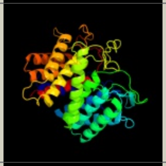
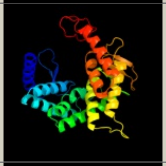
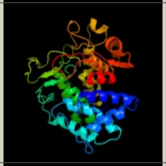
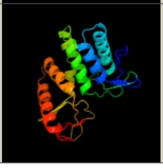
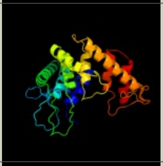
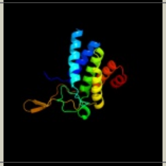
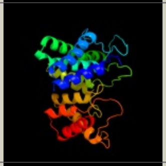
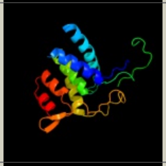
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P32140
Date	Thu Jan 5 11:49:26 GMT 2012
Unique Job ID	22afa0dfe333a0d6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2afaa1	Alignment		100.0	89	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**N-acylglucosamine (NAG) epimerase
2	c3gt5A_	Alignment		100.0	28	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**n-acetylglucosamine 2-epimerase; **PDBTitle:** crystal structure of an n-acetylglucosamine 2-epimerase family protein2 from xylella fastidiosa
3	d1fp3a_	Alignment		100.0	17	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**N-acylglucosamine (NAG) epimerase
4	c2gz6B_	Alignment		100.0	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**n-acetyl-d-glucosamine 2-epimerase; **PDBTitle:** crystal structure of anabaena sp. ch1 n-acetyl-d-glucosamine 2-2 epimerase at 2.0 a
5	c3k7xA_	Alignment		99.7	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin0763 protein; **PDBTitle:** crystal structure of the lin0763 protein from listeria2 innocua. northeast structural genomics consortium target3 lkr23.
6	c2zzrA_	Alignment		99.5	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**unsaturated glucuronyl hydrolase; **PDBTitle:** crystal structure of unsaturated glucuronyl hydrolase from2 streptcoccus agalactiae
7	d2d5ja1	Alignment		99.3	11	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glycosyl Hydrolase Family 88
8	c3pmmA_	Alignment		98.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative cytoplasmic protein; **PDBTitle:** the crystal structure of a possible member of gh105 family from2 klebsiella pneumoniae subsp. pneumoniae mgh 78578
9	c3gzkA_	Alignment		98.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cellulase; **PDBTitle:** structure of a. acidocaldarius cellulase cela
10	d1nc5a_	Alignment		98.5	10	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Hypothetical protein YteR
11	d1wzza1	Alignment		98.5	9	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain

12	d1tf4a1	Alignment		98.3	10	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
13	c1clcA_	Alignment		98.3	10	**PDB header:**glycosyl hydrolase **Chain:** A: **PDB Molecule:**endoglucanase celd; ec: 3.2.1.4; **PDBTitle:** three-dimensional structure of endoglucanase d at 1.92 angstroms resolution
14	d1ut9a1	Alignment		98.2	12	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
15	d1g87a1	Alignment		98.0	10	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
16	c3k11A_	Alignment		97.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative glycosyl hydrolase; **PDBTitle:** crystal structure of putative glycosyl hydrolase (np_813087.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.80 a resolution
17	d1ks8a_	Alignment		97.9	11	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
18	d1ia6a_	Alignment		97.8	8	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
19	c2xfgA_	Alignment		97.8	12	**PDB header:**hydrolase/sugar binding protein **Chain:** A: **PDB Molecule:**endoglucanase 1; **PDBTitle:** reassembly and co-crystallization of a family 9 processive2 endoglucanase from separately expressed gh9 and cbm3c3 modules
20	d1nxca_	Alignment		97.8	12	**Fold:**alpha/alpha toroid **Superfamily:**Seven-hairpin glycosidases **Family:**Class I alpha-1;2-mannosidase, catalytic domain
21	d1wu4a1	Alignment	not modelled	97.6	9	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
22	c1ut9A_	Alignment	not modelled	97.6	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cellulose 1,4-beta-cellobiosidase; **PDBTitle:** structural basis for the exocellulase activity of the2 cellobiohydrolase cbha from c. thermocellum
23	c3h7lC_	Alignment	not modelled	97.6	10	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of endoglucanase-related protein from vibrio2 parahaemolyticus
24	d1v5da_	Alignment	not modelled	97.5	12	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
25	c1g6iA_	Alignment	not modelled	97.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**class i alpha-1,2-mannosidase; **PDBTitle:** crystal structure of the yeast alpha-1,2-mannosidase with bound 1-2 deoxymannojirimycin at 1.59 a resolution
26	c3e6uA_	Alignment	not modelled	97.4	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**lanc-like protein 1; **PDBTitle:** crystal structure of human lancl1
27	d1clca1	Alignment	not modelled	97.4	10	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
28	c1ga2A_	Alignment	not modelled	97.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase 9g; **PDBTitle:** the crystal structure of endoglucanase 9g from clostridium2 cellulolyticum complexed with cellobiose
						Fold:alpha/alpha toroid

29	d1ulva1	Alignment	not modelled	97.2	11	**Superfamily:**Six-hairpin glycosidases **Family:**Bacterial glucoamylase C-terminal domain-like
30	c1w6kA_	Alignment	not modelled	97.1	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**lanosterol synthase; **PDBTitle:** structure of human osc in complex with lanosterol
31	c1js4B_	Alignment	not modelled	97.0	13	**PDB header:**glycosyl hydrolase **Chain:** B: **PDB Molecule:**endo/exocellulase e4; **PDBTitle:** endo/exocellulase:cellobiose from thermomonospora
32	d1kwfa_	Alignment	not modelled	96.7	10	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
33	c2v8kA_	Alignment	not modelled	96.3	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**pectate lyase; **PDBTitle:** structure of a family 2 pectate lyase in complex with2 trigalacturonic acid
34	d1g9ga_	Alignment	not modelled	96.3	16	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
35	d1hcua_	Alignment	not modelled	96.1	15	**Fold:**alpha/alpha toroid **Superfamily:**Seven-hairpin glycosidases **Family:**Class I alpha-1;2-mannosidase, catalytic domain
36	c1lf6A_	Alignment	not modelled	95.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucoamylase; **PDBTitle:** crystal structure of bacterial glucoamylase
37	d2sqca1	Alignment	not modelled	95.4	12	**Fold:**alpha/alpha toroid **Superfamily:**Terpenoid cyclases/Protein prenyltransferases **Family:**Terpene synthases
38	d1dl2a_	Alignment	not modelled	95.1	14	**Fold:**alpha/alpha toroid **Superfamily:**Seven-hairpin glycosidases **Family:**Class I alpha-1;2-mannosidase, catalytic domain
39	c1o79A_	Alignment	not modelled	95.1	8	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**squalene--hopene cyclase; **PDBTitle:** structures of human oxidosqualene cyclase inhibitors bound2 to a homolgous enzyme
40	c1ug9A_	Alignment	not modelled	94.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucodextranase; **PDBTitle:** crystal structure of glucodextranase from arthrobacter globiformis i42
41	c3qxqD_	Alignment	not modelled	94.3	7	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**endoglucanase; **PDBTitle:** structure of the bacterial cellulose synthase subunit z in complex2 with cellopentaose
42	c2a73B_	Alignment	not modelled	94.0	12	**PDB header:**immune system **Chain:** B: **PDB Molecule:**complement c3; **PDBTitle:** human complement component c3
43	c3renB_	Alignment	not modelled	93.9	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycosyl hydrolase, family 8; **PDBTitle:** cpf_2247, a novel alpha-amylase from clostridium perfringens
44	c1x9dA_	Alignment	not modelled	93.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoplasmic reticulum mannosyl-oligosaccharide 1, **PDBTitle:** crystal structure of human class i alpha-1,2-mannosidase in2 complex with thio-disaccharide substrate analogue
45	d1x9da1	Alignment	not modelled	93.8	12	**Fold:**alpha/alpha toroid **Superfamily:**Seven-hairpin glycosidases **Family:**Class I alpha-1;2-mannosidase, catalytic domain
46	d1c3da_	Alignment	not modelled	93.0	12	**Fold:**alpha/alpha toroid **Superfamily:**Terpenoid cyclases/Protein prenyltransferases **Family:**Complement components
47	c3g6jB_	Alignment	not modelled	92.9	12	**PDB header:**immune system **Chain:** B: **PDB Molecule:**complement c3 alpha chain; **PDBTitle:** c3b in complex with a c3b specific fab
48	d1lf6a1	Alignment	not modelled	92.7	10	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Bacterial glucoamylase C-terminal domain-like
49	c3c67B_	Alignment	not modelled	92.5	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**uncharacterized protein ygjk; **PDBTitle:** escherichia coli k12 ygjk in a complexed with glucose
50	d1w6ka1	Alignment	not modelled	92.0	12	**Fold:**alpha/alpha toroid **Superfamily:**Terpenoid cyclases/Protein prenyltransferases **Family:**Terpene synthases
51	c2pn5A_	Alignment	not modelled	91.6	11	**PDB header:**immune system **Chain:** A: **PDB Molecule:**thioester-containing protein i; **PDBTitle:** crystal structure of tep1r
52	d1qqfa_	Alignment	not modelled	91.6	12	**Fold:**alpha/alpha toroid **Superfamily:**Terpenoid cyclases/Protein prenyltransferases **Family:**Complement components
53	d2g0da1	Alignment	not modelled	89.9	10	**Fold:**alpha/alpha toroid **Superfamily:**LanC-like **Family:**LanC-like
54	d2jg0a1	Alignment	not modelled	88.9	14	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Trehalase-like
55	c2jg0A_	Alignment	not modelled	88.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**periplasmic trehalase; **PDBTitle:** family 37 trehalase from escherichia coli in complex with 1-2 thiatrehazolin

56	c2b39B_	Alignment	not modelled	86.2	12	**PDB header:**immune system **Chain:** B: **PDB Molecule:**c3; **PDBTitle:** structure of mammalian c3 with an intact thioester at 3a resolution
57	c3eu8D_	Alignment	not modelled	82.7	10	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative glucoamylase; **PDBTitle:** crystal structure of putative glucoamylase (yp_210071.1) from2 bacteroides fragilis nctc 9343 at 2.12 a resolution
58	d1h12a_	Alignment	not modelled	79.0	11	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
59	c1krfA_	Alignment	not modelled	75.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mannosyl-oligosaccharide alpha-1,2-mannosidase; **PDBTitle:** structure of p. citrinum alpha 1,2-mannosidase reveals the basis for2 differences in specificity of the er and golgi class i enzymes
60	d2ri9a1	Alignment	not modelled	75.9	16	**Fold:**alpha/alpha toroid **Superfamily:**Seven-hairpin glycosidases **Family:**Class I alpha-1;2-mannosidase, catalytic domain
61	c1v7wA_	Alignment	not modelled	73.5	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**chitobiose phosphorylase; **PDBTitle:** crystal structure of vibrio proteolyticus chitobiose phosphorylase in2 complex with glcnac
62	c1l2aD_	Alignment	not modelled	67.6	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cellobiohydrolase; **PDBTitle:** the crystal structure and catalytic mechanism of2 cellobiohydrolase cels, the major enzymatic component of3 the clostridium thermocellum cellulosome
63	d1l1ya_	Alignment	not modelled	67.6	16	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
64	c3cu7A_	Alignment	not modelled	65.2	11	**PDB header:**immune system **Chain:** A: **PDB Molecule:**complement c5; **PDBTitle:** human complement component 5
65	c2z07A_	Alignment	not modelled	61.3	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha0978; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 thermus thermophilus hb8
66	c3nfvA_	Alignment	not modelled	41.1	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**alginate lyase; **PDBTitle:** crystal structure of an alginate lyase (bacova_01668) from bacteroides2 ovatus at 1.95 a resolution
67	d1r76a_	Alignment	not modelled	38.0	16	**Fold:**alpha/alpha toroid **Superfamily:**Family 10 polysaccharide lyase **Family:**Family 10 polysaccharide lyase
68	d1gxma_	Alignment	not modelled	35.7	10	**Fold:**alpha/alpha toroid **Superfamily:**Family 10 polysaccharide lyase **Family:**Family 10 polysaccharide lyase
69	c2konA_	Alignment	not modelled	28.2	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr solution structure of cv_2116 from chromobacterium2 violaceum. northeast structural genomics consortium target3 cvt4(1-82)
70	d1v7wa1	Alignment	not modelled	20.2	10	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glycosyltransferase family 36 C-terminal domain
71	d1qaza_	Alignment	not modelled	18.4	27	**Fold:**alpha/alpha toroid **Superfamily:**Chondroitin AC/alginate lyase **Family:**Alginate lyase A1-III
72	c2eacB_	Alignment	not modelled	18.1	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-fucosidase; **PDBTitle:** crystal structure of 1,2-a-l-fucosidase from2 bifidobacterium bifidum in complex with3 deoxyfuconojirimycin
73	d1ccwb_	Alignment	not modelled	18.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Cobalamin (vitamin B12)-dependent enzymes **Family:**Glutamate mutase, large subunit
74	d2fbaa1	Alignment	not modelled	17.3	11	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glucoamylase
75	c1hzfA_	Alignment	not modelled	10.5	13	**PDB header:**immune system **Chain:** A: **PDB Molecule:**complement factor c4a; **PDBTitle:** c4adg fragment of human complement factor c4a
76	d1hzfa_	Alignment	not modelled	10.5	13	**Fold:**alpha/alpha toroid **Superfamily:**Terpenoid cyclases/Protein prenyltransferases **Family:**Complement components
77	c3cihA_	Alignment	not modelled	9.8	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative alpha-rhamnosidase; **PDBTitle:** crystal structure of a putative alpha-rhamnosidase from2 bacteroides thetaiotaomicron
78	d2diga1	Alignment	not modelled	8.5	38	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
79	c1zr7A_	Alignment	not modelled	8.5	29	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**huntingtin-interacting protein hypa/fbp11; **PDBTitle:** solution structure of the first ww domain of fbp11
80	c2jxwA_	Alignment	not modelled	7.9	17	**PDB header:**formin binding protein **Chain:** A: **PDB Molecule:**ww domain-binding protein 4; **PDBTitle:** solution structure of the tandem ww domains of fbp21
81	c3a0oB	Alignment	not modelled	6.7	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**oligo alginate lyase;

81	c3a00B_	Alignment	not modelled	6.7	11	**PDBTitle:** crystal structure of alginate lyase from agrobacterium tumefaciens c58
82	d2sqca2	Alignment	not modelled	6.5	9	**Fold:**alpha/alpha toroid **Superfamily:**Terpenoid cyclases/Protein prenyltransferases **Family:**Terpene synthases
83	d2dk1a1	Alignment	not modelled	6.4	14	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain