Phyre2

Email	l.a.kelley@imperial.ac.uk
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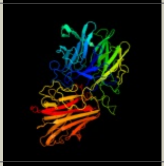
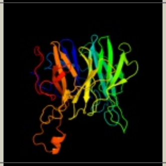
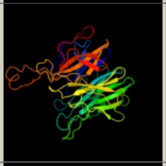
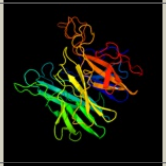
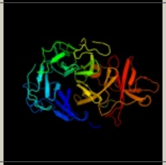
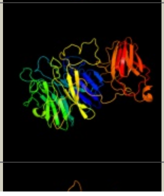
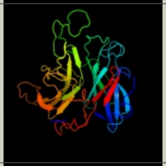
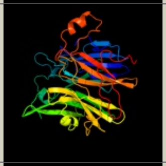
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2exiA_	Alignment		100.0	57	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-d-xylosidase; **PDBTitle:** structure of the family43 beta-xylosidase d15g mutant from geobacillus2 stearothermophilus
2	c1yifC_	Alignment		100.0	54	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**beta-1,4-xylosidase; **PDBTitle:** crystal structure of beta-1,4-xylosidase from bacillus2 subtilis, new york structural genomics consortium
3	c1yrzB_	Alignment		100.0	48	**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
4	c1yi7C_	Alignment		100.0	54	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**beta-xylosidase, family 43 glycosyl hydrolase; **PDBTitle:** beta-d-xylosidase (selenomethionine) xynd from clostridium2 acetobutylicum
5	d2exha2	Alignment		100.0	60	**Fold:**5-bladed beta-propeller **Superfamily:**Arabinanase/levansucrase/invertase **Family:**alpha-L-arabinanase-like
6	d1yifa2	Alignment		100.0	58	**Fold:**5-bladed beta-propeller **Superfamily:**Arabinanase/levansucrase/invertase **Family:**alpha-L-arabinanase-like
7	d1y7ba2	Alignment		100.0	57	**Fold:**5-bladed beta-propeller **Superfamily:**Arabinanase/levansucrase/invertase **Family:**alpha-L-arabinanase-like
8	d1yrza2	Alignment		100.0	54	**Fold:**5-bladed beta-propeller **Superfamily:**Arabinanase/levansucrase/invertase **Family:**alpha-L-arabinanase-like
9	c3lv4B_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycoside hydrolase yxia; **PDBTitle:** crystal structure of the glycoside hydrolase, family 43 yxia2 protein from bacillus licheniformis. northeast structural3 genomics consortium target bir14.
10	c3akgA_	Alignment		100.0	17	**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
11	c3c7hA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-1,4-beta-xylanase; **PDBTitle:** crystal structure of glycoside hydrolase family 43 arabinoxylan2 arabinofuranohydrolase from bacillus subtilis in complex with axos-4-3 0.5.

12	c3cpnA_	Alignment		100.0	18	**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
13	d1gyha_	Alignment		100.0	22	**Fold:**5-bladed beta-propeller **Superfamily:**Arabinanase/levansucrase/invertase **Family:**alpha-L-arabinanase-like
14	c3kstA_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-1,4-beta-xylanase; **PDBTitle:** crystal structure of endo-1,4-beta-xylanase (np_811807.1)2 from bacteroides thetaiotaomicron vpi-5482 at 1.70 a3 resolution
15	d1wl7a1	Alignment		100.0	22	**Fold:**5-bladed beta-propeller **Superfamily:**Arabinanase/levansucrase/invertase **Family:**alpha-L-arabinanase-like
16	d1uv4a1	Alignment		100.0	21	**Fold:**5-bladed beta-propeller **Superfamily:**Arabinanase/levansucrase/invertase **Family:**alpha-L-arabinanase-like
17	c3p2nB_	Alignment		100.0	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'
18	c3qefB_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-xylosidase/alpha-l-arabinfuranosidase, 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
19	c3qz4B_	Alignment		100.0	23	**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
20	d1y7ba1	Alignment		100.0	50	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Beta-D-xylosidase C-terminal domain-like
21	d2exha1	Alignment	not modelled	100.0	54	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Beta-D-xylosidase C-terminal domain-like
22	d1yifa1	Alignment	not modelled	100.0	49	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Beta-D-xylosidase C-terminal domain-like
23	d1yrza1	Alignment	not modelled	100.0	37	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Beta-D-xylosidase C-terminal domain-like
24	c3nqhA_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyl hydrolase; **PDBTitle:** crystal structure of a glycosyl hydrolase (bt_2959) from bacteroides2 thetaiotaomicron vpi-5482 at 2.11 a resolution
25	c3o12A_	Alignment	not modelled	100.0	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yjl217w; **PDBTitle:** the crystal structure of a functionally unknown protein from2 saccharomyces cerevisiae.
26	c1w2tE_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**beta fructosidase; **PDBTitle:** beta-fructosidase from thermotoga maritima in complex with2 raffinose
27	c3mepC_	Alignment	not modelled	99.9	18	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein eca2234; **PDBTitle:** crystal structure of eca2234 protein from erwinia2 carotovora, northeast structural genomics consortium target3 ewr44
28	c3pijA_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-fructofuranosidase; **PDBTitle:** beta-fructofuranosidase from bifidobacterium longum - complex with2 fructose
29	d1uypa2	Alignment	not modelled	99.8	16	**Fold:**5-bladed beta-propeller **Superfamily:**Arabinanase/levansucrase/invertase

						Family: Glycosyl hydrolases family 32 N-terminal domain
30	c1y9gA_	Alignment	not modelled	99.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exo-inulinase; **PDBTitle:** crystal structure of exo-inulinase from aspergillus awamori complexed2 with fructose
31	c3kf5A_	Alignment	not modelled	99.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**invertase; **PDBTitle:** structure of invertase from schwanniomyces occidentalis
32	d1vkda_	Alignment	not modelled	99.8	12	**Fold:**5-bladed beta-propeller **Superfamily:**Arabinanase/levansucrase/invertase **Family:**TM1225-like predicted glycosylases
33	c2aezA_	Alignment	not modelled	99.7	14	**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
34	c3bykA_	Alignment	not modelled	99.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**levansucrase; **PDBTitle:** crystal structure of b. subtilis levansucrase mutant d247a
35	c3ugfB_	Alignment	not modelled	99.7	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sucrose:(sucrose/fructan) 6-fructosyltransferase; **PDBTitle:** crystal structure of a 6-sst/6-sft from pachysandra terminalis
36	c2ac1A_	Alignment	not modelled	99.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**invertase; **PDBTitle:** crystal structure of a cell-wall invertase from arabidopsis thaliana
37	d1oyga_	Alignment	not modelled	99.7	18	**Fold:**5-bladed beta-propeller **Superfamily:**Arabinanase/levansucrase/invertase **Family:**Levansucrase
38	c3lemA_	Alignment	not modelled	99.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fructosyltransferase; **PDBTitle:** crystal structure of fructosyltransferase (d191a) from a. japonicus in2 complex with nystose
39	c2yfrA_	Alignment	not modelled	99.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**levansucrase; **PDBTitle:** crystal structure of inulosucrase from lactobacillus2 johnsonii ncc533
40	d1y4wa2	Alignment	not modelled	99.5	18	**Fold:**5-bladed beta-propeller **Superfamily:**Arabinanase/levansucrase/invertase **Family:**Glycosyl hydrolases family 32 N-terminal domain
41	c3tawA_	Alignment	not modelled	99.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical glycoside hydrolase; **PDBTitle:** crystal structure of a hypothetical glycoside hydrolase (bdi_3141)2 from parabacteroides distasonis atcc 8503 at 1.70 a resolution
42	c3qc2A_	Alignment	not modelled	99.4	17	**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
43	c1w18A_	Alignment	not modelled	99.4	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**levansucrase; **PDBTitle:** crystal structure of levansucrase from gluconacetobacter2 diazotrophicus
44	c3r67A_	Alignment	not modelled	99.3	15	**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
45	c2xcyA_	Alignment	not modelled	95.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**extracellular sialidase/neuraminidase, putative; **PDBTitle:** crystal structure of aspergillus fumigatus sialidase
46	c3a72A_	Alignment	not modelled	95.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exo-arabinanase; **PDBTitle:** high resolution structure of penicillium chrysogenum alpha-l-2 arabinanase complexed with arabinobiose
47	d2ayha_	Alignment	not modelled	94.1	15	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Glycosyl hydrolases family 16
48	c3i4iA_	Alignment	not modelled	93.5	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**1,3-1,4-beta-glucanase; **PDBTitle:** crystal structure of a prokaryotic beta-1,3-1,4-glucanase (lichenase)2 derived from a mouse hindgut metagenome
49	d1gbga_	Alignment	not modelled	91.4	12	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Glycosyl hydrolases family 16
50	c1upsB_	Alignment	not modelled	91.0	17	**PDB header:**glycosyl hydrolase **Chain:** B: **PDB Molecule:**glcnac-alpha-1,4-gal-releasing endo-beta- **PDBTitle:** glcnac[alpha]1-4gal releasing endo-[beta]-galactosidase2 from clostridium perfringens
51	c2w5oA_	Alignment	not modelled	90.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-l-arabinofuranosidase; **PDBTitle:** complex structure of the gh93 alpha-l-arabinofuranosidase2 of fusarium graminearum with arabinobiose
52	c3juuA_	Alignment	not modelled	89.4	18	**PDB header:**hydrolase/carbohydrate **Chain:** A: **PDB Molecule:**porphyranase b; **PDBTitle:** crystal structure of porphyranase b (porb) from zobellia2 galactanivorans
53	c1yo8A_	Alignment	not modelled	88.2	15	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**thrombospondin-2; **PDBTitle:** structure of the c-terminal domain of human thrombospondin-2
54	c3o5sA_	Alignment	not modelled	87.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucanase; **PDBTitle:** crystal structure of the endo-beta-1,3-1,4 glucanase from bacillus2 subtilis (strain 168)

55	c3fbyC_	Alignment	not modelled	85.1	15	**PDB header:**cell adhesion **Chain:** C: **PDB Molecule:**cartilage oligomeric matrix protein; **PDBTitle:** the crystal structure of the signature domain of cartilage oligomeric2 matrix protein.
56	c3rq0A_	Alignment	not modelled	83.6	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyl hydrolases family protein 16; **PDBTitle:** the crystal structure of a glycosyl hydrolases (gh) family protein 162 from mycobacterium smegmatis str. mc2 155
57	d1o4ya_	Alignment	not modelled	82.9	14	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Glycosyl hydrolases family 16
58	c2w38A_	Alignment	not modelled	77.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sialidase; **PDBTitle:** crystal structure of the pseudaminidase from pseudomonas2 aeruginosa
59	d1w8oa3	Alignment	not modelled	76.4	15	**Fold:**6-bladed beta-propeller **Superfamily:**Sialidases **Family:**Sialidases (neuraminidases)
60	c3zr6A_	Alignment	not modelled	75.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**galactocerebrosidase; **PDBTitle:** structure of galactocerebrosidase from mouse in complex with2 galactose
61	c3dgtA_	Alignment	not modelled	72.1	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-1,3-beta-glucanase; **PDBTitle:** the 1.5 a crystal structure of endo-1,3-beta-glucanase from2 streptomyces sioyaensis
62	d1upsa1	Alignment	not modelled	71.7	18	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Glycosyl hydrolases family 16
63	d1o4za_	Alignment	not modelled	67.2	9	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Glycosyl hydrolases family 16
64	c1o4zA_	Alignment	not modelled	67.2	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-agarase b; **PDBTitle:** the three-dimensional structure of beta-agarase b from2 zobellia galactanivorans
65	c2berA_	Alignment	not modelled	66.8	16	**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).
66	d2b4wa1	Alignment	not modelled	64.6	10	**Fold:**5-bladed beta-propeller **Superfamily:**Arabinanase/levansucrase/invertase **Family:**LmjF10.1260-like
67	d1y4wa1	Alignment	not modelled	63.1	12	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Glycosyl hydrolases family 32 C-terminal domain
68	d2ah2a2	Alignment	not modelled	62.8	15	**Fold:**6-bladed beta-propeller **Superfamily:**Sialidases **Family:**Sialidases (neuraminidases)
69	c2w20B_	Alignment	not modelled	59.9	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sialidase a; **PDBTitle:** structure of the catalytic domain of the native nana2 sialidase from streptococcus pneumoniae
70	c1ux6A_	Alignment	not modelled	55.9	14	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**thrombospondin-1; **PDBTitle:** structure of a thrombospondin c-terminal fragment reveals a2 novel calcium core in the type 3 repeats
71	c3h3lB_	Alignment	not modelled	55.0	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative sugar hydrolase; **PDBTitle:** crystal structure of putative sugar hydrolase (yp_001304206.1) from2 parabacteroides distasonis atcc 8503 at 1.59 a resolution
72	c3azyA_	Alignment	not modelled	54.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**laminarinase; **PDBTitle:** crystal structure of the laminarinase catalytic domain from thermotoga2 maritima msb8
73	d1fbla1	Alignment	not modelled	50.1	16	**Fold:**4-bladed beta-propeller **Superfamily:**Hemopexin-like domain **Family:**Hemopexin-like domain
74	c2vk7A_	Alignment	not modelled	44.1	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exo-alpha-sialidase; **PDBTitle:** the structure of clostridium perfringens nani sialidase and2 its catalytic intermediates
75	c3nmbA_	Alignment	not modelled	44.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative sugar hydrolase; **PDBTitle:** crystal structure of a putative sugar hydrolase (bacova_03189) from2 bacteroides ovatus at 2.40 a resolution
76	c3ecqA_	Alignment	not modelled	42.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-alpha-n-acetylgalactosaminidase; **PDBTitle:** endo-alpha-n-acetylgalactosaminidase from streptococcus pneumoniae:2 semet structure
77	d1dypa_	Alignment	not modelled	39.0	13	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Glycosyl hydrolases family 16
78	d1n1ta2	Alignment	not modelled	36.0	15	**Fold:**6-bladed beta-propeller **Superfamily:**Sialidases **Family:**Sialidases (neuraminidases)
79	c3u1xA_	Alignment	not modelled	35.6	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative glycosyl hydrolase; **PDBTitle:** crystal structure of a putative glycosyl hydrolase (bdi_1869) from2 parabacteroides distasonis atcc 8503 at 1.70 a resolution
80	c1su3A_	Alignment	not modelled	35.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**interstitial collagenase; **PDBTitle:** x-ray structure of human prommp-1: new insights into2

						collagenase action
81	d1w0pa3	Alignment	not modelled	35.3	9	**Fold:**6-bladed beta-propeller **Superfamily:**Sialidases **Family:**Sialidases (neuraminidases)
82	c2vvzA_	Alignment	not modelled	34.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sialidase a; **PDBTitle:** structure of the catalytic domain of streptococcus2 pneumoniae sialidase nana
83	d3sila_	Alignment	not modelled	30.5	15	**Fold:**6-bladed beta-propeller **Superfamily:**Sialidases **Family:**Sialidases (neuraminidases)
84	d1ux6a1	Alignment	not modelled	29.1	17	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Thrombospondin C-terminal domain
85	d1pexa_	Alignment	not modelled	28.1	11	**Fold:**4-bladed beta-propeller **Superfamily:**Hemopexin-like domain **Family:**Hemopexin-like domain
86	c3oyoB_	Alignment	not modelled	23.8	11	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**hemopexin fold protein cp4; **PDBTitle:** crystal structure of hemopexin fold protein cp4 from cow pea
87	d2a6za1	Alignment	not modelled	23.5	12	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Lectin leg-like
88	d1gena_	Alignment	not modelled	23.1	9	**Fold:**4-bladed beta-propeller **Superfamily:**Hemopexin-like domain **Family:**Hemopexin-like domain
89	d1su3a2	Alignment	not modelled	20.6	14	**Fold:**4-bladed beta-propeller **Superfamily:**Hemopexin-like domain **Family:**Hemopexin-like domain
90	c1gxdA_	Alignment	not modelled	20.5	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**72 kda type iv collagenase; **PDBTitle:** prommp-2/timp-2 complex
91	c3ilfA_	Alignment	not modelled	19.2	13	**PDB header:**hydrolase/carbohydrate **Chain:** A: **PDB Molecule:**porphyranase a; **PDBTitle:** crystal structure of porphyranase a (pora) in complex with2 neo-porphyrotetraose
92	c3c7xA_	Alignment	not modelled	17.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**matrix metalloproteinase-14; **PDBTitle:** hemopexin-like domain of matrix metalloproteinase 14
93	c3hbkA_	Alignment	not modelled	17.2	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative glycosyl hydrolase; **PDBTitle:** crystal structure of putative glycosyl hydrolase, was domain of2 unknown function (duf1080) (yp_001302580.1) from parabacteroides3 distasonis atcc 8503 at 2.36 a resolution
94	c3eypB_	Alignment	not modelled	16.4	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of putative alpha-l-fucosidase from bacteroides2 thetaiotaomicron
95	c3lp9C_	Alignment	not modelled	16.2	15	**PDB header:**plant protein **Chain:** C: **PDB Molecule:**ls-24; **PDBTitle:** crystal structure of ls24, a seed albumin from lathyrus2 sativus
96	c2v5dA_	Alignment	not modelled	16.2	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**o-glcnacase nagj; **PDBTitle:** structure of a family 84 glycoside hydrolase and a family2 32 carbohydrate-binding module in tandem from clostridium3 perfringens.
97	d1czsa_	Alignment	not modelled	14.5	31	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Discoidin domain (FA58C, coagulation factor 5/8 C-terminal domain)
98	c2xqxB_	Alignment	not modelled	13.8	13	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**endo-beta-n-acetylglucosaminidase d; **PDBTitle:** structure of the family 32 carbohydrate-binding module from2 streptococcus pneumoniae endod
99	c3jtoE_	Alignment	not modelled	13.7	33	**PDB header:**protein binding **Chain:** E: **PDB Molecule:**adapter protein meca 2; **PDBTitle:** crystal structure of the c-terminal domain of ypbh