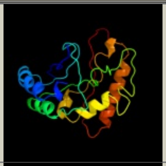
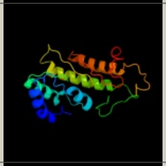
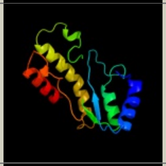
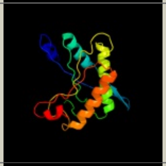
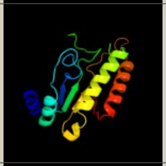
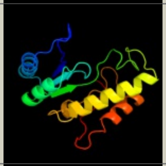
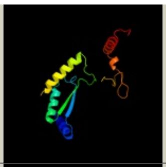
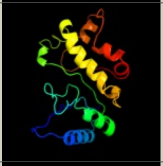
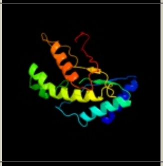
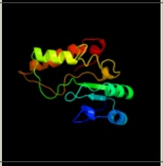
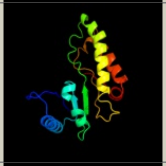
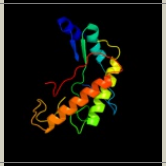
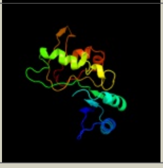
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P37325
Date	Thu Jan 5 11:55:12 GMT 2012
Unique Job ID	462dec9245b8aa71

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2w62A_	Alignment		98.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycolipid-anchored surface protein 2; **PDBTitle:** saccharomyces cerevisiae gas2p in complex with2 laminaripentaose
2	c1kwgA_	Alignment		98.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of thermus thermophilus a4 beta-galactosidase
3	c3u7vA_	Alignment		97.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** the structure of a putative beta-galactosidase from caulobacter2 crescentus cb15.
4	d1bhga3	Alignment		97.5	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
5	c2bs9B_	Alignment		97.4	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-xylosidase; **PDBTitle:** native crystal structure of a gh39 beta-xylosidase xynb12 from geobacillus stearothermophilus
6	d1w91a2	Alignment		97.4	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
7	c3thdD_	Alignment		97.3	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of human beta-galactosidase in complex with 1-2 deoxygalactonojirimycin
8	d1uhva2	Alignment		97.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
9	d1vjza_	Alignment		97.3	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
10	d2vzsa5	Alignment		97.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
11	c1uhvD_	Alignment		97.1	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

12	c1j0yD_	Alignment		97.1	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-amylase; **PDBTitle:** beta-amylase from bacillus cereus var. mycoides in complex2 with glucose
13	c3jugA_	Alignment		97.1	13	**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
14	d1jz8a5	Alignment		97.0	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
15	c3d3aA_	Alignment		96.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of a beta-galactosidase from bacteroides2 thetaiotaomicron
16	d1tg7a5	Alignment		96.8	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Glycosyl hydrolases family 35 catalytic domain
17	d2je8a5	Alignment		96.8	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
18	c1bhgB_	Alignment		96.7	12	**PDB header:**glycosidase **Chain:** B: **PDB Molecule:**beta-glucuronidase; **PDBTitle:** human beta-glucuronidase at 2.6 a resolution
19	d1edga_	Alignment		96.7	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
20	d1yq2a5	Alignment		96.6	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
21	d1wkya2	Alignment	not modelled	96.5	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
22	d2pb1a1	Alignment	not modelled	96.5	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
23	c3lpgA_	Alignment	not modelled	96.3	16	**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
24	d1kwga2	Alignment	not modelled	96.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
25	c3cmgA_	Alignment	not modelled	96.1	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative beta-galactosidase; **PDBTitle:** crystal structure of putative beta-galactosidase from bacteroides2 fragilis
26	c2jepB_	Alignment	not modelled	96.0	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**xyloglucanase; **PDBTitle:** native family 5 xyloglucanase from paenibacillus pabuli
27	d1vema2	Alignment	not modelled	95.8	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
28	c3civA_	Alignment	not modelled	95.5	13	**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

29	d1qnra_	Alignment	not modelled	95.4	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
30	c3mmwB_	Alignment	not modelled	95.3	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of endoglucanase cel5a from the hyperthermophilic2 thermotoga maritima
31	d1rh9a1	Alignment	not modelled	95.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
32	d1ecea_	Alignment	not modelled	95.1	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
33	c3ogrA_	Alignment	not modelled	94.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** complex structure of beta-galactosidase from trichoderma reesei with2 galactose
34	c2vzvB_	Alignment	not modelled	94.3	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exo-beta-d-glucosaminidase; **PDBTitle:** substrate complex of amycolatopsis orientalis exo-2 chitosanase csxa e541a with chitosan
35	c3pzqA_	Alignment	not modelled	94.2	14	**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
36	d1bqca_	Alignment	not modelled	94.2	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
37	d1h4pa_	Alignment	not modelled	94.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
38	d1fh9a_	Alignment		93.6	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
39	c3ncoA_	Alignment	not modelled	93.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase fncel5a; **PDBTitle:** crystal structure of fncel5a from f. nodosum rt17-b1
40	c3ndyA_	Alignment	not modelled	92.8	17	**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
41	c3gm8A_	Alignment	not modelled	92.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycoside hydrolase family 2, candidate beta-glycosidase; **PDBTitle:** crystal structure of a beta-glycosidase from bacteroides vulgatus
42	c3l55B_	Alignment	not modelled	91.8	17	**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
43	d1ur4a_	Alignment	not modelled	91.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
44	d1nq6a_	Alignment	not modelled	91.5	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
45	d1foba_	Alignment	not modelled	91.5	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
46	d1h1na_	Alignment	not modelled	91.2	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
47	d7a3ha_	Alignment	not modelled	91.1	6	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
48	d1v0la_	Alignment	not modelled	90.8	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
49	d1us3a2	Alignment	not modelled	89.8	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
50	c3icgD_	Alignment	not modelled	89.7	17	**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
51	d1n82a_	Alignment	not modelled	89.4	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
52	c2je8B_	Alignment	not modelled	89.1	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-mannosidase; **PDBTitle:** structure of a beta-mannosidase from bacteroides2 thetaiotaomicron
53	c1yq2C_	Alignment	not modelled	88.4	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**beta-galactosidase; **PDBTitle:** beta-galactosidase from arthrobacter sp. c2-2 (isoenzyme c2-2 2-1)

54	d2c0ha1	Alignment	not modelled	86.9	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
55	c3aysA_	Alignment	not modelled	86.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** gh5 endoglucanase from a ruminal fungus in complex with cellotriose
56	c1xc6A_	Alignment	not modelled	86.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** native structure of beta-galactosidase from penicillium sp. in complex2 with galactose
57	d1vbua1	Alignment	not modelled	86.6	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
58	d1v6wa2	Alignment	not modelled	86.6	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
59	d1v6ya_	Alignment	not modelled	86.2	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
60	d1ea9c3	Alignment	not modelled	86.0	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
61	c3fn9B_	Alignment	not modelled	85.8	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative beta-galactosidase; **PDBTitle:** crystal structure of putative beta-galactosidase from bacteroides2 fragilis
62	d1hjsa_	Alignment	not modelled	85.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
63	d1hjqa_	Alignment	not modelled	85.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
64	c2wcsA_	Alignment	not modelled	84.5	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha amylase, catalytic region; **PDBTitle:** crystal structure of debranching enzyme from nostoc2 punctiforme (npde)
65	d1ceoa_	Alignment	not modelled	83.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
66	c1uz4A_	Alignment	not modelled	82.4	12	**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
67	d1uuqa_	Alignment	not modelled	82.4	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
68	c3qr3B_	Alignment	not modelled	82.2	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endoglucanase eg-ii; **PDBTitle:** crystal structure of cel5a (eg2) from hypocrea jecorina (trichoderma2 reesei)
69	c2z1kA_	Alignment	not modelled	82.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**(neo)pullulanase; **PDBTitle:** crystal structure of ttha1563 from thermus thermophilus hb8
70	c2wvsD_	Alignment	not modelled	81.0	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**alpha-l-fucosidase; **PDBTitle:** crystal structure of an alpha-l-fucosidase gh29 trapped2 covalent intermediate from bacteroides thetaiotaomicron in3 complex with 2-fluoro-fucosyl fluoride using an e288q4 mutant
71	c3emzA_	Alignment	not modelled	78.2	16	**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
72	d1ta3b_	Alignment	not modelled	77.3	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
73	d1m7xa3	Alignment	not modelled	75.8	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
74	c3mo4B_	Alignment	not modelled	74.4	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-1,3/4-fucosidase; **PDBTitle:** the crystal structure of an alpha-(1-3,4)-fucosidase from2 bifidobacterium longum subsp. infantis atcc 15697
75	c2zunB_	Alignment	not modelled	74.3	16	**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
76	d1tuxa_	Alignment	not modelled	74.3	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
77	c1hl8B_	Alignment	not modelled	73.5	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of thermotoga maritima alpha-fucosidase
78	c2cksB_	Alignment	not modelled	73.3	15	**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)
79	c2aaaA_	Alignment	not modelled	72.6	19	**PDB header:**glycosidase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** calcium binding in alpha-amylases: an x-ray diffraction2

						study at 2.1 angstroms resolution of two enzymes from3 aspergillus
80	c3pzvB_	Alignment	not modelled	71.6	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endoglucanase; **PDBTitle:** c2 crystal form of the endo-1,4-beta-glucanase from bacillus subtilis2 168
81	d1ua7a2	Alignment	not modelled	70.5	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
82	c3mv14_	Alignment	not modelled	70.2	12	**PDB header:**hydrolase **Chain:** 4: **PDB Molecule:**beta-galactosidase; **PDBTitle:** e.coli (lacz) beta-galactosidase (r599a) in complex with guanidinium
83	d1hl9a2	Alignment	not modelled	70.1	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Putative alpha-L-fucosidase, catalytic domain
84	c2depA_	Alignment	not modelled	68.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**thermostable celloxylanase; **PDBTitle:** crystal structure of xylanase b from clostridium2 stercorarium f9
85	d1ht6a2	Alignment	not modelled	67.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
86	d2csua1	Alignment	not modelled	66.8	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
87	d2guya2	Alignment	not modelled	66.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
88	c1yveK_	Alignment	not modelled	64.6	17	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**acetohydroxy acid isomeroreductase; **PDBTitle:** acetohydroxy acid isomeroreductase complexed with nadph,2 magnesium and inhibitor ipoha (n-hydroxy-n-3 isopropyloxamate)
89	d1w32a_	Alignment	not modelled	62.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
90	d1wzla3	Alignment	not modelled	62.6	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
91	d1ur1a_	Alignment	not modelled	62.2	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
92	d1gnxa_	Alignment	not modelled	59.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Family 1 of glycosyl hydrolase
93	c3obaA_	Alignment	not modelled	58.9	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** structure of the beta-galactosidase from kluyveromyces lactis
94	d1cgta4	Alignment	not modelled	58.8	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
95	d1ug6a_	Alignment	not modelled	58.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Family 1 of glycosyl hydrolase
96	c3th6B_	Alignment	not modelled	58.2	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase from rhipicephalus2 (boophilus) microplus.
97	d1neya_	Alignment	not modelled	58.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
98	c1jz6C_	Alignment	not modelled	57.9	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**beta-galactosidase; **PDBTitle:** e. coli (lacz) beta-galactosidase in complex with galacto-2 tetrazole
99	d1bf2a3	Alignment	not modelled	57.6	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
100	c2j75A_	Alignment	not modelled	57.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucosidase a; **PDBTitle:** beta-glucosidase from thermotoga maritima in complex with2 noeuromycin
101	d1n55a_	Alignment	not modelled	56.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
102	d1o5xa_	Alignment	not modelled	56.8	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
103	d1b9ba_	Alignment	not modelled	56.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
104	d1suxa_	Alignment	not modelled	56.4	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
105	d1lwha2	Alignment	not modelled	56.3	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
106	d1cyga4	Alignment	not modelled	56.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases

						Family: Amylase, catalytic domain
107	c3gzaB_	Alignment	not modelled	55.7	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of putative alpha-l-fucosidase (np_812709.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.60 a resolution
108	d1gcya2	Alignment	not modelled	55.5	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
109	d2aaaa2	Alignment	not modelled	55.1	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
110	d1kv5a_	Alignment	not modelled	54.8	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
111	c3m9yB_	Alignment	not modelled	54.6	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase from methicillin2 resistant staphylococcus aureus at 1.9 angstrom resolution
112	d1m6ja_	Alignment	not modelled	54.2	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
113	c3gvgA_	Alignment	not modelled	53.4	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase from mycobacterium2 tuberculosis
114	c1yyaA_	Alignment	not modelled	53.2	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of tt0473, putative triosephosphate isomerase from2 thermus thermophilus hb8
115	d1ud2a2	Alignment	not modelled	52.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
116	c2oylB_	Alignment	not modelled	52.5	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endoglycoceramidase ii; **PDBTitle:** endo-glycoceramidase ii from rhodococcus sp.: cellobiose-like2 imidazole complex
117	d1eh9a3	Alignment	not modelled	51.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
118	c1e40A_	Alignment	not modelled	51.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** tris/maltotriose complex of chimaeric amylase from b.2 amyloliquefaciens and b. licheniformis at 2.2a
119	c3bmwA_	Alignment	not modelled	50.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cyclomaltodextrin glucanotransferase; **PDBTitle:** cyclodextrin glycosyl transferase from thermoanerobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor
120	d1sw3a_	Alignment	not modelled	50.4	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)