bogh43b; PDBTitle: bacteroides ovatus xyloglucan pul gh43b PDB header: hydrolase

81	c3u1xA_	Alignment	not modelled	85.3	9	Chain: A: PDB Molecule: putative glycosyl hydrolase; PDBTitle: crystal structure of a putative glycosyl hydrolase (bdi_1869) from2 parabacteroides distasonis atcc 8503 at 1.70 a resolution
82	c4qhzC_	Alignment	not modelled	85.0	16	PDB header: hydrolase Chain: C: PDB Molecule: putative glycosyl hydrolase; PDBTitle: crystal structure of a putative glycosyl hydrolase (bdi_3914) from2 parabacteroides distasonis atcc 8503 at 2.13 a resolution
83	c1yrzB_	Alignment	not modelled	83.4	11	PDB header: hydrolase Chain: B: PDB Molecule: xylan beta-1,4-xylosidase; PDBTitle: crystal structure of xylan beta-1,4-xylosidase from bacillus2 halodurans c-125
84	c1fv3B_	Alignment	not modelled	83.0	15	PDB header: toxin Chain: B: PDB Molecule: tetanus toxin heavy chain; PDBTitle: the hc fragment of tetanus toxin complexed with an analogue of its2 ganglioside receptor gt1b
85	c2vxrA_	Alignment	not modelled	81.5	6	PDB header: toxin Chain: A: PDB Molecule: botulinum neurotoxin type g; PDBTitle: crystal structure of the botulinum neurotoxin serotype g2 binding domain
86	c3flpJ_	Alignment	not modelled	79.3	10	PDB header: sugar binding protein Chain: J: PDB Molecule: sap-like pentraxin; PDBTitle: crystal structure of native heptameric sap-like pentraxin2 from limulus polyphemus
87	d3btaa1	Alignment	not modelled	78.6	20	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Clostridium neurotoxins, the second last domain
88	c5ho0A_	Alignment	not modelled	78.2	11	PDB header: hydrolase Chain: A: PDB Molecule: extracellular arabinanase; PDBTitle: crystal structure of abna (closed conformation), a gh43 extracellular2 arabinanase from geobacillus stearothermophilus
89	c3immC_	Alignment	not modelled	77.5	11	PDB header: hydrolase Chain: C: PDB Molecule: putative secreted glycosylhydrolase; PDBTitle: crystal structure of putative glycosyl hydrolase (yp_001301887.1) from2 parabacteroides distasonis atcc 8503 at 2.00 a resolution
90	d1b09a_	Alignment	not modelled	75.5	13	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Pentraxin (pentaxin)
91	d1f9ka_	Alignment	not modelled	74.9	18	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Legume lectins
92	c5fraD_	Alignment	not modelled	73.2	10	PDB header: sugar binding protein Chain: D: PDB Molecule: sialidase; PDBTitle: cbm40_cpf0721-6'sl
93	c1yynA_	Alignment	not modelled	70.8	17	PDB header: hydrolase Chain: A: PDB Molecule: tetanus toxin; PDBTitle: a common binding site for disialyllactose and a tri-peptide2 in the c-fragment of tetanus neurotoxin
94	c1w0pA_	Alignment	not modelled	68.9	13	PDB header: hydrolase Chain: A: PDB Molecule: sialidase; PDBTitle: vibrio cholerae sialidase with alpha-2,6-sialyllactose
95	c3asiA_	Alignment	not modelled	68.5	28	PDB header: cell adhesion Chain: A: PDB Molecule: neurexin-1-alpha; PDBTitle: alpha-neurexin-1 ectodomain fragment; Ins5-egf3-Ins6
96	d1n47a_	Alignment	not modelled	67.6	18	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Legume lectins
97	c4u36A_	Alignment	not modelled	67.4	13	PDB header: sugar binding protein Chain: A: PDB Molecule: seed lectin; PDBTitle: crystal structure of a seed lectin from vatairea macrocarpa complexed2 with tn-antigen
98	c1kitA_	Alignment	not modelled	67.2	13	PDB header: hydrolase Chain: A: PDB Molecule: sialidase; PDBTitle: vibrio cholerae neuraminidase
99	c4pboA_	Alignment	not modelled	66.2	10	PDB header: immune system Chain: A: PDB Molecule: c-reactive protein; PDBTitle: crystal structure of zebrafish short-chain pentraxin protein without2 calcium ions
100	c4m01D_	Alignment	not modelled	66.0	13	PDB header: cell adhesion Chain: D: PDB Molecule: serine-rich adhesin for platelets; PDBTitle: n terminal fragment(residues 245-575) of binding region of srap
101	c4dqaA_	Alignment	not modelled	63.9	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative carbohydrate binding protein2 (bacova_03559) from bacteroides ovatus atcc 8483 at 1.50 a resolution
102	c2bqpA_	Alignment	not modelled	59.2	17	PDB header: sugar binding protein Chain: A: PDB Molecule: protein (pea lectin); PDBTitle: the structure of the pea lectin-d-glucopyranose complex
103	c3n7mA_	Alignment	not modelled	57.4	10	PDB header: toxin Chain: A: PDB Molecule: neurotoxin; PDBTitle: crystal structure of w1252a mutant of hcr d/c vpi 5995
104	c2eigB_	Alignment	not modelled	56.8	13	PDB header: sugar binding protein Chain: B: PDB Molecule: lectin; PDBTitle: lotus tetragonolobus seed lectin (isoform)
105	d2e74d2	Alignment	not modelled	56.6	26	Fold: Single transmembrane helix Superfamily: ISP transmembrane anchor Family: ISP transmembrane anchor
106	d2exha1	Alignment	not modelled	55.1	13	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Beta-D-xylosidase C-terminal domain-like

107	c3fuqA_	Alignment	not modelled	54.3	19	PDB header: toxin Chain: A: PDB Molecule: bont/f (neurotoxin type f); PDBTitle: glycosylated sv2 and gangliosides as dual receptors for2 botulinum neurotoxin serotype f
108	d1d2sa_	Alignment	not modelled	51.8	23	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Laminin G-like module
109	d1g7ya_	Alignment	not modelled	51.1	16	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Legume lectins
110	c3mppG_	Alignment	not modelled	51.1	10	PDB header: toxin Chain: G: PDB Molecule: botulinum neurotoxin type g; PDBTitle: botulinum neurotoxin type g receptor binding domain
111	d1saca_	Alignment	not modelled	50.2	14	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Pentraxin (pentaxin)
112	c2fmdA_	Alignment	not modelled	49.5	17	PDB header: sugar binding protein Chain: A: PDB Molecule: lectin; PDBTitle: structural basis of carbohydrate recognition by bowringia2 milbraedii seed agglutinin
113	d1dhkb_	Alignment	not modelled	48.4	21	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Legume lectins
114	d1gzca_	Alignment	not modelled	45.1	14	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Legume lectins
115	c3ipvC_	Alignment	not modelled	44.4	21	PDB header: sugar binding protein Chain: C: PDB Molecule: lectin alpha chain; PDBTitle: crystal structure of spatholobus parviflorus seed lectin
116	d1fx5a_	Alignment	not modelled	44.0	18	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Legume lectins
117	c2r1dF_	Alignment	not modelled	43.4	28	PDB header: cell adhesion, splicing Chain: F: PDB Molecule: neurexin-1-beta; PDBTitle: crystal structure of rat neurexin 1beta in the ca2+ containing form
118	c3zr6A_	Alignment	not modelled	42.3	8	PDB header: hydrolase Chain: A: PDB Molecule: galactocerebrosidase; PDBTitle: structure of galactocerebrosidase from mouse in complex with galactose
119	d1v6ia_	Alignment	not modelled	41.6	24	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Legume lectins
120	c5zbtA_	Alignment	not modelled	40.4	13	PDB header: unknown function Chain: A: PDB Molecule: lectin-like protein; PDBTitle: structure of legume lectin-like domain from entamoeba histolytica