Phyre²

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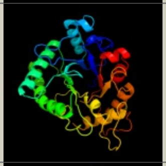
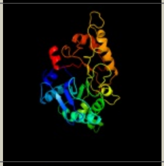
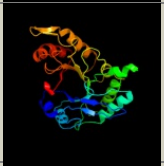
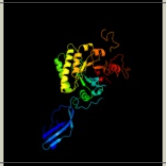
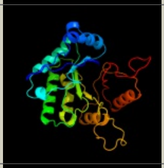
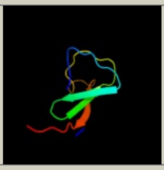
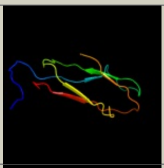
Description	P13656
Date	Thu Jan 5 11:33:39 GMT 2012
Unique Job ID	ada954da858f1b14

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2dskA_	Alignment		100.0	34	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase; **PDBTitle:** crystal structure of catalytic domain of hyperthermophilic chitinase2 from pyrococcus furiosus
2	c3ianA_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase; **PDBTitle:** crystal structure of a chitinase from lactococcus lactis2 subsp. lactis
3	c3ebvA_	Alignment		99.9	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**chinitase a; **PDBTitle:** crystal structure of putative chitinase a from streptomyces2 coelicolor.
4	d2hvma_	Alignment		99.9	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Type II chitinase
5	c3d5hA_	Alignment		99.9	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**haementhin; **PDBTitle:** crystal structure of haementhin from haemanthus multiflorus2 at 2.0a resolution: formation of a novel loop on a tim3 barrel fold and its functional significance
6	c2uy2A_	Alignment		99.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endochitinase; **PDBTitle:** sccts1_apo crystal structure
7	c3n12A_	Alignment		99.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase a; **PDBTitle:** crystal stricture of chitinase in complex with zinc atoms from2 bacillus cereus nctu2
8	c2gsjA_	Alignment		99.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein ppl-2; **PDBTitle:** cdna cloning and 1.75a crystal structure determination of2 ppl2, a novel chimerolectin from parkia platycephala seeds3 exhibiting endochitinolytic activity
9	d1cnva_	Alignment		99.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Type II chitinase
10	c3b9eA_	Alignment		99.7	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase a; **PDBTitle:** crystal structure of inactive mutant e315m chitinase a from2 vibrio harveyi
11	c2xucA_	Alignment		99.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase; **PDBTitle:** natural product-guided discovery of a fungal chitinase2 inhibitor

12	d1itxa1	Alignment		99.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Type II chitinase
13	c1ur8B_	Alignment		99.7	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**chitinase b; **PDBTitle:** interactions of a family 18 chitinase with the designed2 inhibitor hm508, and its degradation product,3 chitobiono-delta-lactone
14	c1rd6A_	Alignment		99.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase a; **PDBTitle:** crystal structure of s. marcescens chitinase a mutant w167a
15	d1edqa2	Alignment		99.6	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Type II chitinase
16	c3co4A_	Alignment		99.6	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase; **PDBTitle:** crystal structure of a chitinase from bacteroides2 thetaiotaomicron
17	d1jnda1	Alignment		99.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Type II chitinase
18	d1w9pa1	Alignment		99.6	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Type II chitinase
19	d1ta3a_	Alignment		99.6	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Type II chitinase
20	c3pohA_	Alignment		99.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-beta-n-acetylglucosaminidase f1; **PDBTitle:** crystal structure of an endo-beta-n-acetylglucosaminidase (bt_3987)2 from bacteroides thetaiotaomicron vpi-5482 at 1.55 a resolution
21	c1wnoB_	Alignment	not modelled	99.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase; **PDBTitle:** crystal structure of a native chitinase from aspergillus fumigatus yj-2 407
22	c1itxA_	Alignment	not modelled	99.5	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyl hydrolase; **PDBTitle:** catalytic domain of chitinase a1 from bacillus circulans wl-12
23	d1goia2	Alignment	not modelled	99.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Type II chitinase
24	d1wb0a1	Alignment	not modelled	99.5	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Type II chitinase
25	d2pi6a1	Alignment	not modelled	99.5	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Type II chitinase
26	c3simA_	Alignment	not modelled	99.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein, family 18 chitinase; **PDBTitle:** crystallographic structure analysis of family 18 chitinase from crocus2 vernus
27	d1hjxa1	Alignment	not modelled	99.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Type II chitinase
28	c1ll4A_	Alignment	not modelled	99.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase 1; **PDBTitle:** structure of c. immitis chitinase 1 complexed with2 allosamidin
						Fold:TIM beta/alpha-barrel

29	d1ll7a1	Alignment	not modelled	99.5	16	**Superfamily:**(Trans)glycosidases **Family:**Type II chitinase
30	c1lq0A_	Alignment	not modelled	99.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitotriosidase; **PDBTitle:** crystal structure of human chitotriosidase at 2.2 angstrom2 resolution
31	c1kfwA_	Alignment	not modelled	99.4	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase b; **PDBTitle:** structure of catalytic domain of psychrophilic chitinase b from2 arthrobacter tad20
32	c3chfA_	Alignment	not modelled	99.4	15	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**chitinase; **PDBTitle:** crystal structure of aspergillus fumigatus chitinase b1 in complex2 with tetrapeptide
33	c1hjvA_	Alignment	not modelled	99.4	15	**PDB header:**lectin **Chain:** A: **PDB Molecule:**chitinase-3 like protein 1; **PDBTitle:** crystal structure of hcgp-39 in complex with chitin2 tetramer
34	d1kfwa1	Alignment	not modelled	99.4	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Type II chitinase
35	c1wb0A_	Alignment	not modelled	99.4	15	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**chitotriosidase 1; **PDBTitle:** specificity and affinity of natural product cyclopentapeptide2 inhibitor argifin against human chitinase
36	c3qokA_	Alignment	not modelled	99.4	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative chitinase ii; **PDBTitle:** crystal structure of putative chitinase ii from klebsiella pneumoniae
37	c3alfA_	Alignment	not modelled	99.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase, class v; **PDBTitle:** crystal structure of class v chitinase from nicotiana tobaccum
38	c1jneA_	Alignment	not modelled	99.4	17	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**imaginal disc growth factor-2; **PDBTitle:** crystal structure of imaginal disc growth factor-2
39	c3fxyA_	Alignment	not modelled	99.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acidic mammalian chitinase; **PDBTitle:** acidic mammalian chinase, catalytic domain
40	d1vf8a1	Alignment	not modelled	99.4	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Type II chitinase
41	c3g6lA_	Alignment	not modelled	99.4	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase; **PDBTitle:** the crystal structure of a chitinase crchi1 from the nematophagous2 fungus clonostachys rosea
42	c4a5qC_	Alignment	not modelled	99.3	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**chi1; **PDBTitle:** crystal structure of the chitinase chi1 fitted into the 3d structure2 of the yersinia entomophaga toxin complex
43	c3oa5A_	Alignment	not modelled	99.3	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chi1; **PDBTitle:** the structure of chi1, a chitinase from yersinia entomophaga
44	d1nara_	Alignment	not modelled	99.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Type II chitinase
45	c3aquD_	Alignment	not modelled	99.3	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**at4g19810; **PDBTitle:** crystal structure of a class v chitinase from arabidopsis thaliana
46	c3bxwB_	Alignment	not modelled	99.3	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**chitinase domain-containing protein 1; **PDBTitle:** crystal structure of stabilin-1 interacting chitinase-like2 protein, si-clp
47	c2d49A_	Alignment		99.2	40	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase c; **PDBTitle:** solution structure of the chitin-binding domain of2 streptomyces griseus chitinase c
48	d1edta_	Alignment	not modelled	99.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Type II chitinase
49	c1e9lA_	Alignment	not modelled	99.2	18	**PDB header:**macrophage secretory protein **Chain:** A: **PDB Molecule:**ym1 secretory protein; **PDBTitle:** the crystal structure of novel mammalian lectin ym12 suggests a saccharide binding site
50	d2ebna_	Alignment	not modelled	99.1	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Type II chitinase
51	c3cz8A_	Alignment	not modelled	99.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative sporulation-specific glycosylase ydhd; **PDBTitle:** crystal structure of putative sporulation-specific glycosylase ydhd2 from bacillus subtilis
52	d1aiwa_	Alignment	not modelled	99.0	28	**Fold:**WW domain-like **Superfamily:**Carbohydrate binding domain **Family:**Carbohydrate binding domain
53	d1goia1	Alignment	not modelled	99.0	22	**Fold:**WW domain-like **Superfamily:**Carbohydrate binding domain **Family:**Carbohydrate binding domain
54	d1eoka_	Alignment	not modelled	98.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases

						Family: Type II chitinase
55	c3b0vD_	Alignment	not modelled	94.6	13	**PDB header:**oxidoreductase/rna **Chain:** D: **PDB Molecule:**trna-dihydrouridine synthase; **PDBTitle:** trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
56	d1ur4a_	Alignment	not modelled	94.6	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
57	d2fiqa1	Alignment	not modelled	90.4	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**GatZ-like
58	d1ed7a_	Alignment	not modelled	90.1	35	**Fold:**WW domain-like **Superfamily:**Carbohydrate binding domain **Family:**Carbohydrate binding domain
59	c3mi6A_	Alignment	not modelled	82.6	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of the alpha-galactosidase from lactobacillus2 brevis, northeast structural genomics consortium target lbr11.
60	d1nq6a_	Alignment	not modelled	81.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
61	c2wwcA_	Alignment	not modelled	80.2	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**1,4-beta-n-acetylmuramidase; **PDBTitle:** 3d-structure of the modular autolysin lytc from2 streptococcus pneumoniae in complex with synthetic3 peptidoglycan ligand
62	c2aamA_	Alignment	not modelled	78.4	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein tm1410; **PDBTitle:** crystal structure of a putative glycosidase (tm1410) from thermotoga2 maritima at 2.20 a resolution
63	d2aama1	Alignment	not modelled	78.4	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**TM1410-like
64	d1i1wa_	Alignment	not modelled	77.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
65	c2yfnA_	Alignment	not modelled	76.5	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase-sucrose kinase agask; **PDBTitle:** galactosidase domain of alpha-galactosidase-sucrose kinase,2 agask
66	c3canA_	Alignment	not modelled	76.0	13	**PDB header:**lyase activator **Chain:** A: **PDB Molecule:**pyruvate-formate lyase-activating enzyme; **PDBTitle:** crystal structure of a domain of pyruvate-formate lyase-activating2 enzyme from bacteroides vulgatus atcc 8482
67	c2i5gB_	Alignment	not modelled	74.8	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**amidohydrolase; **PDBTitle:** crystal strcuture of amidohydrolase from pseudomonas2 aeruginosa
68	c3lu2B_	Alignment	not modelled	72.7	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lmo2462 protein; **PDBTitle:** structure of lmo2462, a listeria monocytogenes amidohydrolase family2 putative dipeptidase
69	d1wgoa_	Alignment		72.2	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PKD domain **Family:**PKD domain
70	c2c26A_	Alignment		68.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** structural basis for the promiscuous specificity of the2 carbohydrate-binding modules from the beta-sandwich super3 family
71	c1uhvD_	Alignment	not modelled	66.3	11	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-xylosidase; **PDBTitle:** crystal structure of beta-d-xylosidase from2 thermoanaerobacterium saccharolyticum, a family 393 glycoside hydrolase
72	d1v6wa2	Alignment	not modelled	65.6	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
73	d1tuxa_	Alignment	not modelled	61.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
74	d1fh9a_	Alignment	not modelled	57.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
75	d1auza_	Alignment	not modelled	55.9	10	**Fold:**SpoIIaa-like **Superfamily:**SpoIIaa-like **Family:**Anti-sigma factor antagonist SpoIIaa
76	d1xrsb2	Alignment	not modelled	55.8	22	**Fold:**Dodecin subunit-like **Superfamily:**D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain **Family:**D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain
77	c2xm5A_	Alignment	not modelled	55.3	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cloq; **PDBTitle:** structural and mechanistic analysis of the magnesium-2

						independent aromatic prenyltransferase cloq from the3 clorobiocin biosynthetic pathway
78	d1qwga_	Alignment	not modelled	52.1	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA **Family:**(2r)-phospho-3-sulfolactate synthase ComA
79	d1bg4a_	Alignment	not modelled	52.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
80	d1sfla_	Alignment	not modelled	51.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
81	c3fdgA_	Alignment	not modelled	49.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidase ac. metallo peptidase. merops family m19; **PDBTitle:** the crystal structure of the dipeptidase ac, metallo peptidase. merops2 family m19
82	c3jugA_	Alignment	not modelled	45.3	12	**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
83	c1l0qC_	Alignment	not modelled	45.2	15	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**surface layer protein; **PDBTitle:** tandem yvtn beta-propeller and pkd domains from an archaeal surface2 layer protein
84	d1w91a2	Alignment	not modelled	43.5	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
85	c2wagA_	Alignment	not modelled	42.8	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme, putative; **PDBTitle:** the structure of a family 25 glycosyl hydrolase from2 bacillus anthracis.
86	d1zdya1	Alignment	not modelled	42.4	21	**Fold:**Antiparallel beta/alpha barrel (PT-barrel) **Superfamily:**Prenyltransferase-like **Family:**Prenyltransferase-like
87	d1vc1a_	Alignment	not modelled	41.8	13	**Fold:**SpoIIaa-like **Superfamily:**SpoIIaa-like **Family:**Anti-sigma factor antagonist SpoIIaa
88	d1tv8a_	Alignment	not modelled	41.1	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**MoCo biosynthesis proteins
89	d1geha1	Alignment	not modelled	41.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
90	c2kzwA_	Alignment	not modelled	40.4	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of q8psa4 from methanosarcina mazei, northeast2 structural genomics consortium target mar143a
91	c2qw5B_	Alignment	not modelled	40.3	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**xylose isomerase-like tim barrel; **PDBTitle:** crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution
92	d1itua_	Alignment	not modelled	39.1	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Renal dipeptidase
93	d1ho8a_	Alignment	not modelled	36.7	12	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**Regulatory subunit H of the V-type ATPase
94	c2o14A_	Alignment	not modelled	35.1	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yxim; **PDBTitle:** x-ray crystal structure of protein yxim_bacsu from bacillus2 subtilis. northeast structural genomics consortium target3 sr595
95	c3emzA_	Alignment	not modelled	34.8	13	**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
96	d1l0qa1	Alignment	not modelled	34.4	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PKD domain **Family:**PKD domain
97	c3itcA_	Alignment	not modelled	33.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**renal dipeptidase; **PDBTitle:** crystal structure of sco3058 with bound citrate and glycerol
98	d1th8b_	Alignment	not modelled	33.6	9	**Fold:**SpoIIaa-like **Superfamily:**SpoIIaa-like **Family:**Anti-sigma factor antagonist SpoIIaa
99	d1ykwa1	Alignment	not modelled	33.4	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
100	d1svda1	Alignment	not modelled	32.6	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
101	c2xn1B_	Alignment	not modelled	31.2	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** structure of alpha-galactosidase from lactobacillus acidophilus ncfm2 with tris
102	d1v0la_	Alignment	not modelled	30.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
						PDB header:cell adhesion **Chain:** A: **PDB Molecule:**collagenase;

103	c3jquA_	Alignment	not modelled	30.8	12	**PDBTitle:** crystal structure of clostridium histolyticum colg collagenase2 polycystic kidney disease domain at 1.4 angstrom resolution
104	c2qygC_	Alignment	not modelled	30.7	18	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**ribulose bisphosphate carboxylase-like protein 2; **PDBTitle:** crystal structure of a rubisco-like protein rlp2 from rhodopseudomonas2 palustris
105	d1rpxa_	Alignment	not modelled	30.3	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
106	c3ndyA_	Alignment	not modelled	29.8	15	**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
107	c2ylaA_	Alignment	not modelled	29.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-n-acetylhexosaminidase; **PDBTitle:** inhibition of the pneumococcal virulence factor strh and2 molecular insights into n-glycan recognition and3 hydrolysis
108	c2j75A_	Alignment	not modelled	29.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucosidase a; **PDBTitle:** beta-glucosidase from thermotoga maritima in complex with2 noeuromycin
109	c2yr1B_	Alignment	not modelled	29.5	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** crystal structure of 3-dehydroquinate dehydratase from geobacillus2 kaustophilus hta426
110	c2zunB_	Alignment	not modelled	29.1	15	**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
111	c3nsnA_	Alignment	not modelled	28.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-acetylglucosaminidase; **PDBTitle:** crystal structure of insect beta-n-acetyl-d-hexosaminidase ofhex12 complexed with tmg-chitotriomycin
112	d1q5ma_	Alignment	not modelled	28.1	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
113	c3e77A_	Alignment	not modelled	27.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoserine aminotransferase; **PDBTitle:** human phosphoserine aminotransferase in complex with plp
114	d1jaka1	Alignment	not modelled	27.5	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain
115	d1n82a_	Alignment	not modelled	27.3	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
116	c2cksB_	Alignment	not modelled	27.3	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)
117	c3qm2A_	Alignment	not modelled	27.1	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoserine aminotransferase; **PDBTitle:** 2.25 angstrom crystal structure of phosphoserine aminotransferase2 (serc) from salmonella enterica subsp. enterica serovar typhimurium
118	d1gqna_	Alignment	not modelled	26.6	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
119	c2ou4C_	Alignment	not modelled	26.3	8	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**d-tagatose 3-epimerase; **PDBTitle:** crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii
120	c3sviA_	Alignment	not modelled	25.5	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**type iii effector hopab2; **PDBTitle:** structure of the pto-binding domain of hoppmal generated by limited2 thermolysin digestion