Phyre2

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Description	P00722
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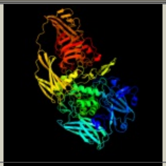
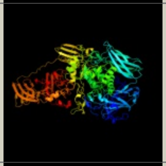
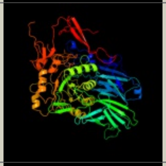
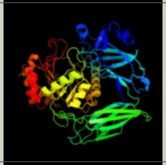
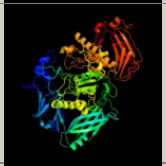
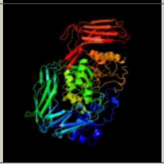
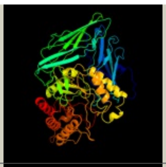
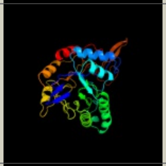
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3mv14_	Alignment		100.0	100	**PDB header:**hydrolase **Chain:** 4: **PDB Molecule:**beta-galactosidase; **PDBTitle:** e.coli (lacz) beta-galactosidase (r599a) in complex with guanidinium
2	c1jz6C_	Alignment		100.0	100	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**beta-galactosidase; **PDBTitle:** e. coli (lacz) beta-galactosidase in complex with galacto-2 tetrazole
3	c3obaA_	Alignment		100.0	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** structure of the beta-galactosidase from kluyveromyces lactis
4	c3bgaB_	Alignment		100.0	33	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of beta-galactosidase from bacteroides2 thetaiotaomicron vpi-5482
5	c1yq2C_	Alignment		100.0	35	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**beta-galactosidase; **PDBTitle:** beta-galactosidase from arthrobacter sp. c2-2 (isoenzyme c2-2 2-1)
6	c3gm8A_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycoside hydrolase family 2, candidate beta-glycosidase; **PDBTitle:** crystal structure of a beta-glycosidase from bacteroides vulgatus
7	c3cmgA_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative beta-galactosidase; **PDBTitle:** crystal structure of putative beta-galactosidase from bacteroides2 fragilis
8	c3fn9B_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative beta-galactosidase; **PDBTitle:** crystal structure of putative beta-galactosidase from bacteroides2 fragilis
9	c3lpgA_	Alignment		100.0	27	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**beta-glucuronidase; **PDBTitle:** 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
10	c2je8B_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-mannosidase; **PDBTitle:** structure of a beta-mannosidase from bacteroides2 thetaiotaomicron
11	c2vzvB_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exo-beta-d-glucosaminidase; **PDBTitle:** substrate complex of amycolatopsis orientalis exo-2 chitosanase csxa e541a with chitosan

12	c1bhgB_	Alignment		100.0	24	**PDB header:**glycosidase **Chain:** B: **PDB Molecule:**beta-glucuronidase; **PDBTitle:** human beta-glucuronidase at 2.6 a resolution
13	d1jz8a4	Alignment		100.0	100	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**beta-Galactosidase, domain 5
14	d1yq2a4	Alignment		100.0	24	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**beta-Galactosidase, domain 5
15	d1jz8a5	Alignment		100.0	100	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
16	d1yq2a5	Alignment		100.0	43	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
17	d1jz8a3	Alignment		100.0	100	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
18	d1yq2a3	Alignment		100.0	44	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
19	d2je8a5	Alignment		100.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
20	d2vzsa5	Alignment		100.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
21	d1bhga3	Alignment	not modelled	100.0	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
22	d1uuqa_	Alignment	not modelled	100.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
23	c1uz4A_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**man5a; **PDBTitle:** common inhibition of beta-glucosidase and beta-mannosidase2 by isofagomine lactam reflects different conformational3 intineraries for glucoside and mannoside hydrolysis
24	d1tg7a5	Alignment	not modelled	100.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Glycosyl hydrolases family 35 catalytic domain
25	d1bhga2	Alignment	not modelled	100.0	22	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
26	c2w62A_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycolipid-anchored surface protein 2; **PDBTitle:** saccharomyces cerevisiae gas2p in complex with2 laminaripentaose
27	d2je8a4	Alignment	not modelled	100.0	21	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
28	d2c0ha1	Alignment	not modelled	100.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases

29	d1wkya2	Alignment	not modelled	100.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
30	d2vzsa4	Alignment	not modelled	100.0	20	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
31	d1qnra_	Alignment	not modelled	100.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
32	d1rh9a1	Alignment	not modelled	100.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
33	c3jugA_	Alignment	not modelled	99.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-mannanase; **PDBTitle:** crystal structure of endo-beta-1,4-mannanase from the alkaliphilic2 bacillus sp. n16-5
34	d1tvna1	Alignment	not modelled	99.9	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
35	d1bqca_	Alignment	not modelled	99.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
36	d7a3ha_	Alignment	not modelled	99.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
37	d1egza_	Alignment	not modelled	99.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
38	c3pzvB_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endoglucanase; **PDBTitle:** c2 crystal form of the endo-1,4-beta-glucanase from bacillus subtilis2 168
39	c2cksB_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endoglucanase e-5; **PDBTitle:** x-ray crystal structure of the catalytic domain of2 thermobifida fusca endoglucanase cel5a (e5)
40	d1jz8a2	Alignment	not modelled	99.9	100	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
41	c3civA_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-beta-1,4-mannanase; **PDBTitle:** crystal structure of the endo-beta-1,4-mannanase from2 alicyclobacillus acidocaldarius
42	d1ecea_	Alignment	not modelled	99.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
43	d1tg7a2	Alignment	not modelled	99.9	14	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Beta-galactosidase LacA, domains 4 and 5
44	c1wkyA_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-beta-1,4-mannanase; **PDBTitle:** crystal structure of alkaline mannanase from bacillus sp. strain jamb-2 602: catalytic domain and its carbohydrate binding module
45	c3thdD_	Alignment	not modelled	99.9	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of human beta-galactosidase in complex with 1-2 deoxygalactonojirimycin
46	d1yq2a1	Alignment	not modelled	99.8	28	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
47	d1jz8a1	Alignment	not modelled	99.8	100	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
48	c2zunB_	Alignment	not modelled	99.8	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**458aa long hypothetical endo-1,4-beta-glucanase; **PDBTitle:** functional analysis of hyperthermophilic endocellulase from2 the archaeon pyrococcus horikoshii
49	d1kwga2	Alignment	not modelled	99.7	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
50	c3d3aA_	Alignment	not modelled	99.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of a beta-galactosidase from bacteroides2 thetaiotaomicron
51	c2oylB_	Alignment	not modelled	99.6	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endoglycoceramidase ii; **PDBTitle:** endo-glycoceramidase ii from rhodococcus sp.: cellobiose-like2 imidazole complex
52	c3ogrA_	Alignment	not modelled	99.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** complex structure of beta-galactosidase from trichoderma reesei with2 galactose
53	d2vzsa1	Alignment	not modelled	99.6	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
54	d1g01a_	Alignment	not modelled	99.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
55	c1xc6A	Alignment	not modelled	99.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase;

						PDBTitle: native structure of beta-galactosidase from penicillium sp. in complex2 with galactose
56	c3pzqA_	Alignment	not modelled	99.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mannan endo-1,4-beta-mannosidase. glycosyl hydrolase family **PDBTitle:** structure of the hyperthermostable endo-1,4-beta-d-mannanase from2 thermotoga petrophila rku-1 with maltose and glycerol
57	c1kwgA_	Alignment	not modelled	99.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of thermus thermophilus a4 beta-galactosidase
58	d1vjza_	Alignment	not modelled	99.5	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
59	d1tg7a3	Alignment	not modelled	99.5	21	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Beta-galactosidase LacA, domains 4 and 5
60	d1yq2a2	Alignment	not modelled	99.5	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
61	d1bhga1	Alignment	not modelled	99.5	22	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
62	d2je8a1	Alignment	not modelled	99.4	21	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
63	d1hjqa_	Alignment	not modelled	99.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
64	c3ncoA_	Alignment	not modelled	99.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase fncel5a; **PDBTitle:** crystal structure of fncel5a from f. nodosum rt17-b1
65	d1ceoa_	Alignment	not modelled	99.3	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
66	c2jepB_	Alignment	not modelled	99.3	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**xyloglucanase; **PDBTitle:** native family 5 xyloglucanase from paenibacillus pabuli
67	c3aysA_	Alignment	not modelled	99.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** gh5 endoglucanase from a ruminal fungus in complex with cellotriose
68	c3mmwB_	Alignment	not modelled	99.2	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of endoglucanase cel5a from the hyperthermophilic2 thermotoga maritima
69	c3icgD_	Alignment	not modelled	99.2	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**endoglucanase d; **PDBTitle:** crystal structure of the catalytic and carbohydrate binding domain of2 endoglucanase d from clostridium cellulovorans
70	d1fh9a_	Alignment	not modelled	99.2	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
71	d1v6wa2	Alignment	not modelled	99.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
72	d1vbua1	Alignment	not modelled	99.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
73	d1w91a2	Alignment	not modelled	99.2	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
74	d1hjsa_	Alignment	not modelled	99.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
75	d2pb1a1	Alignment	not modelled	99.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
76	d1h1na_	Alignment	not modelled	99.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
77	c3l55B_	Alignment	not modelled	99.1	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**b-1,4-endoglucanase/cellulase; **PDBTitle:** crystal structure of a putative beta-1,4-endoglucanase /2 cellulase from prevotella bryantii
78	d1uhva2	Alignment	not modelled	99.1	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
79	d1nq6a_	Alignment	not modelled	99.1	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
80	c3qr3B_	Alignment	not modelled	99.1	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endoglucanase eg-ii; **PDBTitle:** crystal structure of cel5a (eg2) from hypocrea jecorina (trichoderma2 reesei)
81	c3ndyA_	Alignment	not modelled	99.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase d; **PDBTitle:** the structure of the catalytic and carbohydrate binding

						domain of2 endoglucanase d from clostridium cellulovorans
82	c3u7vA_	Alignment	not modelled	99.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** the structure of a putative beta-galactosidase from caulobacter2 crescentus cb15.
83	d1v6ya_	Alignment	not modelled	99.1	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
84	d1v0la_	Alignment	not modelled	99.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
85	d1h4pa_	Alignment	not modelled	98.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
86	d1ur4a_	Alignment	not modelled	98.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
87	c2y8kA_	Alignment	not modelled	98.9	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carbohydrate binding family 6; **PDBTitle:** structure of ctgh5-cbm6, an arabinoxylan-specific xylanase.
88	d1i1wa_	Alignment	not modelled	98.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
89	c3kzsD_	Alignment	not modelled	98.9	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**glycosyl hydrolase family 5; **PDBTitle:** crystal structure of glycosyl hydrolase family 5 (np_809925.1) from2 bacteroides thetaiotaomicron vpi-5482 at 2.10 a resolution
90	d1us3a2	Alignment	not modelled	98.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
91	d1n82a_	Alignment	not modelled	98.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
92	d1ta3b_	Alignment	not modelled	98.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
93	d1w32a_	Alignment	not modelled	98.8	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
94	d1edga_	Alignment	not modelled	98.8	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
95	c2depA_	Alignment	not modelled	98.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**thermostable celloxylanase; **PDBTitle:** crystal structure of xylanase b from clostridium2 stercorarium f9
96	c3emzA_	Alignment	not modelled	98.7	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-1,4-beta-xylanase; **PDBTitle:** crystal structure of xylanase xynb from paenibacillus2 barcinonensis complexed with a conduramine derivative
97	d1tuxa_	Alignment	not modelled	98.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
98	d1bg4a_	Alignment	not modelled	98.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
99	c1xyzA_	Alignment	not modelled	98.7	15	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**1,4-beta-d-xylan-xylanohydrolase; **PDBTitle:** a common protein fold and similar active site in two2 distinct families of beta-glycanases
100	d1xyza_	Alignment	not modelled	98.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
101	c2okxB_	Alignment	not modelled	98.6	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rhamnosidase b; **PDBTitle:** crystal structure of gh78 family rhamnosidase of bacillus sp. gl1 at2 1.9 a
102	d1ur1a_	Alignment	not modelled	98.6	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
103	d1foba_	Alignment	not modelled	98.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
104	c2bs9B_	Alignment	not modelled	98.5	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-xylosidase; **PDBTitle:** native crystal structure of a gh39 beta-xylosidase xynb12 from geobacillus stearothermophilus
105	c2cncA_	Alignment	not modelled	98.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoxylanase; **PDBTitle:** family 10 xylanase
106	c1uhvD_	Alignment	not modelled	98.4	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-xylosidase; **PDBTitle:** crystal structure of beta-d-xylosidase from2 thermoanaerobacterium saccharolyticum, a family 393 glycoside hydrolase
107	d1ug6a_	Alignment	not modelled	98.2	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Family 1 of glycosyl hydrolase
						PDB header:hydrolase

108	c3ahxC_	Alignment	not modelled	98.0	12	**Chain:** C: **PDB Molecule:**beta-glucosidase a; **PDBTitle:** crystal structure of beta-glucosidase a from bacterium clostridium2 cellulovorans
109	d1r85a_	Alignment	not modelled	98.0	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
110	c1iszA_	Alignment	not modelled	98.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-1,4-beta-d-xylanase; **PDBTitle:** crystal structure of xylanase from streptomyces2 olivaceoviridis e-86 complexed with galactose
111	c2vrqB_	Alignment	not modelled	98.0	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-l-arabinofuranosidase; **PDBTitle:** structure of an inactive mutant of arabinofuranosidase from2 thermobacillus xylanilyticus in complex with a3 pentasaccharide
112	c2j75A_	Alignment	not modelled	97.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucosidase a; **PDBTitle:** beta-glucosidase from thermotoga maritima in complex with2 noeuromycin
113	d1aq0a_	Alignment	not modelled	97.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
114	c2w5fB_	Alignment	not modelled	97.8	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endo-1,4-beta-xylanase y; **PDBTitle:** high resolution crystallographic structure of the2 clostridium thermocellum n-terminal endo-1,4-beta-d-3 xylanase 10b (xyn10b) cbm22-1-gh10 modules complexed with4 xylohexaose
115	d1e4ia_	Alignment	not modelled	97.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Family 1 of glycosyl hydrolase
116	c2fglA_	Alignment	not modelled	97.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkaline thermostable endoxylanase; **PDBTitle:** an alkali thermostable f/10 xylanase from alkalophilic2 bacillus sp. ng-27
117	c3fiyA_	Alignment	not modelled	97.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucosidase; **PDBTitle:** crystal structure of bglb
118	d1vffa1	Alignment	not modelled	97.6	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Family 1 of glycosyl hydrolase
119	d2cyga1	Alignment	not modelled	97.5	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
120	d1vema2	Alignment	not modelled	97.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain