


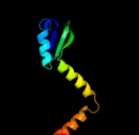



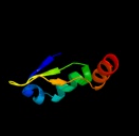



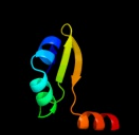










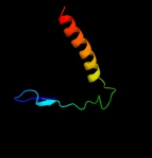

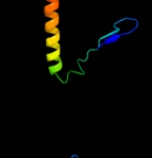

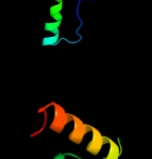
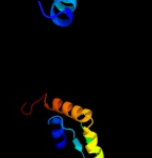


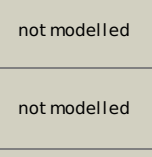


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2a6qa1	 Alignment		100.0	100	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
2	c3g5oA	 Alignment		99.9	27	PDB header: toxin/antitoxin Chain: A: PDB Molecule: uncharacterized protein rv2865; PDBTitle: the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
3	d2a6qb1	 Alignment		99.8	100	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
4	c3hs2H	 Alignment		99.6	29	PDB header: antitoxin Chain: H: PDB Molecule: prevent host death protein; PDBTitle: crystal structure of phd truncated to residue 57 in an orthorhombic2 space group
5	c3hryA	 Alignment		99.5	27	PDB header: antitoxin Chain: A: PDB Molecule: prevent host death protein; PDBTitle: crystal structure of phd in a trigonal space group and partially2 disordered
6	c2odkD	 Alignment		99.2	18	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein; PDBTitle: putative prevent-host-death protein from nitrosomonas europaea
7	d2odka1	 Alignment		99.1	18	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
8	c3k6qB	 Alignment		95.4	27	PDB header: ligand binding protein Chain: B: PDB Molecule: putative ligand binding protein; PDBTitle: crystal structure of an antitoxin part of a putative toxin/antitoxin2 system (swol_0700) from syntrophomonas wolfei subsp. wolfei at 1.80 a3 resolution
9	d1grja1	 Alignment		35.3	21	Fold: Long alpha-hairpin Superfamily: GreA transcript cleavage protein, N-terminal domain Family: GreA transcript cleavage protein, N-terminal domain
10	c2iyfA	 Alignment		30.5	30	PDB header: transferase Chain: A: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
11	d1n0ea	 Alignment		27.2	14	Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: Hypothetical protein MraZ

12	d1ez4a2	Alignment		27.0	16	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
13	c1n0fF_	Alignment		21.8	14	PDB header: biosynthetic protein Chain: F: PDB Molecule: protein mraz; PDBTitle: crystal structure of a cell division and cell wall2 biosynthesis protein upf0040 from mycoplasma pneumoniae:3 indication of a novel fold with a possible new conserved4 sequence motif
14	d1pzga2	Alignment		20.0	23	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
15	c2p6pB_	Alignment		18.5	18	PDB header: transferase Chain: B: PDB Molecule: glycosyl transferase; PDBTitle: x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
16	c2iyaB_	Alignment		16.8	15	PDB header: transferase Chain: B: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
17	d1y0na_	Alignment		16.6	19	Fold: YehU-like Superfamily: YehU-like Family: YehU-like
18	c3o0hB_	Alignment		15.2	15	PDB header: transferase/antibiotic Chain: B: PDB Molecule: calg1; PDBTitle: crystal structure of calg1, calicheamicin glycosyltransferase, tdp2 and calicheamicin alpha3i bound form
19	c3ia7A_	Alignment		15.1	16	PDB header: transferase Chain: A: PDB Molecule: calg4; PDBTitle: crystal structure of calg4, the calicheamicin glycosyltransferase
20	c2qzsA_	Alignment		14.3	12	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)
21	d2iw1a1	Alignment	not modelled	12.7	15	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
22	c3dzcA_	Alignment	not modelled	12.6	23	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: 2.35 angstrom resolution structure of webc (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae.
23	d1f6da_	Alignment	not modelled	11.9	21	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
24	d1g8ma1	Alignment	not modelled	11.9	8	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Inosicase
25	c2p4vA_	Alignment	not modelled	11.8	18	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor greb; PDBTitle: crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
26	c2jjmH_	Alignment	not modelled	11.7	20	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.
27	c1grjA_	Alignment	not modelled	11.6	21	PDB header: transcription regulation Chain: A: PDB Molecule: grea protein; PDBTitle: grea transcript cleavage factor from escherichia coli
28	d2vgna2	Alignment	not modelled	11.6	20	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: ERF1/Dom34 middle domain-like
						PDB header: transferase

29	c3iaaB_	Alignment	not modelled	11.3	15	Chain: B: PDB Molecule: calg2; PDBTitle: crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
30	c1ez4B_	Alignment	not modelled	10.6	16	PDB header: oxidoreductase Chain: B: PDB Molecule: lactate dehydrogenase; PDBTitle: crystal structure of non-allosteric l-lactate dehydrogenase2 from lactobacillus pentosus at 2.3 angstrom resolution
31	c3s29C_	Alignment	not modelled	10.2	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.
32	c2r60A_	Alignment	not modelled	9.0	17	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase, group 1; PDBTitle: structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
33	c3zvkg_	Alignment	not modelled	9.0	3	PDB header: antitoxin/toxin/dna Chain: G: PDB Molecule: antitoxin of toxin-antitoxin system vapb; PDBTitle: crystal structure of vapbc2 from rickettsia felis bound to2 a dna fragment from their promoter
34	d1a5za2	Alignment	not modelled	8.5	21	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
35	c3ot5D_	Alignment	not modelled	8.3	16	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
36	d1o6ca_	Alignment	not modelled	7.7	18	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
37	d1mlda2	Alignment	not modelled	7.6	19	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
38	d2cmda2	Alignment	not modelled	7.5	19	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
39	c2fy2A_	Alignment	not modelled	6.7	16	PDB header: transferase Chain: A: PDB Molecule: choline o-acetyltransferase; PDBTitle: structures of ligand bound human choline acetyltransferase2 provide insight into regulation of acetylcholine synthesis
40	c1zrxA_	Alignment	not modelled	6.7	17	PDB header: antimicrobial protein, antibiotic Chain: A: PDB Molecule: stomoxyn; PDBTitle: solution structure of stomoxyn in h2o/tfe 50%
41	c1smkD_	Alignment	not modelled	6.5	19	PDB header: oxidoreductase Chain: D: PDB Molecule: malate dehydrogenase, glyoxysomal; PDBTitle: mature and translocatable forms of glyoxysomal malate2 dehydrogenase have different activities and stabilities3 but similar crystal structures
42	c1sevA_	Alignment	not modelled	6.5	19	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase, glyoxysomal precursor; PDBTitle: mature and translocatable forms of glyoxysomal malate2 dehydrogenase have different activities and stabilities3 but similar crystal structures
43	d1uxja2	Alignment	not modelled	6.4	23	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
44	d1ghca_	Alignment	not modelled	5.8	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Linker histone H1/H5
45	c1vjqb_	Alignment	not modelled	5.7	14	PDB header: structural genomics, de novo protein Chain: B: PDB Molecule: designed protein; PDBTitle: designed protein based on backbone conformation of2 procarboxypeptidase-a (1aye) with sidechains chosen for maximal3 predicted stability.
46	d1gv0a2	Alignment	not modelled	5.5	18	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
47	c2zqaA_	Alignment	not modelled	5.3	14	PDB header: dna binding protein Chain: A: PDB Molecule: mutS2 protein; PDBTitle: crystal structure of the smr domain of thermus thermophilus mutS2
48	d1pkxa1	Alignment	not modelled	5.1	13	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Inosicase