





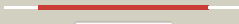


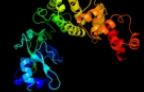














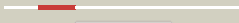
















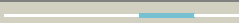

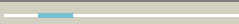
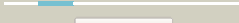
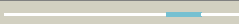




#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3aqpA_	 Alignment		100.0	100	PDB header: transferase Chain: A: PDB Molecule: poly(a) polymerase; PDBTitle: complex structure of bacterial protein (apo form ii)
2	c1miyB_	 Alignment		100.0	28	PDB header: translation, transferase Chain: B: PDB Molecule: trna cca-adding enzyme; PDBTitle: crystal structure of bacillus stearotherophilus cca-adding enzyme in2 complex with ctp
3	c1vfgB_	 Alignment		100.0	24	PDB header: transferase/rna Chain: B: PDB Molecule: poly a polymerase; PDBTitle: crystal structure of trna nucleotidyltransferase complexed2 with a primer trna and an incoming atp analog
4	c3h37B_	 Alignment		100.0	21	PDB header: transferase Chain: B: PDB Molecule: trna nucleotidyl transferase-related protein; PDBTitle: the structure of cca-adding enzyme apo form i
5	c1ou5A_	 Alignment		100.0	26	PDB header: translation, transferase Chain: A: PDB Molecule: trna cca-adding enzyme; PDBTitle: crystal structure of human cca-adding enzyme
6	d1miwa2	 Alignment		100.0	38	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Poly A polymerase head domain-like
7	d1ou5a2	 Alignment		100.0	35	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Poly A polymerase head domain-like
8	d1vfga2	 Alignment		100.0	40	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Poly A polymerase head domain-like
9	d1miwa1	 Alignment		100.0	21	Fold: Poly A polymerase C-terminal region-like Superfamily: Poly A polymerase C-terminal region-like Family: Poly A polymerase C-terminal region-like
10	d1vfga1	 Alignment		100.0	18	Fold: Poly A polymerase C-terminal region-like Superfamily: Poly A polymerase C-terminal region-like Family: Poly A polymerase C-terminal region-like
11	d1ou5a1	 Alignment		100.0	19	Fold: Poly A polymerase C-terminal region-like Superfamily: Poly A polymerase C-terminal region-like Family: Poly A polymerase C-terminal region-like

12	c2la3A_		Alignment		96.7	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the nmr structure of the protein np_344798.1 reveals a cca-adding2 enzyme head domain
13	d2fcla1		Alignment		91.6	22	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: TM1012-like
14	d2qgsa1		Alignment		86.8	10	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
15	d2pq7a1		Alignment		80.8	7	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
16	d1r89a2		Alignment		69.0	20	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Archaeal tRNA CCA-adding enzyme catalytic domain
17	d3djba1		Alignment		63.8	14	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
18	d1y81a1		Alignment		58.2	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
19	d2d59a1		Alignment		46.9	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
20	d1jmsa4		Alignment		43.2	19	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: DNA polymerase beta-like
21	d1iowa1		Alignment	not modelled	39.9	20	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: D-Alanine ligase N-terminal domain
22	c2q14A_		Alignment	not modelled	38.4	7	PDB header: hydrolase Chain: A: PDB Molecule: phosphohydrolase; PDBTitle: crystal structure of phosphohydrolase (bt4208) from bacteroides2 thetaiotaomicron vpi-5482 at 2.20 a resolution
23	c3mdoB_		Alignment	not modelled	34.9	32	PDB header: ligase Chain: B: PDB Molecule: putative phosphoribosylformylglycinamide cyclo-ligase; PDBTitle: crystal structure of a putative phosphoribosylformylglycinamide2 cyclo-ligase (bdi_2101) from parabacteroides distasonis atcc 8503 at3 1.91 a resolution
24	d1b7go1		Alignment	not modelled	34.9	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
25	d2fmpa3		Alignment	not modelled	33.0	26	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: DNA polymerase beta-like
26	c3skdA_		Alignment	not modelled	31.0	11	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein thb187; PDBTitle: crystal structure of the thermus thermophilus cas3 hd domain in the2 presence of ni2+
27	c3fpnA_		Alignment	not modelled	30.3	18	PDB header: dna binding protein Chain: A: PDB Molecule: geobacillus stearothermophilus uvra interaction PDBTitle: crystal structure of uvra-uvrb interaction domains
28	d1n57a_		Alignment	not modelled	29.2	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl

29	c2duwA_	 Alignment	not modelled	28.9	21	PDB header: ligand binding protein Chain: A: PDB Molecule: putative coa-binding protein; PDBTitle: solution structure of putative coa-binding protein of2 klebsiella pneumoniae
30	c1x60A_	 Alignment	not modelled	28.5	30	PDB header: hydrolase Chain: A: PDB Molecule: sporulation-specific n-acetylmuramoyl-l-alanine PDBTitle: solution structure of the peptidoglycan binding domain of2 b. subtilis cell wall lytic enzyme cwlc
31	c2pcnA_	 Alignment	not modelled	28.5	18	PDB header: transferase Chain: A: PDB Molecule: s-adenosylmethionine:2-demethylmenaquinone PDBTitle: crystal structure of s-adenosylmethionine: 2-dimethylmenaquinone2 methyltransferase (gk_1813) from geobacillus kaustophilus hta426
32	c2ze5A_	 Alignment	not modelled	28.0	13	PDB header: transferase Chain: A: PDB Molecule: isopentenyl transferase; PDBTitle: crystal structure of adenosine phosphate-isopentenyltransferase
33	d2bcqa3	 Alignment	not modelled	27.6	23	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: DNA polymerase beta-like
34	c3k4iC_	 Alignment	not modelled	27.0	18	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein pspto_3204 from2 pseudomonas syringae pv. tomato str. dc3000
35	d2bdua1	 Alignment	not modelled	26.9	21	Fold: HAD-like Superfamily: HAD-like Family: Pyrimidine 5'-nucleotidase (UMPH-1)
36	c3c8oB_	 Alignment	not modelled	24.9	32	PDB header: hydrolase regulator Chain: B: PDB Molecule: regulator of ribonuclease activity a; PDBTitle: the crystal structure of rraa from pao1
37	d1vi4a_	 Alignment	not modelled	24.9	27	Fold: The "swivelling" beta/beta/alpha domain Superfamily: RraA-like Family: RraA-like
38	d1no5a_	 Alignment	not modelled	24.0	25	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Catalytic subunit of bi-partite nucleotidyltransferase
39	d1clia2	 Alignment	not modelled	23.9	32	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
40	d1j3la_	 Alignment	not modelled	23.8	32	Fold: The "swivelling" beta/beta/alpha domain Superfamily: RraA-like Family: RraA-like
41	d2vana2	 Alignment	not modelled	23.5	26	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: DNA polymerase beta-like
42	d1q5xa_	 Alignment	not modelled	23.3	18	Fold: The "swivelling" beta/beta/alpha domain Superfamily: RraA-like Family: RraA-like
43	d1iuka_	 Alignment	not modelled	23.3	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
44	c3m5fA_	 Alignment	not modelled	23.2	10	PDB header: hydrolase Chain: A: PDB Molecule: metal dependent phosphohydrolase; PDBTitle: structure of mj0384, a cas3 protein from methanocaldococcus jannaschii
45	c1nxjA_	 Alignment	not modelled	23.1	27	PDB header: unknown function Chain: A: PDB Molecule: probable s-adenosylmethionine:2- PDBTitle: structure of rv3853 from mycobacterium tuberculosis
46	d1nxja_	 Alignment	not modelled	23.1	27	Fold: The "swivelling" beta/beta/alpha domain Superfamily: RraA-like Family: RraA-like
47	c2c5qE_	 Alignment	not modelled	22.7	23	PDB header: structural genomics,unknown function Chain: E: PDB Molecule: rraa-like protein yer010c; PDBTitle: crystal structure of yeast yer010cp
48	c3a8tA_	 Alignment	not modelled	22.6	15	PDB header: transferase Chain: A: PDB Molecule: adenylate isopentenyltransferase; PDBTitle: plant adenylate isopentenyltransferase in complex with atp
49	d1wota_	 Alignment	not modelled	22.5	12	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Catalytic subunit of bi-partite nucleotidyltransferase
50	d2vkqa1	 Alignment	not modelled	22.2	19	Fold: HAD-like Superfamily: HAD-like Family: Pyrimidine 5'-nucleotidase (UMPH-1)
51	d1yt8a4	 Alignment	not modelled	21.9	20	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
52	c3d54l_	 Alignment	not modelled	21.3	22	PDB header: ligase Chain: I: PDB Molecule: phosphoribosylformylglycinamide synthase ii; PDBTitle: structure of purlqs from thermotoga maritima
53	c3g5jA_	 Alignment	not modelled	21.1	22	PDB header: nucleotide binding protein Chain: A: PDB Molecule: putative atp/gtp binding protein; PDBTitle: crystal structure of n-terminal domain of putative atp/gtp binding2 protein from clostridium difficile 630
54	c2w9mB_	 Alignment	not modelled	21.0	19	PDB header: dna replication Chain: B: PDB Molecule: polymerase x; PDBTitle: structure of family x dna polymerase from deinococcus2 radiodurans

55	d2fuea1	Alignment	not modelled	20.0	14	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
56	c3exaD	Alignment	not modelled	19.9	18	PDB header: transferase Chain: D: PDB Molecule: trna delta(2)-isopentenylpyrophosphate PDBTitle: crystal structure of the full-length trna2 isopentenylpyrophosphate transferase (bh2366) from3 bacillus halodurans, northeast structural genomics4 consortium target bhr41.
57	d1wpga2	Alignment	not modelled	19.4	13	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
58	d1vk3a1	Alignment	not modelled	18.7	53	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
59	c3d3qB	Alignment	not modelled	18.1	15	PDB header: transferase Chain: B: PDB Molecule: trna delta(2)-isopentenylpyrophosphate PDBTitle: crystal structure of trna delta(2)-isopentenylpyrophosphate2 transferase (se0981) from staphylococcus epidermidis.3 northeast structural genomics consortium target ser100
60	c3ib6B	Alignment	not modelled	17.6	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from listeria2 monocytogenes serotype 4b
61	d2heka1	Alignment	not modelled	17.4	17	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
62	c2zodB	Alignment	not modelled	16.7	18	PDB header: transferase Chain: B: PDB Molecule: selenide, water dikinase; PDBTitle: crystal structure of selenophosphate synthetase from2 aquifex aeolicus
63	c2cx9C	Alignment	not modelled	16.6	16	PDB header: oxidoreductase Chain: C: PDB Molecule: acyl-coa dehydrogenase; PDBTitle: crystal structure of acyl-coa dehydrogenase
64	c3kizA	Alignment	not modelled	16.2	24	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide cyclo-ligase; PDBTitle: crystal structure of putative phosphoribosylformylglycinamide cyclo-2 ligase (yp_676759.1) from cytophaga hutchinsonii atcc 33406 at 1.50 a3 resolution
65	c3crqA	Alignment	not modelled	16.0	22	PDB header: transferase Chain: A: PDB Molecule: trna delta(2)-isopentenylpyrophosphate PDBTitle: structure of trna dimethylallyltransferase: rna2 modification through a channel
66	c2yxbA	Alignment	not modelled	16.0	25	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
67	c1wv9B	Alignment	not modelled	15.8	32	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: rhodanese homolog tt1651; PDBTitle: crystal structure of rhodanese homolog tt1651 from an2 extremely thermophilic bacterium thermus thermophilus hb8
68	c1sz1A	Alignment	not modelled	15.6	20	PDB header: transferase/rna Chain: A: PDB Molecule: trna nucleotidyltransferase; PDBTitle: mechanism of cca-adding enzymes specificity revealed by crystal2 structures of ternary complexes
69	c3nojA	Alignment	not modelled	15.6	36	PDB header: lyase Chain: A: PDB Molecule: 4-carboxy-4-hydroxy-2-oxoadipate aldolase/oxaloacetate PDBTitle: the structure of hmg/cha aldolase from the protocatechuate degradation2 pathway of pseudomonas putida
70	c2pfrB	Alignment	not modelled	15.5	22	PDB header: transferase Chain: B: PDB Molecule: arylamine n-acetyltransferase 2; PDBTitle: human n-acetyltransferase 2
71	d2b8ea1	Alignment	not modelled	15.5	21	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
72	c3d9wA	Alignment	not modelled	15.0	25	PDB header: transferase Chain: A: PDB Molecule: putative acetyltransferase; PDBTitle: crystal structure analysis of nocardia farcinica arylamine2 n-acetyltransferase
73	d1p49a	Alignment	not modelled	14.6	13	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
74	d1w4ta1	Alignment	not modelled	13.7	40	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Arylamine N-acetyltransferase
75	c2crlA	Alignment	not modelled	12.7	32	PDB header: chaperone Chain: A: PDB Molecule: copper chaperone for superoxide dismutase; PDBTitle: the apo form of hma domain of copper chaperone for2 superoxide dismutase
76	c3ff4A	Alignment	not modelled	12.3	32	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein chu_1412
77	c3lnbA	Alignment	not modelled	12.1	33	PDB header: transferase Chain: A: PDB Molecule: n-acetyltransferase family protein; PDBTitle: crystal structure analysis of arylamine n-acetyltransferase c from2 bacillus anthracis
78	d1r9la	Alignment	not modelled	12.0	19	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
79	d1zpdal	Alignment	not modelled	11.9	16	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain

						Family: Pyruvate oxidase and decarboxylase, middle domain
80	c3ix9B_	Alignment	not modelled	11.9	19	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrofolate reductase; PDBTitle: crystal structure of streptococcus pneumoniae dihydrofolate2 reductase - sp9 mutant
81	c1cliD_	Alignment	not modelled	11.8	32	PDB header: ligase Chain: D: PDB Molecule: protein (phosphoribosyl-aminoimidazole synthetase); PDBTitle: x-ray crystal structure of aminoimidazole ribonucleotide synthetase2 (purm), from the e. coli purine biosynthetic pathway, at 2.5 a3 resolution
82	d1jcea2	Alignment	not modelled	11.5	29	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
83	d1fe0a_	Alignment	not modelled	11.5	21	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
84	d1xpja_	Alignment	not modelled	11.4	8	Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein VC0232
85	d1xbta1	Alignment	not modelled	11.4	10	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Type II thymidine kinase
86	c2pr7A_	Alignment	not modelled	11.3	11	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase/epoxide hydrolase family; PDBTitle: crystal structure of uncharacterized protein (np_599989.1) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.44 a resolution
87	d2b7oa1	Alignment	not modelled	11.2	46	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class-II DAHP synthetase
88	c3u1nC_	Alignment	not modelled	11.0	10	PDB header: hydrolase Chain: C: PDB Molecule: sam domain and hd domain-containing protein 1; PDBTitle: structure of the catalytic core of human samhd1
89	c2jtaA_	Alignment	not modelled	11.0	22	PDB header: transferase Chain: A: PDB Molecule: phage shock protein e; PDBTitle: rhodanese from e.coli
90	c3fozB_	Alignment	not modelled	11.0	27	PDB header: transferase/rna Chain: B: PDB Molecule: trna delta(2)-isopentenylpyrophosphate transferase; PDBTitle: structure of e. coli isopentenyl-trna transferase in complex with e.2 coli trna(phe)
91	c3fryB_	Alignment	not modelled	11.0	35	PDB header: hydrolase Chain: B: PDB Molecule: probable copper-exporting p-type atpase a; PDBTitle: crystal structure of the copa c-terminal metal binding domain
92	c2i7dB_	Alignment	not modelled	10.9	15	PDB header: hydrolase Chain: B: PDB Molecule: 5'(3')-deoxyribonucleotidase, cytosolic type; PDBTitle: structure of human cytosolic deoxyribonucleotidase in2 complex with deoxyuridine, alf4 and mg2+
93	d1z5ga1	Alignment	not modelled	10.8	21	Fold: HAD-like Superfamily: HAD-like Family: Class B acid phosphatase, AphA
94	c2kmvA_	Alignment	not modelled	10.7	21	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 1; PDBTitle: solution structure of the nucleotide binding domain of the2 human menkes protein in the atp-free form
95	c2v9yA_	Alignment	not modelled	10.7	23	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide cyclo-ligase; PDBTitle: human aminoimidazole ribonucleotide synthetase
96	c2z01A_	Alignment	not modelled	10.7	27	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide cyclo-ligase; PDBTitle: crystal structure of phosphoribosylaminoimidazole2 synthetase from geobacillus kaustophilus
97	d1nlna_	Alignment	not modelled	10.5	13	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Adenain-like
98	d2bsza1	Alignment	not modelled	10.4	27	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Arylamine N-acetyltransferase
99	d1u6za1	Alignment	not modelled	10.3	10	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: Ppx associated domain