






















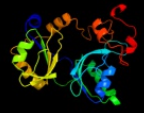






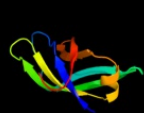


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1vlyA_	 Alignment		100.0	97	PDB header: transferase Chain: A: PDB Molecule: unknown protein from 2d-page; PDBTitle: crystal structure of a putative aminomethyltransferase (ygfz) from <i>escherichia coli</i> at 1.30 a resolution
2	c3girA_	 Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: aminomethyltransferase; PDBTitle: crystal structure of glycine cleavage system2 aminomethyltransferase t from <i>bartonella henselae</i>
3	c1vloA_	 Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: aminomethyltransferase; PDBTitle: crystal structure of aminomethyltransferase (t protein;2 tetrahydrofolate-dependent) of glycine cleavage system (np417381)3 from <i>escherichia coli</i> k12 at 1.70 a resolution
4	c1pj6A_	 Alignment		100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: n,n-dimethylglycine oxidase; PDBTitle: crystal structure of dimethylglycine oxidase of <i>arthrobacter2 globiformis</i> in complex with folic acid
5	d1vlya2	 Alignment		100.0	98	Fold: Folate-binding domain Superfamily: Folate-binding domain Family: Aminomethyltransferase folate-binding domain
6	c1yx2B_	 Alignment		100.0	19	PDB header: transferase Chain: B: PDB Molecule: aminomethyltransferase; PDBTitle: crystal structure of the probable aminomethyltransferase2 from <i>bacillus subtilis</i>
7	c1v5vA_	 Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: aminomethyltransferase; PDBTitle: crystal structure of a component of glycine cleavage system: t-protein2 from <i>pyrococcus horikoshii</i> ot3 at 1.5 a resolution
8	c1worA_	 Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: aminomethyltransferase; PDBTitle: crystal structure of t-protein of the glycine cleavage2 system
9	c1x31A_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: sarcosine oxidase alpha subunit; PDBTitle: crystal structure of heterotetrameric sarcosine oxidase from <i>corynebacterium</i> sp. u-96
10	c1wsrA_	 Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: aminomethyltransferase; PDBTitle: crystal structure of human t-protein of glycine cleavage2 system
11	c3tfhB_	 Alignment		100.0	13	PDB header: transferase Chain: B: PDB Molecule: gcvt-like aminomethyltransferase protein; PDBTitle: dmsp-dependent demethylase from <i>p. ubiquus</i> - apo

12	dlvla2	Alignment		100.0	17	Fold: Folate-binding domain Superfamily: Folate-binding domain Family: Aminomethyltransferase folate-binding domain
13	d1pj5a4	Alignment		100.0	15	Fold: Folate-binding domain Superfamily: Folate-binding domain Family: Aminomethyltransferase folate-binding domain
14	d1v5va2	Alignment		100.0	16	Fold: Folate-binding domain Superfamily: Folate-binding domain Family: Aminomethyltransferase folate-binding domain
15	d1wosa2	Alignment		100.0	15	Fold: Folate-binding domain Superfamily: Folate-binding domain Family: Aminomethyltransferase folate-binding domain
16	c2gagC	Alignment		99.8	9	PDB header: oxidoreductase Chain: C: PDB Molecule: heterotetrameric sarcosine oxidase gamma-subunit; PDBTitle: heterotetrameric sarcosine: structure of a diflavin metalloenzyme at2 1.85 a resolution
17	d1vlya1	Alignment		99.5	96	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: Aminomethyltransferase beta-barrel domain Family: Aminomethyltransferase beta-barrel domain
18	d1v5va1	Alignment		99.1	14	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: Aminomethyltransferase beta-barrel domain Family: Aminomethyltransferase beta-barrel domain
19	d1wosa1	Alignment		99.0	19	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: Aminomethyltransferase beta-barrel domain Family: Aminomethyltransferase beta-barrel domain
20	d1vla1	Alignment		98.9	7	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: Aminomethyltransferase beta-barrel domain Family: Aminomethyltransferase beta-barrel domain
21	d1pj5a1	Alignment	not modelled	98.8	12	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: Aminomethyltransferase beta-barrel domain Family: Aminomethyltransferase beta-barrel domain
22	c1xzqA	Alignment	not modelled	95.3	15	PDB header: hydrolase Chain: A: PDB Molecule: probable trna modification gtpase trme; PDBTitle: structure of the gtp-binding protein trme from thermotoga2 maritima complexed with 5-formyl-thf
23	c3gehA	Alignment	not modelled	95.0	11	PDB header: hydrolase Chain: A: PDB Molecule: trna modification gtpase mnme; PDBTitle: crystal structure of mnme from nostoc in complex with gdp, folinic2 acid and zn
24	c1xzqB	Alignment	not modelled	94.3	15	PDB header: hydrolase Chain: B: PDB Molecule: probable trna modification gtpase trme; PDBTitle: structure of the gtp-binding protein trme from thermotoga2 maritima complexed with 5-formyl-thf
25	d1xzpa3	Alignment	not modelled	94.0	15	Fold: Folate-binding domain Superfamily: Folate-binding domain Family: TrmE formyl-THF-binding domain
26	c3geiB	Alignment	not modelled	93.9	14	PDB header: hydrolase Chain: B: PDB Molecule: trna modification gtpase mnme; PDBTitle: crystal structure of mnme from chlorobium tepidum in complex2 with gcp
27	d3bzka5	Alignment	not modelled	58.3	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Tex RuvX-like domain-like
28	d1w4ma	Alignment	not modelled	25.3	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DEP domain
						PDB header: signaling protein

29	c2ysrA	Alignment	not modelled	16.4	40	Chain: A: PDB Molecule: dep domain-containing protein 1; PDBTitle: solution structure of the dep domain from human dep domain-2 containing protein 1
30	d2bhua2	Alignment	not modelled	14.9	15	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
31	c3brcA	Alignment	not modelled	13.6	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein of unknown function; PDBTitle: crystal structure of a conserved protein of unknown function from2 methanobacterium thermoautotrophicum
32	d2hjsa1	Alignment	not modelled	13.0	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
33	d1uhwa	Alignment	not modelled	12.4	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DEP domain
34	c2vqaC	Alignment	not modelled	12.1	8	PDB header: metal-binding protein Chain: C: PDB Molecule: sli1358 protein; PDBTitle: protein-folding location can regulate mn versus cu- or zn-2 binding. crystal structure of mnca.
35	c1nnoA	Alignment	not modelled	10.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: nitrite reductase; PDBTitle: conformational changes occurring upon no binding in nitrite2 reductase from pseudomonas aeruginosa
36	d1fsha	Alignment	not modelled	10.1	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DEP domain
37	d1xqba	Alignment	not modelled	9.8	15	Fold: YaeB-like Superfamily: YaeB-like Family: YaeB-like
38	c2imuA	Alignment	not modelled	9.7	58	PDB header: viral protein Chain: A: PDB Molecule: structural polyprotein (pp) p1; PDBTitle: nmr structure of pep46 from the infectious bursal disease2 virus (ibdv) in dodecylphosphocholin (dpc).
39	d2csoa1	Alignment	not modelled	9.4	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DEP domain
40	c2gw4C	Alignment	not modelled	7.9	50	PDB header: luminescent protein Chain: C: PDB Molecule: kaede; PDBTitle: crystal structure of stony coral fluorescent protein kaede, red form
41	c2qlcC	Alignment	not modelled	7.2	21	PDB header: dna binding protein Chain: C: PDB Molecule: dna repair protein radc homolog; PDBTitle: the crystal structure of dna repair protein radc from chlorobium2 tepidum t1s
42	d1uika2	Alignment	not modelled	6.6	10	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
43	d2o3la1	Alignment	not modelled	6.5	23	Fold: Left-handed superhelix Superfamily: BH3980-like Family: BH3980-like
44	d1v3fa	Alignment	not modelled	6.4	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DEP domain
45	d1o7fa1	Alignment	not modelled	6.1	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DEP domain
46	c2oceA	Alignment	not modelled	6.1	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa5201; PDBTitle: crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
47	c2nv4A	Alignment	not modelled	5.9	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0066 protein af_0241; PDBTitle: crystal structure of upf0066 protein af0241 in complex with2 s-adenosylmethionine. northeast structural genomics3 consortium target gr27
48	c2nyiB	Alignment	not modelled	5.9	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: unknown protein; PDBTitle: crystal structure of an unknown protein from galdieria2 sulphuraria
49	d1mb4a1	Alignment	not modelled	5.6	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
50	d1u8sa1	Alignment	not modelled	5.4	21	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor
51	d1vqod1	Alignment	not modelled	5.3	19	Fold: RL5-like Superfamily: RL5-like Family: Ribosomal protein L5
52	d2hh6a1	Alignment	not modelled	5.2	14	Fold: Left-handed superhelix Superfamily: BH3980-like Family: BH3980-like
53	c2a56A	Alignment	not modelled	5.1	50	PDB header: luminescent protein Chain: A: PDB Molecule: gfp-like non-fluorescent chromoprotein fp595 chain 1; PDBTitle: fluorescent protein asfp595, a143s, on-state, 5min irradiation