
























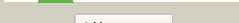


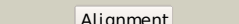
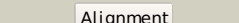
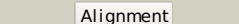
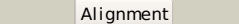
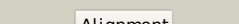

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pswa_	 Alignment		100.0	96	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: ADP-heptose LPS heptosyltransferase II
2	c3tovB_	 Alignment		100.0	23	PDB header: transferase Chain: B: PDB Molecule: glycosyl transferase family 9; PDBTitle: the crystal structure of the glycosyl transferase family 9 from2 veillonella parvula dsm 2008
3	c2h1fB_	 Alignment		100.0	20	PDB header: transferase Chain: B: PDB Molecule: lipopolysaccharide heptosyltransferase-1; PDBTitle: e. coli heptosyltransferase waac with adp
4	c3ot5D_	 Alignment		99.4	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
5	d1v4va_	 Alignment		99.1	15	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
6	d1f6da_	 Alignment		99.0	15	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
7	d1o6ca_	 Alignment		98.9	13	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
8	c2p6pB_	 Alignment		98.8	12	PDB header: transferase Chain: B: PDB Molecule: glycosyl transferase; PDBTitle: x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
9	c3dzcA_	 Alignment		98.7	12	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: 2.35 angstrom resolution structure of wecb (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae.
10	c2xcuC_	 Alignment		98.6	12	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
11	c2gejA_	 Alignment		98.4	14	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

12	c2x6rA_	Alignment		98.4	11	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
13	d1f0ka_	Alignment		98.4	10	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Peptidoglycan biosynthesis glycosyltransferase MurG
14	c3oy2A_	Alignment		98.4	9	PDB header: viral protein,transferase Chain: A: PDB Molecule: glycosyltransferase b736l; PDBTitle: crystal structure of a putative glycosyltransferase from paramecium2 bursaria chlorella virus ny2a
15	c2xmpB_	Alignment		98.4	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
16	c3c4vB_	Alignment		98.3	12	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.
17	d1iira_	Alignment		98.2	12	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
18	c3iaaB_	Alignment		98.2	12	PDB header: transferase Chain: B: PDB Molecule: calg2; PDBTitle: crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
19	c3othB_	Alignment		98.2	15	PDB header: transferase/antibiotic Chain: B: PDB Molecule: calg1; PDBTitle: crystal structure of calg1, calicheamicin glycosyltransferase, tdp2 and calicheamicin alpha3i bound form
20	d1pn3a_	Alignment		98.2	16	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
21	d1rrva_	Alignment	not modelled	98.0	13	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
22	c2jimH_	Alignment	not modelled	97.9	12	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.
23	c3hbmA_	Alignment	not modelled	97.8	11	PDB header: hydrolase Chain: A: PDB Molecule: udp-sugar hydrolase; PDBTitle: crystal structure of pseg from campylobacter jejuni
24	c2iyfA_	Alignment	not modelled	97.8	14	PDB header: transferase Chain: A: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
25	d2acva1	Alignment	not modelled	97.7	13	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
26	c3okaA_	Alignment	not modelled	97.7	14	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)
27	d2bisa1	Alignment	not modelled	97.6	13	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
28	c3d0qB_	Alignment	not modelled	97.6	14	PDB header: transferase Chain: B: PDB Molecule: protein calg3; PDBTitle: crystal structure of calg3 from micromonospora echinospora determined2 in space group i222

29	c2r60A_	Alignment	not modelled	97.6	13	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase, group 1; PDBTitle: structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
30	c2iyaB_	Alignment	not modelled	97.5	11	PDB header: transferase Chain: B: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
31	c2vsnB_	Alignment	not modelled	97.3	13	PDB header: transferase Chain: B: PDB Molecule: xcogt; PDBTitle: structure and topological arrangement of an o-glcna2 transferase homolog: insight into molecular control of3 intracellular glycosylation
32	dlrzuA_	Alignment	not modelled	97.0	16	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
33	c3pe3D_	Alignment	not modelled	96.9	8	PDB header: transferase Chain: D: PDB Molecule: udp-n-acetylglucosamine--peptide n- PDBTitle: structure of human o-glcna2 transferase and its complex with a peptide2 substrate
34	c3q3hA_	Alignment	not modelled	96.6	7	PDB header: transferase Chain: A: PDB Molecule: hmw1c-like glycosyltransferase; PDBTitle: crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
35	c2x0dA_	Alignment	not modelled	96.6	12	PDB header: transferase Chain: A: PDB Molecule: wsaf; PDBTitle: apo structure of wsaf
36	c3hbjA_	Alignment	not modelled	96.3	9	PDB header: transferase Chain: A: PDB Molecule: flavonoid 3-o-glucosyltransferase; PDBTitle: structure of ugt78g1 complexed with udp
37	c2qzsA_	Alignment	not modelled	95.9	14	PDB header: transferase Chain: A: PDB Molecule: glycogen synthase; PDBTitle: crystal structure of wild-type e.coli gs in complex with adp2 and glucose(wtgsb)
38	dluqta_	Alignment	not modelled	95.6	11	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Trehalose-6-phosphate synthase, OtsA
39	c3ia7A_	Alignment	not modelled	95.2	14	PDB header: transferase Chain: A: PDB Molecule: calg4; PDBTitle: crystal structure of calg4, the calicheamicin glycosyltransferase
40	d2c1xa1	Alignment	not modelled	95.0	12	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
41	c1uquB_	Alignment	not modelled	94.8	11	PDB header: synthase Chain: B: PDB Molecule: alpha, alpha-trehalose-phosphate synthase; PDBTitle: trehalose-6-phosphate from e. coli bound with udp-glucose.
42	d2iw1a1	Alignment	not modelled	94.6	10	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
43	d2pq6a1	Alignment	not modelled	94.5	15	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
44	d2f9fa1	Alignment	not modelled	94.5	11	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
45	c2o6lA_	Alignment	not modelled	93.1	13	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
46	c3l7mC_	Alignment	not modelled	90.8	12	PDB header: structural protein Chain: C: PDB Molecule: teichoic acid biosynthesis protein f; PDBTitle: structure of the wall teichoic acid polymerase tagf, h548a
47	c2khzB_	Alignment	not modelled	89.9	24	PDB header: nuclear protein Chain: B: PDB Molecule: c-myc-responsive protein rcl; PDBTitle: solution structure of rcl
48	c3gjzB_	Alignment	not modelled	87.0	14	PDB header: immune system Chain: B: PDB Molecule: microcin immunity protein mccf; PDBTitle: crystal structure of microcin immunity protein mccf from bacillus2 anthracis str. ames
49	c3ehdA_	Alignment	not modelled	86.9	32	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized conserved protein; PDBTitle: crystal structure of conserved protein from enterococcus faecalis v583
50	d2f62a1	Alignment	not modelled	86.8	29	Fold: Flavodoxin-like Superfamily: N-(deoxy)riboseyltransferase-like Family: N-deoxyriboseyltransferase
51	c3qhpB_	Alignment	not modelled	85.7	11	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 glucosyltransferase from helicobacter pylori
52	dlS2da_	Alignment	not modelled	84.8	16	Fold: Flavodoxin-like Superfamily: N-(deoxy)riboseyltransferase-like Family: N-deoxyriboseyltransferase
53	d1cfza_	Alignment	not modelled	84.6	22	Fold: Phosphorylase/hydrolase-like Superfamily: HybD-like Family: Hydrogenase maturing endopeptidase HybD
54	c2iuzB_	Alignment	not modelled	84.4	17	PDB header: transferase Chain: B: PDB Molecule: glycosyltransferase;

54	c2lv3B	Alignment	not modelled	84.4	17	PDBTitle: crystal structure of avigt4, a glycosyltransferase involved2 in avilamycin a biosynthesis
55	c2q6vA	Alignment	not modelled	83.9	17	PDB header: transferase Chain: A: PDB Molecule: glucuronosyltransferase gumk; PDBTitle: crystal structure of gumk in complex with udp
56	d1f8ya	Alignment	not modelled	83.3	16	Fold: Flavodoxin-like Superfamily: N-(deoxy)ribosyltransferase-like Family: N-deoxyribosyltransferase
57	c3dcjA	Alignment	not modelled	83.1	13	PDB header: transferase Chain: A: PDB Molecule: probable 5'-phosphoribosylglycinamide PDBTitle: crystal structure of glycinamide formyltransferase (purn)2 from mycobacterium tuberculosis in complex with 5-methyl-5,3,6,7,8-tetrahydrofolic acid derivative
58	c3cwcB	Alignment	not modelled	80.3	22	PDB header: transferase Chain: B: PDB Molecule: putative glycerate kinase 2; PDBTitle: crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2
59	c2ywrA	Alignment	not modelled	80.3	10	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of gar transformylase from aquifex2 aeolicus
60	d1n2sa	Alignment	not modelled	79.9	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
61	c2qytA	Alignment	not modelled	79.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of 2-dehydropantoate 2-reductase from porphyromonas2 gingivalis w83
62	c3s29C	Alignment	not modelled	78.4	14	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.
63	d1jkxa	Alignment	not modelled	76.9	11	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
64	c1b74A	Alignment	not modelled	75.3	22	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: glutamate racemase from aquifex pyrophilus
65	d1zl0a2	Alignment	not modelled	74.8	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: LD-carboxypeptidase A N-terminal domain-like
66	d1ks9a2	Alignment	not modelled	74.7	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
67	c3ghyA	Alignment	not modelled	73.6	24	PDB header: oxidoreductase Chain: A: PDB Molecule: ketopantoate reductase protein; PDBTitle: crystal structure of a putative ketopantoate reductase from ralstonia2 solanacearum molk2
68	d1qcza	Alignment	not modelled	73.4	13	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
69	c3lp8A	Alignment	not modelled	72.9	16	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine-glycine ligase; PDBTitle: crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis
70	c1wnfA	Alignment	not modelled	72.5	13	PDB header: hydrolase Chain: A: PDB Molecule: l-asparaginase; PDBTitle: crystal structure of ph0066 from pyrococcus horikoshii
71	c3g17H	Alignment	not modelled	71.7	21	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: similar to 2-dehydropantoate 2-reductase; PDBTitle: structure of putative 2-dehydropantoate 2-reductase from2 staphylococcus aureus
72	d1kjna	Alignment	not modelled	70.9	17	Fold: Hypothetical protein MTH777 (MT0777) Superfamily: Hypothetical protein MTH777 (MT0777) Family: Hypothetical protein MTH777 (MT0777)
73	c2e85B	Alignment	not modelled	70.8	7	PDB header: hydrolase Chain: B: PDB Molecule: hydrogenase 3 maturation protease; PDBTitle: crystal structure of the hydrogenase 3 maturation protease
74	d1txga2	Alignment	not modelled	70.7	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
75	c2iz6A	Alignment	not modelled	70.7	16	PDB header: metal transport Chain: A: PDB Molecule: molybdenum cofactor carrier protein; PDBTitle: structure of the chlamydomonas reinhardtii moco carrier2 protein
76	c3qvjB	Alignment	not modelled	70.6	22	PDB header: isomerase Chain: B: PDB Molecule: putative hydantoin racemase; PDBTitle: allantoin racemase from klebsiella pneumoniae
77	d2vcha1	Alignment	not modelled	69.3	12	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
78	d1vl0a	Alignment	not modelled	69.2	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
79	d1to6a	Alignment	not modelled	68.5	16	Fold: Glycerate kinase I Superfamily: Glycerate kinase I Family: Glycerate kinase I
						PDB header: structural genomics, unknown function

80	c3pu6A	Alignment	not modelled	68.5	18	Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of an uncharacterized protein from wolinella2 succinogenes
81	c2fw9A	Alignment	not modelled	68.3	17	PDB header: lyase Chain: A: PDB Molecule: n5-carboxyaminimidazole ribonucleotide mutase; PDBTitle: structure of pure (n5-carboxyaminimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8
82	d1b74a1	Alignment	not modelled	67.7	20	Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
83	c2jfbB	Alignment	not modelled	67.7	17	PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of helicobacter pylori glutamate racemase2 in complex with d-glutamate and an inhibitor
84	c1nhqA	Alignment	not modelled	65.8	29	PDB header: oxidoreductase (h2o2(a)) Chain: A: PDB Molecule: nadh peroxidase; PDBTitle: crystallographic analyses of nadh peroxidase cys42ala and cys42ser2 mutants: active site structure, mechanistic implications, and an3 unusual environment of arg303
85	d1u11a	Alignment	not modelled	65.8	17	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminimidazole carboxylase, PurE)
86	c3trhl	Alignment	not modelled	64.1	13	PDB header: lyase Chain: I: PDB Molecule: phosphoribosylaminimidazole carboxylase PDBTitle: structure of a phosphoribosylaminimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
87	c3gjaA	Alignment	not modelled	63.7	18	PDB header: transferase Chain: A: PDB Molecule: spermidine synthase; PDBTitle: crystal structure of a probable spermidine synthase from2 corynebacterium glutamicum atcc 13032
88	c3lp6D	Alignment	not modelled	63.4	23	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
89	d1u7pa	Alignment	not modelled	61.8	11	Fold: HAD-like Superfamily: HAD-like Family: Magnesium-dependent phosphatase-1, Mdp1
90	c2ofpB	Alignment	not modelled	61.3	21	PDB header: oxidoreductase Chain: B: PDB Molecule: ketopantoate reductase; PDBTitle: crystal structure of escherichia coli ketopantoate2 reductase in a ternary complex with nadp+ and pantoate
91	c2cduB	Alignment	not modelled	61.2	23	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh oxidase; PDBTitle: the crystal structure of water-forming nad(p)h oxidase from2 lactobacillus sanfranciscensis
92	d1miob	Alignment	not modelled	60.4	15	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
93	c3orsD	Alignment	not modelled	59.9	20	PDB header: isomerase,biosynthetic protein Chain: D: PDB Molecule: n5-carboxyaminimidazole ribonucleotide mutase; PDBTitle: crystal structure of n5-carboxyaminimidazole ribonucleotide mutase2 from staphylococcus aureus
94	c3shoA	Alignment	not modelled	59.6	14	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, rpir family; PDBTitle: crystal structure of rpir transcription factor from spharobacter2 thermophilus (sugar isomerase domain)
95	c2ys6A	Alignment	not modelled	59.3	19	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylglycinamide synthetase; PDBTitle: crystal structure of gar synthetase from geobacillus kaustophilus
96	c3oc4A	Alignment	not modelled	58.5	35	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, pyridine nucleotide-disulfide family; PDBTitle: crystal structure of a pyridine nucleotide-disulfide family2 oxidoreductase from the enterococcus faecalis v583
97	c2xd4A	Alignment	not modelled	58.3	16	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase
98	d1o4va	Alignment	not modelled	58.0	15	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminimidazole carboxylase, PurE)
99	c3sc6F	Alignment	not modelled	57.6	20	PDB header: oxidoreductase Chain: F: PDB Molecule: ddtp-4-dehydrorhamnose reductase; PDBTitle: 2.65 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 reductase (rfd) from bacillus anthracis str. ames in complex with3 nadp
100	c3rhzb	Alignment	not modelled	57.5	10	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
101	d1a9xa3	Alignment	not modelled	57.2	11	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
102	d2auna2	Alignment	not modelled	56.7	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: LD-carboxypeptidase A N-terminal domain-like
103	c1zrsB	Alignment	not modelled	56.5	16	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein;

						PDBTitle: wild-type Id-carboxypeptidase
104	d1xmpa_	 Alignment	not modelled	56.1	20	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
105	d2f1ka2	 Alignment	not modelled	55.9	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
106	c2ejbA_	 Alignment	not modelled	54.4	19	PDB header: lyase Chain: A: PDB Molecule: probable aromatic acid decarboxylase; PDBTitle: crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
107	c3rggD_	 Alignment	not modelled	53.8	18	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase, pure protein; PDBTitle: crystal structure of treponema denticola pure bound to air
108	c3ic5A_	 Alignment	not modelled	53.6	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative saccharopine dehydrogenase; PDBTitle: n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
109	d2c5aa1	 Alignment	not modelled	53.1	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
110	c1xpuB_	 Alignment	not modelled	52.5	12	PDB header: transcription/rna Chain: B: PDB Molecule: rho transcription termination factor; PDBTitle: structural mechanism of inhibition of the rho transcription2 termination factor by the antibiotic 5a-(3-formylphenylsulfanyl)-3 dihydrobicyclomycin (fpdb)
111	c3pfnB_	 Alignment	not modelled	52.5	12	PDB header: transferase Chain: B: PDB Molecule: nad kinase; PDBTitle: crystal structure of human nad kinase
112	c2x4gA_	 Alignment	not modelled	52.3	19	PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate-sugar epimerase; PDBTitle: crystal structure of pa4631, a nucleoside-diphosphate-sugar2 epimerase from pseudomonas aeruginosa
113	c1txgA_	 Alignment	not modelled	52.2	13	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad(p)+]; PDBTitle: structure of glycerol-3-phosphate dehydrogenase from archaeoglobus2 fulgidus
114	d1udca_	 Alignment	not modelled	51.5	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
115	d1s3ia2	 Alignment	not modelled	51.4	13	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
116	c3jzdA_	 Alignment	not modelled	51.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: iron-containing alcohol dehydrogenase; PDBTitle: crystal structure of putative alcohol dehydrogenase (yp_298327.1) from2 ralstonia eutropha jmp134 at 2.10 a resolution
117	d2g8la1	 Alignment	not modelled	50.9	11	Fold: AF1104-like Superfamily: AF1104-like Family: AF1104-like
118	c3l0oB_	 Alignment	not modelled	50.6	13	PDB header: hydrolase Chain: B: PDB Molecule: transcription termination factor rho; PDBTitle: structure of rna-free rho transcription termination factor from2 thermotoga maritima
119	c3pdiG_	 Alignment	not modelled	49.3	17	PDB header: protein binding Chain: G: PDB Molecule: nitrogenase mofe cofactor biosynthesis protein nife; PDBTitle: precursor bound nifen
120	c2vrcD_	 Alignment	not modelled	49.1	24	PDB header: oxidoreductase Chain: D: PDB Molecule: triphenylmethane reductase; PDBTitle: crystal structure of the citrobacter sp. triphenylmethane2 reductase complexed with nadp(h)