




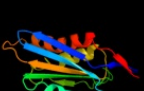

















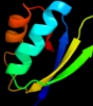



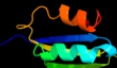

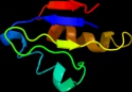



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1vi7A_	 Alignment		100.0	100	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein yigz; PDBTitle: crystal structure of an hypothetical protein
2	c2cveA_	 Alignment		100.0	35	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein ttha1053; PDBTitle: crystal structure of a conserved hypothetical protein tt1547 from2 thermus thermophilus hb8
3	d1vi7a1	 Alignment		100.0	100	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: YigZ N-terminal domain-like
4	d2cvea1	 Alignment		100.0	45	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: YigZ N-terminal domain-like
5	d1vi7a2	 Alignment		99.0	100	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: YigZ C-terminal domain-like
6	c2xexA_	 Alignment		97.6	10	PDB header: translation Chain: A; PDB Molecule: elongation factor g; PDBTitle: crystal structure of staphylococcus aureus elongation factor2 g
7	c2bm0A_	 Alignment		97.6	14	PDB header: elongation factor Chain: A; PDB Molecule: elongation factor g; PDBTitle: ribosomal elongation factor g (ef-g) fusidic acid resistant2 mutant t84a
8	c3b8hA_	 Alignment		97.6	14	PDB header: biosynthetic protein/transferase Chain: A; PDB Molecule: elongation factor 2; PDBTitle: structure of the eef2-exoa(e546a)-nad+ complex
9	c2dy1A_	 Alignment		97.5	12	PDB header: signaling protein, translation Chain: A; PDB Molecule: elongation factor g; PDBTitle: crystal structure of ef-g-2 from thermus thermophilus
10	c2rdo7_	 Alignment		97.5	11	PDB header: ribosome Chain: 7; PDB Molecule: elongation factor g; PDBTitle: 50s subunit with ef-g(gdpnp) and rrf bound
11	c1zn0B_	 Alignment		97.0	14	PDB header: translation/biosynthetic protein/rna Chain: B; PDB Molecule: elongation factor g; PDBTitle: coordinates of rrf and ef-g fitted into cryo-em map of the2 50s subunit bound with both ef-g (gdpnp) and rrf

12	d2dy1a5	Alignment		97.0	15	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: EF-G/eEF-2 domains III and V
13	d1n0ua5	Alignment		96.9	18	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: EF-G/eEF-2 domains III and V
14	d2bv3a5	Alignment		96.9	13	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: EF-G/eEF-2 domains III and V
15	c2ywfA_	Alignment		96.7	22	PDB header: translation Chain: A: PDB Molecule: gtp-binding protein lepa; PDBTitle: crystal structure of gmppnp-bound lepa from aquifex aeolicus
16	d2cvea2	Alignment		96.4	19	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: YigZ C-terminal domain-like
17	c3cb4D_	Alignment		96.3	26	PDB header: translation Chain: D: PDB Molecule: gtp-binding protein lepa; PDBTitle: the crystal structure of lepa
18	c3degC_	Alignment		96.3	26	PDB header: ribosome Chain: C: PDB Molecule: gtp-binding protein lepa; PDBTitle: complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmppnp
19	c2kdoA_	Alignment		95.6	11	PDB header: rna binding protein Chain: A: PDB Molecule: ribosome maturation protein sbds; PDBTitle: structure of the human shwachman-bodian-diamond syndrome protein, sbds
20	d1p9qc3	Alignment		95.5	10	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: Hypothetical protein AF0491, C-terminal domain
21	c1t95A_	Alignment	not modelled	95.0	9	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein af0491; PDBTitle: crystal structure of the shwachman-bodian-diamond syndrome2 protein orthologue from archaeoglobus fulgidus
22	d1t95a3	Alignment	not modelled	94.5	11	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: Hypothetical protein AF0491, C-terminal domain
23	c2wbmA_	Alignment	not modelled	93.5	18	PDB header: rna-binding protein Chain: A: PDB Molecule: ribosome maturation protein sdo1 homolog; PDBTitle: crystal structure of mthsbs, the homologue of the2 shwachman-bodian-diamond syndrome protein in the3 euriarchaeon methanothermobacter thermautotrophicus
24	c1jqscC_	Alignment	not modelled	93.5	13	PDB header: ribosome Chain: C: PDB Molecule: elongation factor g; PDBTitle: fitting of l11 protein and elongation factor g (domain g'2 and v) in the cryo-em map of e. coli 70s ribosome bound3 with ef-g and gmppcp, a nonhydrolysable gtp analog
25	d1lrza2	Alignment	not modelled	57.4	17	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: FemXAB nonribosomal peptidyltransferases
26	d1kona_	Alignment	not modelled	52.9	5	Fold: YebC-like Superfamily: YebC-like Family: YebC-like
27	d1mw7a_	Alignment	not modelled	47.9	9	Fold: YebC-like Superfamily: YebC-like Family: YebC-like
28	d1lfpa_	Alignment	not modelled	35.2	9	Fold: YebC-like Superfamily: YebC-like

						Family: YebC-like
29	c2p5xB	Alignment	not modelled	35.1	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: n-acetylserotonin o-methyltransferase-like protein; PDBTitle: crystal structure of maf domain of human n-acetylserotonin o-2 methyltransferase-like protein
30	d1tzfa	Alignment	not modelled	25.1	24	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylytransferase
31	dlex2a	Alignment	not modelled	22.6	19	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: Maf-like
32	d2cz4a1	Alignment	not modelled	20.7	12	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
33	d2c71a1	Alignment	not modelled	20.5	27	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
34	d1v4aa1	Alignment	not modelled	19.3	50	Fold: Four-helical up-and-down bundle Superfamily: Nucleotidyltransferase substrate binding subunit/domain Family: Glutamine synthase adenyllyltransferase GlnE, domain 2
35	c3polA	Alignment	not modelled	17.6	21	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidylyltransferase; PDBTitle: 2.3 angstrom crystal structure of 3-deoxy-manno-octulosonate2 cytidylyltransferase (kdsb) from acinetobacter baumannii.
36	c3okrA	Alignment	not modelled	16.5	29	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; PDBTitle: structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
37	c3tl8D	Alignment	not modelled	16.2	10	PDB header: transferase Chain: D: PDB Molecule: aminotransferase class i and ii; PDBTitle: crystal structure of aminotransferase from anaerococcus prevotii dsm2 20548.
38	c3q3jA	Alignment	not modelled	15.3	22	PDB header: membrane protein/protein binding Chain: A: PDB Molecule: plexin-a2; PDBTitle: crystal structure of plexin a2 rbd in complex with rnd1
39	d2f1fa2	Alignment	not modelled	15.3	16	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
40	c2qs0A	Alignment	not modelled	14.2	11	PDB header: biosynthetic protein Chain: A: PDB Molecule: quinolinate synthetase a; PDBTitle: quinolinate synthase from pyrococcus furiosus
41	d1vh3a	Alignment	not modelled	14.0	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylytransferase
42	d2amha1	Alignment	not modelled	13.0	17	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: Maf-like
43	c2vshB	Alignment	not modelled	12.1	21	PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate PDBTitle: synthesis of cdp-activated ribitol for teichoic acid2 precursors in streptococcus pneumoniae
44	d2fgca1	Alignment	not modelled	12.1	18	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
45	d1qwja	Alignment	not modelled	11.7	27	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylytransferase
46	d1vh1a	Alignment	not modelled	11.1	29	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylytransferase
47	c3e3xA	Alignment	not modelled	11.1	17	PDB header: hydrolase Chain: A: PDB Molecule: bipa; PDBTitle: the c-terminal part of bipa protein from vibrio parahaemolyticus rimd2 2210633
48	d1vgwa	Alignment	not modelled	10.9	27	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylytransferase
49	c3lkwA	Alignment	not modelled	10.8	45	PDB header: viral protein,hydrolase Chain: A: PDB Molecule: fusion protein of nonstructural protein 2b and PDBTitle: crystal structure of dengue virus 1 ns2b/ns3 protease active2 site mutant
50	c2kr6A	Alignment	not modelled	10.7	36	PDB header: hydrolase Chain: A: PDB Molecule: presenilin-1; PDBTitle: solution structure of presenilin-1 ctf subunit
51	d1v3aa	Alignment	not modelled	10.7	20	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
52	d1rxda	Alignment	not modelled	9.9	18	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
53	d2ijob1	Alignment	not modelled	9.9	45	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
54	c2nn2A	Alignment	not modelled	9.8	43	PDB header: transcription Chain: A: PDB Molecule: putative tetr-family regulator;

54	c2tp3A	Alignment	not modelled	9.8	43	PDBTitle: crystal structure of tet-family regulator (sco0857) from streptomyces2 coelicolor a3.
55	c2exeA	Alignment	not modelled	9.7	8	PDB header: transferase Chain: A: PDB Molecule: dual specificity protein kinase clk3; PDBTitle: crystal structure of the phosphorylated clk3
56	d2fomb1	Alignment	not modelled	9.6	26	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
57	c3e90B	Alignment	not modelled	9.4	45	PDB header: hydrolase Chain: B: PDB Molecule: ns3 protease; PDBTitle: west nile vi rus ns2b-ns3protease in complexed with2 inhibitor naph-kr-h
58	d1t41b	Alignment	not modelled	8.9	39	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
59	d1befa	Alignment	not modelled	8.8	36	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
60	d1ny1a	Alignment	not modelled	8.5	19	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
61	d1t4oa	Alignment	not modelled	8.3	38	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
62	c1t4oA	Alignment	not modelled	8.3	38	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease iii; PDBTitle: crystal structure of rnt1p dsrbd
63	d2fp7b1	Alignment	not modelled	8.0	45	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
64	d1pnoa	Alignment	not modelled	7.9	30	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Transhydrogenase domain III (dIII)
65	c2gv1A	Alignment	not modelled	7.7	8	PDB header: hydrolase Chain: A: PDB Molecule: probable acylphosphatase; PDBTitle: nmr solution structure of the acylphosphatase from2 eschaerichia coli
66	c2w3zA	Alignment	not modelled	7.6	21	PDB header: hydrolase Chain: A: PDB Molecule: putative deacetylase; PDBTitle: structure of a streptococcus mutans ce4 esterase
67	c1up6F	Alignment	not modelled	7.6	26	PDB header: hydrolase Chain: F: PDB Molecule: 6-phospho-beta-glucosidase; PDBTitle: structure of the 6-phospho-beta glucosidase from thermotoga2 maritima at 2.55 angstrom resolution in the tetragonal form3 with manganese, nad+ and glucose-6-phosphate
68	d1eyra	Alignment	not modelled	7.4	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
69	c1l2yA	Alignment	not modelled	7.4	56	PDB header: de novo protein Chain: A: PDB Molecule: tc5b; PDBTitle: nmr structure of trp-cage miniprotein construct tc5b
70	c3b4oB	Alignment	not modelled	7.4	13	PDB header: biosynthetic protein Chain: B: PDB Molecule: phenazine biosynthesis protein a/b; PDBTitle: crystal structure of phenazine biosynthesis protein phza/b2 from burkholderia cepacia r18194, apo form
71	c2wv9A	Alignment	not modelled	7.3	41	PDB header: hydrolase Chain: A: PDB Molecule: flavivirin protease ns2b regulatory subunit, flavivirin PDBTitle: crystal structure of the ns3 protease-helicase from murray2 valley encephalitis virus
72	d1jo0a	Alignment	not modelled	7.2	14	Fold: IF3-like Superfamily: YhbY-like Family: YhbY-like
73	c2hfuB	Alignment	not modelled	7.2	17	PDB header: transferase Chain: B: PDB Molecule: mevalonate kinase, putative; PDBTitle: crystal structure of l. major mevalonate kinase in complex2 with r-mevalonate
74	d1d4oa	Alignment	not modelled	6.9	27	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Transhydrogenase domain III (dIII)
75	c2kduB	Alignment	not modelled	6.8	25	PDB header: metal binding protein/exocytosis Chain: B: PDB Molecule: protein unc-13 homolog a; PDBTitle: structural basis of the munc13-1/ca2+-calmodulin2 interaction: a novel 1-26 calmodulin binding motif with a3 bipartite binding mode
76	c3oamD	Alignment	not modelled	6.8	33	PDB header: transferase Chain: D: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: crystal structure of cytidyltransferase from vibrio cholerae
77	c2jphA	Alignment	not modelled	6.7	25	PDB header: signaling protein, protein binding Chain: A: PDB Molecule: plexin-b1; PDBTitle: nmr solution structure of the rho gtpase binding domain of2 human plexin-b1
78	c2jofA	Alignment	not modelled	6.6	56	PDB header: de novo protein Chain: A: PDB Molecule: trp-cage; PDBTitle: the trp-cage: optimizing the stability of a globular2 miniprotein
79	d1tmka	Alignment	not modelled	6.4	9	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
						Fold: Ferredoxin-like

80	d2pc6a1	Alignment	not modelled	6.4	11	Superfamily: ACT-like Family: IlvH-like
81	c1s6yA	Alignment	not modelled	6.4	30	PDB header: hydrolase Chain: A: PDB Molecule: 6-phospho-beta-glucosidase; PDBTitle: 2.3a crystal structure of phospho-beta-glucosidase
82	c1v4aA	Alignment	not modelled	6.3	50	PDB header: transferase Chain: A: PDB Molecule: glutamate-ammonia-ligase adenylyltransferase; PDBTitle: structure of the n-terminal domain of escherichia coli2 glutamine synthetase adenylyltransferase
83	d1vm6a2	Alignment	not modelled	6.3	80	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C- terminal domain Family: Dihydrodipicolinate reductase-like
84	d1f61a	Alignment	not modelled	6.3	50	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
85	d1h7ea	Alignment	not modelled	6.2	23	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: Cytidylyltransferase
86	c1uv7A	Alignment	not modelled	6.2	14	PDB header: transport Chain: A: PDB Molecule: general secretion pathway protein m; PDBTitle: periplasmic domain of epsm from vibrio cholerae
87	d1uv7a	Alignment	not modelled	6.2	14	Fold: RRF/tRNA synthetase additional domain-like Superfamily: General secretion pathway protein M, EpsM Family: General secretion pathway protein M, EpsM
88	c3k7dA	Alignment	not modelled	6.1	30	PDB header: transferase Chain: A: PDB Molecule: glutamate-ammonia-ligase adenylyltransferase; PDBTitle: c-terminal (adenylation) domain of e.coli glutamine synthetase2 adenylyltransferase
89	c2vbcA	Alignment	not modelled	6.0	36	PDB header: hydrolase Chain: A: PDB Molecule: dengue 4 ns3 full-length protein; PDBTitle: crystal structure of the ns3 protease-helicase from dengue2 virus
90	d1w55a1	Alignment	not modelled	5.9	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: Cytidylyltransferase
91	c2ux8G	Alignment	not modelled	5.8	14	PDB header: transferase Chain: G: PDB Molecule: glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of sphingomonas elodea atcc 31461 glucose-2 1-phosphate uridylyltransferase in complex with glucose-3 1-phosphate.
92	c2xw1B	Alignment	not modelled	5.8	39	PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; PDBTitle: crystal structure of ispd from mycobacterium smegmatis in complex2 with ctp and mg
93	c2bruC	Alignment	not modelled	5.8	33	PDB header: oxidoreductase Chain: C: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: complex of the domain i and domain iii of escherichia coli2 transhydrogenase
94	c3rz2B	Alignment	not modelled	5.7	16	PDB header: hydrolase Chain: B: PDB Molecule: protein tyrosine phosphatase type iva 1; PDBTitle: crystal of prl-1 complexed with peptide
95	d2ieca1	Alignment	not modelled	5.7	57	Fold: MK0786-like Superfamily: MK0786-like Family: MK0786-like
96	c3pnnA	Alignment	not modelled	5.6	20	PDB header: transferase Chain: A: PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
97	d2f06a1	Alignment	not modelled	5.6	9	Fold: Ferredoxin-like Superfamily: ACT-like Family: BT0572-like
98	c3okrC	Alignment	not modelled	5.5	35	PDB header: transferase Chain: C: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; PDBTitle: structure of mtb apo 2-c-methyl-d-erythritol 4- phosphate2 cytidyltransferase (ispd)
99	d1diha2	Alignment	not modelled	5.5	80	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C- terminal domain Family: Dihydrodipicolinate reductase-like