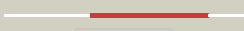
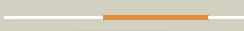
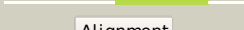
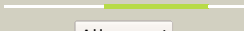


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3oy2A_	 Alignment		93.9	19	PDB header: viral protein,transferase Chain: A: PDB Molecule: glycosyltransferase b736l; PDBTitle: crystal structure of a putative glycosyltransferase from paramecium2 bursaria chlorella virus ny2a
2	c2gejA_	 Alignment		91.2	10	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol mannosyltransferase (pima); PDBTitle: crystal structure of phosphatidylinositol mannosyltransferase (pima)2 from mycobacterium smegmatis in complex with gdp-man
3	c3c4vB_	 Alignment		89.4	10	PDB header: transferase Chain: B: PDB Molecule: predicted glycosyltransferases; PDBTitle: structure of the retaining glycosyltransferase msha:the2 first step in mycothiol biosynthesis. organism:3 corynebacterium glutamicum : complex with udp and 1l-ins-1-4 p.
4	c2x0dA_	 Alignment		86.2	11	PDB header: transferase Chain: A: PDB Molecule: wsaf; PDBTitle: apo structure of wsaf
5	c3rhzB_	 Alignment		85.1	7	PDB header: transferase Chain: B: PDB Molecule: nucleotide sugar synthetase-like protein; PDBTitle: structure and functional analysis of a new subfamily of2 glycosyltransferases required for glycosylation of serine-rich3 streptococcal adhesions
6	c2xmpB_	 Alignment		85.1	14	PDB header: sugar binding protein Chain: B: PDB Molecule: trehalose-synthase tret; PDBTitle: crystal structure of trehalose synthase tret mutant e326a2 from p.horishiki in complex with udp
7	c2r60A_	 Alignment		69.6	7	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase, group 1; PDBTitle: structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
8	d2bisa1	 Alignment		64.4	14	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
9	c1uquB_	 Alignment		63.1	16	PDB header: synthase Chain: B: PDB Molecule: alpha, alpha-trehalose-phosphate synthase; PDBTitle: trehalose-6-phosphate from e. coli bound with udp-glucose.
10	c2x6rA_	 Alignment		59.5	13	PDB header: isomerase Chain: A: PDB Molecule: trehalose-synthase tret; PDBTitle: crystal structure of trehalose synthase tret from p.2 horikoshi produced by soaking in trehalose
11	c2jimH_	 Alignment		55.0	14	PDB header: transferase Chain: H: PDB Molecule: glycosyl transferase, group 1 family protein; PDBTitle: crystal structure of a family gt4 glycosyltransferase from2 bacillus anthracis orf ba1558.

12	dluqta_	Alignment		47.9	14	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Trehalose-6-phosphate synthase, OtsA
13	c3okaA_	Alignment		34.3	12	PDB header: transferase Chain: A: PDB Molecule: gdp-mannose-dependent alpha-(1-6)-phosphatidylinositol PDBTitle: crystal structure of corynebacterium glutamicum pimb' in complex with2 gdp-man (triclinic crystal form)
14	dlrzua_	Alignment		30.7	16	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
15	c3pe3D_	Alignment		29.8	15	PDB header: transferase Chain: D: PDB Molecule: udp-n-acetylglucosamine--peptide n- PDBTitle: structure of human o-glcnae transferase and its complex with a peptide2 substrate
16	c2xcuC_	Alignment		27.0	14	PDB header: transferase Chain: C: PDB Molecule: 3-deoxy-d-manno-2-octulosonic acid transferase; PDBTitle: membrane-embedded monofunctional glycosyltransferase waaa of aquifex2 aeolicus, comlex with cmp
17	c2khzB_	Alignment		26.8	17	PDB header: nuclear protein Chain: B: PDB Molecule: c-myc-responsive protein rcl; PDBTitle: solution structure of rcl
18	d2f9fa1	Alignment		26.6	15	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
19	c2q6vA_	Alignment		26.0	10	PDB header: transferase Chain: A: PDB Molecule: glucuronosyltransferase gumk; PDBTitle: crystal structure of gumk in complex with udp
20	dljixa_	Alignment		23.4	19	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: beta-Glycosyltransferase (DNA-modifying)
21	c2vsnB_	Alignment	not modelled	21.5	11	PDB header: transferase Chain: B: PDB Molecule: xcogt; PDBTitle: structure and topological arrangement of an o-glcnae2 transferase homolog: insight into molecular control of3 intracellular glycosylation
22	c3h16A_	Alignment	not modelled	16.2	14	PDB header: signaling protein Chain: A: PDB Molecule: tir protein; PDBTitle: crystal structure of a bacteria tir domain, pdtir from2 paracoccus denitrificans
23	dlr0ka2	Alignment	not modelled	12.9	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
24	dlq0qa2	Alignment	not modelled	12.3	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
25	d2iw1a1	Alignment	not modelled	11.0	14	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
26	c2eghA_	Alignment	not modelled	10.1	21	PDB header: oxidoreductase Chain: A: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: crystal structure of 1-deoxy-d-xylulose 5-phosphate reductoisomerase2 complexed with a magnesium ion, nadph and fosmidomycin
27	c3a14B_	Alignment	not modelled	9.6	14	PDB header: oxidoreductase Chain: B: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: crystal structure of dxr from thermotoga maritima, in complex with2 nadph

28	d1o6ca_	Alignment	not modelled	7.9	11	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
29	d1ipaa1	Alignment	not modelled	7.2	19	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
30	c1q2lA_	Alignment	not modelled	6.9	13	PDB header: hydrolase Chain: A: PDB Molecule: protease iii; PDBTitle: crystal structure of pitrilysin
31	d1m53a1	Alignment	not modelled	6.2	12	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
32	c2i6dA_	Alignment	not modelled	6.1	11	PDB header: transferase Chain: A: PDB Molecule: rna methyltransferase, trmh family; PDBTitle: the structure of a putative rna methyltransferase of the trmh family2 from porphyromonas gingivalis.
33	c2f06B_	Alignment	not modelled	5.9	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of protein bt0572 from bacteroides thetaiotaomicron
34	c2hlqA_	Alignment	not modelled	5.4	44	PDB header: plant protein Chain: A: PDB Molecule: fruit-specific protein; PDBTitle: nmr solution structure of a new tomato peptide