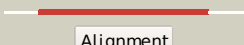

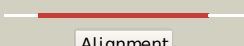

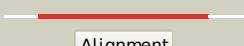
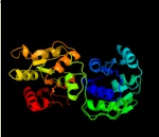
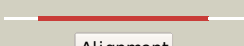











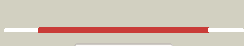





#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3tovB_</a>	 Alignment		100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl transferase family 9; <b>PDBTitle:</b> the crystal structure of the glycosyl transferase family 9 from2 veillonella parvula dsm 2008
2	<a href="#">d1pswa_</a>	 Alignment		100.0	24	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> ADP-heptose LPS heptosyltransferase II
3	<a href="#">c2h1fB_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> lipopolysaccharide heptosyltransferase-1; <b>PDBTitle:</b> e. coli heptosyltransferase waac with adp
4	<a href="#">d1v4va_</a>	 Alignment		99.4	13	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDP-N-acetylglucosamine 2-epimerase
5	<a href="#">c3ot5D_</a>	 Alignment		99.3	13	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> udp-n-acetylglucosamine 2-epimerase; <b>PDBTitle:</b> 2.2 angstrom resolution crystal structure of putative udp-n-2 acetylglucosamine 2-epimerase from listeria monocytogenes
6	<a href="#">d1f6da_</a>	 Alignment		99.1	11	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDP-N-acetylglucosamine 2-epimerase
7	<a href="#">d1o6ca_</a>	 Alignment		99.0	13	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDP-N-acetylglucosamine 2-epimerase
8	<a href="#">c2xcuC_</a>	 Alignment		98.7	11	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-deoxy-d-manno-2-octulosonic acid transferase; <b>PDBTitle:</b> membrane-embedded monofunctional glycosyltransferase waaa of aquifex2 aeolicus, complex with cmp
9	<a href="#">c3dzcA_</a>	 Alignment		98.6	12	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine 2-epimerase; <b>PDBTitle:</b> 2.35 angstrom resolution structure of webc (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae.
10	<a href="#">c2gejA_</a>	 Alignment		98.1	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol mannosyltransferase (pima); <b>PDBTitle:</b> crystal structure of phosphatidylinositol mannosyltransferase (pima)2 from mycobacterium smegmatis in complex with gdp-man
11	<a href="#">c2xmpB_</a>	 Alignment		98.1	11	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> trehalose-synthase tret; <b>PDBTitle:</b> crystal structure of trehalose synthase tret mutant e326a2 from p.horishiki in complex with udp

12	<a href="#">c3oy2A_</a>	Alignment		98.0	9	<b>PDB header:</b> viral protein,transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyltransferase b736l; <b>PDBTitle:</b> crystal structure of a putative glycosyltransferase from paramecium2 bursaria chlorella virus ny2a
13	<a href="#">c2vsnB_</a>	Alignment		97.9	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> xcogt; <b>PDBTitle:</b> structure and topological arrangement of an o-glcna2 transferase homolog: insight into molecular control of3 intracellular glycosylation
14	<a href="#">d1pn3a_</a>	Alignment		97.8	16	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Gtf glycosyltransferase
15	<a href="#">d1f0ka_</a>	Alignment		97.7	11	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Peptidoglycan biosynthesis glycosyltransferase MurG
16	<a href="#">c3c4vB_</a>	Alignment		97.7	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> predicted glycosyltransferases; <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.
17	<a href="#">c3okaA_</a>	Alignment		97.7	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gdp-mannose-dependent alpha-(1-6)-phosphatidylinositol <b>PDBTitle:</b> crystal structure of corynebacterium glutamicum pimb' in complex with2 gdp-man (triclinic crystal form)
18	<a href="#">c2x6rA_</a>	Alignment		97.6	11	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> trehalose-synthase tret; <b>PDBTitle:</b> crystal structure of trehalose synthase tret from p.2 horikoshi produced by soaking in trehalose
19	<a href="#">c3othB_</a>	Alignment		97.5	16	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> B: <b>PDB Molecule:</b> calg1; <b>PDBTitle:</b> crystal structure of calg1, calicheamicin glycosyltransferase, tdp2 and calicheamicin alpha3i bound form
20	<a href="#">c3q3hA_</a>	Alignment		97.3	8	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hmw1c-like glycosyltransferase; <b>PDBTitle:</b> crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
21	<a href="#">c3iaaB_</a>	Alignment	not modelled	97.3	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> calg2; <b>PDBTitle:</b> crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
22	<a href="#">c3hbmA_</a>	Alignment	not modelled	97.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-sugar hydrolase; <b>PDBTitle:</b> crystal structure of pseg from campylobacter jejuni
23	<a href="#">c3pe3D_</a>	Alignment	not modelled	97.3	11	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> udp-n-acetylglucosamine--peptide n- <b>PDBTitle:</b> structure of human o-glcna2 transferase and its complex with a peptide2 substrate
24	<a href="#">c2p6pB_</a>	Alignment	not modelled	97.2	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl transferase; <b>PDBTitle:</b> x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
25	<a href="#">c2jjmH_</a>	Alignment	not modelled	97.1	10	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> glycosyl transferase, group 1 family protein; <b>PDBTitle:</b> crystal structure of a family gt4 glycosyltransferase from2 bacillus anthracis orf ba1558.
26	<a href="#">c2x0dA_</a>	Alignment	not modelled	97.1	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> wsaf; <b>PDBTitle:</b> apo structure of wsaf
27	<a href="#">c2r60A_</a>	Alignment	not modelled	96.9	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyl transferase, group 1; <b>PDBTitle:</b> structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
28	<a href="#">d1rrva_</a>	Alignment	not modelled	96.6	14	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Gtf glycosyltransferase

29	<a href="#">dliira_</a>	Alignment	not modelled	96.5	17	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Gtf glycosyltransferase
30	<a href="#">d2f9fa1</a>	Alignment	not modelled	96.1	14	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Glycosyl transferases group 1
31	<a href="#">c2o6lA_</a>	Alignment	not modelled	96.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-glucuronosyltransferase 2b7; <b>PDBTitle:</b> crystal structure of the udp-glucuronic acid binding domain2 of the human drug metabolizing udp-glucuronosyltransferase3 2b7
32	<a href="#">d2iwl1a1</a>	Alignment	not modelled	95.9	8	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Glycosyl transferases group 1
33	<a href="#">c3qhpB_</a>	Alignment	not modelled	95.9	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> type 1 capsular polysaccharide biosynthesis protein j <b>PDBTitle:</b> crystal structure of the catalytic domain of cholesterol-alpha-2 glucosyltransferase from helicobacter pylori
34	<a href="#">c2iyfA_</a>	Alignment	not modelled	95.7	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> oleanomycin glycosyltransferase; <b>PDBTitle:</b> the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
35	<a href="#">c1uquB_</a>	Alignment	not modelled	95.6	14	<b>PDB header:</b> synthase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha, alpha-trehalose-phosphate synthase; <b>PDBTitle:</b> trehalose-6-phosphate from e. coli bound with udp-glucose.
36	<a href="#">d2bisa1</a>	Alignment	not modelled	95.4	12	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Glycosyl transferases group 1
37	<a href="#">d1uqta_</a>	Alignment	not modelled	93.7	14	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Trehalose-6-phosphate synthase, OtsA
38	<a href="#">c2q6vA_</a>	Alignment	not modelled	93.7	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucuronosyltransferase gumk; <b>PDBTitle:</b> crystal structure of gumk in complex with udp
39	<a href="#">c3hbjA_</a>	Alignment	not modelled	92.5	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> flavonoid 3-o-glucosyltransferase; <b>PDBTitle:</b> structure of ugt78g1 complexed with udp
40	<a href="#">c2iyaB_</a>	Alignment	not modelled	92.3	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> oleanomycin glycosyltransferase; <b>PDBTitle:</b> the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
41	<a href="#">d2acva1</a>	Alignment	not modelled	92.3	12	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDPGT-like
42	<a href="#">c2khzB_</a>	Alignment	not modelled	92.0	22	<b>PDB header:</b> nuclear protein <b>Chain:</b> B: <b>PDB Molecule:</b> c-myc-responsive protein rcl; <b>PDBTitle:</b> solution structure of rcl
43	<a href="#">d2bfwa1</a>	Alignment	not modelled	91.8	12	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Glycosyl transferases group 1
44	<a href="#">c3ia7A_</a>	Alignment	not modelled	89.2	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> calg4; <b>PDBTitle:</b> crystal structure of calg4, the calicheamicin glycosyltransferase
45	<a href="#">c3d0qB_</a>	Alignment	not modelled	89.0	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein calg3; <b>PDBTitle:</b> crystal structure of calg3 from micromonospora echinospora determined2 in space group i222
46	<a href="#">c3ehdA_</a>	Alignment	not modelled	87.9	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized conserved protein; <b>PDBTitle:</b> crystal structure of conserved protein from enterococcus faecalis v583
47	<a href="#">c2qzsA_</a>	Alignment	not modelled	87.8	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycogen synthase; <b>PDBTitle:</b> crystal structure of wild-type e.coli gs in complex with adp2 and glucose(wtgsb)
48	<a href="#">d2f62a1</a>	Alignment	not modelled	87.7	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> N-(deoxy)ribosyltransferase-like <b>Family:</b> N-deoxyribosyltransferase
49	<a href="#">d2c1xa1</a>	Alignment	not modelled	86.4	10	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDPGT-like
50	<a href="#">d1f8ya_</a>	Alignment	not modelled	84.5	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> N-(deoxy)ribosyltransferase-like <b>Family:</b> N-deoxyribosyltransferase
51	<a href="#">c3rhzb_</a>	Alignment	not modelled	81.9	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> nucleotide sugar synthetase-like protein; <b>PDBTitle:</b> structure and functional analysis of a new subfamily of2 glycosyltransferases required for glycosylation of serine-rich3 streptococcal adhesions
52	<a href="#">d1s2da_</a>	Alignment	not modelled	81.6	26	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> N-(deoxy)ribosyltransferase-like <b>Family:</b> N-deoxyribosyltransferase
53	<a href="#">d2pq6a1</a>	Alignment	not modelled	77.6	10	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDPGT-like
54	<a href="#">d1qh8a_</a>	Alignment	not modelled	73.8	10	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein

55	<a href="#">dlrzua_</a>	Alignment	not modelled	71.1	9	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Glycosyl transferases group 1
56	<a href="#">dlm1na_</a>	Alignment	not modelled	69.9	15	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
57	<a href="#">c3cwcB_</a>	Alignment	not modelled	68.7	34	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative glycerate kinase 2; <b>PDBTitle:</b> crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2
58	<a href="#">c3l7mC_</a>	Alignment	not modelled	68.1	9	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> teichoic acid biosynthesis protein f; <b>PDBTitle:</b> structure of the wall teichoic acid polymerase tagf, h548a
59	<a href="#">d2vcha1</a>	Alignment	not modelled	67.4	9	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDPGT-like
60	<a href="#">c2akmA_</a>	Alignment	not modelled	66.8	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> gamma enolase; <b>PDBTitle:</b> fluoride inhibition of enolase: crystal structure of the2 inhibitory complex
61	<a href="#">c3afoB_</a>	Alignment	not modelled	66.2	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> nadh kinase pos5; <b>PDBTitle:</b> crystal structure of yeast nadh kinase complexed with nadh
62	<a href="#">c2jzcA_</a>	Alignment	not modelled	64.3	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine transferase subunit <b>PDBTitle:</b> nmr solution structure of alg13: the sugar donor subunit of2 a yeast n-acetylglucosamine transferase. northeast3 structural genomics consortium target yg1
63	<a href="#">c2lqcA_</a>	Alignment	not modelled	63.1	14	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative toxin vapc6; <b>PDBTitle:</b> solution structure of the endonuclease nob1 from p.horikoshii
64	<a href="#">c3pdiG_</a>	Alignment	not modelled	62.7	13	<b>PDB header:</b> protein binding <b>Chain:</b> G: <b>PDB Molecule:</b> nitrogenase mofe cofactor biosynthesis protein nife; <b>PDBTitle:</b> precursor bound nifen
65	<a href="#">dlo94c_</a>	Alignment	not modelled	54.7	11	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
66	<a href="#">c2iz6A_</a>	Alignment	not modelled	54.7	12	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> molybdenum cofactor carrier protein; <b>PDBTitle:</b> structure of the chlamydomonas reinhardtii moco carrier2 protein
67	<a href="#">c3s29C_</a>	Alignment	not modelled	54.5	11	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sucrose synthase 1; <b>PDBTitle:</b> the crystal structure of sucrose synthase-1 from arabidopsis thaliana2 and its functional implications.
68	<a href="#">c3gjzB_</a>	Alignment	not modelled	51.1	16	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> microcin immunity protein mccf; <b>PDBTitle:</b> crystal structure of microcin immunity protein mccf from bacillus2 anthracis str. ames
69	<a href="#">c3cf4G_</a>	Alignment	not modelled	47.4	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> acetyl-coa decarboxylase/synthase epsilon subunit; <b>PDBTitle:</b> structure of the codh component of the m. barkeri acids complex
70	<a href="#">c2hlhA_</a>	Alignment	not modelled	47.1	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nodulation fucosyltransferase; <b>PDBTitle:</b> crystal structure of fucosyltransferase nodz from bradyrhizobium
71	<a href="#">d2akza1</a>	Alignment	not modelled	44.9	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> Enolase
72	<a href="#">d1to6a_</a>	Alignment	not modelled	41.7	23	<b>Fold:</b> Glycerate kinase I <b>Superfamily:</b> Glycerate kinase I <b>Family:</b> Glycerate kinase I
73	<a href="#">c3tqpA_</a>	Alignment	not modelled	39.4	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enolase; <b>PDBTitle:</b> structure of an enolase (eno) from coxiella burnetii
74	<a href="#">c2qv7A_</a>	Alignment	not modelled	38.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> diacylglycerol kinase dgkb; <b>PDBTitle:</b> crystal structure of diacylglycerol kinase dgkb in complex with adp2 and mg
75	<a href="#">d1to0a_</a>	Alignment	not modelled	37.1	18	<b>Fold:</b> alpha/beta knot <b>Superfamily:</b> alpha/beta knot <b>Family:</b> YbeA-like
76	<a href="#">dlm1nb_</a>	Alignment	not modelled	34.2	20	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
77	<a href="#">c1l8pC_</a>	Alignment	not modelled	33.7	14	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> enolase 1; <b>PDBTitle:</b> mg-phosphonoacetohydroxamate complex of s39a yeast enolase 1
78	<a href="#">d2jgra1</a>	Alignment	not modelled	33.5	17	<b>Fold:</b> NAD kinase/diacylglycerol kinase-like <b>Superfamily:</b> NAD kinase/diacylglycerol kinase-like <b>Family:</b> Diacylglycerol kinase-like
79	<a href="#">d2qv7a1</a>	Alignment	not modelled	33.0	14	<b>Fold:</b> NAD kinase/diacylglycerol kinase-like <b>Superfamily:</b> NAD kinase/diacylglycerol kinase-like <b>Family:</b> Diacylglycerol kinase-like
80	<a href="#">c3fxaA_</a>	Alignment	not modelled	31.1	10	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sis domain protein; <b>PDBTitle:</b> crystal structure of a putative sugar-phosphate isomerase2 (lmof2365_0531) from listeria monocytogenes str. 4b

					f2365 at 1.60 a3 resolution
81	<a href="#">c3pfnB_</a>	Alignment	not modelled	29.8	15 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> nad kinase; <b>PDBTitle:</b> crystal structure of human nad kinase
82	<a href="#">dlzl0a2</a>	Alignment	not modelled	29.1	17 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> LD-carboxypeptidase A N-terminal domain-like
83	<a href="#">dlylqa1</a>	Alignment	not modelled	28.7	13 <b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Catalytic subunit of bi-partite nucleotidyltransferase
84	<a href="#">clezaA_</a>	Alignment	not modelled	28.6	20 <b>PDB header:</b> phosphotransferase <b>Chain:</b> A: <b>PDB Molecule:</b> enzyme i; <b>PDBTitle:</b> amino terminal domain of enzyme i from escherichia coli nmr,2 restrained regularized mean structure
85	<a href="#">c2pa6A_</a>	Alignment	not modelled	27.5	13 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enolase; <b>PDBTitle:</b> crystal structure of mj0232 from methanococcus jannaschii
86	<a href="#">dlh6za2</a>	Alignment	not modelled	27.4	18 <b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> Phosphohistidine domain <b>Family:</b> Pyruvate phosphate dikinase, central domain
87	<a href="#">dlkbla2</a>	Alignment	not modelled	26.1	15 <b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> Phosphohistidine domain <b>Family:</b> Pyruvate phosphate dikinase, central domain
88	<a href="#">dlgeqa_</a>	Alignment	not modelled	25.6	19 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
89	<a href="#">c2an1D_</a>	Alignment	not modelled	25.5	16 <b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> putative kinase; <b>PDBTitle:</b> structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
90	<a href="#">d2bona1</a>	Alignment	not modelled	25.4	17 <b>Fold:</b> NAD kinase/diacylglycerol kinase-like <b>Superfamily:</b> NAD kinase/diacylglycerol kinase-like <b>Family:</b> Diacylglycerol kinase-like
91	<a href="#">dlybha1</a>	Alignment	not modelled	25.3	9 <b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
92	<a href="#">c3aerB_</a>	Alignment	not modelled	25.1	15 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit b; <b>PDBTitle:</b> structure of the light-independent protochlorophyllide reductase2 catalyzing a key reduction for greening in the dark
93	<a href="#">c2w36B_</a>	Alignment	not modelled	25.0	17 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endonuclease v; <b>PDBTitle:</b> structures of endonuclease v with dna reveal initiation of2 deaminated adenine repair
94	<a href="#">clqgeD_</a>	Alignment	not modelled	25.0	13 <b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> protein (triacylglycerol hydrolase); <b>PDBTitle:</b> new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
95	<a href="#">d2ez9a1</a>	Alignment	not modelled	24.8	7 <b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
96	<a href="#">c3qn3B_</a>	Alignment	not modelled	24.5	15 <b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> enolase; <b>PDBTitle:</b> phosphopyruvate hydratase from campylobacter jejuni.
97	<a href="#">c3bzaA_</a>	Alignment	not modelled	24.1	29 <b>PDB header:</b> membrane protein, protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> escu; <b>PDBTitle:</b> crystal structure of escu c-terminal domain with n262d mutation, space2 group p 41 21 2
98	<a href="#">d3bzra1</a>	Alignment	not modelled	24.1	29 <b>Fold:</b> EscU C-terminal domain-like <b>Superfamily:</b> EscU C-terminal domain-like <b>Family:</b> EscU C-terminal domain-like
99	<a href="#">dlzyma2</a>	Alignment	not modelled	23.8	20 <b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> Phosphohistidine domain <b>Family:</b> N-terminal domain of enzyme I of the PEP:sugar phosphotransferase system
100	<a href="#">dl06da_</a>	Alignment	not modelled	23.6	13 <b>Fold:</b> alpha/beta knot <b>Superfamily:</b> alpha/beta knot <b>Family:</b> YbeA-like
101	<a href="#">dlqh8b_</a>	Alignment	not modelled	23.6	14 <b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
102	<a href="#">dlz6na1</a>	Alignment	not modelled	23.6	9 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
103	<a href="#">dlpdza1</a>	Alignment	not modelled	23.3	11 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> Enolase
104	<a href="#">c3kosA_</a>	Alignment	not modelled	23.0	17 <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional activator ampr; <b>PDBTitle:</b> structure of the ampr effector binding domain from citrobacter2 freundii
105	<a href="#">d2p1ra1</a>	Alignment	not modelled	22.9	15 <b>Fold:</b> NAD kinase/diacylglycerol kinase-like <b>Superfamily:</b> NAD kinase/diacylglycerol kinase-like <b>Family:</b> Diacylglycerol kinase-like
106	<a href="#">c2bonB_</a>	Alignment	not modelled	21.7	16 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> lipid kinase; <b>PDBTitle:</b> structure of an escherichia coli lipid kinase (yegs)
107	<a href="#">d2h1qa1</a>	Alignment	not modelled	21.4	9 <b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> Dhaf3308-like

					<b>Family:</b> Dhaf3308-like
108	<a href="#">c1powA_</a>	Alignment	not modelled	21.0	7
				<b>PDB header:</b> oxidoreductase(oxygen as acceptor) <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate oxidase; <b>PDBTitle:</b> the refined structures of a stabilized mutant and of wild-type2 pyruvate oxidase from lactobacillus plantarum	