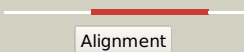





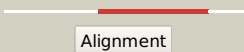











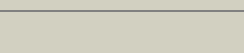











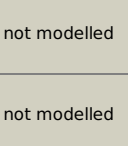


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1754c_(-)_1984986_1986677
Date	Fri Aug 2 13:30:36 BST 2019
Unique Job ID	0a90a6110d66f56f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4hbsA_	 Alignment		99.8	13	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of a putative hydrolase (bacova_04882) from <i>Bacteroides ovatus</i> ATCC 8483 at 2.80 Å resolution
2	d1so7a_	 Alignment		97.6	14	Fold: 6-bladed beta-propeller Superfamily: Sialidases Family: Sialidases (neuraminidases)
3	c5hx0A_	 Alignment		97.6	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein dfer_1899; PDBTitle: crystal structure of unknown function protein dfer_18992 from <i>Dyadobacter fermentans</i> DSM 18053
4	c3a72A_	 Alignment		97.6	14	PDB header: hydrolase Chain: A: PDB Molecule: exo-arabinanase; PDBTitle: high resolution structure of <i>Penicillium chrysogenum</i> alpha-L-2 arabinanase complexed with arabinobiose
5	d2ah2a2	 Alignment		97.5	21	Fold: 6-bladed beta-propeller Superfamily: Sialidases Family: Sialidases (neuraminidases)
6	c4fj6C_	 Alignment		97.4	20	PDB header: hydrolase Chain: C: PDB Molecule: glycoside hydrolase family 33, candidate sialidase; PDBTitle: crystal structure of a glycoside hydrolase family 33, candidate 2 sialidase (bdi_2946) from <i>Parabacteroides distasonis</i> ATCC 8503 at 3.190 Å resolution
7	c3nqhA_	 Alignment		97.4	17	PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolase; PDBTitle: crystal structure of a glycosyl hydrolase (bt_2959) from <i>Bacteroides thetaiotaomicron</i> VPI-5482 at 2.11 Å resolution
8	c2sliA_	 Alignment		97.3	18	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
9	c4bbwA_	 Alignment		97.2	18	PDB header: hydrolase Chain: A: PDB Molecule: sialidase (neuraminidase); PDBTitle: the crystal structure of sialidase VPI 5482 (btsa) from <i>Bacteroides thetaiotaomicron</i>
10	d1n1ta2	 Alignment		97.2	18	Fold: 6-bladed beta-propeller Superfamily: Sialidases Family: Sialidases (neuraminidases)
11	c1n1vA_	 Alignment		97.2	18	PDB header: hydrolase Chain: A: PDB Molecule: sialidase; PDBTitle: <i>Trypanosoma rangeli</i> sialidase in complex with DANA

12	c3qc2A	Alignment		97.1	14	PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolase; PDBTitle: crystal structure of a glycosyl hydrolase (bacova_03624) from2 bacteroides ovatus at 2.30 a resolution
13	c4u6dB	Alignment		97.1	21	PDB header: hydrolase Chain: B: PDB Molecule: conserved hypothetical periplasmic protein; PDBTitle: zg3615, a family 117 glycoside hydrolase in complex with beta-3,6-2 anhydro-l-galactose
14	c4u6bC	Alignment		97.1	17	PDB header: hydrolase Chain: C: PDB Molecule: conserved hypothetical lipoprotein; PDBTitle: zg3597, a family 117 glycoside hydrolase, produced by the marine2 bacterium zobellia galactanivorans
15	c3tawA	Alignment		97.1	17	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical glycoside hydrolase; PDBTitle: crystal structure of a putative glycoside hydrolase (bdi_3141) from2 parabacteroides distasonis atcc 8503 at 1.70 a resolution
16	c2xcyA	Alignment		97.1	16	PDB header: hydrolase Chain: A: PDB Molecule: extracellular sialidase/neuraminidase, putative; PDBTitle: crystal structure of aspergillus fumigatus sialidase
17	d1w0pa3	Alignment		96.9	12	Fold: 6-bladed beta-propeller Superfamily: Sialidases Family: Sialidases (neuraminidases)
18	c2vk7A	Alignment		96.9	20	PDB header: hydrolase Chain: A: PDB Molecule: exo-alpha-sialidase; PDBTitle: the structure of clostridium perfringens nani sialidase and2 its catalytic intermediates
19	c5a8dA	Alignment		96.9	14	PDB header: hydrolase Chain: A: PDB Molecule: carbohydrate binding family 6; PDBTitle: the high resolution structure of a novel alpha-l-arabinofuranosidase2 (ctgh43) from clostridium thermocellum atcc 27405
20	c5joxA	Alignment		96.9	15	PDB header: hydrolase Chain: A: PDB Molecule: non-reducing end alpha-l-arabinofuranosidase bogh43a; PDBTitle: bacteroides ovatus xyloglucan pul gh43a in complex with aradnj
21	c2jkbA	Alignment	not modelled	96.9	17	PDB header: lyase Chain: A: PDB Molecule: sialidase b; PDBTitle: crystal structure of streptococcus pneumoniae nanb in2 complex with 2,7-anhydro-neu5ac
22	c2w5oA	Alignment	not modelled	96.8	15	PDB header: hydrolase Chain: A: PDB Molecule: alpha-l-arabinofuranosidase; PDBTitle: complex structure of the gh93 alpha-l-arabinofuranosidase2 of fusarium graminearum with arabinobiose
23	c2berA	Alignment	not modelled	96.8	17	PDB header: hydrolase Chain: A: PDB Molecule: bacterial sialidase; PDBTitle: y370g active site mutant of the sialidase from2 micromonospora viridifaciens in complex with beta-neu5ac3 (sialic acid).
24	c3r4zA	Alignment	not modelled	96.7	17	PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolase family 32, n terminal; PDBTitle: crystal structure of alpha-neoagarobiose hydrolase (alpha-nabh) in2 complex with alpha-d-galactopyranose from saccharophagus degradans 2-3 40
25	d1yifa2	Alignment	not modelled	96.7	14	Fold: 5-bladed beta-propeller Superfamily: Arabinanase/levansucrase/invertase Family: alpha-L-arabinanase-like
26	c3p2nB	Alignment	not modelled	96.6	18	PDB header: hydrolase Chain: B: PDB Molecule: 3,6-anhydro-alpha-l-galactosidase; PDBTitle: discovery and structural characterization of a new glycoside hydrolase2 family abundant in coastal waters that was annotated as 'hypothetical3 protein'
27	c4n2rA	Alignment	not modelled	96.5	16	PDB header: hydrolase Chain: A: PDB Molecule: alpha-l-arabinofuranosidase umabf62a; PDBTitle: crystal structure of the alpha-l-arabinofuranosidase umabf62a from2 ustilago maydis in complex with l-arabinofuranose
						PDB header: hydrolase Chain: A: PDB Molecule: endo-1,4-beta-xylanase;

28	c3c7hA	Alignment	not modelled	96.5	17	PDBTitle: crystal structure of glycoside hydrolase family 43 arabinoxylan2 arabinofuranohydrolase from bacillus subtilis in complex with axos-4-3 0.5. PDB header: transferase Chain: B; PDB Molecule: uhgb_mp; PDBTitle: crystal structure of b-1,4-mannopyranosyl-chitobiose2 phosphorylase at 1.60 angstrom in complex with n-3 acetylglucosamine and inorganic phosphate
29	c4udgB	Alignment	not modelled	96.5	13	Fold: 6-bladed beta-propeller Superfamily: Sialidases Family: Endo-alpha-sialidase
30	d1v0ea1	Alignment	not modelled	96.4	32	PDB header: hydrolase Chain: A; PDB Molecule: sialidase; PDBTitle: vibrio cholerae sialidase with alpha-2,6-sialyllactose
31	c1w0pA	Alignment	not modelled	96.3	18	Fold: 6-bladed beta-propeller Superfamily: Sialidases Family: Sialidases (neuraminidases)
32	d1w8oa3	Alignment	not modelled	96.2	15	PDB header: hydrolase Chain: A; PDB Molecule: beta-xylosidase; PDBTitle: crystal structure of a thermostable glycoside hydrolase family 432 {beta}-1,4-xylosidase from geobacillus thermoleovorans it-08 in3 complex with d-xylose
33	c5z5hA	Alignment	not modelled	96.2	12	PDB header: hydrolase Chain: A; PDB Molecule: alpha-l-arabinofuranosidase axha-2; PDBTitle: structure of an alpha-l-arabinofuranosidase (gh62) from aspergillus2 nidulans
34	c5ubjA	Alignment	not modelled	96.2	14	PDB header: hydrolase Chain: A; PDB Molecule: neuraminidase c; PDBTitle: crystal structure of streptococcus pneumoniae nanc, complex with2 oseltamivir carboxylate
35	c4yw5A	Alignment	not modelled	96.0	15	PDB header: hydrolase Chain: A; PDB Molecule: putative secreted alpha l- arabinofuranosidase ii; PDBTitle: crystal structure of exo-1,5-alpha-l-arabinofuranosidase complexed2 with alpha-1,5-l-arabinofuranobiose
36	c3akgA	Alignment	not modelled	95.9	14	PDB header: hydrolase Chain: A; PDB Molecule: beta-galactosidase; PDBTitle: glycoside hydrolase bt_0996
37	c5muiA	Alignment	not modelled	95.9	14	Fold: 5-bladed beta-propeller Superfamily: Arabinanase/levansucrase/invertase Family: alpha-L-arabinanase-like
38	d2exha2	Alignment	not modelled	95.8	14	PDB header: hydrolase Chain: B; PDB Molecule: sialidase a; PDBTitle: structure of the catalytic domain of the native nana2 sialidase from streptococcus pneumoniae
39	c2w20B	Alignment	not modelled	95.7	17	PDB header: hydrolase Chain: A; PDB Molecule: putative glycosidase; PDBTitle: crystal structure of a putative glycosidase (bt_4094) from bacteroides2 thetaiotaomicron vpi-5482 at 2.30 a resolution
40	c3r67A	Alignment	not modelled	95.7	12	PDB header: hydrolase,viral protein Chain: A; PDB Molecule: endosialidase; PDBTitle: phage phi92 endosialidase
41	c4hizA	Alignment	not modelled	95.6	34	PDB header: hydrolase Chain: B; PDB Molecule: beta-xylosidase/alpha-l- arabinofuranosidase, gly43n; PDBTitle: the structure and function of an arabinan-specific alpha-1,2-2 arabinofuranosidase identified from screening the activities of3 bacterial gh43 glycoside hydrolases
42	c3qefB	Alignment	not modelled	95.5	12	PDB header: hydrolase Chain: A; PDB Molecule: beta-d-xylosidase; PDBTitle: structure of the family43 beta-xylosidase d15g mutant from geobacillus2 steartothermophilus
43	c2exiA	Alignment	not modelled	95.5	14	PDB header: transferase Chain: A; PDB Molecule: sialidase; PDBTitle: crystal structure of the pseudaminidase from pseudomonas aeruginosa
44	c2w38A	Alignment	not modelled	95.5	17	PDB header: hydrolase Chain: A; PDB Molecule: xylosidase/arabinofuranosidase xsa43e; PDBTitle: xsa43e, a gh43 family enzyme from butyrivibrio proteoclasticus
45	c4novA	Alignment	not modelled	95.2	12	PDB header: hydrolase Chain: B; PDB Molecule: endo-alpha-sialidase; PDBTitle: endosialidase of bacteriophage k1f
46	c1v0eB	Alignment	not modelled	95.2	37	PDB header: hydrolase Chain: A; PDB Molecule: sialidase a; PDBTitle: structure of the catalytic domain of streptococcus pneumoniae2 sialidase nana
47	c2vvzA	Alignment	not modelled	94.7	17	Fold: 6-bladed beta-propeller Superfamily: Sialidases Family: Sialidases (neuraminidases)
48	d2sli2	Alignment	not modelled	94.7	14	PDB header: hydrolase Chain: A; PDB Molecule: extracellular invertase; PDBTitle: aspergillus kawachii beta-fructofuranosidase
49	c5xh9A	Alignment	not modelled	94.6	19	PDB header: hydrolase Chain: A; PDB Molecule: putative glycoside hydrolase; PDBTitle: crystal structure of a putative glycoside hydrolase (bacova_02161)2 from bacteroides ovatus atcc 8483 at 1.85 a resolution
50	c4onzA	Alignment	not modelled	94.6	14	Fold: 5-bladed beta-propeller Superfamily: Arabinanase/levansucrase/invertase Family: alpha-L-arabinanase-like
51	d1yrza2	Alignment	not modelled	94.6	15	Fold: 5-bladed beta-propeller Superfamily: Arabinanase/levansucrase/invertase Family: alpha-L-arabinanase-like
52	d1gyha	Alignment	not modelled	94.4	9	PDB header: hydrolase

53	c4mlgF_	Alignment	not modelled	94.3	15	Chain: F: PDB Molecule: beta-xylosidase; PDBTitle: structure of rs223-beta-xylosidase
54	c4eqvA_	Alignment	not modelled	94.1	12	PDB header: hydrolase Chain: A: PDB Molecule: invertase 2; PDBTitle: structure of saccharomyces cerevisiae invertase
55	d1vkda_	Alignment	not modelled	93.4	14	Fold: 5-bladed beta-propeller Superfamily: Arabinanase/levansucrase/invertase Family: TM1225-like predicted glycosylases
56	c6euiA_	Alignment	not modelled	93.3	15	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucanase; PDBTitle: the gh43, beta 1,3 galactosidase, bt3683 with galactose
57	c6eujC_	Alignment	not modelled	93.2	14	PDB header: hydrolase Chain: C: PDB Molecule: beta-glucanase; PDBTitle: the gh43, beta 1,3 galactosidase, bt0265
58	c5fk8B_	Alignment	not modelled	93.1	19	PDB header: hydrolase Chain: B: PDB Molecule: beta-fructofuranosidase; PDBTitle: structure of d80a-fructofuranosidase from xanthophyllomyces2 dendrorhous complexed with neo-erlose
59	d3sila_	Alignment	not modelled	93.1	11	Fold: 6-bladed beta-propeller Superfamily: Sialidases Family: Sialidases (neuraminidases)
60	c1yrzB_	Alignment	not modelled	92.7	16	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
61	d2ebsa2	Alignment	not modelled	92.6	28	Fold: 7-bladed beta-propeller Superfamily: Oligoxyloglucan reducing end-specific cellobiohydrolase Family: Oligoxyloglucan reducing end-specific cellobiohydrolase
62	c3qz4B_	Alignment	not modelled	92.4	16	PDB header: hydrolase Chain: B: PDB Molecule: endo-1,4-beta-xylanase d; PDBTitle: crystal structure of an endo-1,4-beta-xylanase d (bt_3675) from2 bacteroides thetaiotaomicron vpi-5482 at 1.74 a resolution
63	c5flwB_	Alignment	not modelled	92.2	8	PDB header: hydrolase Chain: B: PDB Molecule: exo-beta-1,3-galactanase; PDBTitle: crystal structure of putative exo-beta-1,3-galactanase from2 bifidobacterium bifidum s17
64	c3lemA_	Alignment	not modelled	92.2	17	PDB header: hydrolase Chain: A: PDB Molecule: fructosyltransferase; PDBTitle: crystal structure of fructosyltransferase (d191a) from a japonicus in2 complex with nystose
65	d1uv4a1	Alignment	not modelled	92.2	11	Fold: 5-bladed beta-propeller Superfamily: Arabinanase/levansucrase/invertase Family: alpha-L-arabinanase-like
66	c3kf5A_	Alignment	not modelled	91.4	13	PDB header: hydrolase Chain: A: PDB Molecule: invertase; PDBTitle: structure of invertase from schwanniomyces occidentalis
67	d1y7ba2	Alignment	not modelled	91.4	15	Fold: 5-bladed beta-propeller Superfamily: Arabinanase/levansucrase/invertase Family: alpha-L-arabinanase-like
68	c4qqsB_	Alignment	not modelled	90.6	17	PDB header: hydrolase Chain: B: PDB Molecule: glycoside hydrolase family 43; PDBTitle: crystal structure of a thermostable family-43 glycoside hydrolase
69	c5fzpB_	Alignment	not modelled	90.3	27	PDB header: signaling protein Chain: B: PDB Molecule: dispase autolysis-inducing protein; PDBTitle: structure of the dispase autolysis inducing protein from2 streptomyces mobaraensis
70	c3vt2B_	Alignment	not modelled	90.3	16	PDB header: sugar binding protein Chain: B: PDB Molecule: ricin b lectin; PDBTitle: crystal structure of ct1,3gal43a in complex with isopropyl-beta-d-2 thiogalactoside
71	c1kitA_	Alignment	not modelled	90.3	10	PDB header: hydrolase Chain: A: PDB Molecule: sialidase; PDBTitle: vibrio cholerae neuraminidase
72	c3cpnA_	Alignment	not modelled	90.1	14	PDB header: hydrolase Chain: A: PDB Molecule: beta-xylosidase, family 43 glycosyl hydrolase; PDBTitle: crystal structure of beta-xylosidase, family 43 glycosyl2 hydrolase from clostridium acetobutylicum
73	c3wsxA_	Alignment	not modelled	89.5	16	PDB header: protein binding Chain: A: PDB Molecule: sortilin-related receptor; PDBTitle: sorla vps10p domain in ligand-free form
74	c5uasA_	Alignment	not modelled	89.4	14	PDB header: lyase Chain: A: PDB Molecule: ulvanlyase-pl25; PDBTitle: structure of a new family of polysaccharide lyase pl25-ulvanlyase2 bound to -[glca(1-4)rha3s]-
75	c2aezA_	Alignment	not modelled	89.2	13	PDB header: hydrolase Chain: A: PDB Molecule: fructan 1-exohydrolase iia; PDBTitle: crystal structure of fructan 1-exohydrolase iia (e201q) from cichorium2 intybus in complex with 1-kestose
76	d1uypa2	Alignment	not modelled	88.9	17	Fold: 5-bladed beta-propeller Superfamily: Arabinanase/levansucrase/invertase Family: Glycosyl hydrolases family 32 N-terminal domain
77	c5glkB_	Alignment	not modelled	88.6	17	PDB header: hydrolase Chain: B: PDB Molecule: glycoside hydrolase family 43; PDBTitle: crystal structure of coxyl43, gh43 beta-xylosidase/alpha-2 arabinofuranosidase from a compost microbial metagenome, calcium-free3 form.
78	c4pviA_	Alignment	not modelled	88.4	15	PDB header: hydrolase Chain: A: PDB Molecule: gh62 hydrolase; PDBTitle: crystal structure of gh62 hydrolase in complex with xylotriose PDB header: hydrolase

79	c4n2zA_	Alignment	not modelled	88.3	18	Chain: A; PDB Molecule: gh62 arabinofuranosidase; PDBTitle: crystal structure of the alpha-l-arabinofuranosidase paabf62a from2 podospira anserina in complex with cellobiose
80	c3a0fA_	Alignment	not modelled	87.5	19	PDB header: hydrolase Chain: A; PDB Molecule: xyloglucanase; PDBTitle: the crystal structure of geotrichum sp. m128 xyloglucanase
81	c5ho0A_	Alignment	not modelled	87.5	15	PDB header: hydrolase Chain: A; PDB Molecule: extracellular arabinanase; PDBTitle: crystal structure of abna (closed conformation), a gh43 extracellular2 arabinanase from geobacillus stearothermophilus
82	c1yifC_	Alignment	not modelled	87.4	15	PDB header: hydrolase Chain: C; PDB Molecule: beta-1,4-xylosidase; PDBTitle: crystal structure of beta-1,4-xylosidase from bacillus subtilis, new2 york structural genomics consortium
83	c5j0zB_	Alignment	not modelled	87.4	23	PDB header: hydrolase Chain: B; PDB Molecule: non-reducing end alpha-l-arabinofuranosidase bogh43b; PDBTitle: bacteroides ovatus xyloglucan pul gh43b
84	c4lgnA_	Alignment	not modelled	86.5	31	PDB header: cellulose binding protein Chain: A; PDB Molecule: cellulose-binding, family ii; PDBTitle: the structure of acidothermus cellulolyticus family 74 glycoside2 hydrolase
85	c3wszA_	Alignment	not modelled	86.4	16	PDB header: protein binding Chain: A; PDB Molecule: sortilin-related receptor; PDBTitle: sorla vps10p domain in complex with abeta-derived peptide
86	c1w2tE_	Alignment	not modelled	86.3	17	PDB header: hydrolase Chain: E; PDB Molecule: beta fructosidase; PDBTitle: beta-fructosidase from thermotoga maritima in complex with raffinose
87	c5oj3A_	Alignment	not modelled	85.7	20	PDB header: photosynthesis Chain: A; PDB Molecule: photosystem ii stability/assembly factor hcf136; PDBTitle: ycf48 from cyanidioschyzon merolae
88	c5aycA_	Alignment	not modelled	84.8	15	PDB header: transferase Chain: A; PDB Molecule: 4-o-beta-d-mannosyl-d-glucose phosphorylase; PDBTitle: crystal structure of ruminococcus albus 4-o-beta-d-mannosyl-d-glucose2 phosphorylase (ramp1) in complexes with sulfate and 4-o-beta-d-3 mannosyl-d-glucose
89	d2ebsa1	Alignment	not modelled	84.7	11	Fold: 7-bladed beta-propeller Superfamily: Oligoxyloglucan reducing end-specific cellobiohydrolase Family: Oligoxyloglucan reducing end-specific cellobiohydrolase
90	c2y38A_	Alignment	not modelled	84.2	28	PDB header: structural protein Chain: A; PDB Molecule: laminin subunit alpha-5; PDBTitle: laminin alpha5 chain n-terminal fragment
91	c3f6kA_	Alignment	not modelled	83.9	21	PDB header: signaling protein Chain: A; PDB Molecule: sortilin; PDBTitle: crystal structure of the vps10p domain of human sortilin/nts3 in2 complex with neurotensin
92	c3ugfB_	Alignment	not modelled	83.6	17	PDB header: transferase Chain: B; PDB Molecule: sucrose:(sucrose/fructan) 6-fructosyltransferase; PDBTitle: crystal structure of a 6-sst/6-sft from pachysandra terminalis
93	c4ploA_	Alignment	not modelled	83.1	31	PDB header: protein binding Chain: A; PDB Molecule: netrin-1; PDBTitle: crystal structure of chicken netrin-1 (ln-le3) in complex with mouse2 dcc (fn4-5)
94	d1wl7a1	Alignment	not modelled	82.6	14	Fold: 5-bladed beta-propeller Superfamily: Arabinanase/levansucrase/invertase Family: alpha-L-arabinanase-like
95	c4aqsA_	Alignment	not modelled	82.5	19	PDB header: cell adhesion Chain: A; PDB Molecule: laminin subunit beta-1; PDBTitle: laminin beta1 ln-le1-4 structure
96	c6ms3A_	Alignment	not modelled	82.0	14	PDB header: hydrolase Chain: A; PDB Molecule: glycoside hydrolase family 43; PDBTitle: crystal structure of the gh43 protein blxynb mutant (k247s) from2 bacillus licheniformis
97	c4wnxA_	Alignment	not modelled	81.9	19	PDB header: laminin binding protein Chain: A; PDB Molecule: netrin-4; PDBTitle: netrin 4 lacking the c-terminal domain
98	c2xbgA_	Alignment	not modelled	81.3	27	PDB header: photosynthesis Chain: A; PDB Molecule: ycf48-like protein; PDBTitle: crystal structure of ycf48 from thermosynechococcus elongatus
99	c2ebsB_	Alignment	not modelled	80.0	11	PDB header: hydrolase Chain: B; PDB Molecule: oligoxyloglucan reducing end-specific PDBTitle: crystal structure analysis of oligoxyloglucan reducing-end-2 specific cellobiohydrolase (oxg-rcbh) d465n mutant3 complexed with a xyloglucan heptasaccharide
100	c3kstA_	Alignment	not modelled	79.3	14	PDB header: hydrolase Chain: A; PDB Molecule: endo-1,4-beta-xylanase; PDBTitle: crystal structure of endo-1,4-beta-xylanase (np_811807.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.70 a resolution
101	c5nmrA_	Alignment	not modelled	75.9	17	PDB header: protein transport Chain: A; PDB Molecule: sortilin; PDBTitle: monomeric mouse sortilin extracellular domain
102	c3tbdA_	Alignment	not modelled	74.4	25	PDB header: cell adhesion Chain: A; PDB Molecule: netrin-g2; PDBTitle: crystal structure of domain vi and le1 of human netrin-g2
103	c3zyiB_	Alignment	not modelled	74.0	28	PDB header: cell adhesion Chain: B; PDB Molecule: netrin-g2; PDBTitle: netring2 in complex with ngl2
104	c6ffyA_	Alignment	not modelled	73.7	17	PDB header: apoptosis Chain: A; PDB Molecule: vps10 domain-containing receptor sorcs2;

						PDBTitle: structure of the mouse sorcs2-ngf complex
105	c6n1bA_	Alignment	not modelled	71.9	17	PDB header: hydrolase Chain: A; PDB Molecule: carbohydrate-binding protein; PDBTitle: crystal structure of an n-acetylgalactosamine deacetylase from f.2 plautii in complex with blood group b trisaccharide
106	c1y9gA_	Alignment	not modelled	70.7	13	PDB header: hydrolase Chain: A; PDB Molecule: exo-inulinase; PDBTitle: crystal structure of exo-inulinase from aspergillus awamori complexed2 with fructose
107	c3zyjB_	Alignment	not modelled	69.7	25	PDB header: cell adhesion Chain: B; PDB Molecule: netrin-g1; PDBTitle: netring1 in complex with ngl1
108	c5g5oC_	Alignment	not modelled	69.4	19	PDB header: viral protein Chain: C; PDB Molecule: lh3 hexon-interlacing capsid protein; PDBTitle: structure of the snake adenovirus 1 hexon-interlacing lh3 protein,2 native
109	c4nl6C_	Alignment	not modelled	68.8	17	PDB header: splicing Chain: C; PDB Molecule: survival motor neuron protein; PDBTitle: structure of the full-length form of the protein smn found in healthy2 patients
110	c4ffhA_	Alignment	not modelled	68.0	16	PDB header: transferase Chain: A; PDB Molecule: levan fructotransferase; PDBTitle: crystal structure of levan fructotransferase d54n mutant from2 arthrobacter ureafaciens in complex with sucrose
111	c6mgkB_	Alignment	not modelled	67.2	10	PDB header: hydrolase Chain: B; PDB Molecule: xyloglucanase; PDBTitle: crystal structure of the catalytic domain from gh74 enzyme pogh74 from2 paenibacillus odorifer, in complex with xlx xyloglucan
112	c5b0rA_	Alignment	not modelled	65.1	20	PDB header: transferase Chain: A; PDB Molecule: lin0857 protein; PDBTitle: beta-1,2-mannobiose phosphorylase from listeria innocua - beta-1,2-2 mannobiose complex
113	c2cn2C_	Alignment	not modelled	64.8	11	PDB header: hydrolase Chain: C; PDB Molecule: beta-1,4-xyloglucan hydrolase; PDBTitle: crystal structures of clostridium thermocellum2 xyloglucanase
114	c4aqtA_	Alignment	not modelled	64.1	14	PDB header: cell adhesion Chain: A; PDB Molecule: laminin subunit gamma-1; PDBTitle: laminin gamma1 ln-le1-2 structure
115	c5yjeA_	Alignment	not modelled	61.7	20	PDB header: gene regulation Chain: A; PDB Molecule: protein hira; PDBTitle: crystal structure of hira(644-1017)
116	c6r3uA_	Alignment	not modelled	60.3	12	PDB header: hydrolase Chain: A; PDB Molecule: glycoside hydrolase family 32; PDBTitle: endo-levanase bt1760 mutant e221a from bacteroides thetaiotaomicron2 complexed with levantetraose
117	c3watA_	Alignment	not modelled	60.2	13	PDB header: transferase Chain: A; PDB Molecule: 4-o-beta-d-mannosyl-d-glucose phosphorylase; PDBTitle: crystal structure of 4-o-beta-d-mannosyl-d-glucose phosphorylase mgp2 complexed with man+glc
118	c5jwzA_	Alignment	not modelled	58.2	10	PDB header: hydrolase Chain: A; PDB Molecule: cellulose-binding family ii; PDBTitle: structure of a putative xyloglucanase from the cellulolytic bacteria2 streptomyces sp. sirexaa-e
119	c3lv4B_	Alignment	not modelled	58.2	13	PDB header: hydrolase Chain: B; PDB Molecule: glycoside hydrolase yxia; PDBTitle: crystal structure of the glycoside hydrolase, family 43 yxia protein2 from bacillus licheniformis. northeast structural genomics consortium3 target bir14.
120	c5c0pA_	Alignment	not modelled	56.6	11	PDB header: hydrolase Chain: A; PDB Molecule: endo-arabinase; PDBTitle: the crystal structure of endo-arabinase from bacteroides2 thetaiotaomicron vpi-5482