























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3tovB_	 Alignment		100.0	18	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
2	c2h1fB_	 Alignment		100.0	92	PDB header: transferase Chain: B: PDB Molecule: lipopolysaccharide heptosyltransferase-1; PDBTitle: e. coli heptosyltransferase waac with adp
3	d1pswa_	 Alignment		100.0	22	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: ADP-heptose LPS heptosyltransferase II
4	c3ot5D_	 Alignment		99.4	12	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		99.3	12	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
6	d1o6ca_	 Alignment		99.1	10	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
7	d1f6da_	 Alignment		99.0	14	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
8	c2gejA_	 Alignment		98.8	12	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
9	d1pn3a_	 Alignment		98.8	17	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
10	c3dzca_	 Alignment		98.8	13	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.
11	c3c4vB_	 Alignment		98.8	13	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.

12	c3iaaB_	Alignment		98.7	16	PDB header: transferase Chain: B: PDB Molecule: calg2; PDBTitle: crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
13	d1f0ka_	Alignment		98.7	13	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Peptidoglycan biosynthesis glycosyltransferase MurG
14	d1rrva_	Alignment		98.6	11	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
15	c3o3thB_	Alignment		98.6	15	PDB header: transferase/antibiotic Chain: B: PDB Molecule: calg1; PDBTitle: crystal structure of calg1, calicheamicin glycosyltransferase, tdp2 and calicheamicin alpha3i bound form
16	c2p6pB_	Alignment		98.6	14	PDB header: transferase Chain: B: PDB Molecule: glycosyl transferase; PDBTitle: x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
17	c3oy2A_	Alignment		98.6	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
18	c2jimH_	Alignment		98.5	11	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.
19	c3hbmA_	Alignment		98.5	13	PDB header: hydrolase Chain: A: PDB Molecule: udp-sugar hydrolase; PDBTitle: crystal structure of pseg from campylobacter jejuni
20	d1iira_	Alignment		98.4	11	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
21	c2iyaB_	Alignment	not modelled	98.4	12	PDB header: transferase Chain: B: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
22	c2xcuC_	Alignment	not modelled	98.3	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
23	c2iyfA_	Alignment	not modelled	98.1	14	PDB header: transferase Chain: A: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
24	c3d0qB_	Alignment	not modelled	98.1	16	PDB header: transferase Chain: B: PDB Molecule: protein calg3; PDBTitle: crystal structure of calg3 from micromonospora echinospora determined2 in space group i222
25	c2x6rA_	Alignment	not modelled	98.1	10	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
26	c2xmpB_	Alignment	not modelled	98.0	11	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
27	c2vsnB_	Alignment	not modelled	98.0	11	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
28	d2acva1	Alignment	not modelled	97.9	14	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase

					Family: UDPGT-like
29	c2r60A	Alignment	not modelled	97.8	11 PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase, group 1; PDBTitle: structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
30	c3ia7A	Alignment	not modelled	97.8	16 PDB header: transferase Chain: A: PDB Molecule: calg4; PDBTitle: crystal structure of calg4, the calicheamicin glycosyltransferase
31	c2qzsA	Alignment	not modelled	97.8	15 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)
32	d1rzua	Alignment	not modelled	97.7	13 Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
33	c3okaA	Alignment	not modelled	97.6	13 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)
34	c3hbjA	Alignment	not modelled	97.4	10 PDB header: transferase Chain: A: PDB Molecule: flavonoid 3-o-glucosyltransferase; PDBTitle: structure of ugt78g1 complexed with udp
35	d2bisa1	Alignment	not modelled	97.3	14 Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
36	c3pe3D	Alignment	not modelled	97.0	11 PDB header: transferase Chain: D: PDB Molecule: udp-n-acetylglucosamine--peptide n- PDBTitle: structure of human o-glcnae transferase and its complex with a peptide2 substrate
37	c2x0dA	Alignment	not modelled	97.0	16 PDB header: transferase Chain: A: PDB Molecule: wsaf; PDBTitle: apo structure of wsaf
38	d2c1xa1	Alignment	not modelled	96.8	11 Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
39	d2iwl1a1	Alignment	not modelled	96.6	9 Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
40	d2f9fa1	Alignment	not modelled	95.9	14 Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
41	c2iv3B	Alignment	not modelled	95.6	17 PDB header: transferase Chain: B: PDB Molecule: glycosyltransferase; PDBTitle: crystal structure of avigt4, a glycosyltransferase involved2 in avilamycin a biosynthesis
42	c3qhpB	Alignment	not modelled	95.6	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
43	d2pq6a1	Alignment	not modelled	95.1	9 Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
44	c3q3hA	Alignment	not modelled	95.0	9 PDB header: transferase Chain: A: PDB Molecule: hmw1c-like glycosyltransferase; PDBTitle: crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
45	c2o6lA	Alignment	not modelled	94.7	10 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	c2q6vA	Alignment	not modelled	94.1	9 PDB header: transferase Chain: A: PDB Molecule: glucuronosyltransferase gumk; PDBTitle: crystal structure of gumk in complex with udp
47	c2khzB	Alignment	not modelled	93.7	26 PDB header: nuclear protein Chain: B: PDB Molecule: c-myc-responsive protein rcl; PDBTitle: solution structure of rcl
48	d2vcha1	Alignment	not modelled	93.0	10 Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
49	c3ehdA	Alignment	not modelled	91.9	16 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	91.8	16 Fold: Flavodoxin-like Superfamily: N-(deoxy)ribosyltransferase-like Family: N-deoxyribosyltransferase
51	d1m1na	Alignment	not modelled	89.6	10 Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
52	c1uquB	Alignment	not modelled	89.0	5 PDB header: synthase Chain: B: PDB Molecule: alpha, alpha-trehalose-phosphate synthase; PDBTitle: trehalose-6-phosphate from e. coli bound with udp-glucose.
53	c3l7mC	Alignment	not modelled	88.3	14 PDB header: structural protein Chain: C: PDB Molecule: teichoic acid biosynthesis protein f; PDBTitle: structure of the wall teichoic acid polymerase tagf, h548a
					Fold: Chelatase-like

54	d1qh8a_	Alignment	not modelled	88.0	13	Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
55	d1f8ya_	Alignment	not modelled	88.0	11	Fold: Flavodoxin-like Superfamily: N-(deoxy)ribosyltransferase-like Family: N-deoxyribosyltransferase
56	d1b74a1	Alignment	not modelled	86.5	16	Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
57	d1s2da_	Alignment	not modelled	85.6	23	Fold: Flavodoxin-like Superfamily: N-(deoxy)ribosyltransferase-like Family: N-deoxyribosyltransferase
58	c1b74A_	Alignment	not modelled	82.3	16	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: glutamate racemase from aquifex pyrophilus
59	d1cfza_	Alignment	not modelled	82.2	14	Fold: Phosphorylase/hydrolase-like Superfamily: HybD-like Family: Hydrogenase maturing endopeptidase HybD
60	d1uqta_	Alignment	not modelled	79.7	11	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Trehalose-6-phosphate synthase, OtsA
61	c2qytA_	Alignment	not modelled	76.1	9	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of 2-dehydropantoate 2-reductase from porphyromonas2 gingivalis w83
62	c3uhjE_	Alignment	not modelled	75.7	17	PDB header: oxidoreductase Chain: E: PDB Molecule: probable glycerol dehydrogenase; PDBTitle: crystal structure of a probable glycerol dehydrogenase from2 sinorhizobium meliloti 1021
63	c3qviB_	Alignment	not modelled	74.3	16	PDB header: isomerase Chain: B: PDB Molecule: putative hydantoin racemase; PDBTitle: allantoin racemase from klebsiella pneumoniae
64	c2jfbB_	Alignment	not modelled	73.6	15	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
65	c3afoB_	Alignment	not modelled	72.6	14	PDB header: transferase Chain: B: PDB Molecule: nadh kinase pos5; PDBTitle: crystal structure of yeast nadh kinase complexed with nadh
66	c3cwcB_	Alignment	not modelled	70.8	26	PDB header: transferase Chain: B: PDB Molecule: putative glycerate kinase 2; PDBTitle: crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2
67	d1uana_	Alignment	not modelled	69.4	17	Fold: LmbE-like Superfamily: LmbE-like Family: LmbE-like
68	d1a9xa3	Alignment	not modelled	67.9	18	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
69	d1ks9a2	Alignment	not modelled	67.8	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
70	d1m1nb_	Alignment	not modelled	67.8	12	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
71	d1vl0a_	Alignment	not modelled	67.7	7	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
72	c3icpA_	Alignment	not modelled	67.7	13	PDB header: isomerase Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of udp-galactose 4-epimerase
73	c3rhzb_	Alignment	not modelled	67.6	18	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
74	c2p5uC_	Alignment	not modelled	66.8	18	PDB header: isomerase Chain: C: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: crystal structure of thermus thermophilus hb8 udp-glucose 4-2 epimerase complex with nad
75	d1vbga2	Alignment	not modelled	66.4	11	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Phosphohistidine domain Family: Pyruvate phosphate dikinase, central domain
76	c2e85B_	Alignment	not modelled	66.4	14	PDB header: hydrolase Chain: B: PDB Molecule: hydrogenase 3 maturation protease; PDBTitle: crystal structure of the hydrogenase 3 maturation protease
77	d1n2sa_	Alignment	not modelled	64.9	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
78	d1kbla2	Alignment	not modelled	64.9	16	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Phosphohistidine domain Family: Pyruvate phosphate dikinase, central domain
79	c3g17H_	Alignment	not modelled	64.5	15	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
80	c3m2pD_	Alignment	not modelled	64.5	3	PDB header: isomerase Chain: D: PDB Molecule: udp-n-acetylglucosamine 4-epimerase; PDBTitle: the crystal structure of udp-n-acetylglucosamine 4-

						epimerase2 from bacillus cereus
81	c2h31A_	Alignment	not modelled	64.2	15	PDB header: ligase, lyase Chain: A: PDB Molecule: multifunctional protein ade2; PDBTitle: crystal structure of human paics, a bifunctional carboxylase and2 synthetase in purine biosynthesis
82	c3fhIC_	Alignment	not modelled	64.2	16	PDB header: oxidoreductase Chain: C: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from bacteroides2 fragilis nctc 9343
83	d2c5aa1	Alignment	not modelled	64.2	6	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
84	d1udca_	Alignment	not modelled	63.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
85	c3ghyA_	Alignment	not modelled	61.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: ketopantoate reductase protein; PDBTitle: crystal structure of a putative ketopantoate reductase from ralstonia2 solanacearum molk2
86	c3gfgB_	Alignment	not modelled	61.8	15	PDB header: oxidoreductase Chain: B: PDB Molecule: uncharacterized oxidoreductase yvaa; PDBTitle: structure of putative oxidoreductase yvaa from bacillus subtilis in2 triclinic form
87	c3lp8A_	Alignment	not modelled	61.6	13	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine-glycine ligase; PDBTitle: crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis
88	c3lp6D_	Alignment	not modelled	61.2	28	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
89	d1o4va_	Alignment	not modelled	61.1	20	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
90	c2x4gA_	Alignment	not modelled	60.9	12	PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate-sugar epimerase; PDBTitle: crystal structure of pa4631, a nucleoside-diphosphate-sugar2 epimerase from pseudomonas aeruginosa
91	c2ggsB_	Alignment	not modelled	60.5	15	PDB header: oxidoreductase Chain: B: PDB Molecule: 273aa long hypothetical dtdp-4-dehydrorhamnose PDBTitle: crystal structure of hypothetical dtdp-4-dehydrorhamnose2 reductase from sulfolobus tokodaii
92	c2ofpB_	Alignment	not modelled	60.5	15	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
93	c2ejbA_	Alignment	not modelled	60.0	14	PDB header: lyase Chain: A: PDB Molecule: probable aromatic acid decarboxylase; PDBTitle: crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
94	c3pu6A_	Alignment	not modelled	59.7	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of an uncharacterized protein from wolinella2 succinogenes
95	c3pdiG_	Alignment	not modelled	59.7	12	PDB header: protein binding Chain: G: PDB Molecule: nitrogenase mofe cofactor biosynthesis protein nife; PDBTitle: precursor bound nifen
96	d1miob_	Alignment	not modelled	59.1	12	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
97	d2bfwa1	Alignment	not modelled	59.1	12	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
98	c3sc6F_	Alignment	not modelled	58.8	8	PDB header: oxidoreductase Chain: F: PDB Molecule: dtdp-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
99	d1txga2	Alignment	not modelled	58.6	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
100	c2v4oB_	Alignment	not modelled	57.3	15	PDB header: hydrolase Chain: B: PDB Molecule: multifunctional protein sur e; PDBTitle: crystal structure of salmonella typhimurium sure at 2.752 angstrom resolution in monoclinic form
101	c3rggD_	Alignment	not modelled	57.0	15	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase, pure protein; PDBTitle: crystal structure of treponema denticola pure bound to air
102	d2f1ka2	Alignment	not modelled	56.4	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
103	c2pzlB_	Alignment	not modelled	56.3	16	PDB header: sugar binding protein Chain: B: PDB Molecule: putative nucleotide sugar epimerase/dehydratase; PDBTitle: crystal structure of the bordetella bronchiseptica enzyme2 wbmj in complex with nad and udp
104	c2jzcA_	Alignment	not modelled	55.8	21	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine transferase subunit PDBTitle: nmr solution structure of alg13: the sugar donor subunit

						of2 a yeast n-acetylglucosamine transferase. northeast3 structural genomics consortium target yg1
105	c2xd4A_	 Alignment	not modelled	51.4	16	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase
106	c3evnA_	 Alignment	not modelled	51.3	13	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of putative oxidoreductase from streptococcus2 agalactiae 2603v/r
107	c2pk3B_	 Alignment	not modelled	51.1	11	PDB header: oxidoreductase Chain: B: PDB Molecule: gdp-6-deoxy-d-lyxo-4-hexulose reductase; PDBTitle: crystal structure of a gdp-4-keto-6-deoxy-d-mannose reductase
108	c3kuxA_	 Alignment	not modelled	50.2	13	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of the ypo2259 putative oxidoreductase from yersinia pestis
109	d1mioa_	 Alignment	not modelled	50.0	10	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
110	d1qh8b_	 Alignment	not modelled	49.9	15	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
111	c1ks9A_	 Alignment	not modelled	48.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: ketopantoate reductase from escherichia coli
112	c2vrcD_	 Alignment	not modelled	48.5	9	PDB header: oxidoreductase Chain: D: PDB Molecule: triphenylmethane reductase; PDBTitle: crystal structure of the citrobacter sp. triphenylmethane2 reductase complexed with nadp(h)
113	c3orsD_	 Alignment	not modelled	47.2	15	PDB header: isomerase,biosynthetic protein Chain: D: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
114	c3pfnB_	 Alignment	not modelled	47.0	10	PDB header: transferase Chain: B: PDB Molecule: nad kinase; PDBTitle: crystal structure of human nad kinase
115	c3qtpB_	 Alignment	not modelled	46.1	16	PDB header: lyase Chain: B: PDB Molecule: enolase 1; PDBTitle: crystal structure analysis of entamoeba histolytica enolase
116	c2ys6A_	 Alignment	not modelled	45.9	21	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylglycinamide synthetase; PDBTitle: crystal structure of gar synthetase from geobacillus kaustophilus
117	d1to6a_	 Alignment	not modelled	45.4	17	Fold: Glycerate kinase I Superfamily: Glycerate kinase I Family: Glycerate kinase I
118	c3pdiB_	 Alignment	not modelled	45.3	17	PDB header: protein binding Chain: B: PDB Molecule: nitrogenase mofe cofactor biosynthesis protein nifn; PDBTitle: precursor bound nifen
119	c1kblA_	 Alignment	not modelled	45.1	16	PDB header: transferase Chain: A: PDB Molecule: pyruvate phosphate dikinase; PDBTitle: pyruvate phosphate dikinase
120	c1txgA_	 Alignment	not modelled	44.8	21	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad(p)+]; PDBTitle: structure of glycerol-3-phosphate dehydrogenase from archaeoglobus2 fulgidus