


























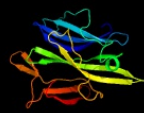







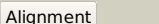
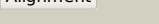


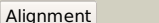
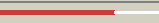
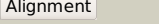



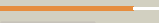
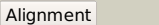

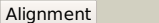

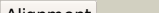
# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3707c_(-)_4150208_4151218
Date	Fri Aug 9 18:20:40 BST 2019
Unique Job ID	f8202c65c5ca1092

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4hbsA_</a>	 Alignment		100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hydrolase; <b>PDBTitle:</b> crystal structure of a putative hydrolase (bacova_04882) from <i>Bacteroides ovatus</i> ATCC 8483 at 2.80 Å resolution
2	<a href="#">d1gyha_</a>	 Alignment		97.6	11	<b>Fold:</b> 5-bladed beta-propeller <b>Superfamily:</b> Arabinanase/levansucrase/invertase <b>Family:</b> alpha-L-arabinanase-like
3	<a href="#">c3p2nB_</a>	 Alignment		97.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 3,6-anhydro-alpha-L-galactosidase; <b>PDBTitle:</b> discovery and structural characterization of a new glycoside hydrolase2 family abundant in coastal waters that was annotated as 'hypothetical3 protein'
4	<a href="#">c5z5hA_</a>	 Alignment		97.2	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-xylosidase; <b>PDBTitle:</b> crystal structure of a thermostable glycoside hydrolase family 432 {beta}-1,4-xylosidase from <i>Geobacillus thermoleovorans</i> IT-08 in 3 complex with D-xylose
5	<a href="#">c5a8dA_</a>	 Alignment		97.1	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carbohydrate binding family 6; <b>PDBTitle:</b> the high resolution structure of a novel alpha-L-arabinofuranosidase2 (ctgh43) from <i>Clostridium thermocellum</i> ATCC 27405
6	<a href="#">d1vkda_</a>	 Alignment		97.0	15	<b>Fold:</b> 5-bladed beta-propeller <b>Superfamily:</b> Arabinanase/levansucrase/invertase <b>Family:</b> TM1225-like predicted glycosylases
7	<a href="#">c3r4zA_</a>	 Alignment		97.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyl hydrolase family 32, N-terminal; <b>PDBTitle:</b> crystal structure of alpha-neoagarobiose hydrolase (alpha-NabH) in 2 complex with alpha-D-galactopyranose from <i>Saccharophagus degradans</i> 2-3 40
8	<a href="#">d2exha2</a>	 Alignment		96.6	15	<b>Fold:</b> 5-bladed beta-propeller <b>Superfamily:</b> Arabinanase/levansucrase/invertase <b>Family:</b> alpha-L-arabinanase-like
9	<a href="#">c5joxA_</a>	 Alignment		96.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> non-reducing end alpha-L-arabinofuranosidase bogh43a; <b>PDBTitle:</b> <i>Bacteroides ovatus</i> xyloglucan pul gh43a in complex with aradnj
10	<a href="#">c2exiA_</a>	 Alignment		96.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-D-xylosidase; <b>PDBTitle:</b> structure of the family43 beta-xylosidase d15g mutant from <i>Geobacillus stearothermophilus</i>
11	<a href="#">c4mlgF_</a>	 Alignment		96.1	9	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> beta-xylosidase; <b>PDBTitle:</b> structure of rs223-beta-xylosidase

12	<a href="#">c3akgA</a>	Alignment		95.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative secreted alpha l-arabinofuranosidase ii; <b>PDBTitle:</b> crystal structure of exo-1,5-alpha-l-arabinofuranosidase complexed2 with alpha-1,5-l-arabinofuranobiose
13	<a href="#">c4novA</a>	Alignment		95.7	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> xylosidase/arabinofuranosidase xsa43e; <b>PDBTitle:</b> xsa43e, a gh43 family enzyme from butyrivibrio proteoclasticus
14	<a href="#">c4udgB</a>	Alignment		95.6	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> uhgb_mp; <b>PDBTitle:</b> crystal structure of b-1,4-mannopyranosyl-chitobiose2 phosphorylase at 1.60 angstrom in complex with n-3 acetylglucosamine and inorganic phosphate
15	<a href="#">d1uv4a1</a>	Alignment		95.6	12	<b>Fold:</b> 5-bladed beta-propeller <b>Superfamily:</b> Arabinanase/levansucrase/invertase <b>Family:</b> alpha-L-arabinanase-like
16	<a href="#">c3lv4B</a>	Alignment		95.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycoside hydrolase xyia; <b>PDBTitle:</b> crystal structure of the glycoside hydrolase, family 43 xyia protein2 from bacillus licheniformis. northeast structural genomics consortium3 target bir14.
17	<a href="#">c3tawA</a>	Alignment		95.6	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical glycoside hydrolase; <b>PDBTitle:</b> crystal structure of a putative glycoside hydrolase (bdi_3141) from2 parabacteroides distazonis atcc 8503 at 1.70 a resolution
18	<a href="#">c4n2rA</a>	Alignment		95.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-l-arabinofuranosidase umabf62a; <b>PDBTitle:</b> crystal structure of the alpha-l-arabinofuranosidase umabf62a from2 ustilago maydis in complex with l-arabinofuranose
19	<a href="#">c4qqsB</a>	Alignment		95.5	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycoside hydrolase family 43; <b>PDBTitle:</b> crystal structure of a thermostable family-43 glycoside hydrolase
20	<a href="#">d1y7ba2</a>	Alignment		94.7	10	<b>Fold:</b> 5-bladed beta-propeller <b>Superfamily:</b> Arabinanase/levansucrase/invertase <b>Family:</b> alpha-L-arabinanase-like
21	<a href="#">c3qz4B</a>	Alignment	not modelled	94.4	9	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endo-1,4-beta-xylanase d; <b>PDBTitle:</b> crystal structure of an endo-1,4-beta-xylanase d (bt_3675) from2 bacteroides thetaiotaomicron vpi-5482 at 1.74 a resolution
22	<a href="#">c5qlkB</a>	Alignment	not modelled	94.4	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycoside hydrolase family 43; <b>PDBTitle:</b> crystal structure of coxyl43, gh43 beta-xylosidase/alpha-2 arabinofuranosidase from a compost microbial metagenome, calcium-free3 form.
23	<a href="#">c1yifC</a>	Alignment	not modelled	94.2	12	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> beta-1,4-xylosidase; <b>PDBTitle:</b> crystal structure of beta-1,4-xylosidase from bacillus subtilis, new2 york structural genomics consortium
24	<a href="#">c4u6bC</a>	Alignment	not modelled	94.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> conserved hypothetical lipoprotein; <b>PDBTitle:</b> zg3597, a family 117 glycoside hydrolase, produced by the marine2 bacterium zobellia galactanivorans
25	<a href="#">d1wl7a1</a>	Alignment	not modelled	93.9	14	<b>Fold:</b> 5-bladed beta-propeller <b>Superfamily:</b> Arabinanase/levansucrase/invertase <b>Family:</b> alpha-L-arabinanase-like
26	<a href="#">c5ho0A</a>	Alignment	not modelled	93.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> extracellular arabinanase; <b>PDBTitle:</b> crystal structure of abna (closed conformation), a gh43 extracellular2 arabinanase from geobacillus stearothermophilus
27	<a href="#">c3kstA</a>	Alignment	not modelled	93.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-1,4-beta-xylanase; <b>PDBTitle:</b> crystal structure of endo-1,4-beta-xylanase (np_811807.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.70 a resolution
28	<a href="#">c1yrzB</a>	Alignment	not modelled	93.4	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> xylan beta-1,4-xylosidase; <b>PDBTitle:</b> crystal structure of xylan beta-1,4-xylosidase from bacillus2 halodurans c-125

29	<a href="#">c4u6dB</a>	 Alignment	not modelled	93.4	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> conserved hypothetical periplasmic protein; <b>PDBTitle:</b> zg3615, a family 117 glycoside hydrolase in complex with beta-3,6-2 anhydro-l-galactose
30	<a href="#">c3qefB</a>	 Alignment	not modelled	93.3	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-xylosidase/alpha-l-arabinofuranosidase, gly43n; <b>PDBTitle:</b> the structure and function of an arabinan-specific alpha-1,2-2 arabinofuranosidase identified from screening the activities of 3 bacterial gh43 glycoside hydrolases
31	<a href="#">c3vt2B</a>	 Alignment	not modelled	93.3	11	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> ricin b lectin; <b>PDBTitle:</b> crystal structure of ct1,3gal43a in complex with isopropyl-beta-d-2 thiogalactoside
32	<a href="#">c2sliA</a>	 Alignment	not modelled	93.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> intramolecular trans-sialidase; <b>PDBTitle:</b> leech intramolecular trans-sialidase complexed with 2,7-2 anhydro-neu5ac, the reaction product
33	<a href="#">c1w0pA</a>	 Alignment	not modelled	93.1	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sialidase; <b>PDBTitle:</b> vibrio cholerae sialidase with alpha-2,6-sialyllactose
34	<a href="#">c5jozB</a>	 Alignment	not modelled	93.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> non-reducing end alpha-l-arabinofuranosidase bogh43b; <b>PDBTitle:</b> bacteroides ovatus xyloglucan pul gh43b
35	<a href="#">d1yrza2</a>	 Alignment	not modelled	92.7	12	<b>Fold:</b> 5-bladed beta-propeller <b>Superfamily:</b> Arabinanase/levansucrase/invertase <b>Family:</b> alpha-L-arabinanase-like
36	<a href="#">c4pviA</a>	 Alignment	not modelled	92.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gh62 hydrolase; <b>PDBTitle:</b> crystal structure of gh62 hydrolase in complex with xylotriase
37	<a href="#">d1uypa2</a>	 Alignment	not modelled	92.4	14	<b>Fold:</b> 5-bladed beta-propeller <b>Superfamily:</b> Arabinanase/levansucrase/invertase <b>Family:</b> Glycosyl hydrolases family 32 N-terminal domain
38	<a href="#">d1n1ta2</a>	 Alignment	not modelled	92.3	16	<b>Fold:</b> 6-bladed beta-propeller <b>Superfamily:</b> Sialidases <b>Family:</b> Sialidases (neuraminidases)
39	<a href="#">c6euiA</a>	 Alignment	not modelled	92.2	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucanase; <b>PDBTitle:</b> the gh43, beta 1,3 galactosidase, bt3683 with galactose
40	<a href="#">c3c7hA</a>	 Alignment	not modelled	91.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-1,4-beta-xylanase; <b>PDBTitle:</b> crystal structure of glycoside hydrolase family 43 arabinoxylan2 arabinofuranohydrolase from bacillus subtilis in complex with axos-4-3 0.5.
41	<a href="#">c1n1vA</a>	 Alignment	not modelled	91.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sialidase; <b>PDBTitle:</b> trypanosoma rangeli sialidase in complex with dana
42	<a href="#">c1yi7C</a>	 Alignment	not modelled	90.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> beta-xylosidase, family 43 glycosyl hydrolase; <b>PDBTitle:</b> beta-d-xylosidase (selenomethionine) xynd from clostridium2 acetobutylicum
43	<a href="#">c5ubjA</a>	 Alignment	not modelled	90.4	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-l-arabinofuranosidase axha-2; <b>PDBTitle:</b> structure of an alpha-l-arabinofuranosidase (gh62) from aspergillus2 nidulans
44	<a href="#">c3qc2A</a>	 Alignment	not modelled	89.3	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyl hydrolase; <b>PDBTitle:</b> crystal structure of a glycosyl hydrolase (bacova_03624) from2 bacteroides ovatus at 2.30 a resolution
45	<a href="#">d1vifa2</a>	 Alignment	not modelled	89.1	9	<b>Fold:</b> 5-bladed beta-propeller <b>Superfamily:</b> Arabinanase/levansucrase/invertase <b>Family:</b> alpha-L-arabinanase-like
46	<a href="#">c5aydB</a>	 Alignment	not modelled	88.9	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-1,4-mannooligosaccharide phosphorylase; <b>PDBTitle:</b> crystal structure of ruminococcus albus beta-(1,4)-2 mannoooligosaccharide phosphorylase (ramp2) in complexes with3 phosphate
47	<a href="#">c4n2zA</a>	Alignment	not modelled	88.5	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gh62 arabinofuranosidase; <b>PDBTitle:</b> crystal structure of the alpha-l-arabinofuranosidase paabf62a from2 podospora anserina in complex with celotriose
48	<a href="#">c4hizA</a>	Alignment	not modelled	88.0	18	<b>PDB header:</b> hydrolase,viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> endosialidase; <b>PDBTitle:</b> phage phi92 endosialidase
49	<a href="#">c5c0pA</a>	Alignment	not modelled	86.6	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-arabinase; <b>PDBTitle:</b> the crystal structure of endo-arabinase from bacteroides2 thetaiotaomicron vpi-5482
50	<a href="#">c3cpnA</a>	Alignment	not modelled	85.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-xylosidase, family 43 glycosyl hydrolase; <b>PDBTitle:</b> crystal structure of beta-xylosidase, family 43 glycosyl2 hydrolase from clostridium acetobutylicum
51	<a href="#">d2ah2a2</a>	Alignment	not modelled	83.3	17	<b>Fold:</b> 6-bladed beta-propeller <b>Superfamily:</b> Sialidases <b>Family:</b> Sialidases (neuraminidases)
52	<a href="#">c3nqhA</a>	Alignment	not modelled	81.6	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyl hydrolase; <b>PDBTitle:</b> crystal structure of a glycosyl hydrolase (bt_2959) from bacteroides2 thetaiotaomicron vpi-5482 at 2.11 a resolution
53	<a href="#">c6mc2A</a>	Alignment	not modelled	81.4	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycoside hydrolase family 43;

53	<a href="#">c0ms9A</a>	Alignment	not modelled	81.4	12	<b>PDBTitle:</b> crystal structure of the gh43 protein blxybn mutant (k247s) from2 bacillus licheniformis <b>PDB header:</b> hydrolase
54	<a href="#">c4onzA</a>	Alignment	not modelled	78.3	7	<b>Chain:</b> A; <b>PDB Molecule:</b> putative glycoside hydrolase; <b>PDBTitle:</b> crystal structure of a putative glycoside hydrolase (bacova_02161)2 from bacteroides ovatus atcc 8483 at 1.85 a resolution <b>PDB header:</b> hydrolase
55	<a href="#">c5fk8B</a>	Alignment	not modelled	78.3	15	<b>Chain:</b> B; <b>PDB Molecule:</b> beta-fructofuranosidase; <b>PDBTitle:</b> structure of d80a-fructofuranosidase from xanthophyllomyces2 dendrorhous complexed with neo-erlose <b>PDB header:</b> hydrolase
56	<a href="#">c1w2tE</a>	Alignment	not modelled	78.2	11	<b>Chain:</b> E; <b>PDB Molecule:</b> beta fructosidase; <b>PDBTitle:</b> beta-fructosidase from thermotoga maritima in complex with raffinose <b>PDB header:</b> hydrolase
57	<a href="#">c2vk7A</a>	Alignment	not modelled	78.0	17	<b>Chain:</b> A; <b>PDB Molecule:</b> exo-alpha-sialidase; <b>PDBTitle:</b> the structure of clostridium perfringens nani sialidase and2 its catalytic intermediates <b>PDB header:</b> hydrolase
58	<a href="#">c2aezA</a>	Alignment	not modelled	76.4	18	<b>Chain:</b> A; <b>PDB Molecule:</b> fructan 1-exohydrolase iia; <b>PDBTitle:</b> crystal structure of putative 1-exohydrolase iia (e201q) from cichorium2 intybus in complex with 1-kestose <b>PDB header:</b> lyase
59	<a href="#">c2jkbA</a>	Alignment	not modelled	75.6	12	<b>Chain:</b> A; <b>PDB Molecule:</b> sialidase b; <b>PDBTitle:</b> crystal structure of streptococcus pneumoniae nanb in2 complex with 2,7-anhydro-neu5ac <b>PDB header:</b> hydrolase
60	<a href="#">c1v0eB</a>	Alignment	not modelled	74.6	15	<b>Chain:</b> B; <b>PDB Molecule:</b> endo-alpha-sialidase; <b>PDBTitle:</b> endosialidase of bacteriophage k1f <b>PDB header:</b> hydrolase
61	<a href="#">c6r3uA</a>	Alignment	not modelled	70.9	13	<b>Chain:</b> A; <b>PDB Molecule:</b> glycoside hydrolase family 32; <b>PDBTitle:</b> endo-levanase bt1760 mutant e221a from bacteroides thetaiotaomicron2 complexed with levantetraose <b>PDB header:</b> hydrolase
62	<a href="#">c6eujC</a>	Alignment	not modelled	67.0	8	<b>Chain:</b> C; <b>PDB Molecule:</b> beta-glucanase; <b>PDBTitle:</b> the gh43, beta 1,3 galactosidase, bt0265 <b>PDB header:</b> hydrolase
63	<a href="#">c2w5oA</a>	Alignment	not modelled	65.2	11	<b>Chain:</b> A; <b>PDB Molecule:</b> alpha-l-arabinofuranosidase; <b>PDBTitle:</b> complex structure of the gh93 alpha-l-arabinofuranosidase2 of fusarium graminearum with arabinobiose <b>PDB header:</b> hydrolase
64	<a href="#">c5flwB</a>	Alignment	not modelled	64.9	12	<b>Chain:</b> B; <b>PDB Molecule:</b> exo-beta-1,3-galactanase; <b>PDBTitle:</b> crystal structure of putative exo-beta-1,3-galactanase from2 bifidobacterium bifidum s17 <b>PDB header:</b> transferase
65	<a href="#">c2w38A</a>	Alignment	not modelled	64.9	11	<b>Chain:</b> A; <b>PDB Molecule:</b> sialidase; <b>PDBTitle:</b> crystal structure of the pseudaminidase from pseudomonas aeruginosa <b>PDB header:</b> structural genomics, unknown function
66	<a href="#">c5hx0A</a>	Alignment	not modelled	63.5	19	<b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein dfer_1899; <b>PDBTitle:</b> crystal structure of unknown function protein dfer_18992 fromdyadobacter fermentans dsm 18053 <b>PDB header:</b> hydrolase
67	<a href="#">c2w20B</a>	Alignment	not modelled	62.7	11	<b>Chain:</b> B; <b>PDB Molecule:</b> sialidase a; <b>PDBTitle:</b> structure of the catalytic domain of the native nana2 sialidase from streptococcus pneumoniae <b>PDB header:</b> hydrolase
68	<a href="#">c4yw5A</a>	Alignment	not modelled	59.2	13	<b>Chain:</b> A; <b>PDB Molecule:</b> neuraminidase c; <b>PDBTitle:</b> crystal structure of streptococcus pneumoniae nanc, complex with2 oseltamivir carboxylate <b>PDB header:</b> hydrolase
69	<a href="#">c2vzvA</a>	Alignment	not modelled	57.1	11	<b>Chain:</b> A; <b>PDB Molecule:</b> sialidase a; <b>PDBTitle:</b> structure of the catalytic domain of streptococcus pneumoniae2 sialidase nana <b>PDB header:</b> hydrolase
70	<a href="#">c2berA</a>	Alignment	not modelled	45.6	16	<b>Chain:</b> A; <b>PDB Molecule:</b> bacterial sialidase; <b>PDBTitle:</b> y370g active site mutant of the sialidase from2 micromonospora viridifaciens in complex with beta-neu5ac3 (sialic acid). <b>PDB header:</b> hydrolase
71	<a href="#">c4fj6C</a>	Alignment	not modelled	44.2	12	<b>Chain:</b> C; <b>PDB Molecule:</b> glycoside hydrolase family 33, candidate sialidase; <b>PDBTitle:</b> crystal structure of a glycoside hydrolase family 33, candidate2 sialidase (bdi_2946) from parabacteroides distasonis atcc 8503 at3 1.90 a resolution <b>PDB header:</b> transferase
72	<a href="#">c3watA</a>	Alignment	not modelled	42.3	14	<b>Chain:</b> A; <b>PDB Molecule:</b> 4-o-beta-d-mannosyl-d-glucose phosphorylase; <b>PDBTitle:</b> crystal structure of 4-o-beta-d-mannosyl-d-glucose phosphorylase mgp2 complexed with man+glc <b>PDB header:</b> hydrolase
73	<a href="#">c3r67A</a>	Alignment	not modelled	42.1	8	<b>Chain:</b> A; <b>PDB Molecule:</b> putative glycosidase; <b>PDBTitle:</b> crystal structure of a putative glycosidase (bt_4094) from bacteroides2 thetaiotaomicron vpi-5482 at 2.30 a resolution <b>PDB header:</b> transferase
74	<a href="#">c5aycA</a>	Alignment	not modelled	41.4	14	<b>Chain:</b> A; <b>PDB Molecule:</b> 4-o-beta-d-mannosyl-d-glucose phosphorylase; <b>PDBTitle:</b> 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 <b>Fold:</b> 6-bladed beta-propeller <b>Superfamily:</b> Sialidas <b>Family:</b> Sialidas (neuraminidas)
75	<a href="#">d2sli2</a>	Alignment	not modelled	39.9	14	<b>PDB header:</b> hydrolase
76	<a href="#">c4bbwA</a>	Alignment	not modelled	39.9	14	<b>Chain:</b> A; <b>PDB Molecule:</b> sialidase (neuraminidase); <b>PDBTitle:</b> the crystal structure of sialidase vpi 5482 (btsa) from bacteroides2 thetaiotaomicron <b>PDB header:</b> hydrolase
77	<a href="#">c3lemA</a>	Alignment	not modelled	38.1	14	<b>Chain:</b> A; <b>PDB Molecule:</b> fructosyltransferase; <b>PDBTitle:</b> crystal structure of fructosyltransferase (d191a) from a.

						japonicus in2 complex with nystose
78	<a href="#">d1qtra2</a>	Alignment	not modelled	36.7	11	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
79	<a href="#">c3a72A</a>	Alignment	not modelled	33.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exo-arabinanase; <b>PDBTitle:</b> high resolution structure of penicillium chrysogenum alpha-l-2 arabinanase complexed with arabinobiose
80	<a href="#">c6dkuA</a>	Alignment	not modelled	31.0	38	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> vp35; <b>PDBTitle:</b> crystal structure of myotis vp35 mutant of interferon inhibitory2 domain
81	<a href="#">c4r3zC</a>	Alignment	not modelled	30.8	16	<b>PDB header:</b> protein binding/ligase <b>Chain:</b> C: <b>PDB Molecule:</b> glutamine--trna ligase; <b>PDBTitle:</b> crystal structure of human argrs-glnrs-aimp1 complex
82	<a href="#">c3aiiA</a>	Alignment	not modelled	30.7	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase; <b>PDBTitle:</b> archaeal non-discriminating glutamyl-trna synthetase from2 methanothermobacter thermautotrophicus
83	<a href="#">c1kitA</a>	Alignment	not modelled	30.6	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sialidase; <b>PDBTitle:</b> vibrio cholerae neuraminidase
84	<a href="#">c5mqrA</a>	Alignment	not modelled	30.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-l-arabinobiosidase; <b>PDBTitle:</b> sialidase bt_1020
85	<a href="#">c1y9gA</a>	Alignment	not modelled	30.4	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exo-inulinase; <b>PDBTitle:</b> crystal structure of exo-inulinase from aspergillus awamori complexed2 with fructose
86	<a href="#">c3kf5A</a>	Alignment	not modelled	29.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> invertase; <b>PDBTitle:</b> structure of invertase from schwanniomyces occidentalis
87	<a href="#">c2ebsB</a>	Alignment	not modelled	29.7	7	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> oligoxyloglucan reducing end-specific <b>PDBTitle:</b> crystal structure anaalysis of oligoxyloglucan reducing-end-2 specific cellobiohydrolase (oxg-rcbh) d465n mutant3 complexed with a xyloglucan heptasaccharide
88	<a href="#">c5xh9A</a>	Alignment	not modelled	25.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> extracellular invertase; <b>PDBTitle:</b> aspergillus kawachii beta-fructofuranosidase
89	<a href="#">c4p2bA</a>	Alignment	not modelled	25.2	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine aminoacyl-trna synthetase; <b>PDBTitle:</b> crystal structure of the apo form of the glutaminyl-trna synthetase2 catalytic domain from toxoplasma gondii.
90	<a href="#">c1exdA</a>	Alignment	not modelled	24.2	11	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> glutaminyl-trna synthetase; <b>PDBTitle:</b> crystal structure of a tight-binding glutamine trna bound2 to glutamine aminoacyl trna synthetase
91	<a href="#">c4h3sA</a>	Alignment	not modelled	21.9	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine-trna ligase; <b>PDBTitle:</b> the structure of glutaminyl-trna synthetase from saccharomyces2 cerevisiae
92	<a href="#">d1y4wa2</a>	Alignment	not modelled	20.2	13	<b>Fold:</b> 5-bladed beta-propeller <b>Superfamily:</b> Arabinanase/levansucrase/invertase <b>Family:</b> Glycosyl hydrolases family 32 N-terminal domain
93	<a href="#">c3ugfB</a>	Alignment	not modelled	20.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sucrose:(sucrose/fructan) 6-fructosyltransferase; <b>PDBTitle:</b> crystal structure of a 6-sst/6-sft from pachysandra terminalis
94	<a href="#">c5zdoA</a>	Alignment	not modelled	19.6	11	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine-trna ligase; <b>PDBTitle:</b> crystal structure analysis of ttqrs in co-crystallised with atp
95	<a href="#">c3sc7X</a>	Alignment	not modelled	19.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> inulinase; <b>PDBTitle:</b> first crystal structure of an endo-inulinase, from aspergillus ficuum:2 structural analysis and comparison with other gh32 enzymes.
96	<a href="#">c6mgkB</a>	Alignment	not modelled	19.2	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> xyloglucanase; <b>PDBTitle:</b> crystal structure of the catalytic domain from gh74 enzyme pogh74 from2 paenibacillus odorifer, in complex with xlx xyloglucan
97	<a href="#">c2hz7A</a>	Alignment	not modelled	18.8	11	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaminyl-trna synthetase; <b>PDBTitle:</b> crystal structure of the glutaminyl-trna synthetase from deinococcus2 radiodurans
98	<a href="#">d1v0ea1</a>	Alignment	not modelled	17.9	15	<b>Fold:</b> 6-bladed beta-propeller <b>Superfamily:</b> Sialidases <b>Family:</b> Endo-alpha-sialidase
99	<a href="#">c4ffhA</a>	Alignment	not modelled	17.3	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> levan fructotransferase; <b>PDBTitle:</b> crystal structure of levan fructotransferase d54n mutant from2 arthrobacter ureafaciens in complex with sucrose