























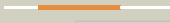





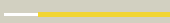










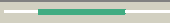





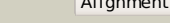


Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P27128
Date	Thu Jan 5 11:43:15 GMT 2012
Unique Job ID	1f83a12794b1eadd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ga8A_	 Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: galactosyl transferase lgtc; PDBTitle: crystal structure of galactosyltransferase lgtc in complex2 with donor and acceptor sugar analogs.
2	d1ga8a_	 Alignment		100.0	20	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Galactosyltransferase LgtC
3	c3tztB_	 Alignment		100.0	21	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	18	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	18	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		97.2	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	c2ffuA_	 Alignment		96.2	16	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 2; PDBTitle: crystal structure of human ppgalnact-2 complexed with udp2 and ea2
9	c2d7iA_	 Alignment		95.8	13	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylgalactosaminyltransferase 10; PDBTitle: crsytal structure of pp-galnac-t10 with udp, galnac and mn2+
10	d1o7qa_	 Alignment		94.9	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: alpha-1,3-galactosyltransferase-like
11	c2z86D_	 Alignment		92.3	12	PDB header: transferase Chain: D: PDB Molecule: chondroitin synthase; PDBTitle: crystal structure of chondroitin polymerase from2 escherichia coli strain k4 (k4cp) complexed with udp-glucua3 and udp

12	d1xhba2	 Alignment		88.4	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Polypeptide N-acetyl galactosaminyltransferase 1, N-terminal domain
13	d1qg8a_	 Alignment		84.9	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Spore coat polysaccharide biosynthesis protein SpsA
14	c2p73A_	 Alignment		76.0	12	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
15	d1fo8a_	 Alignment		75.6	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: N-acetylglucosaminyltransferase I
16	d1lzia_	 Alignment		74.1	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: alpha-1,3-galactosyltransferase-like
17	d2py5a2	 Alignment		68.6	17	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I
18	d1s4na_	 Alignment		67.4	12	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Glycolipid 2-alpha-mannosyltransferase
19	c2ex3l_	 Alignment		55.2	16	PDB header: transferase/replication Chain: I: PDB Molecule: dna polymerase; PDBTitle: bacteriophage phi29 dna polymerase bound to terminal protein
20	d1omza_	 Alignment		54.8	11	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Exostosin
21	c2nplB_	 Alignment	not modelled	51.9	16	PDB header: transcription Chain: B: PDB Molecule: protein clp1; PDBTitle: clp1-atp-pcf11 complex
22	c3ckvA_	 Alignment	not modelled	49.0	15	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a mycobacterial protein
23	d1w7pd2	 Alignment	not modelled	39.5	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
24	c1omxB_	 Alignment	not modelled	30.6	9	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)
25	c3ew8A_	 Alignment	not modelled	24.8	25	PDB header: hydrolase Chain: A: PDB Molecule: histone deacetylase 8; PDBTitle: crystal structure analysis of human hdac8 d101l variant
26	c3maxB_	 Alignment	not modelled	20.4	30	PDB header: hydrolase Chain: B: PDB Molecule: histone deacetylase 2; PDBTitle: crystal structure of human hdac2 complexed with an n-(2-aminophenyl)2 benzamide
27	c3bcvA_	 Alignment	not modelled	20.0	15	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase protein; PDBTitle: crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
28	d1libia1	 Alignment	not modelled	20.0	55	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain

29	d1t64a_	Alignment	not modelled	19.9	25	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Histone deacetylase, HDAC
30	d1v9fa_	Alignment	not modelled	18.9	12	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase RsuA/RluD
31	c1v9fa_	Alignment	not modelled	18.9	12	PDB header: lyase Chain: A: PDB Molecule: ribosomal large subunit pseudouridine synthase d; PDBTitle: crystal structure of catalytic domain of pseudouridine2 synthase rluD from escherichia coli
32	c1qyuA_	Alignment	not modelled	17.2	12	PDB header: lyase Chain: A: PDB Molecule: ribosomal large subunit pseudouridine synthase d; PDBTitle: structure of the catalytic domain of 23s rrna pseudouridine2 synthase rluD
33	c4a69A_	Alignment	not modelled	16.0	40	PDB header: transcription Chain: A: PDB Molecule: histone deacetylase 3;; PDBTitle: structure of hdac3 bound to corepressor and inositol tetraphosphate
34	c3lmaC_	Alignment	not modelled	14.7	11	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.
35	c1hf2A_	Alignment	not modelled	14.7	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
36	c2w3zA_	Alignment	not modelled	14.5	10	PDB header: hydrolase Chain: A: PDB Molecule: putative deacetylase; PDBTitle: structure of a streptococcus mutans ce4 esterase
37	d1c3pa_	Alignment	not modelled	13.5	24	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Histone deacetylase, HDAC
38	c3lznA_	Alignment	not modelled	12.9	20	PDB header: transport protein Chain: A: PDB Molecule: p19 protein; PDBTitle: crystal structure analysis of the apo p19 protein from campylobacter2 jejuni at 1.59 a at ph 9
39	d1hf2a1	Alignment	not modelled	11.4	17	Fold: Single-stranded right-handed beta-helix Superfamily: Cell-division inhibitor MinC, C-terminal domain Family: Cell-division inhibitor MinC, C-terminal domain
40	d1u5tb1	Alignment	not modelled	11.1	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
41	c3menC_	Alignment	not modelled	9.9	25	PDB header: hydrolase Chain: C: PDB Molecule: acetyl polyamine aminohydrolase; PDBTitle: crystal structure of acetyl polyamine aminohydrolase from burkholderia2 pseudomallei, iodide soak
42	c3kk1B_	Alignment	not modelled	8.9	16	PDB header: transferase/dna Chain: B: PDB Molecule: reverse transcriptase p51 subunit; PDBTitle: hiv-1 reverse transcriptase-dna complex with nucleotide inhibitor gs-2 9148-diphosphate bound in nucleotide site
43	d2f5ka1	Alignment	not modelled	8.6	53	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo barrel domain
44	c3m9qA_	Alignment	not modelled	8.0	20	PDB header: dna binding protein Chain: A: PDB Molecule: protein male-specific lethal-3; PDBTitle: drosophila msl3 chromodomain
45	d2q3ra2	Alignment	not modelled	7.8	33	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
46	d1vhib_	Alignment	not modelled	7.7	12	Fold: Ferredoxin-like Superfamily: Viral DNA-binding domain Family: Viral DNA-binding domain
47	d2c71a1	Alignment	not modelled	7.6	10	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
48	c2o6dB_	Alignment	not modelled	7.4	27	PDB header: membrane protein, protein binding Chain: B: PDB Molecule: 34 kda membrane antigen; PDBTitle: structure of native rtp34 from treponema pallidum
49	c3m9pA_	Alignment	not modelled	6.8	33	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
50	d1xbta1	Alignment	not modelled	6.1	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Type II thymidine kinase
51	d1ny1a_	Alignment	not modelled	6.0	13	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
52	d1b3ta_	Alignment	not modelled	6.0	12	Fold: Ferredoxin-like Superfamily: Viral DNA-binding domain Family: Viral DNA-binding domain
53	c2rffA_	Alignment	not modelled	5.7	4	PDB header: transferase Chain: A: PDB Molecule: putative nucleotidyltransferase; PDBTitle: crystal structure of a putative nucleotidyltransferase2 (np_343093.1) from sulfolobus solfataricus at 1.40 a3 resolution
54	d2buda1	Alignment	not modelled	5.1	27	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo barrel domain