

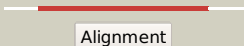

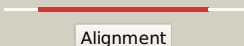







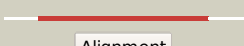









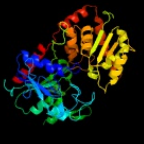



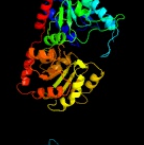
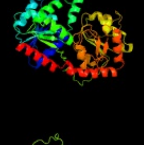

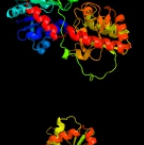
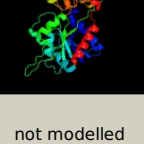


Phyre2

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|---------------|------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD3032_(-)_3391545_3392789 |
| Date | Thu Aug 8 16:20:20 BST 2019 |
| Unique Job ID | 87d75272336a320a |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c3c4vB_ |  Alignment |  | 100.0 | 27 | 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. |
| 2 | c2r60A_ |  Alignment |  | 100.0 | 17 | PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase, group 1; PDBTitle: structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii |
| 3 | d2bisa1 |  Alignment |  | 100.0 | 23 | Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1 |
| 4 | c3s29C_ |  Alignment |  | 100.0 | 17 | PDB header: transferase Chain: C: PDB Molecule: sucrose synthase 1; PDBTitle: the crystal structure of sucrose synthase-1 from arabidopsis thaliana2 and its functional implications. |
| 5 | c6gneB_ |  Alignment |  | 100.0 | 21 | PDB header: transferase Chain: B: PDB Molecule: probable starch synthase 4, chloroplastic/amyloplastic; PDBTitle: catalytic domain of starch synthase iv from arabidopsis thaliana bound2 to adp and acarbose |
| 6 | c2qzsA_ |  Alignment |  | 100.0 | 25 | PDB header: transferase Chain: A: PDB Molecule: glycogen synthase; PDBTitle: crystal structure of wild-type e.coli gs in complex with adp and2 glucose(wtgsb) |
| 7 | c5d00A_ |  Alignment |  | 100.0 | 21 | PDB header: transferase Chain: A: PDB Molecule: n-acetyl-alpha-d-glucosaminyl l-malate synthase; PDBTitle: crystal structure of bsha from b. subtilis complexed with n-2 acetylglucosaminyl-malate and ump |
| 8 | c6d9tA_ |  Alignment |  | 100.0 | 17 | PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase; PDBTitle: bsha from staphylococcus aureus complexed with udp |
| 9 | c2gejA_ |  Alignment |  | 100.0 | 26 | 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 |
| 10 | c2jimH_ |  Alignment |  | 100.0 | 21 | PDB header: transferase Chain: H: PDB Molecule: glycosyl transferase, group 1 family protein; PDBTitle: crystal structure of a family gt4 glycosyltransferase from bacillus2 anthracis orf ba1558. |
| 11 | c3vufA_ |  Alignment |  | 100.0 | 26 | PDB header: transferase Chain: A: PDB Molecule: granule-bound starch synthase 1, PDBTitle: crystal structure of rice granule bound starch synthase i catalytic2 domain in complex with adp |

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|----|-------------------------|-----------|---|-------|----|---|
| 12 | c6gnfC_ | Alignment |  | 100.0 | 19 | PDB header: transferase Chain: C: PDB Molecule: glycogen synthase; PDBTitle: granule bound starch synthase from cyanobacterium sp. clg1 bound to2 acarbose and adp |
| 13 | c4rbnD_ | Alignment |  | 100.0 | 19 | PDB header: transferase Chain: D: PDB Molecule: sucrose synthase:glycosyl transferases group 1; PDBTitle: the crystal structure of nitrosomonas europaea sucrose synthase:2 insights into the evolutionary origin of sucrose metabolism in3 prokaryotes |
| 14 | d1rzua_ | Alignment |  | 100.0 | 24 | Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1 |
| 15 | c4hlnA_ | Alignment |  | 100.0 | 23 | PDB header: transferase Chain: A: PDB Molecule: starch synthase i; PDBTitle: structure of barley starch synthase i in complex with2 maltoooligosaccharide |
| 16 | c6gngB_ | Alignment |  | 100.0 | 21 | PDB header: transferase Chain: B: PDB Molecule: granule-bound starch synthase; PDBTitle: granule bound starch synthase i from cyanophora paradoxa bound to2 acarbose and adp |
| 17 | c6ejia_ | Alignment |  | 100.0 | 16 | PDB header: transferase Chain: A: PDB Molecule: wlac protein; PDBTitle: structure of a glycosyltransferase |
| 18 | c3okaA_ | Alignment |  | 100.0 | 21 | 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) |
| 19 | c4xsuB_ | Alignment |  | 100.0 | 18 | PDB header: transferase Chain: B: PDB Molecule: alr3699 protein; PDBTitle: crystal structure of anabaena alr3699/hepe in complex with udp and2 glucose |
| 20 | c3oy2A_ | Alignment |  | 100.0 | 15 | PDB header: viral protein,transferase Chain: A: PDB Molecule: glycosyltransferase b736i; PDBTitle: crystal structure of a putative glycosyltransferase from paramecium2 bursaria chlorella virus ny2a |
| 21 | c2xmpB_ | Alignment | not modelled | 100.0 | 17 | 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 |
| 22 | d2iw1a1 | Alignment | not modelled | 100.0 | 19 | Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1 |
| 23 | c2x6rA_ | Alignment | not modelled | 100.0 | 16 | 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 |
| 24 | c5zesA_ | Alignment | not modelled | 100.0 | 22 | PDB header: transferase Chain: A: PDB Molecule: udp-glucose:tetrahydrobiopterin glycosyltransferase; PDBTitle: udp glucose alpha tetrahydrobiopterin glycosyltransferase from2 synechococcus species pcc 7942 - udp complex |
| 25 | c4x7pB_ | Alignment | not modelled | 100.0 | 14 | PDB header: transferase Chain: B: PDB Molecule: tarm; PDBTitle: crystal structure of apo s. aureus tarm |
| 26 | c5v0tB_ | Alignment | not modelled | 100.0 | 21 | PDB header: transferase Chain: B: PDB Molecule: alpha,alpha-trehalose-phosphate synthase (udp-forming); PDBTitle: crystal structure of an alpha,alpha-trehalose-phosphate synthase (udp-2 forming) from burkholderia xenovorans in complex with glucose-6-3 phosphate |
| 27 | c5n80A_ | Alignment | not modelled | 100.0 | 13 | PDB header: transferase Chain: A: PDB Molecule: lipopolysaccharide 1,6-galactosyltransferase; PDBTitle: glycosyltransferase lps biosynthesis in complex with udp |
| 28 | c4xuuA_ | Alignment | not modelled | 100.0 | 18 | PDB header: transferase Chain: A: PDB Molecule: o-antigen biosynthesis glycosyltransferase |

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|----|-------------------------|-----------|--------------|-------|----|--|
| 28 | c4xywA_ | Alignment | not modelled | 100.0 | 18 | wbnh; PDB header: glycosyltransferases wbnh |
| 29 | c1uquB_ | Alignment | not modelled | 100.0 | 18 | PDB header: synthase Chain: B: PDB Molecule: alpha, alpha-trehalose-phosphate synthase; PDBTitle: trehalose-6-phosphate from e. coli bound with udp-glucose. |
| 30 | c2iv3B_ | Alignment | not modelled | 100.0 | 20 | PDB header: transferase Chain: B: PDB Molecule: glycosyltransferase; PDBTitle: crystal structure of avigt4, a glycosyltransferase involved2 in avilamycin a biosynthesis |
| 31 | c3nb0A_ | Alignment | not modelled | 100.0 | 22 | PDB header: transferase Chain: A: PDB Molecule: glycogen [starch] synthase isoform 2; PDBTitle: glucose-6-phosphate activated form of yeast glycogen synthase |
| 32 | c5hxaA_ | Alignment | not modelled | 100.0 | 18 | PDB header: protein binding Chain: A: PDB Molecule: alpha,alpha-trehalose-phosphate synthase (udp-forming); PDBTitle: crystal structure of an udp-forming alpha, alpha-terhalose-phosphate2 synthase from burkholderia xenovorans |
| 33 | c3o3cD_ | Alignment | not modelled | 100.0 | 21 | PDB header: transferase Chain: D: PDB Molecule: glycogen [starch] synthase isoform 2; PDBTitle: glycogen synthase basal state udp complex |
| 34 | c4pqgB_ | Alignment | not modelled | 100.0 | 16 | PDB header: transferase Chain: B: PDB Molecule: glycosyltransferase gtf1; PDBTitle: crystal structure of the pneumococcal o-glcnaC transferase gtfA in2 complex with udp and glcnaC |
| 35 | d1uqta_ | Alignment | not modelled | 100.0 | 18 | Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Trehalose-6-phosphate synthase, OtsA |
| 36 | c2x0dA_ | Alignment | not modelled | 100.0 | 11 | PDB header: transferase Chain: A: PDB Molecule: wsaf; PDBTitle: apo structure of wsaf |
| 37 | c5e9tA_ | Alignment | not modelled | 100.0 | 18 | PDB header: transferase/chaperone Chain: A: PDB Molecule: glycosyltransferase gtf1; PDBTitle: crystal structure of gtfA/b complex |
| 38 | c5jijA_ | Alignment | not modelled | 100.0 | 17 | PDB header: transferase Chain: A: PDB Molecule: alpha,alpha-trehalose-phosphate synthase; PDBTitle: structure of mycobacterium thermoresistibile trehalose-6-phosphate2 synthase (apo form). |
| 39 | c4qlbD_ | Alignment | not modelled | 100.0 | 20 | PDB header: transferase Chain: D: PDB Molecule: probable glycogen [starch] synthase; PDBTitle: structural basis for the recruitment of glycogen synthase by2 glycogenin |
| 40 | c5hutB_ | Alignment | not modelled | 100.0 | 15 | PDB header: transferase Chain: B: PDB Molecule: alpha,alpha-trehalose-phosphate synthase [udp-forming]; PDBTitle: structure of candida albicans trehalose-6-phosphate synthase in2 complex with udp-glucose |
| 41 | c3ot5D_ | Alignment | not modelled | 100.0 | 11 | PDB header: isomerase Chain: D: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: 2.2 angstrom resolution crystal structure of putative udp-n-2 acetylglucosamine 2-epimerase from listeria monocytogenes |
| 42 | c2q6vA_ | Alignment | not modelled | 100.0 | 14 | PDB header: transferase Chain: A: PDB Molecule: glucuronosyltransferase gumk; PDBTitle: crystal structure of gumk in complex with udp |
| 43 | c3s2uA_ | Alignment | not modelled | 100.0 | 18 | PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine--n-acetylmuramyl-(pentapeptide) PDBTitle: crystal structure of the pseudomonas aeruginosa murg:udp-glcnaC2 substrate complex |
| 44 | c5enzA_ | Alignment | not modelled | 100.0 | 11 | PDB header: isomerase Chain: A: PDB Molecule: udp-glcnaC 2-epimerase; PDBTitle: s. aureus mnaa-udp co-structure |
| 45 | d1f6da_ | Alignment | not modelled | 100.0 | 14 | Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase |
| 46 | c3beoA_ | Alignment | not modelled | 100.0 | 11 | PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: a structural basis for the allosteric regulation of non-2 hydrolyzing udp-glcnaC 2-epimerases |
| 47 | c6fj3A_ | Alignment | not modelled | 100.0 | 23 | PDB header: membrane protein Chain: A: PDB Molecule: parathyroid hormone/parathyroid hormone-related peptide PDBTitle: high resolution crystal structure of parathyroid hormone 1 receptor in2 complex with a peptide agonist. |
| 48 | c4hwgA_ | Alignment | not modelled | 100.0 | 10 | PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: structure of udp-n-acetylglucosamine 2-epimerase from rickettsia2 bellii |
| 49 | c4w6qC_ | Alignment | not modelled | 100.0 | 13 | PDB header: transferase Chain: C: PDB Molecule: glycosyltransferase; PDBTitle: glycosyltransferase c from streptococcus agalactiae |
| 50 | c3dzcA_ | Alignment | not modelled | 99.9 | 13 | PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: 2.35 angstrom resolution structure of webc (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae. |
| 51 | c3rhzB_ | Alignment | not modelled | 99.9 | 14 | 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 |
| 52 | c5dldA_ | Alignment | not modelled | 99.9 | 16 | PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: crystal structure of a udp-n-acetylglucosamine 2-epimerase from2 burkholderia vietnamiensis complexed with udp- |

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|----|-------------------------|-----------|--------------|------|----|---|
| | | | | | | glnac and udp |
| 53 | c4nesA_ | Alignment | not modelled | 99.9 | 13 | PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: crystal structure of methanocaldococcus jannaschii udp-glnac 2-2 epimerase in complex with udp-glnac and udp |
| 54 | c3ia7A_ | Alignment | not modelled | 99.9 | 15 | PDB header: transferase Chain: A: PDB Molecule: calg4; PDBTitle: crystal structure of calg4, the calicheamicin glycosyltransferase |
| 55 | d1v4va_ | Alignment | not modelled | 99.9 | 17 | Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase |
| 56 | c5w8sA_ | Alignment | not modelled | 99.9 | 14 | PDB header: transferase Chain: A: PDB Molecule: lipid-a-disaccharide synthase; PDBTitle: lipid a disaccharide synthase (lpxb)-7 solubilizing mutations |
| 57 | c5dxfa_ | Alignment | not modelled | 99.9 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: trehalose-6-phosphate phosphatase; PDBTitle: structure of candida albicans trehalose-6-phosphate phosphatase n-2 terminal domain |
| 58 | c3iaaB_ | Alignment | not modelled | 99.9 | 15 | PDB header: transferase Chain: B: PDB Molecule: calg2; PDBTitle: crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form |
| 59 | c3t5ta_ | Alignment | not modelled | 99.9 | 14 | PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase; PDBTitle: vall from streptomyces hygroscopicus in apo form |
| 60 | c5vafD_ | Alignment | not modelled | 99.9 | 13 | PDB header: cell adhesion Chain: D: PDB Molecule: accessory sec system protein asp1; PDBTitle: crystal structure of accessory secretion protein 1 |
| 61 | c5xvmB_ | Alignment | not modelled | 99.9 | 12 | PDB header: transferase Chain: B: PDB Molecule: sterol 3-beta-glucosyltransferase; PDBTitle: sterol 3-beta-glucosyltransferase (ugt51) from saccharomyces2 cerevisiae (strain atcc 204508 / s288c) |
| 62 | c3tsaA_ | Alignment | not modelled | 99.9 | 16 | PDB header: transferase Chain: A: PDB Molecule: ndp-rhamnosyltransferase; PDBTitle: spinosyn rhamnosyltransferase spng |
| 63 | c3wadA_ | Alignment | not modelled | 99.9 | 13 | PDB header: transferase Chain: A: PDB Molecule: glycosyltransferase; PDBTitle: crystal structure of glycosyltransferase vinc involved in the2 biosynthesis of vicienistatin |
| 64 | d1f0ka_ | Alignment | not modelled | 99.9 | 16 | Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Peptidoglycan biosynthesis glycosyltransferase MurG |
| 65 | c2xcuC_ | Alignment | not modelled | 99.9 | 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, complex with cmp |
| 66 | c5xvsA_ | Alignment | not modelled | 99.9 | 12 | PDB header: hydrolase Chain: A: PDB Molecule: gdp/udp-n,n'-diacetyl bacillosamine 2-epimerase PDBTitle: crystal structure of udp-glnac 2-epimerase neuc complexed with udp |
| 67 | d1o6ca_ | Alignment | not modelled | 99.9 | 13 | Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase |
| 68 | c4ambB_ | Alignment | not modelled | 99.9 | 17 | PDB header: transferase Chain: B: PDB Molecule: snogd; PDBTitle: crystal structure of the glycosyltransferase snogd from streptomyces2 nogalater |
| 69 | c4rieB_ | Alignment | not modelled | 99.9 | 15 | PDB header: transferase Chain: B: PDB Molecule: glycosyl transferase homolog; PDBTitle: landomycin glycosyltransferase langt2 |
| 70 | c5hvoD_ | Alignment | not modelled | 99.9 | 16 | PDB header: transferase Chain: D: PDB Molecule: alpha,alpha-trehalose-phosphate synthase (udp-forming); PDBTitle: structure of aspergillus fumigatus trehalose-6-phosphate synthase b in2 complex with udp and validoxylamine a |
| 71 | c5lqdB_ | Alignment | not modelled | 99.9 | 18 | PDB header: transferase Chain: B: PDB Molecule: alpha,alpha-trehalose-phosphate synthase; PDBTitle: trehalose-6-phosphate synthase, gdp-glucose-dependent otsa |
| 72 | c4x1tA_ | Alignment | not modelled | 99.9 | 10 | PDB header: transferase Chain: A: PDB Molecule: monogalactosyldiacylglycerol synthase 1, chloroplastic; PDBTitle: the crystal structure of arabidopsis thaliana galactolipid synthase2 mgd1 in complex with udp |
| 73 | c2iyaB_ | Alignment | not modelled | 99.9 | 12 | PDB header: transferase Chain: B: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a blueprint2 for antibiotic engineering |
| 74 | c4leiB_ | Alignment | not modelled | 99.9 | 15 | PDB header: transferase Chain: B: PDB Molecule: ndp-forosamyltransferase; PDBTitle: spinosyn forosaminyltransferase spnp |
| 75 | c2vsnB_ | Alignment | not modelled | 99.9 | 19 | PDB header: transferase Chain: B: PDB Molecule: xcogt; PDBTitle: structure and topological arrangement of an o-glnac2 transferase homolog: insight into molecular control of3 intracellular glycosylation |
| 76 | c2p6pB_ | Alignment | not modelled | 99.9 | 19 | PDB header: transferase Chain: B: PDB Molecule: glycosyl transferase; PDBTitle: x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2 |
| 77 | c3nthB_ | Alignment | not modelled | 99.9 | 13 | PDB header: transferase/antibiotic Chain: B: PDB Molecule: calg1; |

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|-----|-------------------------|-----------|--------------|------|----|---|
| 77 | c50tlB | Alignment | not modelled | 99.9 | 13 | PDBTitle: crystal structure of calg1, calicheamicin glycosyltransferase, tdp2 and calicheamicin alpha3i bound form PDB header: transferase Chain: A: PDB Molecule: glycosyl transferases group 1 family protein; |
| 78 | c5i45A | Alignment | not modelled | 99.9 | 21 | PDBTitle: 1.35 angstrom crystal structure of c-terminal domain of glycosyl2 transferase group 1 family protein (lpcc) from francisella3 tularensis. PDB header: transferase Chain: A: PDB Molecule: oleandomycin glycosyltransferase; |
| 79 | c2iyfA | Alignment | not modelled | 99.9 | 11 | PDBTitle: the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering PDB header: transferase Chain: B: PDB Molecule: sterol 3-beta-glycosyltransferase; |
| 80 | c5gl5B | Alignment | not modelled | 99.9 | 15 | PDBTitle: sterol 3-beta-glycosyltransferase (ugt51) from saccharomyces2 cerevisiae (strain atcc 204508 / s288c): udpg complex PDB header: transferase Chain: A: PDB Molecule: tetratricopeptide tpr_2 repeat protein; |
| 81 | c5djsA | Alignment | not modelled | 99.8 | 16 | PDBTitle: thermobaculum terrenum o-glcnac transferase mutant - k341m Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1 |
| 82 | d2f9fa1 | Alignment | not modelled | 99.8 | 23 | PDB header: transferase Chain: B: PDB Molecule: espg2 glycosyltransferase; PDBTitle: structural analysis of espg2 glycosyltransferase |
| 83 | c5du2B | Alignment | not modelled | 99.8 | 14 | PDB header: transferase Chain: D: PDB Molecule: udp-n-acetylglucosamine--peptide n- PDBTitle: structure of human o-glcnac transferase and its complex with a peptide2 substrate |
| 84 | c3pe3D | Alignment | not modelled | 99.8 | 11 | Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1 |
| 85 | d2bfwa1 | Alignment | not modelled | 99.8 | 25 | PDB header: transferase Chain: B: PDB Molecule: protein calg3; PDBTitle: crystal structure of calg3 from micromonospora echinospora determined2 in space group i222 |
| 86 | c3d0qB | Alignment | not modelled | 99.8 | 13 | PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-d-manno-octulosonic-acid transferase; PDBTitle: crystal structure of the c-terminal cmp-kdo binding domain of waaa2 from acinetobacter baumannii |
| 87 | c4bfcA | Alignment | not modelled | 99.7 | 14 | PDB header: transferase/chaperone Chain: B: PDB Molecule: glycosyltransferase-stabilizing protein gtf2; PDBTitle: crystal structure of gtfa/b complex bound to udp and glcnac |
| 88 | c5e9uB | Alignment | not modelled | 99.7 | 8 | Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase |
| 89 | d1iira | Alignment | not modelled | 99.7 | 13 | PDB header: transferase Chain: B: PDB Molecule: type 1 capsular polysaccharide biosynthesis protein j PDBTitle: crystal structure of the catalytic domain of cholesterol-alpha-2 glycosyltransferase from helicobacter pylori |
| 90 | c3qhpB | Alignment | not modelled | 99.7 | 21 | Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase |
| 91 | d1pn3a | Alignment | not modelled | 99.7 | 14 | Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase |
| 92 | d1rrva | Alignment | not modelled | 99.6 | 13 | Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase |
| 93 | c4fzrA | Alignment | not modelled | 99.6 | 18 | PDB header: transferase Chain: A: PDB Molecule: ssf6; PDBTitle: crystal structure of ssf6, streptomyces sp. sf25752 glycosyltransferase |
| 94 | c4zhtB | Alignment | not modelled | 99.4 | 10 | PDB header: isomerase Chain: B: PDB Molecule: bifunctional udp-n-acetylglucosamine 2-epimerase/n- PDBTitle: crystal structure of udp-glcnac 2-epimerase |
| 95 | c6o86A | Alignment | not modelled | 99.3 | 15 | PDB header: transferase Chain: A: PDB Molecule: udp-glycosyltransferase 76g1; PDBTitle: crystal structure of semet udp-dependent glycosyltransferases (ugt)2 from stevia rebaudiana in complex with udp |
| 96 | c3hbjA | Alignment | not modelled | 99.2 | 11 | PDB header: transferase Chain: A: PDB Molecule: flavonoid 3-o-glycosyltransferase; PDBTitle: structure of ugt78g1 complexed with udp |
| 97 | c5nlmB | Alignment | not modelled | 99.2 | 11 | PDB header: transferase Chain: B: PDB Molecule: indoxyl udp-glycosyltransferase; PDBTitle: complex between a udp-glycosyltransferase from polygonum tinctorium2 capable of glucosylating indoxyl and indoxyl sulfate |
| 98 | d2acva1 | Alignment | not modelled | 99.2 | 11 | Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like |
| 99 | c3wc4A | Alignment | not modelled | 99.1 | 9 | PDB header: transferase Chain: A: PDB Molecule: udp-glucose:anthocyanidin 3-o-glycosyltransferase; PDBTitle: crystal structure of udp-glucose: anthocyanidin 3-o-2 glycosyltransferase from clitoria ternatea |
| 100 | d2c1xa1 | Alignment | not modelled | 99.0 | 11 | Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like |
| 101 | c5tmdA | Alignment | not modelled | 98.9 | 14 | PDB header: transferase Chain: A: PDB Molecule: glycosyltransferase, os79; PDBTitle: crystal structure of os79 from o. sativa in complex with u2f and2 trichothecene. |

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|-----|-------------------------|-----------|--------------|------|----|---|
| 102 | c5v2kA_ | Alignment | not modelled | 98.8 | 9 | PDB header: transferase Chain: A: PDB Molecule: udp-glycosyltransferase 74f2; PDBTitle: crystal structure of udp-glucosyltransferase, ugt74f2 (t15a), with udp2 and 2-bromobenzoic acid |
| 103 | c6jtdB_ | Alignment | not modelled | 98.7 | 11 | PDB header: transferase Chain: B: PDB Molecule: rc-glycosyltransferase; PDBTitle: crystal structure of tccg1 in complex with udp |
| 104 | d2pq6a1 | Alignment | not modelled | 98.7 | 9 | Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like |
| 105 | d2vcha1 | Alignment | not modelled | 98.6 | 13 | Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like |
| 106 | c3q3hA_ | Alignment | not modelled | 98.6 | 12 | PDB header: transferase Chain: A: PDB Molecule: hmw1c-like glycosyltransferase; PDBTitle: crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc |
| 107 | c3hbmA_ | Alignment | not modelled | 98.2 | 12 | PDB header: hydrolase Chain: A: PDB Molecule: udp-sugar hydrolase; PDBTitle: crystal structure of pseg from campylobacter jejuni |
| 108 | c4bqeA_ | Alignment | not modelled | 97.8 | 16 | PDB header: transferase Chain: A: PDB Molecule: alpha-glucan phosphorylase 2,4-glucan phosphorylase; PDBTitle: arabidopsis thaliana cytosolic alpha-1,4-glucan phosphorylase (phs2) |
| 109 | c2c4mA_ | Alignment | not modelled | 97.7 | 15 | PDB header: transferase Chain: A: PDB Molecule: glycogen phosphorylase; PDBTitle: starch phosphorylase: structural studies explain oxyanion-dependent2 kinetic stability and regulatory control. |
| 110 | c3ddsB_ | Alignment | not modelled | 97.6 | 15 | PDB header: transferase Chain: B: PDB Molecule: glycogen phosphorylase, liver form; PDBTitle: crystal structure of glycogen phosphorylase complexed with an2 anthranilimide based inhibitor gsk261 |
| 111 | d2gj4a1 | Alignment | not modelled | 97.5 | 14 | Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Oligosaccharide phosphorylase |
| 112 | d1ygpa_ | Alignment | not modelled | 97.5 | 11 | Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Oligosaccharide phosphorylase |
| 113 | c5lrbB_ | Alignment | not modelled | 97.5 | 14 | PDB header: transferase Chain: B: PDB Molecule: alpha-1,4 glucan phosphorylase; PDBTitle: plastidial phosphorylase from barley in complex with acarbose |
| 114 | c2h1fB_ | Alignment | not modelled | 97.4 | 15 | PDB header: transferase Chain: B: PDB Molecule: lipopolysaccharide heptosyltransferase-1; PDBTitle: e. coli heptosyltransferase waac with adp |
| 115 | d2atia1 | Alignment | not modelled | 97.1 | 17 | Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Oligosaccharide phosphorylase |
| 116 | c4l22A_ | Alignment | not modelled | 97.1 | 13 | PDB header: transferase Chain: A: PDB Molecule: phosphorylase; PDBTitle: crystal structure of putative glycogen phosphorylase from2 streptococcus mutans |
| 117 | d1l5wa_ | Alignment | not modelled | 97.1 | 19 | Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Oligosaccharide phosphorylase |
| 118 | c2o6lA_ | Alignment | not modelled | 97.0 | 12 | PDB header: transferase Chain: A: PDB Molecule: udp-glucuronosyltransferase 2b7; PDBTitle: crystal structure of the udp-glucuronic acid binding domain2 of the human drug metabolizing udp-glucuronosyltransferase3 2b7 |
| 119 | c5l0uA_ | Alignment | not modelled | 96.6 | 9 | PDB header: transferase Chain: A: PDB Molecule: protein o-glycosyltransferase 1; PDBTitle: human poglut1 in complex with egf(+) and udp-phosphono-glucose |
| 120 | c3l7mC_ | Alignment | not modelled | 96.5 | 11 | PDB header: structural protein Chain: C: PDB Molecule: teichoic acid biosynthesis protein f; PDBTitle: structure of the wall teichoic acid polymerase tagf, h548a |