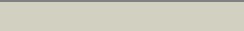


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ecjB_	 Alignment		100.0	19	PDB header: transferase Chain: B: PDB Molecule: glutamine phosphoribosylpyrophosphate PDBTitle: escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
2	c1gph1_	 Alignment		100.0	25	PDB header: transferase(glutamine amidotransferase) Chain: 1: PDB Molecule: glutamine phosphoribosyl-pyrophosphate amidotransferase; PDBTitle: structure of the allosteric regulatory enzyme of purine biosynthesis
3	c1jxaA_	 Alignment		100.0	34	PDB header: transferase Chain: A: PDB Molecule: glucosamine 6-phosphate synthase; PDBTitle: glucosamine 6-phosphate synthase with glucose 6-phosphate
4	d1xffa_	 Alignment		100.0	36	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
5	d1ecfa2	 Alignment		100.0	20	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
6	d1gph12	 Alignment		100.0	25	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
7	c1ct9D_	 Alignment		100.0	25	PDB header: ligase Chain: D: PDB Molecule: asparagine synthetase b; PDBTitle: crystal structure of asparagine synthetase b from2 escherichia coli
8	d1ofda3	 Alignment		100.0	20	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
9	d1ct9a2	 Alignment		100.0	26	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
10	d1ea0a3	 Alignment		100.0	23	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
11	d1te5a_	 Alignment		100.0	17	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases

12	c3mdnD_	Alignment		99.9	17	PDB header: transferase Chain: D: PDB Molecule: glutamine aminotransferase class-ii domain protein; PDBTitle: structure of glutamine aminotransferase class-ii domain protein2 (spo2029) from silicibacter pomeroyi
13	c1q15A_	Alignment		99.9	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: cara; PDBTitle: carbapenam synthetase
14	c1mlzB_	Alignment		99.9	14	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactam synthetase; PDBTitle: beta-lactam synthetase apo enzyme
15	d1q15a2	Alignment		99.9	17	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
16	d1jgta2	Alignment		99.8	15	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
17	c1lm1A_	Alignment		99.6	22	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin-dependent glutamate synthase; PDBTitle: structural studies on the synchronization of catalytic centers in2 glutamate synthase: native enzyme
18	c2vdcF_	Alignment		99.5	23	PDB header: oxidoreductase Chain: F: PDB Molecule: glutamate synthase [nadph] large chain; PDBTitle: the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
19	c2rprA_	Alignment		48.3	14	PDB header: metal binding protein Chain: A: PDB Molecule: flywch-type zinc finger-containing protein 1; PDBTitle: solution structure of the fifth flywch domain of flywch-type2 zinc finger-containing protein 1
20	c1skoA_	Alignment		39.6	16	PDB header: signaling protein Chain: A: PDB Molecule: mitogen-activated protein kinase kinase 1 PDBTitle: mp1-p14 complex
21	d2outa1	Alignment	not modelled	39.0	42	Fold: LEM/SAP HeH motif Superfamily: Rho N-terminal domain-like Family: YqbF C-terminal domain-like
22	d3cpta1	Alignment	not modelled	38.9	15	Fold: Profilin-like Superfamily: Roadblock/LC7 domain Family: Roadblock/LC7 domain
23	c3sipC_	Alignment	not modelled	32.3	13	PDB header: hydrolase/ligase/hydrolase Chain: C: PDB Molecule: caspase; PDBTitle: crystal structure of drice and diap1-bir1 complex
24	c2oqbA_	Alignment	not modelled	32.0	26	PDB header: transferase,gene regulation Chain: A: PDB Molecule: histone-arginine methyltransferase carm1; PDBTitle: crystal structure of the n-terminal domain of coactivator-associated2 methyltransferase 1 (carm1)
25	c2jz8A_	Alignment	not modelled	29.0	38	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bh09830; PDBTitle: solution nmr structure of bh09830 from bartonella henselae2 modeled with one zn+2 bound. northeast structural genomics3 consortium target bnr55
26	d2naca2	Alignment	not modelled	26.9	20	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
27	d1vk9a_	Alignment	not modelled	17.4	22	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Hypothetical protein TM1506
28	c2l3mA_	Alignment	not modelled	17.0	13	PDB header: metal binding protein Chain: A: PDB Molecule: copper-ion-binding protein; PDBTitle: solution structure of the putative copper-ion-binding protein from2 bacillus anthracis str. ames

29	d2c71a1	Alignment	not modelled	16.0	18	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
30	c1y8aA	Alignment	not modelled	15.8	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af1437; PDBTitle: structure of gene product af1437 from archaeoglobus fulgidus
31	c1nh1A	Alignment	not modelled	15.8	38	PDB header: avirulence protein Chain: A: PDB Molecule: avirulence b protein; PDBTitle: crystal structure of the type iii effector avrb from2 pseudomonas syringae.
32	d1nh1a	Alignment	not modelled	15.8	38	Fold: Antivirulence factor Superfamily: Antivirulence factor Family: Antivirulence factor
33	c2a45L	Alignment	not modelled	14.5	30	PDB header: hydrolase/hydrolase inhibitor Chain: L: PDB Molecule: fibrinogen gamma chain; PDBTitle: crystal structure of the complex between thrombin and the central "e"2 region of fibrin
34	d1k94a	Alignment	not modelled	12.6	9	Fold: EF Hand-like Superfamily: EF-hand Family: Penta-EF-hand proteins
35	c2loja	Alignment	not modelled	12.4	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative cytoplasmic protein; PDBTitle: solution nmr structure of tstm1273 from salmonella typhimurium lt2,2 nesg target stt322, csgid target idp01027 and ocsf target tstm1273
36	d2nlyal	Alignment	not modelled	12.1	15	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: Divergent polysaccharide deacetylase
37	c2jraB	Alignment	not modelled	11.9	25	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein rpa2121; PDBTitle: a novel domain-swapped solution nmr structure of protein rpa2121 from2 rhodopseudomonas palustris. northeast structural genomics target rpt6
38	d1nlyal	Alignment	not modelled	11.2	24	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
39	c3h11A	Alignment	not modelled	11.1	8	PDB header: apoptosis Chain: A: PDB Molecule: casp8 and fadd-like apoptosis regulator; PDBTitle: zymogen caspase-8:c-flip protease domain complex
40	c2hl7A	Alignment	not modelled	10.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c-type biogenesis protein ccmh; PDBTitle: crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
41	c2kw0A	Alignment	not modelled	10.1	6	PDB header: oxidoreductase Chain: A: PDB Molecule: ccmh protein; PDBTitle: solution structure of n-terminal domain of ccmh from escherichia.coli
42	c2rmlA	Alignment	not modelled	9.9	19	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting p-type atpase copa; PDBTitle: solution structure of the n-terminal soluble domains of2 bacillus subtilis copa
43	d1isia	Alignment	not modelled	9.6	17	Fold: Flavodoxin-like Superfamily: N-(deoxy)ribosyltransferase-like Family: ADP ribosyl cyclase-like
44	c2rdsA	Alignment	not modelled	9.6	13	PDB header: oxidoreductase Chain: A: PDB Molecule: 1-deoxypentalenic acid 11-beta hydroxylase; fe(ii)/alpha- PDBTitle: crystal structure of pth with fe/oxalylglycine and ent-1-2 deoxypentalenic acid bound
45	c2qpnA	Alignment	not modelled	9.2	12	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase ges-1; PDBTitle: ges-1 beta-lactamase
46	c2w3zA	Alignment	not modelled	8.7	16	PDB header: hydrolase Chain: A: PDB Molecule: putative deacetylase; PDBTitle: structure of a streptococcus mutans ce4 esterase
47	d1tygb	Alignment	not modelled	8.5	11	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
48	c2funB	Alignment	not modelled	8.4	8	PDB header: apoptosis/hydrolase Chain: B: PDB Molecule: caspase-8; PDBTitle: alternative p35-caspase-8 complex
49	d1e25a	Alignment	not modelled	8.3	5	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
50	c2kq6A	Alignment	not modelled	7.9	38	PDB header: transport protein Chain: A: PDB Molecule: polycystin-2; PDBTitle: the structure of the ef-hand domain of polycystin-2 suggests a2 mechanism for ca2+-dependent regulation of polycystin-2 channel3 activity
51	c2kl0A	Alignment	not modelled	7.8	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative thiamin biosynthesis this; PDBTitle: solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
52	c2an1D	Alignment	not modelled	7.8	13	PDB header: transferase Chain: D: PDB Molecule: putative kinase; PDBTitle: structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurium lt2
53	c2kleA	Alignment	not modelled	7.7	38	PDB header: membrane protein Chain: A: PDB Molecule: polycystin-2; PDBTitle: isic refined solution structure of the calcium binding2 domain of the c-terminal cytosolic domain of polycystin-2
						Fold: Ribonuclease H-like motif

54	dly97a1	Alignment	not modelled	7.4	28	Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
55	cli3oC_	Alignment	not modelled	7.3	18	PDB header: apoptosis Chain: C: PDB Molecule: caspase 3; PDBTitle: crystal structure of the complex of xiap-bir2 and caspase 3
56	c2kKhA_	Alignment	not modelled	7.3	19	PDB header: metal transport Chain: A: PDB Molecule: putative heavy metal transporter; PDBTitle: structure of the zinc binding domain of the atpase hma4
57	clqduL_	Alignment	not modelled	7.1	9	PDB header: hydrolase/hydrolase inhibitor Chain: I: PDB Molecule: caspase-8 alpha-chain; PDBTitle: crystal structure of the complex of caspase-8 with the tripeptide2 ketone inhibitor zevd-dcbmk
58	d2j13a1	Alignment	not modelled	6.9	32	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
59	cly3kA_	Alignment	not modelled	6.9	11	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 1; PDBTitle: solution structure of the apo form of the fifth domain of2 menkes protein
60	c2ldiA_	Alignment	not modelled	6.7	13	PDB header: hydrolase Chain: A: PDB Molecule: zinc-transporting atpase; PDBTitle: nmr solution structure of ziaan sub mutant
61	d1xi8a3	Alignment	not modelled	6.5	17	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
62	c2wdpA_	Alignment	not modelled	6.2	5	PDB header: hydrolase Chain: A: PDB Molecule: caspase-6; PDBTitle: crystal structure of ligand free human caspase-6
63	c3dxsX_	Alignment	not modelled	6.1	17	PDB header: hydrolase Chain: X: PDB Molecule: copper-transporting atpase ran1; PDBTitle: crystal structure of a copper binding domain from hma7, a p-2 type atpase
64	clabzA_	Alignment	not modelled	5.8	37	PDB header: de novo design Chain: A: PDB Molecule: alpha-t-alpha; PDBTitle: alpha-t-alpha, a de novo designed peptide, nmr, 232 structures
65	clnmqB_	Alignment	not modelled	5.7	12	PDB header: apoptosis, hydrolase Chain: B: PDB Molecule: caspase-3; PDBTitle: extendend tethering: in situ assembly of inhibitors
66	dlm40a_	Alignment	not modelled	5.6	9	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
67	clvliA_	Alignment	not modelled	5.5	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: spore coat polysaccharide biosynthesis protein spse; PDBTitle: crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
68	dlidy6a_	Alignment	not modelled	5.5	8	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
69	clyx7A_	Alignment	not modelled	5.2	19	PDB header: metal binding protein Chain: A: PDB Molecule: calsensin; PDBTitle: nmr structure of calsensin, energy minimized average2 structure.
70	dlaxxa_	Alignment	not modelled	5.2	14	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Cytochrome b5
71	dlk78a2	Alignment	not modelled	5.2	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
72	dlp94a_	Alignment	not modelled	5.2	16	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
73	dlbsga_	Alignment	not modelled	5.0	12	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
74	clw17A_	Alignment	not modelled	5.0	24	PDB header: hydrolase Chain: A: PDB Molecule: probable polysaccharide deacetylase pdaa; PDBTitle: structure of bacillus subtilis pdaa, a family 42 carbohydrate esterase.