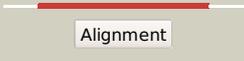
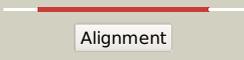
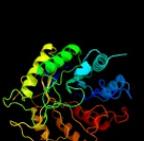


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3096 (-)_3464544_3465683
Date	Thu Aug 8 16:20:27 BST 2019
Unique Job ID	55af8d7a210056d6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1uuqa_</a>	 Alignment		100.0	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
2	<a href="#">c1uz4A_</a>	 Alignment		100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> man5a; <b>PDBTitle:</b> common inhibition of beta-glucosidase and beta-mannosidase2 by isofagomine lactam reflects different conformational3 itineraries for glucoside and mannoside hydrolysis
3	<a href="#">c6mp2B_</a>	 Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> blman5b; <b>PDBTitle:</b> crystal structure of blman5b solved by siras
4	<a href="#">c3obaA_</a>	 Alignment		100.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> structure of the beta-galactosidase from kluyveromyces lactis
5	<a href="#">c3jugA_</a>	 Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-mannanase; <b>PDBTitle:</b> crystal structure of endo-beta-1,4-mannanase from the alkaliphilic2 bacillus sp. n16-5
6	<a href="#">c6gvbC_</a>	 Alignment		100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> exo-beta-1,4-mannosidase; <b>PDBTitle:</b> crystal structure of cutibacterium acnes exo-beta-1,4-mannosidase
7	<a href="#">c4tufC_</a>	 Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> major extracellular endoglucanase; <b>PDBTitle:</b> catalytic domain of the major endoglucanase from xanthomonas2 campestris pv. campestris
8	<a href="#">d1wkya2</a>	 Alignment		100.0	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
9	<a href="#">c1yq2C_</a>	 Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> beta-galactosidase from arthrobacter sp. c2-2 (isozyme c2-2 2-1)
10	<a href="#">c6etzA_</a>	 Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> cold-adapted beta-d-galactosidase from arthrobacter sp. 32cb
11	<a href="#">c1wkya_</a>	 Alignment		100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-beta-1,4-mannanase; <b>PDBTitle:</b> crystal structure of alkaline mannanase from bacillus sp. strain jamb-2 602: catalytic domain and its carbohydrate binding module

12	<a href="#">c1jz6C_</a>	Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> e. coli (lacZ) beta-galactosidase in complex with galacto-2 tetrazole
13	<a href="#">c3mv14_</a>	Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> 4: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> e.coli (lacZ) beta-galactosidase (r599a) in complex with guanidinium
14	<a href="#">c4ee9A_</a>	Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoglucanase; <b>PDBTitle:</b> crystal structure of the rbc11 endo-1,4-glucanase
15	<a href="#">c2oylB_</a>	Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endoglycoceramidase ii; <b>PDBTitle:</b> endo-glycoceramidase ii from rhodococcus sp.: cellobiose-like2 imidazole complex
16	<a href="#">d1bqca_</a>	Alignment		100.0	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
17	<a href="#">c4fk9A_</a>	Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulose-binding family ii; <b>PDBTitle:</b> high resolution structure of the catalytic domain of mannanase2 sacte_2347 from streptomyces sp. sirexaa-e
18	<a href="#">c5ccuA_</a>	Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative secreted endoglycosylceramidase; <b>PDBTitle:</b> crystal structure of endoglycoceramidase i from rhodococ-cus equi
19	<a href="#">c5y6tA_</a>	Alignment		100.0	17	<b>PDB header:</b> carbohydrate <b>Chain:</b> A: <b>PDB Molecule:</b> endo-1,4-beta-mannanase; <b>PDBTitle:</b> crystal structure of endo-1,4-beta-mannanase from eisenia fetida
20	<a href="#">c4oouB_</a>	Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-1,4-mannanase; <b>PDBTitle:</b> crystal structure of beta-1,4-d-mannanase from cryptopygus antarcticus
21	<a href="#">c2zunB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 458aa long hypothetical endo-1,4-beta-glucanase; <b>PDBTitle:</b> functional analysis of hyperthermophilic endocellulase from2 the archaeon pyrococcus horikoshii
22	<a href="#">c3vupB_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-1,4-mannanase; <b>PDBTitle:</b> beta-1,4-mannanase from the common sea hare aplysia kurodai
23	<a href="#">c3wflA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-mannanase; <b>PDBTitle:</b> crstal structure of glycoside hydrolase family 5 beta-mannanase from2 talaromyces trachyspermus
24	<a href="#">c4lx4D_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> endoglucanase(endo-1,4-beta-glucanase)protein; <b>PDBTitle:</b> crystal structure determination of pseudomonas stutzeri endoglucanase2 cel5a using a twinned data set
25	<a href="#">c5fipA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gh5 cellulase; <b>PDBTitle:</b> discovery and characterization of a novel thermostable and2 highly halotolerant gh5 cellulase from an icelandic hot3 spring isolate
26	<a href="#">d1ecea_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
27	<a href="#">c3wh9A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-beta-1,4-mannanase; <b>PDBTitle:</b> the ligand-free structure of manbk from aspergillus niger bk01
						<b>Fold:</b> TIM beta/alpha-barrel

28	<a href="#">d2c0ha1</a>	Alignment	not modelled	100.0	18	<b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
29	<a href="#">c5e09A</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulase; <b>PDBTitle:</b> structural insight of a trimodular halophilic cellulase with a family2 46 carbohydrate-binding module
30	<a href="#">c4im4F</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> endoglucanase e; <b>PDBTitle:</b> multifunctional cellulase, xylanase, mannanase
31	<a href="#">c5uhxA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carbohydrate-active enzyme; <b>PDBTitle:</b> structure of cellulase cel5c_1
32	<a href="#">d1egza</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
33	<a href="#">c4yheB</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> gh5; <b>PDBTitle:</b> native bacteroidetes-affiliated gh5 cellulase linked with a2 polysaccharide utilization locus
34	<a href="#">c4w7wA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulase; <b>PDBTitle:</b> high-resolution structure of xaccel5a in complex with cellopentaose
35	<a href="#">c4htyA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulase; <b>PDBTitle:</b> crystal structure of a metagenome-derived cellulase cel5a
36	<a href="#">c4lypA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exo-beta-1,4-mannosidase; <b>PDBTitle:</b> crystal structure of glycoside hydrolase family 5 mannosidase from2 rhizomucor miehei
37	<a href="#">c3bgaB</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> crystal structure of beta-galactosidase from bacteroides2 thetaiotaomicron vpi-5482
38	<a href="#">c3l55B</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> b-1,4-endoglucanase/cellulase; <b>PDBTitle:</b> crystal structure of a putative beta-1,4-endoglucanase / cellulase2 from prevotella bryantii
39	<a href="#">d1tvna1</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
40	<a href="#">c5hosA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulase; <b>PDBTitle:</b> crystal structure of the endo-beta-1,4-glucanase xac0029 from2 xanthomonas axonopodis pv. citri
41	<a href="#">c4u5iB</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endoglucanase h; <b>PDBTitle:</b> complex structure of mutant ctcel5e (e314a) with xylobiose
42	<a href="#">d1yq2a5</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
43	<a href="#">c4xzbA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cela; <b>PDBTitle:</b> endo-glucanase gscela p1
44	<a href="#">c5ihsA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoglucanase, glycoside hydrolase family 5 protein; <b>PDBTitle:</b> structure of chu_2103 from cytophaga hutchinsonii
45	<a href="#">c3zizA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gh5 endo-beta-1,4-mannanase; <b>PDBTitle:</b> crystal structure of podospira anserina gh5 beta-(1,4)-mannanase
46	<a href="#">c3aysA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoglucanase; <b>PDBTitle:</b> gh5 endoglucanase from a ruminal fungus in complex with cellotriose
47	<a href="#">c4v2xA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-beta-1,4-glucanase (cellulase b); <b>PDBTitle:</b> high resolution structure of the full length tri-modular2 endo-beta-1,4-glucanase b (cel5b) from bacillus halodurans
48	<a href="#">c5a94B</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative retaining b-glycosidase; <b>PDBTitle:</b> crystal structure of beta-glucanase sdgluc5_26a from saccharophagus2 degradans in complex with tetrasaccharide a, form 1
49	<a href="#">c6nczB</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-glucuronidase; <b>PDBTitle:</b> crystal structure of hybrid beta-glucuronidase/beta-galacturonidase2 from fusicatenibacter saccharivorans bound to phenyl-thio-beta-d-3 glucuronide
50	<a href="#">d1edga</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
51	<a href="#">c3qr3B</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endoglucanase eg-ii; <b>PDBTitle:</b> crystal structure of cel5a (eg2) from hypocreia jecorina (trichoderma2 reesei)
52	<a href="#">c3pzvB</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endoglucanase; <b>PDBTitle:</b> c2 crystal form of the endo-1,4-beta-glucanase from bacillus subtilis2 168
53	<a href="#">c4aweA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-beta-d-1,4-mannanase; <b>PDBTitle:</b> the crystal structure of chrysonilia sitophila endo-beta-d-2 1,4-mannanase
						<b>PDB header:</b> hydrolase

54	<a href="#">c4yztA</a>	Alignment	not modelled	100.0	16	<b>Chain:</b> A: <b>PDB Molecule:</b> cellulose hydrolase; <b>PDBTitle:</b> crystal structure of a tri-modular gh5 (subfamily 4) endo-beta-1, 4-2 glucanase from bacillus licheniformis complexed with cellotetraose
55	<a href="#">c3icqD</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> endoglucanase d; <b>PDBTitle:</b> crystal structure of the catalytic and carbohydrate binding domain of2 endoglucanase d from clostridium cellulovorans
56	<a href="#">c5i2uB</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cellulase; <b>PDBTitle:</b> crystal structure of a novel halo-tolerant cellulase from soil2 metagenome
57	<a href="#">c4nf7A</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-1,4-beta-glucanase cel5c; <b>PDBTitle:</b> crystal structure of the gh5 family catalytic domain of endo-1,4-beta-2 glucanase cel5c from butyrivibrio proteoclasticus.
58	<a href="#">c3lpgA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucuronidase; <b>PDBTitle:</b> structure of e. coli beta-glucuronidase bound with a novel, potent2 inhibitor 3-(2-fluorophenyl)-1-(2-hydroxyethyl)-1-((6-methyl-2-oxo-1,3 2-dihydroquinolin-3-yl)methyl)urea
59	<a href="#">c4w8aA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exo-xyloglucanase; <b>PDBTitle:</b> crystal structure of xeg5b, a gh5 xyloglucan-specific beta-1,4-2 glucanase from ruminal metagenomic library, in the native form
60	<a href="#">c5c70B</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glucuronidase; <b>PDBTitle:</b> the structure of aspergillus oryzae beta-glucuronidase
61	<a href="#">c3zmrA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulase (glycosyl hydrolase family 5); <b>PDBTitle:</b> bacteroides ovatus gh5 xyloglucanase in complex with a xxxg2 heptasaccharide
62	<a href="#">d1rh9a1</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
63	<a href="#">c6d4oA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucuronidase; <b>PDBTitle:</b> eubacterium eligens beta-glucuronidase bound to an amoxapine-2 glucuronide conjugate
64	<a href="#">d1vjza</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
65	<a href="#">c2cksB</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endoglucanase e-5; <b>PDBTitle:</b> x-ray crystal structure of the catalytic domain of thermobifida fusca2 endoglucanase cel5a (e5)
66	<a href="#">c4l3mA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-beta-mannanase; <b>PDBTitle:</b> structure of the endo-1,4-beta-mannanase from thermophilic fungus2 rhizomucor miehei
67	<a href="#">d1g01a</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
68	<a href="#">c2jepB</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> xyloglucanase; <b>PDBTitle:</b> native family 5 xyloglucanase from paenibacillus pabuli
69	<a href="#">c4x0vH</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> beta-1,3-1,4-glucanase; <b>PDBTitle:</b> structure of a gh5 family lichenase from caldicellulosiruptor sp. f32
70	<a href="#">c2w62A</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycolipid-anchored surface protein 2; <b>PDBTitle:</b> saccharomyces cerevisiae gas2p in complex with2 laminaripentaose
71	<a href="#">d7a3ha</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
72	<a href="#">c3pzaA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mannan endo-1,4-beta-mannosidase. glycosyl hydrolase family <b>PDBTitle:</b> structure of the hyperthermostable endo-1,4-beta-d-mannanase from2 thermotoga petrophila rku-1 with maltose and glycerol
73	<a href="#">d1jz8a5</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
74	<a href="#">d1h1na</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
75	<a href="#">c3ncoA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoglucanase fncel5a; <b>PDBTitle:</b> crystal structure of fncel5a from f. nodosum rt17-b1
76	<a href="#">c6d8kA</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyl hydrolase family 2, sugar binding domain protein; <b>PDBTitle:</b> bacteroides multiple species beta-glucuronidase
77	<a href="#">d1qnra</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
78	<a href="#">c3ndyA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoglucanase d; <b>PDBTitle:</b> the structure of the catalytic and carbohydrate binding domain of2 endoglucanase d from clostridium cellulovorans
79	<a href="#">c5oydA</a>	Alianment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulase, putative, cel5d;

						<b>PDBTitle:</b> gh5 endo-xyloglucanase from cellvibrio japonicus
80	<a href="#">c5z19F_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> F; <b>PDB Molecule:</b> beta-glucuronidase; <b>PDBTitle:</b> the crystal structure of ruminococcus gnavus beta-glucuronidase in2 complex with uronic isofagomine
81	<a href="#">c6d89B_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> beta-galactosidase/beta-glucuronidase; <b>PDBTitle:</b> bacteroides uniformis beta-glucuronidase 1 with n-terminal loop2 deletion
82	<a href="#">c4w86B_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> xyloglucan-specific endo-beta-1,4-glucanase; <b>PDBTitle:</b> crystal structure of xeg5a, a gh5 xyloglucan-specific endo-beta-1,4-2 glucanase from ruminal metagenomic library, in complex with glucose3 and tris
83	<a href="#">c6ed1B_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> glycosyl hydrolase family 2, sugar binding domain protein; <b>PDBTitle:</b> bacteroides dorei beta-glucuronidase
84	<a href="#">c6ecaA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> beta-glucuronidase; <b>PDBTitle:</b> lactobacillus rhamnosus beta-glucuronidase
85	<a href="#">c2w61A_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> glycoprotein <b>Chain:</b> A; <b>PDB Molecule:</b> glycolipid-anchored surface protein 2; <b>PDBTitle:</b> saccharomyces cerevisiae gas2p apostructure (e176q mutant)
86	<a href="#">c4jkmB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> beta-glucuronidase; <b>PDBTitle:</b> crystal structure of clostridium perfringens beta-glucuronidase
87	<a href="#">d1ceoa_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
88	<a href="#">c5z1bC_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> glycosyl hydrolase family 2, tim barrel domain protein; <b>PDBTitle:</b> structure of bifidobacterium dentium beta-glucuronidase complexed with2 coumarin-3-o-glucuronide
89	<a href="#">c6ed2A_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> glycosyl hydrolase family 2, tim barrel domain protein; <b>PDBTitle:</b> faecalibacterium prausnitzii beta-glucuronidase
90	<a href="#">c1bhgB_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> glycosidase <b>Chain:</b> B; <b>PDB Molecule:</b> beta-glucuronidase; <b>PDBTitle:</b> human beta-glucuronidase at 2.6 a resolution
91	<a href="#">c5i6sA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> endoglucanase; <b>PDBTitle:</b> crystal structure of an endoglucanase from penicillium verrucosum
92	<a href="#">c3w0kA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> bifunctional endomannanase/endoglucanase; <b>PDBTitle:</b> crystal structure of a glycoside hydrolase
93	<a href="#">c5e9aB_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> crystal structure analysis of the cold-adamped beta-galactosidase from2 rahnella sp. r3
94	<a href="#">c6gl2A_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> endoglucanase, family gh5; <b>PDBTitle:</b> structure of z gengagh5_4 wild type at 1.2 angstrom resolution
95	<a href="#">c4jkiA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> beta-glucuronidase; <b>PDBTitle:</b> crystal structure of streptococcus agalactiae beta-glucuronidase in2 space group p21212
96	<a href="#">d1bhga3</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
97	<a href="#">c6ncxB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> beta-galacturonidase; <b>PDBTitle:</b> crystal structure of gh2 beta-galacturonidase from eisenbergiella tayi2 bound to galacturonate
98	<a href="#">c5uj6A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> glycosyl hydrolases family 2, sugar binding domain protein; <b>PDBTitle:</b> crystal structure of bacteroides uniformis beta-glucuronidase
99	<a href="#">c4uzsB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> crystal structure of bifidobacterium bifidum beta-galactosidase
100	<a href="#">c6mvgB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> beta-glucuronidase; <b>PDBTitle:</b> crystal structure of fmn-binding beta-glucuronidase from ruminococcus2 gnavus
101	<a href="#">c4uozC_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> beta-(1,6)-galactosidase from bifidobacterium animalis subsp. lactis2 bl-04 nucleophile mutant e324a in complex with galactose
102	<a href="#">c5jvkB_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structural insights into a family 39 glycoside hydrolase from the gut2 symbiont bacteroides cellulosilyticus wh2.
103	<a href="#">c4ojyA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> 3d structure of the e323a catalytic mutant of gan42b, a gh42 beta-2 galactosidase from g. stearothermophilus
104	<a href="#">c6mvfA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> beta-galactosidase/beta-glucuronidase;

104	<a href="#">c0mv1A_</a>	Alignment	not modelled	100.0	15	<b>PDBTitle:</b> crystal structure of fmn-binding beta-glucuronidase from2 facaelibacterium prausnitzii I2-6 <b>PDB header:</b> hydrolase
105	<a href="#">c2y8kA_</a>	Alignment	not modelled	100.0	17	<b>Chain:</b> A; <b>PDB Molecule:</b> carbohydrate binding family 6; <b>PDBTitle:</b> structure of ctgh5-cbm6, an arabinoxylan-specific xylanase.
106	<a href="#">c5bx9A_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> pslg; <b>PDBTitle:</b> structure of pslg from pseudomonas aeruginosa
107	<a href="#">c3mmwB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> endoglucanase; <b>PDBTitle:</b> crystal structure of endoglucanase cel5a from the hyperthermophilic2 thermotoga maritima
108	<a href="#">c5dmyA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> beta-galactosidase - construct 33-930
109	<a href="#">d1kwga2</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
110	<a href="#">c3cmgA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative beta-galactosidase; <b>PDBTitle:</b> crystal structure of putative beta-galactosidase from bacteroides2 fragilis
111	<a href="#">c5t98B_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> glycoside hydrolase; <b>PDBTitle:</b> crystal structure of bugh2awt
112	<a href="#">d2pb1a1</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
113	<a href="#">c4cucA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> unravelling the multiple functions of the architecturally intricate2 streptococcus pneumoniae beta-galactosidase, bgaa.
114	<a href="#">c3ttsD_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> crystal structure of beta-galactosidase from bacillus circulans sp.2 alkalophilus
115	<a href="#">c1kwgA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> crystal structure of thermus thermophilus a4 beta- galactosidase
116	<a href="#">c5xb7E_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> E; <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> gh42 alpha-l-arabinopyranosidase from bifidobacterium animalis subsp.2 lactis bl-04
117	<a href="#">c4ypjB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> beta galactosidase; <b>PDBTitle:</b> x-ray structure of the mutant of glycoside hydrolase
118	<a href="#">c3civA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> endo-beta-1,4-mannanase; <b>PDBTitle:</b> crystal structure of the endo-beta-1,4-mannanase from2 alicyclobacillus acidocaldarius
119	<a href="#">c3fn9B_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> putative beta-galactosidase; <b>PDBTitle:</b> crystal structure of putative beta-galactosidase from bacteroides2 fragilis
120	<a href="#">d1h4pa_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases