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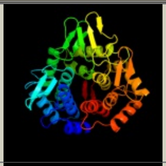
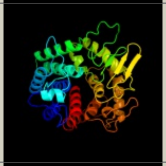
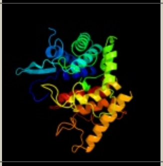
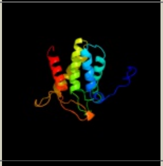
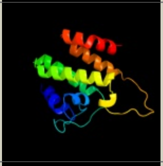
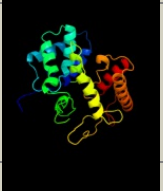
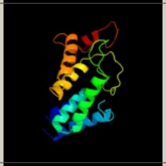
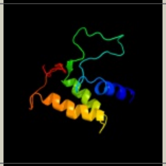
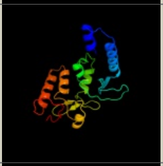
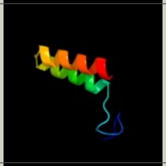
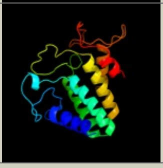
Description	P37651
Date	Thu Jan 5 11:56:23 GMT 2012
Unique Job ID	8eba1720deea65bb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qxqD_	Alignment		100.0	100	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**endoglucanase; **PDBTitle:** structure of the bacterial cellulose synthase subunit z in complex2 with cellopentaose
2	d1wzza1	Alignment		100.0	26	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
3	d1wu4a1	Alignment		100.0	22	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
4	d1h12a_	Alignment		100.0	22	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
5	d1kwfa_	Alignment		100.0	22	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
6	d1v5da_	Alignment		100.0	18	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
7	c3renB_	Alignment		100.0	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycosyl hydrolase, family 8; **PDBTitle:** cpf_2247, a novel alpha-amylase from clostridium perfringens
8	c2zzrA_	Alignment		94.2	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**unsaturated glucuronyl hydrolase; **PDBTitle:** crystal structure of unsaturated glucuronyl hydrolase from2 streptcoccus agalactiae
9	d1fp3a_	Alignment		93.9	12	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**N-acylglucosamine (NAG) epimerase
10	d2afaa1	Alignment		93.3	8	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**N-acylglucosamine (NAG) epimerase
11	c3pmmA_	Alignment		90.2	11	**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

12	c3k11A_	Alignment		88.9	7	**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
13	d1nxca_	Alignment		83.2	15	**Fold:**alpha/alpha toroid **Superfamily:**Seven-hairpin glycosidases **Family:**Class I alpha-1;2-mannosidase, catalytic domain
14	c3k7xA_	Alignment		74.6	10	**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.
15	c3eu8D_	Alignment		69.7	14	**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
16	c3qspB_	Alignment		68.0	15	**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
17	d1g9ga_	Alignment		55.3	30	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
18	c1x9dA_	Alignment		47.2	14	**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
19	d1x9da1	Alignment		47.2	14	**Fold:**alpha/alpha toroid **Superfamily:**Seven-hairpin glycosidases **Family:**Class I alpha-1;2-mannosidase, catalytic domain
20	c2gz6B_	Alignment		42.9	7	**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
21	c3e6uA_	Alignment	not modelled	37.6	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**lanc-like protein 1; **PDBTitle:** crystal structure of human lancl1
22	d1hcua_	Alignment	not modelled	34.1	12	**Fold:**alpha/alpha toroid **Superfamily:**Seven-hairpin glycosidases **Family:**Class I alpha-1;2-mannosidase, catalytic domain
23	d2p0va1	Alignment	not modelled	31.2	14	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**CPF0428-like
24	c2p0vA_	Alignment	not modelled	31.2	14	**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
25	c3okfA_	Alignment	not modelled	21.6	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-dehydroquinate synthase; **PDBTitle:** 2.5 angstrom resolution crystal structure of 3-dehydroquinate synthase2 (arob) from vibrio cholerae
26	d2g0da1	Alignment	not modelled	18.0	14	**Fold:**alpha/alpha toroid **Superfamily:**LanC-like **Family:**LanC-like
27	c3rbbA_	Alignment	not modelled	17.4	30	**PDB header:**viral protein, protein binding **Chain:** A: **PDB Molecule:**protein nef; **PDBTitle:** hiv-1 nef protein in complex with engineered hck sh3 domain
28	d2nvpa1	Alignment	not modelled	16.9	14	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**CPF0428-like
29	d1l1ya_	Alignment	not modelled	15.8	16	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain

30	c1l2aD_	Alignment	not modelled	15.8	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
31	d2nefa_	Alignment	not modelled	15.8	29	**Fold:**Regulatory factor Nef **Superfamily:**Regulatory factor Nef **Family:**Regulatory factor Nef
32	c3jtgA_	Alignment	not modelled	15.7	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ets-related transcription factor elf-3; **PDBTitle:** crystal structure of mouse elf3 c-terminal dna-binding domain in2 complex with type ii tgf-beta receptor promoter dna
33	c3gt5A_	Alignment	not modelled	15.1	10	**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
34	d1nc5a_	Alignment	not modelled	13.7	14	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Hypothetical protein YteR
35	c1p0oA_	Alignment	not modelled	13.0	30	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**19-mer peptide from 50s ribosomal protein l1; **PDBTitle:** hp (2-20) substitution of trp for gln and asp at position2 17 and 19 modification in sds-d25 micelles
36	c3l55B_	Alignment	not modelled	12.7	15	**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
37	c3ik5A_	Alignment	not modelled	12.6	25	**PDB header:**viral protein/signaling protein **Chain:** A: **PDB Molecule:**protein nef; **PDBTitle:** sivmac239 nef in complex with tcr zeta itam 1 polypeptide2 (a63-r80)
38	c2d3wB_	Alignment	not modelled	12.1	29	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**probable atp-dependent transporter sufc; **PDBTitle:** crystal structure of escherichia coli sufc, an atpase2 compenent of the suf iron-sulfur cluster assembly machinery
39	c2dcoA_	Alignment	not modelled	10.8	63	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**s1p4 first extracellular loop peptidomimetic; **PDBTitle:** s1p4 first extracellular loop peptidomimetic
40	c2xi1A_	Alignment	not modelled	10.0	30	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**nef; **PDBTitle:** crystal structure of the hiv-1 nef sequenced from a patient's sample
41	d1jb7a1	Alignment	not modelled	9.8	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
42	c3nfvA_	Alignment	not modelled	9.0	13	**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
43	d1efnb_	Alignment	not modelled	8.9	30	**Fold:**Regulatory factor Nef **Superfamily:**Regulatory factor Nef **Family:**Regulatory factor Nef
44	d1puee_	Alignment	not modelled	8.4	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ets domain
45	d1lm7a_	Alignment	not modelled	8.3	20	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Plakin repeat **Family:**Plakin repeat
46	c2oylB_	Alignment	not modelled	7.9	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endoglycoceramidase ii; **PDBTitle:** endo-glycoceramidase ii from rhodococcus sp.: cellobiose-like2 imidazole complex
47	d1rmva_	Alignment	not modelled	6.8	24	**Fold:**Four-helical up-and-down bundle **Superfamily:**TMV-like viral coat proteins **Family:**TMV-like viral coat proteins
48	d1g99a2	Alignment	not modelled	6.6	31	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
49	d1pgl21	Alignment	not modelled	6.6	19	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Comoviridae-like VP
50	d1pgw21	Alignment	not modelled	6.5	19	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Comoviridae-like VP
51	d1ny721	Alignment	not modelled	6.4	13	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Comoviridae-like VP
52	d1xjva1	Alignment	not modelled	6.3	12	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
53	d1ei7a_	Alignment	not modelled	6.2	21	**Fold:**Four-helical up-and-down bundle **Superfamily:**TMV-like viral coat proteins **Family:**TMV-like viral coat proteins
54	c1lf6A_	Alignment	not modelled	6.1	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucoamylase; **PDBTitle:** crystal structure of bacterial glucoamylase
55	c3pdmP_	Alignment	not modelled	6.1	24	**PDB header:**virus **Chain:** P: **PDB Molecule:**coat protein; **PDBTitle:** hibiscus latent singapore virus
						Fold:alpha/alpha toroid

56	d2d5ja1	Alignment	not modelled	5.9	10	**Superfamily:**Six-hairpin glycosidases **Family:**Glycosyl Hydrolase Family 88
57	d1vtmp_	Alignment	not modelled	5.9	17	**Fold:**Four-helical up-and-down bundle **Superfamily:**TMV-like viral coat proteins **Family:**TMV-like viral coat proteins
58	c3sm3A_	Alignment	not modelled	5.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sam-dependent methyltransferases; **PDBTitle:** crystal structure of sam-dependent methyltransferases q8puk2_metma2 from methanosarcina mazei. northeast structural genomics consortium3 target mar262.
59	c3mtiA_	Alignment	not modelled	5.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rrna methylase; **PDBTitle:** the crystal structure of a rrna methylase from streptococcus2 thermophilus to 1.95a
60	c2bfuL_	Alignment	not modelled	5.6	10	**PDB header:**virus **Chain:** L: **PDB Molecule:**cowpea mosaic virus, large (l) subunit; **PDBTitle:** x-ray structure of cpmv top component
61	c1bmv2_	Alignment	not modelled	5.4	14	**PDB header:**virus/rna **Chain:** 2: **PDB Molecule:**protein (icosahedral virus - b and c domain); **PDBTitle:** protein-rna interactions in an icosahedral virus at 3.02 angstroms resolution
62	c1ta9A_	Alignment	not modelled	5.2	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol dehydrogenase; **PDBTitle:** crystal structure of glycerol dehydrogenase from schizosaccharomyces2 pombe
63	c2ov2O_	Alignment	not modelled	5.1	29	**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)
64	c2yfvC_	Alignment	not modelled	5.0	35	**PDB header:**cell cycle **Chain:** C: **PDB Molecule:**scm3; **PDBTitle:** the heterotrimeric complex of kluyveromyces lactis scm3, cse4 and h4