
















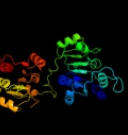













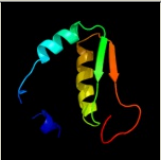


| #  | Template                | Alignment Coverage   | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|--|---|------------|--------|--|
| 1  | <a href="#">c3tovB_</a> | <br>Alignment   |    | 100.0      | 14     | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl transferase family 9;<br><b>PDBTitle:</b> the crystal structure of the glycosyl transferase family 9 from2 veillonella parvula dsm 2008                               |
| 2  | <a href="#">d1pswa_</a> | <br>Alignment   |    | 100.0      | 13     | <b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Family:</b> ADP-heptose LPS heptosyltransferase II   |
| 3  | <a href="#">c2h1fB_</a> | <br>Alignment   |    | 100.0      | 12     | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> lipopolysaccharide heptosyltransferase-1;<br><b>PDBTitle:</b> e. coli heptosyltransferase waac with adp  |
| 4  | <a href="#">d1v4va_</a> | <br>Alignment   |   | 99.2       | 12     | <b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Family:</b> UDP-N-acetylglucosamine 2-epimerase  |
| 5  | <a href="#">c3ot5D_</a> | <br>Alignment |  | 99.1       | 11     | <b>PDB header:</b> isomerase<br><b>Chain:</b> D: <b>PDB Molecule:</b> udp-n-acetylglucosamine 2-epimerase;<br><b>PDBTitle:</b> 2.2 angstrom resolution crystal structure of putative udp-n-2 acetylglucosamine 2-epimerase from listeria monocytogenes |
| 6  | <a href="#">d1o6ca_</a> | <br>Alignment |  | 98.6       | 10     | <b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Family:</b> UDP-N-acetylglucosamine 2-epimerase  |
| 7  | <a href="#">d1f6da_</a> | <br>Alignment |  | 98.6       | 10     | <b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Family:</b> UDP-N-acetylglucosamine 2-epimerase  |
| 8  | <a href="#">c3dzcA_</a> | <br>Alignment |  | 98.4       | 12     | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine 2-epimerase;<br><b>PDBTitle:</b> 2.35 angstrom resolution structure of wecb (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae.      |
| 9  | <a href="#">c2xcuC_</a> | <br>Alignment |  | 97.8       | 11     | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> 3-deoxy-d-manno-2-octulosonic acid transferase;<br><b>PDBTitle:</b> membrane-embedded monofunctional glycosyltransferase waaa of aquifex2 aeolicus, complex with cmp           |
| 10 | <a href="#">c3hbmA_</a> | <br>Alignment |  | 97.3       | 12     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> udp-sugar hydrolase;<br><b>PDBTitle:</b> crystal structure of pseg from campylobacter jejuni   |
| 11 | <a href="#">c2vsnB_</a> | <br>Alignment |  | 97.2       | 9      | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> xcogt;<br><b>PDBTitle:</b> structure and topological arrangement of an o-glcna2 transferase homolog: insight into molecular control of3 intracellular glycosylation            |

|    |                         |           |   |      |    |   |
|----|-------------------------|-----------|---|------|----|---|
| 12 | <a href="#">d1pn3a_</a> | Alignment |     | 97.1 | 11 | <b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Family:</b> Gtf glycosyltransferase   |
| 13 | <a href="#">c3c4vB_</a> | Alignment |    | 96.7 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> predicted glycosyltransferases;<br><b>PDBTitle:</b> 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. |
| 14 | <a href="#">c2o6lA_</a> | Alignment |    | 96.3 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> udp-glucuronosyltransferase 2b7;<br><b>PDBTitle:</b> crystal structure of the udp-glucuronic acid binding domain2 of the human drug metabolizing udp-glucuronosyltransferase3 2b7   |
| 15 | <a href="#">c2gejA_</a> | Alignment |    | 96.1 | 13 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol mannosyltransferase (pima);<br><b>PDBTitle:</b> crystal structure of phosphatidylinositol mannosyltransferase (pima)2 from mycobacterium smegmatis in complex with gdp-man                               |
| 16 | <a href="#">c2xmpB_</a> | Alignment |    | 95.9 | 10 | <b>PDB header:</b> sugar binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> trehalose-synthase tret;<br><b>PDBTitle:</b> crystal structure of trehalose synthase tret mutant e326a2 from p.horishiki in complex with udp  |
| 17 | <a href="#">c3o0hB_</a> | Alignment |    | 95.5 | 14 | <b>PDB header:</b> transferase/antibiotic<br><b>Chain:</b> B: <b>PDB Molecule:</b> calg1;<br><b>PDBTitle:</b> crystal structure of calg1, calicheamicin glycosyltransferase, tdp2 and calicheamicin alpha3i bound form  |
| 18 | <a href="#">c3okaA_</a> | Alignment |  | 95.3 | 13 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> gdp-mannose-dependent alpha-(1-6)-phosphatidylinositol<br><b>PDBTitle:</b> crystal structure of corynebacterium glutamicum pimb' in complex with2 gdp-man (triclinic crystal form)  |
| 19 | <a href="#">d1rrva_</a> | Alignment |  | 95.3 | 13 | <b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Family:</b> Gtf glycosyltransferase   |
| 20 | <a href="#">d1f0ka_</a> | Alignment |  | 95.3 | 9  | <b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Family:</b> Peptidoglycan biosynthesis glycosyltransferase MurG   |
| 21 | <a href="#">c2x6rA_</a> | Alignment | not modelled  | 95.2 | 10 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> trehalose-synthase tret;<br><b>PDBTitle:</b> crystal structure of trehalose synthase tret from p.2 horikoshi produced by soaking in trehalose   |
| 22 | <a href="#">c3iaaB_</a> | Alignment | not modelled  | 95.2 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> calg2;<br><b>PDBTitle:</b> crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form   |
| 23 | <a href="#">c3pe3D_</a> | Alignment | not modelled  | 95.1 | 11 | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> udp-n-acetylglucosamine--peptide n-<br><b>PDBTitle:</b> structure of human o-glcnae transferase and its complex with a peptide2 substrate   |
| 24 | <a href="#">c2r60A_</a> | Alignment | not modelled  | 95.1 | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glycosyl transferase, group 1;<br><b>PDBTitle:</b> structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii   |
| 25 | <a href="#">c2jjmH_</a> | Alignment | not modelled  | 94.1 | 11 | <b>PDB header:</b> transferase<br><b>Chain:</b> H: <b>PDB Molecule:</b> glycosyl transferase, group 1 family protein;<br><b>PDBTitle:</b> crystal structure of a family gt4 glycosyltransferase from2 bacillus anthracis orf ba1558.  |
| 26 | <a href="#">c3q3hA_</a> | Alignment | not modelled  | 91.7 | 8  | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> hmw1c-like glycosyltransferase;<br><b>PDBTitle:</b> crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc   |
| 27 | <a href="#">d2c1xa1</a> | Alignment | not modelled  | 91.1 | 9  | <b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Family:</b> UDPGT-like  |
| 28 | <a href="#">c3qhpB_</a> | Alignment | not modelled  | 90.9 | 12 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> type 1 capsular polysaccharide biosynthesis protein j<br><b>PDBTitle:</b> crystal structure of the catalytic domain of cholesterol-   |

|    |                         |           |   |      |  |
|----|-------------------------|-----------|---|------|--|
|    |                         |           |   |      | alpha-2 glucosyltransferase from helicobacter pylori   |
| 29 | <a href="#">c2q6vA</a>  | Alignment | not modelled  | 90.2 | 14<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glucuronosyltransferase gumk;<br><b>PDBTitle:</b> crystal structure of gumk in complex with udp  |
| 30 | <a href="#">d2f9fa1</a> | Alignment | not modelled  | 90.1 | 16<br><b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Family:</b> Glycosyl transferases group 1  |
| 31 | <a href="#">c3ehdA</a>  | Alignment | not modelled  | 89.4 | 28<br><b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized conserved protein;<br><b>PDBTitle:</b> crystal structure of conserved protein from enterococcus faecalis v583        |
| 32 | <a href="#">c2x0dA</a>  | Alignment | not modelled  | 89.3 | 11<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> wsaf;<br><b>PDBTitle:</b> apo structure of wsaf  |
| 33 | <a href="#">d1o6da</a>  | Alignment | not modelled  | 88.6 | 8<br><b>Fold:</b> alpha/beta knot<br><b>Superfamily:</b> alpha/beta knot<br><b>Family:</b> YbeA-like   |
| 34 | <a href="#">d1vh0a</a>  | Alignment | not modelled  | 88.1 | 8<br><b>Fold:</b> alpha/beta knot<br><b>Superfamily:</b> alpha/beta knot<br><b>Family:</b> YbeA-like   |
| 35 | <a href="#">c2khzB</a>  | Alignment | not modelled  | 87.4 | 18<br><b>PDB header:</b> nuclear protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> c-myc-responsive protein rcl;<br><b>PDBTitle:</b> solution structure of rcl  |
| 36 | <a href="#">c3d0qB</a>  | Alignment | not modelled  | 87.4 | 11<br><b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> protein calg3;<br><b>PDBTitle:</b> crystal structure of calg3 from micromonospora echinospora determined2 in space group i222                                  |
| 37 | <a href="#">d1to0a</a>  | Alignment | not modelled  | 87.2 | 10<br><b>Fold:</b> alpha/beta knot<br><b>Superfamily:</b> alpha/beta knot<br><b>Family:</b> YbeA-like  |
| 38 | <a href="#">c2p6pB</a>  | Alignment | not modelled  | 86.7 | 12<br><b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl transferase;<br><b>PDBTitle:</b> x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2                                       |
| 39 | <a href="#">c2iyaB</a>  | Alignment | not modelled  | 86.1 | 10<br><b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> oleandomycin glycosyltransferase;<br><b>PDBTitle:</b> the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering         |
| 40 | <a href="#">d2f62a1</a> | Alignment | not modelled  | 85.8 | 32<br><b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> N-(deoxy)ribosyltransferase-like<br><b>Family:</b> N-deoxyribosyltransferase   |
| 41 | <a href="#">c3ia7A</a>  | Alignment | not modelled  | 85.3 | 11<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> calg4;<br><b>PDBTitle:</b> crystal structure of calg4, the calicheamicin glycosyltransferase   |
| 42 | <a href="#">d1ns5a</a>  | Alignment | not modelled  | 84.7 | 7<br><b>Fold:</b> alpha/beta knot<br><b>Superfamily:</b> alpha/beta knot<br><b>Family:</b> YbeA-like   |
| 43 | <a href="#">d1iira</a>  | Alignment | not modelled  | 84.6 | 10<br><b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Family:</b> Gtf glycosyltransferase  |
| 44 | <a href="#">c3oy2A</a>  | Alignment | not modelled  | 84.4 | 9<br><b>PDB header:</b> viral protein,transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glycosyltransferase b736l;<br><b>PDBTitle:</b> crystal structure of a putative glycosyltransferase from paramecium2 bursaria chlorella virus ny2a |
| 45 | <a href="#">d2g8la1</a> | Alignment |  | 82.5 | 9<br><b>Fold:</b> AF1104-like<br><b>Superfamily:</b> AF1104-like<br><b>Family:</b> AF1104-like   |
| 46 | <a href="#">c3gjzB</a>  | Alignment | not modelled  | 81.6 | 13<br><b>PDB header:</b> immune system<br><b>Chain:</b> B: <b>PDB Molecule:</b> microcin immunity protein mccf;<br><b>PDBTitle:</b> crystal structure of microcin immunity protein mccf from bacillus2 anthracis str. ames                   |
| 47 | <a href="#">d1s2da</a>  | Alignment | not modelled  | 81.4 | 19<br><b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> N-(deoxy)ribosyltransferase-like<br><b>Family:</b> N-deoxyribosyltransferase   |
| 48 | <a href="#">d1f8ya</a>  | Alignment | not modelled  | 81.2 | 22<br><b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> N-(deoxy)ribosyltransferase-like<br><b>Family:</b> N-deoxyribosyltransferase   |
| 49 | <a href="#">c2iyfA</a>  | Alignment | not modelled  | 78.5 | 8<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> oleandomycin glycosyltransferase;<br><b>PDBTitle:</b> the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering          |
| 50 | <a href="#">d1to6a</a>  | Alignment | not modelled  | 78.0 | 16<br><b>Fold:</b> Glycerate kinase I<br><b>Superfamily:</b> Glycerate kinase I<br><b>Family:</b> Glycerate kinase I   |
| 51 | <a href="#">c3l7mC</a>  | Alignment | not modelled  | 76.2 | 16<br><b>PDB header:</b> structural protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> teichoic acid biosynthesis protein f;<br><b>PDBTitle:</b> structure of the wall teichoic acid polymerase tagf, h548a                                    |
| 52 | <a href="#">d1w6ta1</a> | Alignment | not modelled  | 75.4 | 16<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Enolase C-terminal domain-like<br><b>Family:</b> Enolase   |
| 53 | <a href="#">c2qzsA</a>  | Alignment | not modelled  | 73.3 | 11<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glycogen synthase;<br><b>PDBTitle:</b> crystal structure of wild-type e.coli gs in complex with adp2 and glucose(wtgsb)  |
| 54 | <a href="#">d2bisa1</a> | Alignment | not modelled  | 73.2 | 12<br><b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase  |

|    |                         |           |              |      |  |
|----|-------------------------|-----------|--------------|------|--|
|    |                         |           |              |      | <b>Family:</b> Glycosyl transferases group 1   |
| 55 | <a href="#">d2iw1a1</a> | Alignment | not modelled | 72.4 | 14<br><b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Family:</b> Glycosyl transferases group 1  |
| 56 | <a href="#">c3uj2C_</a> | Alignment | not modelled | 69.1 | 20<br><b>PDB header:</b> lyase<br><b>Chain:</b> C: <b>PDB Molecule:</b> enolase 1;<br><b>PDBTitle:</b> crystal structure of an enolase from anaerostipes cacciae (efi target2 efi-502054) with bound mg and sulfate  |
| 57 | <a href="#">dliyxal</a> | Alignment | not modelled | 66.5 | 19<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Enolase C-terminal domain-like<br><b>Family:</b> Enolase   |
| 58 | <a href="#">c3pdiG_</a> | Alignment | not modelled | 66.0 | 11<br><b>PDB header:</b> protein binding<br><b>Chain:</b> G: <b>PDB Molecule:</b> nitrogenase mofe cofactor biosynthesis protein nife;<br><b>PDBTitle:</b> precursor bound nifen   |
| 59 | <a href="#">c2h31A_</a> | Alignment | not modelled | 65.0 | 8<br><b>PDB header:</b> ligase, lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> multifunctional protein ade2;<br><b>PDBTitle:</b> crystal structure of human paics, a bifunctional carboxylase and2 synthetase in purine biosynthesis   |
| 60 | <a href="#">c2fymA_</a> | Alignment | not modelled | 63.3 | 19<br><b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> enolase;<br><b>PDBTitle:</b> crystal structure of e. coli enolase complexed with the2 minimal binding segment of rnase e.  |
| 61 | <a href="#">c3cwcB_</a> | Alignment | not modelled | 62.0 | 21<br><b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative glycerate kinase 2;<br><b>PDBTitle:</b> crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2   |
| 62 | <a href="#">d2fyma1</a> | Alignment | not modelled | 59.3 | 18<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Enolase C-terminal domain-like<br><b>Family:</b> Enolase   |
| 63 | <a href="#">c3rggD_</a> | Alignment | not modelled | 56.6 | 13<br><b>PDB header:</b> lyase<br><b>Chain:</b> D: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase, pure protein;<br><b>PDBTitle:</b> crystal structure of treponema denticola pure bound to air   |
| 64 | <a href="#">dlybha1</a> | Alignment | not modelled | 55.6 | 10<br><b>Fold:</b> DHS-like NAD/FAD-binding domain<br><b>Superfamily:</b> DHS-like NAD/FAD-binding domain<br><b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain  |
| 65 | <a href="#">dlrzua_</a> | Alignment | not modelled | 55.5 | 13<br><b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Family:</b> Glycosyl transferases group 1  |
| 66 | <a href="#">d2acva1</a> | Alignment | not modelled | 54.4 | 8<br><b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Family:</b> UDPGT-like  |
| 67 | <a href="#">c3tqpA_</a> | Alignment | not modelled | 54.3 | 17<br><b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> enolase;<br><b>PDBTitle:</b> structure of an enolase (eno) from coxiella burnetii  |
| 68 | <a href="#">c2jzcA_</a> | Alignment | not modelled | 52.8 | 12<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine transferase subunit<br><b>PDBTitle:</b> nmr solution structure of alg13: the sugar donor subunit of2 a yeast n-acetylglucosamine transferase. northeast3 structural genomics consortium target yg1             |
| 69 | <a href="#">d1mlna_</a> | Alignment | not modelled | 50.7 | 6<br><b>Fold:</b> Chelatase-like<br><b>Superfamily:</b> "Helical backbone" metal receptor<br><b>Family:</b> Nitrogenase iron-molybdenum protein  |
| 70 | <a href="#">c2xdqB_</a> | Alignment | not modelled | 49.7 | 11<br><b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit b;<br><b>PDBTitle:</b> dark operative protochlorophyllide oxidoreductase (chlN-2 chlB)2 complex   |
| 71 | <a href="#">c3l8mA_</a> | Alignment | not modelled | 49.0 | 16<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable thiamine pyrophosphokinase;<br><b>PDBTitle:</b> crystal structure of a probable thiamine pyrophosphokinase2 from staphylococcus saprophyticus subsp. saprophyticus.3 northeast structural genomics consortium target id syr86 |
| 72 | <a href="#">c2h9aA_</a> | Alignment | not modelled | 40.8 | 13<br><b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> carbon monoxide dehydrogenase corrinoid/iron-<br><b>PDBTitle:</b> corrinoid iron-sulfur protein   |
| 73 | <a href="#">c3k94A_</a> | Alignment | not modelled | 40.2 | 17<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> thiamin pyrophosphokinase;<br><b>PDBTitle:</b> crystal structure of thiamin pyrophosphokinase from geobacillus2 thermodenitrificans, northeast structural genomics consortium target3 gtr2   |
| 74 | <a href="#">d1qh8a_</a> | Alignment | not modelled | 38.9 | 10<br><b>Fold:</b> Chelatase-like<br><b>Superfamily:</b> "Helical backbone" metal receptor<br><b>Family:</b> Nitrogenase iron-molybdenum protein   |
| 75 | <a href="#">c3qtpB_</a> | Alignment | not modelled | 38.8 | 14<br><b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> enolase 1;<br><b>PDBTitle:</b> crystal structure analysis of entamoeba histolytica enolase   |
| 76 | <a href="#">c2axqA_</a> | Alignment | not modelled | 36.4 | 12<br><b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine dehydrogenase;<br><b>PDBTitle:</b> apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae  |
| 77 | <a href="#">d2ptza1</a> | Alignment | not modelled | 33.3 | 17<br><b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Enolase C-terminal domain-like<br><b>Family:</b> Enolase   |
| 78 | <a href="#">c3qn3B_</a> | Alignment | not modelled | 32.6 | 17<br><b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> enolase;<br><b>PDBTitle:</b> phosphopyruvate hydratase from campylobacter jejuni.  |
| 79 | <a href="#">c3ou7A_</a> | Alignment | not modelled | 32.3 | 13<br><b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> biotin carboxylase;   |

|     |                         |           |              |      |    |   |
|-----|-------------------------|-----------|--------------|------|----|---|
| 79  | <a href="#">c3u02A</a>  | Alignment | not modelled | 32.3 | 13 | <b>PDBTitle:</b> crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni   |
| 80  | <a href="#">d1w3ia</a>  | Alignment | not modelled | 32.2 | 7  | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Aldolase<br><b>Family:</b> Class I aldolase   |
| 81  | <a href="#">d1z6na1</a> | Alignment | not modelled | 31.8 | 12 | <b>Fold:</b> Thioredoxin fold<br><b>Superfamily:</b> Thioredoxin-like<br><b>Family:</b> Thioltransferase  |
| 82  | <a href="#">d2bfwa1</a> | Alignment | not modelled | 31.6 | 10 | <b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase<br><b>Family:</b> Glycosyl transferases group 1   |
| 83  | <a href="#">d1t9ba1</a> | Alignment | not modelled | 31.2 | 7  | <b>Fold:</b> DHS-like NAD/FAD-binding domain<br><b>Superfamily:</b> DHS-like NAD/FAD-binding domain<br><b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain   |
| 84  | <a href="#">c3cq9C</a>  | Alignment | not modelled | 31.2 | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein Ip_1622;<br><b>PDBTitle:</b> crystal structure of the Ip_1622 protein from lactobacillus2 plantarum. northeast structural genomics consortium target3 lpr114                    |
| 85  | <a href="#">c3lm8D</a>  | Alignment | not modelled | 30.4 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> thiamine pyrophosphokinase;<br><b>PDBTitle:</b> crystal structure of thiamine pyrophosphokinase from2 bacillus subtilis, northeast structural genomics consortium3 target sr677                         |
| 86  | <a href="#">c3afoB</a>  | Alignment | not modelled | 28.9 | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> nadh kinase pos5;<br><b>PDBTitle:</b> crystal structure of yeast nadh kinase complexed with nadh  |
| 87  | <a href="#">c3cf4G</a>  | Alignment | not modelled | 28.0 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> G: <b>PDB Molecule:</b> acetyl-coa decarboxylase/synthase epsilon subunit;<br><b>PDBTitle:</b> structure of the codh component of the m. barkeri acds complex  |
| 88  | <a href="#">d2ez9a1</a> | Alignment | not modelled | 28.0 | 13 | <b>Fold:</b> DHS-like NAD/FAD-binding domain<br><b>Superfamily:</b> DHS-like NAD/FAD-binding domain<br><b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain   |
| 89  | <a href="#">c3aerB</a>  | Alignment | not modelled | 26.7 | 11 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit b;<br><b>PDBTitle:</b> structure of the light-independent protochlorophyllide reductase2 catalyzing a key reduction for greening in the dark |
| 90  | <a href="#">d1m1nb</a>  | Alignment | not modelled | 26.2 | 13 | <b>Fold:</b> Chelatase-like<br><b>Superfamily:</b> "Helical backbone" metal receptor<br><b>Family:</b> Nitrogenase iron-molybdenum protein  |
| 91  | <a href="#">c3d3aA</a>  | Alignment | not modelled | 26.0 | 6  | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> beta-galactosidase;<br><b>PDBTitle:</b> crystal structure of a beta-galactosidase from bacteroides2 thetaiotaomicron  |
| 92  | <a href="#">c2j0wA</a>  | Alignment | not modelled | 25.5 | 22 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> lysine-sensitive aspartokinase 3;<br><b>PDBTitle:</b> crystal structure of e. coli aspartokinase iii in complex2 with aspartate and adp (r-state)   |
| 93  | <a href="#">c1zrsB</a>  | Alignment | not modelled | 25.3 | 14 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein;<br><b>PDBTitle:</b> wild-type ld-carboxypeptidase   |
| 94  | <a href="#">c3b8kA</a>  | Alignment | not modelled | 24.9 | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoyllysine-residue acetyltransferase;<br><b>PDBTitle:</b> structure of the truncated human dihydrolipoyl2 acetyltransferase (e2)   |
| 95  | <a href="#">d2fgea3</a> | Alignment | not modelled | 24.5 | 16 | <b>Fold:</b> LuxS/MPP-like metallohydrolase<br><b>Superfamily:</b> LuxS/MPP-like metallohydrolase<br><b>Family:</b> MPP-like  |
| 96  | <a href="#">c2hlhA</a>  | Alignment | not modelled | 24.1 | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> modulation fucosyltransferase;<br><b>PDBTitle:</b> crystal structure of fucosyltransferase nodz from bradyrhizobium   |
| 97  | <a href="#">c3aerC</a>  | Alignment | not modelled | 24.0 | 6  | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit n;<br><b>PDBTitle:</b> structure of the light-independent protochlorophyllide reductase2 catalyzing a key reduction for greening in the dark |
| 98  | <a href="#">d2h1qa1</a> | Alignment | not modelled | 23.5 | 9  | <b>Fold:</b> PLP-dependent transferase-like<br><b>Superfamily:</b> Dhaf3308-like<br><b>Family:</b> Dhaf3308-like  |
| 99  | <a href="#">c3thdD</a>  | Alignment | not modelled | 23.3 | 6  | <b>PDB header:</b> hydrolase<br><b>Chain:</b> D: <b>PDB Molecule:</b> beta-galactosidase;<br><b>PDBTitle:</b> crystal structure of human beta-galactosidase in complex with 1-2 deoxygalactonojirimycin   |
| 100 | <a href="#">c3hbjA</a>  | Alignment | not modelled | 23.2 | 10 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> flavonoid 3-o-glucosyltransferase;<br><b>PDBTitle:</b> structure of ugt78g1 complexed with udp  |
| 101 | <a href="#">d2jdid3</a> | Alignment | not modelled | 23.1 | 8  | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> RecA protein-like (ATPase-domain)   |
| 102 | <a href="#">d2djia1</a> | Alignment | not modelled | 22.9 | 9  | <b>Fold:</b> DHS-like NAD/FAD-binding domain<br><b>Superfamily:</b> DHS-like NAD/FAD-binding domain<br><b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain   |
| 103 | <a href="#">c3ihkC</a>  | Alignment | not modelled | 22.8 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> thiamin pyrophosphokinase;<br><b>PDBTitle:</b> crystal structure of thiamin pyrophosphokinase from2 s.mutans, northeast structural genomics consortium target3 smr83                                    |
| 104 | <a href="#">c3otrC</a>  | Alignment | not modelled | 22.0 | 15 | <b>PDB header:</b> lyase<br><b>Chain:</b> C: <b>PDB Molecule:</b> enolase;  |

|     |                         |           |              |      |    |  |
|-----|-------------------------|-----------|--------------|------|----|--|
| 104 | <a href="#">c3vuc_</a>  | Alignment | not modelled | 22.0 | 15 | <b>PDBTitle:</b> 2.75 angstrom crystal structure of enolase 1 from toxoplasma gondii   |
| 105 | <a href="#">d1miob_</a> | Alignment | not modelled | 21.8 | 17 | <b>Fold:</b> Chelatase-like<br><b>Superfamily:</b> "Helical backbone" metal receptor<br><b>Family:</b> Nitrogenase iron-molybdenum protein   |
| 106 | <a href="#">c3rhzb_</a> | Alignment | not modelled | 21.3 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> nucleotide sugar synthetase-like protein;<br><b>PDBTitle:</b> structure and functional analysis of a new subfamily of2 glycosyltransferases required for glycosylation of serine-rich3 streptococcal adhesions |