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Description	P27129
Date	Thu Jan 5 11:43:17 GMT 2012
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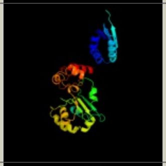
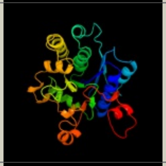
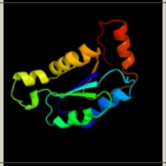
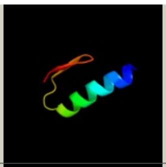
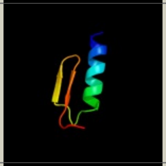
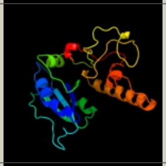
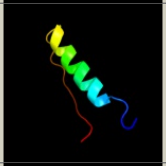
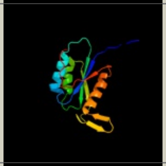
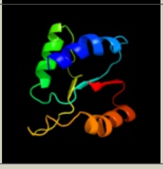
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ga8a_	Alignment		100.0	19	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Galactosyltransferase LgtC
2	c1ga8A_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**galactosyl transferase lgtc; **PDBTitle:** crystal structure of galacosyltransferase lgtc in complex2 with donor and acceptor sugar analogs.
3	c3tztB_	Alignment		100.0	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyl transferase family 8; **PDBTitle:** the structure of a protein in glycosyl transferase family 8 from2 anaerococcus prevotii.
4	c1zcyA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycogenin-1; **PDBTitle:** apo form of a mutant of glycogenin in which asp159 is replaced by ser
5	d1ll2a_	Alignment		100.0	17	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Glycogenin
6	c1zctB_	Alignment		100.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycogenin-1; **PDBTitle:** structure of glycogenin truncated at residue 270 in a2 complex with udp
7	c1xhbA_	Alignment		95.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 1; **PDBTitle:** the crystal structure of udp-galnac: polypeptide alpha-n-2 acetylgalactosaminyltransferase-t1
8	d1o7qa_	Alignment		92.7	15	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**alpha-1,3-galactosyltransferase-like
9	c2d7iA_	Alignment		88.9	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 10; **PDBTitle:** crsytal structure of pp-galnac-t10 with udp, galnac and mn2+
10	c2ffuA_	Alignment		85.2	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 2; **PDBTitle:** crystal structure of human ppgalnact-2 complexed with udp2 and ea2
11	d1fo8a_	Alignment		70.8	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**N-acetylglucosaminyltransferase I

12	d2py5a2	Alignment		67.9	20	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**DNA polymerase I
13	c2ex3I_	Alignment		57.2	18	**PDB header:**transferase/replication **Chain:** I: **PDB Molecule:**dna polymerase; **PDBTitle:** bacteriophage phi29 dna polymerase bound to terminal protein
14	d1lzia_	Alignment		45.3	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**alpha-1,3-galactosyltransferase-like
15	d1w7pd2	Alignment		42.8	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
16	c2npiB_	Alignment		30.2	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**protein clp1; **PDBTitle:** clp1-atp-pcf11 complex
17	c2z86D_	Alignment		26.5	6	**PDB header:**transferase **Chain:** D: **PDB Molecule:**chondroitin synthase; **PDBTitle:** crystal structure of chondroitin polymerase from2 escherichia coli strain k4 (k4cp) complexed with udp-glcua3 and udp
18	c2p73A_	Alignment		24.2	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative glycosyltransferase (mannosyltransferase) involved **PDBTitle:** crystal structure of a glycosyltransferase involved in the2 glycosylation of the major capsid of pbcv-1
19	d1qg8a_	Alignment		23.4	20	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Spore coat polysaccharide biosynthesis protein SpsA
20	c3lmaC_	Alignment		23.3	12	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**stage v sporulation protein ad (spovad); **PDBTitle:** crystal structure of the stage v sporulation protein ad2 (spovad) from bacillus licheniformis. northeast structural3 genomics consortium target bir6.
21	d1ibia1	Alignment	not modelled	22.6	64	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
22	d1s4na_	Alignment	not modelled	18.4	16	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Glycolipid 2-alpha-mannosyltransferase
23	c2w3zA_	Alignment	not modelled	18.0	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deacetylase; **PDBTitle:** structure of a streptococcus mutans ce4 esterase
24	d1acoa2	Alignment	not modelled	16.7	14	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
25	c3ew8A_	Alignment	not modelled	15.5	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**histone deacetylase 8; **PDBTitle:** crystal structure analysis of human hdac8 d101l variant
26	d2c71a1	Alignment	not modelled	12.6	14	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
27	c3maxB_	Alignment	not modelled	12.5	35	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**histone deacetylase 2; **PDBTitle:** crystal structure of human hdac2 complexed with an n-(2-aminophenyl)2 benzamide
28	c2ktvA_	Alignment	not modelled	11.7	18	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic peptide chain release factor subunit 1; **PDBTitle:** human erf1 c-domain, "open" conformer
29	c4a69A_	Alignment	not modelled	11.6	30	**PDB header:**transcription **Chain:** A: **PDB Molecule:**histone deacetylase 3,;

29	c4a69A_	Alignment	not modelled	11.6	30	**PDBTitle:** structure of hdac3 bound to corepressor and inositol tetraphosphate
30	d1xhba2	Alignment	not modelled	11.3	15	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
31	c3ckvA_	Alignment	not modelled	11.0	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a mycobacterial protein
32	c3m9qA_	Alignment	not modelled	10.7	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein male-specific lethal-3; **PDBTitle:** drosophila msl3 chromodomain
33	c1hf2A_	Alignment	not modelled	10.6	17	**PDB header:**cell division protein **Chain:** A: **PDB Molecule:**septum site-determining protein minc; **PDBTitle:** crystal structure of the bacterial cell-division inhibitor2 minc from t. maritima
34	d1u5tb1	Alignment	not modelled	10.3	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
35	c3e20C_	Alignment	not modelled	10.1	24	**PDB header:**translation **Chain:** C: **PDB Molecule:**eukaryotic peptide chain release factor subunit 1; **PDBTitle:** crystal structure of s.pombe erf1/erf3 complex
36	c3m9pA_	Alignment	not modelled	9.5	40	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**male-specific lethal 3 homolog; **PDBTitle:** human msl3 chromodomain bound to dna and h4k20me1 peptide
37	d1hf2a1	Alignment	not modelled	8.9	17	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Cell-division inhibitor MinC, C-terminal domain **Family:**Cell-division inhibitor MinC, C-terminal domain
38	d1t64a_	Alignment	not modelled	6.9	18	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Histone deacetylase, HDAC
39	d1dt9a2	Alignment	not modelled	6.6	18	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
40	c1w17A_	Alignment	not modelled	6.4	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable polysaccharide deacetylase pdaa; **PDBTitle:** structure of bacillus subtilis pdaa, a family 42 carbohydrate esterase.
41	d1c3pa_	Alignment	not modelled	6.1	29	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Histone deacetylase, HDAC
42	c3menC_	Alignment	not modelled	5.9	35	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**acetylpolyamine aminohydrolase; **PDBTitle:** crystal structure of acetylpolyamine aminohydrolase from burkholderia2 pseudomallei, iodide soak
43	c2zmeB_	Alignment	not modelled	5.8	26	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**vacuolar protein-sorting-associated protein 36; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
44	d1ctla1	Alignment	not modelled	5.8	55	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
45	d2f5ka1	Alignment	not modelled	5.6	47	**Fold:**SH3-like barrel **Superfamily:**Chromo domain-like **Family:**Chromo barrel domain
46	d2g3ra2	Alignment	not modelled	5.5	56	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
47	c3bcvA_	Alignment	not modelled	5.4	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative glycosyltransferase protein; **PDBTitle:** crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
48	c3ir9A_	Alignment	not modelled	5.4	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**peptide chain release factor subunit 1; **PDBTitle:** c-terminal domain of peptide chain release factor from2 methanosarcina mazei.
49	c1omxB_	Alignment	not modelled	5.3	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**alpha-1,4-n-acetylhexosaminyltransferase extl2; **PDBTitle:** crystal structure of mouse alpha-1,4-n-2 acetylhexosaminyltransferase (extl2)