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Description	P77154
Date	Thu Jan 5 12:25:42 GMT 2012
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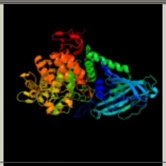
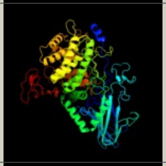
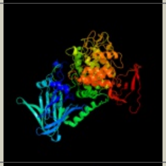
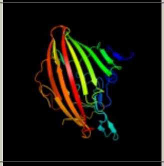
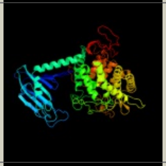
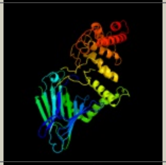
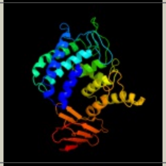
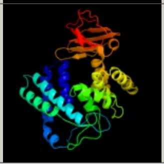
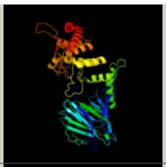
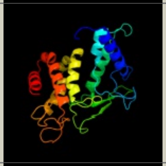
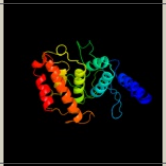
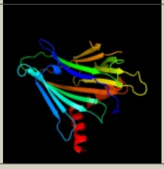
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1h54B_	Alignment		100.0	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**maltose phosphorylase; **PDBTitle:** maltose phosphorylase from lactobacillus brevis
2	c2rdyB_	Alignment		100.0	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**bh0842 protein; **PDBTitle:** crystal structure of a putative glycoside hydrolase family2 protein from bacillus halodurans
3	c2eacB_	Alignment		100.0	15	**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
4	d1h54a1	Alignment		100.0	32	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glycosyltransferase family 36 C-terminal domain
5	d1h54a2	Alignment		100.0	23	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Glycosyltransferase family 36 N-terminal domain
6	c2cqtA_	Alignment		100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cellobiose phosphorylase; **PDBTitle:** crystal structure of cellvibrio gilvus cellobiose phosphorylase2 crystallized from sodium/potassium phosphate
7	c1v7wA_	Alignment		100.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**chitobiose phosphorylase; **PDBTitle:** crystal structure of vibrio proteolyticus chitobiose phosphorylase in2 complex with glcnac
8	d1v7wa1	Alignment		100.0	13	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glycosyltransferase family 36 C-terminal domain
9	c1ug9A_	Alignment		99.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucodextranase; **PDBTitle:** crystal structure of glucodextranase from arthrobacter globiformis i42
10	c2okxB_	Alignment		99.7	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rhamnosidase b; **PDBTitle:** crystal structure of gh78 family rhamnosidase of bacillus sp. gl1 at2 1.9 a
11	c3cihA_	Alignment		99.6	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative alpha-rhamnosidase; **PDBTitle:** crystal structure of a putative alpha-rhamnosidase from2 bacteroides thetaiotaomicron

12	c1lf6A_	Alignment		99.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucoamylase; **PDBTitle:** crystal structure of bacterial glucoamylase
13	c3c67B_	Alignment		99.1	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**uncharacterized protein ygjk; **PDBTitle:** escherichia coli k12 ygjk in a complexed with glucose
14	d1lf6a1	Alignment		98.1	15	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Bacterial glucoamylase C-terminal domain-like
15	c2ww1B_	Alignment		97.6	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-1,2-mannosidase; **PDBTitle:** structure of the family gh92 inverting mannosidase bt39902 from bacteroides thetaiotaomicron vpi-5482 in complex with3 thiomannobioside
16	c2zzrA_	Alignment		97.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**unsaturated glucuronyl hydrolase; **PDBTitle:** crystal structure of unsaturated glucuronyl hydrolase from2 streptcoccus agalactiae
17	c2jg0A_	Alignment		97.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**periplasmic trehalase; **PDBTitle:** family 37 trehalase from escherichia coli in complex with 1-2 thiatrehazolin
18	d2jg0a1	Alignment		97.5	15	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Trehalase-like
19	d1ulva1	Alignment		97.2	18	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Bacterial glucoamylase C-terminal domain-like
20	d1ulva4	Alignment		96.8	14	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Bacterial glucoamylase N-terminal domain-like
21	d1lf6a2	Alignment	not modelled	96.7	12	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Bacterial glucoamylase N-terminal domain-like
22	d2d5ja1	Alignment	not modelled	96.5	17	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glycosyl Hydrolase Family 88
23	c2vn4A_	Alignment	not modelled	95.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucoamylase; **PDBTitle:** glycoside hydrolase family 15 glucoamylase from hypocrea2 jecorina
24	c3qspB_	Alignment	not modelled	94.6	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** analysis of a new family of widely distributed metal-independent alpha2 mannosidases provides unique insight into the processing of n-linked3 glycans, streptococcus pneumoniae sp_2144 non-productive substrate4 complex with alpha-1,6-mannobiose
25	d2fbaa1	Alignment	not modelled	93.1	17	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glucoamylase
26	c2z07A_	Alignment	not modelled	93.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha0978; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 thermus thermophilus hb8
27	c2wvyA_	Alignment	not modelled	92.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-1,2-mannosidase; **PDBTitle:** structure of the family gh92 inverting mannosidase bt21992 from bacteroides thetaiotaomicron vpi-5482
						Fold:alpha/alpha toroid

28	d1gaia_	Alignment	not modelled	87.4	17	**Superfamily:**Six-hairpin glycosidases **Family:**Glucoamylase
29	c2p0vA_	Alignment	not modelled	78.2	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein bt3781; **PDBTitle:** crystal structure of bt3781 protein from bacteroides2 thetaiotaomicron, northeast structural genomics target3 btr58
30	d2p0va1	Alignment	not modelled	78.2	19	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**CPF0428-like
31	d2nvpa1	Alignment	not modelled	70.2	16	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**CPF0428-like
32	c3gt5A_	Alignment	not modelled	31.3	8	**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
33	c3d82A_	Alignment	not modelled	22.6	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**cupin 2, conserved barrel domain protein; **PDBTitle:** crystal structure of a cupin-2 domain containing protein (sfri_3543)2 from shewanella frigidimarina ncimb 400 at 2.05 a resolution
34	c2ky8A_	Alignment	not modelled	22.2	35	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**methyl-cpg-binding domain protein 2; **PDBTitle:** solution structure and dynamic analysis of chicken mbd2 methyl binding2 domain bound to a target methylated dna sequence
35	c3nuqA_	Alignment	not modelled	17.2	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative nucleotide phosphatase; **PDBTitle:** structure of a putative nucleotide phosphatase from saccharomyces2 cerevisiae
36	d2pyta1	Alignment	not modelled	16.4	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**EutQ-like
37	c3lwcA_	Alignment	not modelled	15.9	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of structural genomics, unknown function2 (yp_766765.1) from rhizobium leguminosarum bv. viciae 3841 at 1.40 a3 resolution
38	d1ig4a_	Alignment	not modelled	15.2	26	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**Methyl-CpG-binding domain, MBD
39	d1fp3a_	Alignment	not modelled	14.9	13	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**N-acylglucosamine (NAG) epimerase
40	d2e45a1	Alignment	not modelled	14.6	20	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
41	c2avpA_	Alignment	not modelled	13.8	14	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**synthetic consensus tpr protein; **PDBTitle:** crystal structure of an 8 repeat consensus tpr superhelix
42	c1na3A_	Alignment	not modelled	12.5	15	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**designed protein ctpr2; **PDBTitle:** design of stable alpha-helical arrays from an idealized tpr2 motif
43	d1blaa_	Alignment	not modelled	12.4	24	**Fold:**beta-Trefoil **Superfamily:**Cytokine **Family:**Fibroblast growth factors (FGF)
44	c2gz6B_	Alignment	not modelled	11.7	13	**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
45	c3fjsC_	Alignment	not modelled	11.1	17	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**uncharacterized protein with rmlc-like cupin fold; **PDBTitle:** crystal structure of a putative biosynthetic protein with rmlc-like2 cupin fold (reut_b4087) from ralstonia eutropha jmp134 at 1.90 a3 resolution
46	d1ok0a_	Alignment	not modelled	10.8	40	**Fold:**alpha-Amylase inhibitor tendamistat **Superfamily:**alpha-Amylase inhibitor tendamistat **Family:**alpha-Amylase inhibitor tendamistat
47	d2ysca1	Alignment	not modelled	10.6	33	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
48	c2ov2O_	Alignment	not modelled	9.9	75	**PDB header:**protein binding/transferase **Chain:** O: **PDB Molecule:**serine/threonine-protein kinase pak 4; **PDBTitle:** the crystal structure of the human rac3 in complex with the crib2 domain of human p21-activated kinase 4 (pak4)
49	d1sfua_	Alignment	not modelled	9.3	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
50	c3ecqA_	Alignment	not modelled	9.2	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-alpha-n-acetylgalactosaminidase; **PDBTitle:** endo-alpha-n-acetylgalactosaminidase from streptococcus pneumoniae:2 semet structure
51	d1tueb_	Alignment	not modelled	9.0	12	**Fold:**E2 regulatory, transactivation domain **Superfamily:**E2 regulatory, transactivation domain **Family:**E2 regulatory, transactivation domain
52	d3d37a1	Alignment	not modelled	8.5	6	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like
53	c2vt8B_	Alignment	not modelled	8.1	24	**PDB header:**hydrolase inhibitor **Chain:** B: **PDB Molecule:**proteasome inhibitor pi31 subunit; **PDBTitle:** structure of a conserved dimerisation domain within fbox72 and pi31

54	c1wr4A_	Alignment	not modelled	7.8	36	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ubiquitin-protein ligase nedd4-2; **PDBTitle:** solution structure of the second ww domain of nedd4-2
55	d1qk9a_	Alignment	not modelled	7.5	50	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**Methyl-CpG-binding domain, MBD
56	d2fug33	Alignment	not modelled	7.5	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
57	d1ub1a_	Alignment	not modelled	7.1	32	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**Methyl-CpG-binding domain, MBD
58	c2k85A_	Alignment	not modelled	7.0	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**glucocorticoid receptor dna-binding factor 1; **PDBTitle:** p190-a rhogap ff1 domain
59	c2kywA_	Alignment	not modelled	7.0	9	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**adhesion exoprotein; **PDBTitle:** solution nmr structure of a domain of adhesion exoprotein from2 pediococcus pentosaceus, northeast structural genomics consortium3 target ptr41o
60	c3k7xA_	Alignment	not modelled	6.8	14	**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.
61	d1tjca_	Alignment	not modelled	6.6	14	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
62	d2ho2a1	Alignment	not modelled	6.6	33	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
63	d1kwga1	Alignment	not modelled	6.5	11	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
64	c2odbB_	Alignment	not modelled	6.4	63	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase pak 6; **PDBTitle:** the crystal structure of human cdc42 in complex with the crib domain2 of human p21-activated kinase 6 (pak6)
65	c2zxqA_	Alignment	not modelled	6.4	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-alpha-n-acetylgalactosaminidase; **PDBTitle:** crystal structure of endo-alpha-n-acetylgalactosaminidase2 from bifidobacterium longum (engbf)
66	d2arca_	Alignment	not modelled	6.1	3	**Fold:**Double-stranded beta-helix **Superfamily:**Regulatory protein AraC **Family:**Regulatory protein AraC
67	c1e0aB_	Alignment	not modelled	5.7	63	**PDB header:**signalling protein **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase pak-alpha; **PDBTitle:** cdc42 complexed with the gtpase binding domain of p212 activated kinase
68	c3mpbA_	Alignment	not modelled	5.6	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar isomerase; **PDBTitle:** z5688 from e. coli o157:h7 bound to fructose
69	c3j08A_	Alignment	not modelled	5.6	20	**PDB header:**hydrolase, metal transport **Chain:** A: **PDB Molecule:**copper-exporting p-type atpase a; **PDBTitle:** high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
70	c2v8kA_	Alignment	not modelled	5.6	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**pectate lyase; **PDBTitle:** structure of a family 2 pectate lyase in complex with2 trigalacturonic acid
71	d1qqha_	Alignment	not modelled	5.4	12	**Fold:**E2 regulatory, transactivation domain **Superfamily:**E2 regulatory, transactivation domain **Family:**E2 regulatory, transactivation domain
72	d1xuba2	Alignment	not modelled	5.2	9	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like
73	d2gj4a1	Alignment	not modelled	5.2	26	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Oligosaccharide phosphorylase
74	c2vc8A_	Alignment	not modelled	5.2	18	**PDB header:**protein-binding **Chain:** A: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of the lsm domain of human edc3 (enhancer2 of decapping 3)
75	d1p9ka_	Alignment	not modelled	5.2	12	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**YbcJ-like
76	c2hc8A_	Alignment	not modelled	5.1	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation-transporting atpase, p-type; **PDBTitle:** structure of the a. fulgidus copa a-domain
77	c2hyzA_	Alignment	not modelled	5.1	15	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**synthetic consensus tpr protein; **PDBTitle:** crystal structure of an 8 repeat consensus tpr superhelix2 (orthorombic crystal form)
78	d2atia1	Alignment	not modelled	5.1	26	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Oligosaccharide phosphorylase
79	d1ljma_	Alignment	not modelled	5.0	19	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**RUNT domain