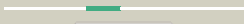
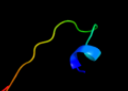
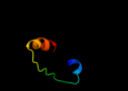
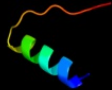
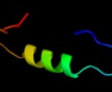
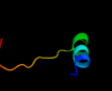


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ltxA_	 Alignment		61.4	19	PDB header: transferase/protein binding Chain: A: PDB Molecule: rab geranylgeranyltransferase alpha subunit; PDBTitle: structure of rab escort protein-1 in complex with rab2 geranylgeranyl transferase and isoprenoid
2	c2j5bA_	 Alignment		48.5	11	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: structure of the tyrosyl trna synthetase from acanthamoeba2 polyphaga mimivirus complexed with tyrosynol
3	c3lubE_	 Alignment		48.4	18	PDB header: hydrolase Chain: E: PDB Molecule: putative creatinine amidohydrolase; PDBTitle: crystal structure of putative creatinine amidohydrolase2 (yp_211512.1) from bacteroides fragilis nctc 9343 at 2.11 a3 resolution
4	c3no4A_	 Alignment		44.3	7	PDB header: hydrolase Chain: A: PDB Molecule: creatinine amidohydrolase; PDBTitle: crystal structure of a creatinine amidohydrolase (npun_f1913) from2 nostoc punctiforme pcc 73102 at 2.00 a resolution
5	d1hrua_	 Alignment		42.8	25	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: YrdC-like
6	d1v7za_	 Alignment		38.1	17	Fold: Creatininase Superfamily: Creatininase Family: Creatininase
7	c1tcvB_	 Alignment		36.1	18	PDB header: transferase Chain: B: PDB Molecule: purine-nucleoside phosphorylase; PDBTitle: crystal structure of the purine nucleoside phosphorylase2 from schistosoma mansoni in complex with non-detergent3 sulfofetaine 195 and acetate
8	c3khsB_	 Alignment		35.9	15	PDB header: hydrolase Chain: B: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of grouper iridovirus purine nucleoside2 phosphorylase
9	c3f6tA_	 Alignment		34.4	15	PDB header: transferase Chain: A: PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of aspartate aminotransferase (e.c. 2.6.1.1)2 (yp_194538.1) from lactobacillus acidophilus ncfm at 2.15 a3 resolution
10	c3cwcB_	 Alignment		26.2	8	PDB header: transferase Chain: B: PDB Molecule: putative glycerate kinase 2; PDBTitle: crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2
11	d1jcua_	 Alignment		25.2	30	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: YrdC-like

12	dlg9sa_	Alignment		23.2	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
13	dlk7ja_	Alignment		20.6	22	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: YrdC-like
14	dlnj8a2	Alignment		20.2	33	Fold: IF3-like Superfamily: C-terminal domain of ProRS Family: C-terminal domain of ProRS
15	c2h3oA_	Alignment		19.4	18	PDB header: membrane protein Chain: A: PDB Molecule: merf; PDBTitle: structure of merft, a membrane protein with two trans-2 membrane helices
16	dljixa_	Alignment		19.2	3	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: beta-Glycosyltransferase (DNA-modifying)
17	c2advB_	Alignment		18.9	31	PDB header: hydrolase Chain: B: PDB Molecule: glutaryl 7- aminocephalosporanic acid acylase; PDBTitle: crystal structures of glutaryl 7-aminocephalosporanic acid acylase:2 mutational study of activation mechanism
18	dlld8da_	Alignment		16.6	33	Fold: alpha-alpha superhelix Superfamily: Protein prenyltransferase Family: Protein prenyltransferase
19	clr6uB_	Alignment		16.3	27	PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of an active fragment of human tryptophanyl-trna2 synthetase with cytokine activity
20	c2cycB_	Alignment		16.3	23	PDB header: ligase Chain: B: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: crystal structure of tyrosyl-trna synthetase complexed with l-tyrosine2 from pyrococcus horikoshii
21	c2b8eB_	Alignment	not modelled	15.6	30	PDB header: membrane protein Chain: B: PDB Molecule: cation-transporting atpase; PDBTitle: copa atp binding domain
22	dlvmka_	Alignment	not modelled	15.4	13	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
23	dlj7ja_	Alignment	not modelled	14.7	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
24	c3ihjA_	Alignment	not modelled	14.6	19	PDB header: transferase Chain: A: PDB Molecule: alanine aminotransferase 2; PDBTitle: human alanine aminotransferase 2 in complex with plp
25	dlnjla2	Alignment	not modelled	14.5	27	Fold: IF3-like Superfamily: C-terminal domain of ProRS Family: C-terminal domain of ProRS
26	c2zy3A_	Alignment	not modelled	14.3	9	PDB header: lyase Chain: A: PDB Molecule: l-aspartate beta-decarboxylase; PDBTitle: dodecameric l-aspartate beta-decarboxylase
27	dlregx_	Alignment	not modelled	14.0	13	Fold: Ferredoxin-like Superfamily: Translational regulator protein regA Family: Translational regulator protein regA
28	dlpq4a_	Alignment	not modelled	13.2	11	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: TroA-like
29	dltuwa_	Alignment	not modelled	13.2	11	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel

						Family: Polyketide synthesis cyclase
30	c2rjnA	Alignment	not modelled	13.1	7	PDB header: hydrolase Chain: A: PDB Molecule: response regulator receiver:metal-dependent PDBTitle: crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
31	d2pi8a1	Alignment	not modelled	12.3	20	Fold: Double psi beta-barrel Superfamily: Barwin-like endoglucanases Family: MLTA-like
32	c3l6gA	Alignment	not modelled	12.2	12	PDB header: glycine betaine-binding protein Chain: A: PDB Molecule: betaine abc transporter permease and substrate binding PDBTitle: crystal structure of lactococcal opuac in its open conformation
33	c2eqaA	Alignment	not modelled	12.2	19	PDB header: rna binding protein Chain: A: PDB Molecule: hypothetical protein st1526; PDBTitle: crystal structure of the hypothetical sua5 protein from2 sulfolobus tokodaii
34	d1jlua	Alignment	not modelled	11.8	25	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
35	d1v4na	Alignment	not modelled	11.7	16	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
36	d3eeqa2	Alignment	not modelled	11.5	13	Fold: CbiG N-terminal domain-like Superfamily: CbiG N-terminal domain-like Family: CbiG N-terminal domain-like
37	d1cb0a	Alignment	not modelled	11.4	15	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
38	d2h6fa1	Alignment	not modelled	10.9	33	Fold: alpha-alpha superhelix Superfamily: Protein prenilyltransferase Family: Protein prenilyltransferase
39	d1pyfa	Alignment	not modelled	10.8	10	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
40	c2cyaA	Alignment	not modelled	10.6	19	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: crystal structure of tyrosyl-trna synthetase from aeropyrum pernix
41	d2dvta1	Alignment	not modelled	10.5	22	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
42	d2ae0x1	Alignment	not modelled	10.4	19	Fold: Double psi beta-barrel Superfamily: Barwin-like endoglucanases Family: MLTA-like
43	d1r6ta2	Alignment	not modelled	10.4	24	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
44	d1a9xb1	Alignment	not modelled	10.3	17	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Carbamoyl phosphate synthetase, small subunit N-terminal domain Family: Carbamoyl phosphate synthetase, small subunit N-terminal domain
45	d1d7ya2	Alignment	not modelled	10.3	15	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
46	d1p3qq	Alignment	not modelled	10.2	14	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: CUE domain
47	d1snna	Alignment	not modelled	10.2	26	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
48	c1fcuA	Alignment	not modelled	10.1	21	PDB header: hydrolase Chain: A: PDB Molecule: hyaluronoglucosaminidase; PDBTitle: crystal structure (trigonal) of bee venom hyaluronidase
49	c3tmgA	Alignment	not modelled	9.9	17	PDB header: transport protein Chain: A: PDB Molecule: glycine betaine, l-proline abc transporter, PDBTitle: crystal structure of glycine betaine, l-proline abc transporter,2 glycine/betaine/l-proline-binding protein (prox) from borrelia3 burgdorferi
50	c1yr3A	Alignment	not modelled	9.8	11	PDB header: transferase Chain: A: PDB Molecule: xanthosine phosphorylase; PDBTitle: escherichia coli purine nucleoside phosphorylase ii, the2 product of the xpa gene
51	c2cybA	Alignment	not modelled	9.6	32	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: crystal structure of tyrosyl-trna synthetase complexed with2 l-tyrosine from archaeoglobus fulgidus
52	d1fcqa	Alignment	not modelled	9.6	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Bee venom hyaluronidase
53	d1iyjb4	Alignment	not modelled	9.4	33	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
54	c2quiB	Alignment	not modelled	9.4	28	PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structures of human tryptophanyl-trna synthetase in2 complex with tryptophanamide and atp PDB header: transport protein

55	c1wazA	Alignment	not modelled	9.3	18	Chain: A: PDB Molecule: merf; PDBTitle: nmr structure determination of the bacterial mercury2 transporter, merf, in micelles
56	d2b8ea1	Alignment	not modelled	9.0	18	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
57	c2yztA	Alignment	not modelled	9.0	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein ttha1756; PDBTitle: crystal structure of uncharacterized conserved protein from thermus2 thermophilus hb8
58	d2g0ia1	Alignment	not modelled	8.8	15	Fold: elF1-like Superfamily: TM1457-like Family: TM1457-like
59	c3ggsA	Alignment	not modelled	8.7	14	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: human purine nucleoside phosphorylase double mutant e201q,n243d2 complexed with 2-fluoro-2'-deoxyadenosine
60	c3ktsA	Alignment	not modelled	8.4	5	PDB header: transcriptional regulator Chain: A: PDB Molecule: glycerol uptake operon antiterminator regulatory protein; PDBTitle: crystal structure of glycerol uptake operon antiterminator regulatory2 protein from listeria monocytogenes str. 4b f2365
61	c2pe4A	Alignment	not modelled	8.4	8	PDB header: hydrolase Chain: A: PDB Molecule: hyaluronidase-1; PDBTitle: structure of human hyaluronidase 1, a hyaluronan hydrolyzing enzyme2 involved in tumor growth and angiogenesis
62	d2o34a1	Alignment	not modelled	8.4	7	Fold: T-fold Superfamily: ApbE-like Family: DVU1097-like
63	c1tnol	Alignment	not modelled	8.3	28	PDB header: transferase Chain: I: PDB Molecule: geranylgeranyltransferase type i alpha subunit; PDBTitle: rat protein geranylgeranyltransferase type-i complexed with2 a ggpp analog and a kkskstkcvim peptide derived from k-3 ras4b
64	d2lfba	Alignment	not modelled	8.2	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
65	d1xdfa1	Alignment	not modelled	8.2	15	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
66	d1ubea1	Alignment	not modelled	8.1	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
67	d1nkt4	Alignment	not modelled	8.1	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
68	c3j08A	Alignment	not modelled	8.1	32	PDB header: hydrolase, metal transport Chain: A: PDB Molecule: copper-exporting p-type atpase a; PDBTitle: high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
69	c3hbcA	Alignment	not modelled	7.9	32	PDB header: hydrolase Chain: A: PDB Molecule: choloylglycine hydrolase; PDBTitle: crystal structure of choloylglycine hydrolase from bacteroides2 thetaiotaomicron vpi
70	d1fl2a2	Alignment	not modelled	7.7	14	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
71	c3kdvB	Alignment	not modelled	7.5	35	PDB header: dna binding protein Chain: B: PDB Molecule: dna damage response b protein; PDBTitle: crystal structure of dna damage response b (ddrb) from deinococcus2 geothermalis
72	c3iraA	Alignment	not modelled	7.4	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein; PDBTitle: the crystal structure of one domain of the conserved protein from2 methanosarcina mazei go1
73	c3m8yC	Alignment	not modelled	7.3	23	PDB header: isomerase Chain: C: PDB Molecule: phosphopentomutase; PDBTitle: phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
74	d1t6ia1	Alignment	not modelled	7.0	35	Fold: DNA clamp Superfamily: DNA clamp Family: DNA polymerase processivity factor
75	d1mkya3	Alignment	not modelled	7.0	13	Fold: Alpha-lytic protease prodomain-like Superfamily: Probable GTPase Der, C-terminal domain Family: Probable GTPase Der, C-terminal domain
76	d1xhca2	Alignment	not modelled	6.9	10	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
77	c2ip1A	Alignment	not modelled	6.8	24	PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure analysis of s. cerevisiae tryptophanyl trna2 synthetase
78	c3bgwD	Alignment	not modelled	6.8	10	PDB header: replication Chain: D: PDB Molecule: dnab-like replicative helicase; PDBTitle: the structure of a dnab-like replicative helicase and its interactions2 with primase
79	d1qgna	Alignment	not modelled	6.8	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
80	d1dcea1	Alignment	not modelled	6.7	33	Fold: alpha-alpha superhelix Superfamily: Protein prenyltransferase

					Family: Protein prenyltransferase
81	d1gm5a4	Alignment	not modelled	6.5	6 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
82	c3hh1D	Alignment	not modelled	6.5	21 PDB header: transferase Chain: D: PDB Molecule: tetrapyrrole methylase family protein; PDBTitle: the structure of a tetrapyrrole methylase family protein domain from2 chlorobium tepidum t1s
83	d1iuqa	Alignment	not modelled	6.5	17 Fold: Glycerol-3-phosphate (1)-acyltransferase Superfamily: Glycerol-3-phosphate (1)-acyltransferase Family: Glycerol-3-phosphate (1)-acyltransferase
84	c2dhyA	Alignment	not modelled	6.5	12 PDB header: immune system Chain: A: PDB Molecule: cue domain-containing protein 1; PDBTitle: solution structure of the cue domain in the human cue2 domain containing protein 1 (cuedc1)
85	d1a3ca	Alignment	not modelled	6.4	10 Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
86	c2ogxB	Alignment	not modelled	6.3	12 PDB header: metal binding protein Chain: B: PDB Molecule: molybdenum storage protein subunit beta; PDBTitle: the crystal structure of the molybdenum storage protein from2 azotobacter vinelandii loaded with polyoxotungstates (wsto)
87	d1fa2a	Alignment	not modelled	6.3	18 Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
88	d1vdca2	Alignment	not modelled	6.3	7 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
89	d1uyra1	Alignment	not modelled	6.3	13 Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
90	c3focB	Alignment	not modelled	6.2	14 PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: tryptophanyl-trna synthetase from giardia lamblia
91	d1vzya2	Alignment	not modelled	6.1	20 Fold: HSP33 redox switch-like Superfamily: HSP33 redox switch-like Family: HSP33 redox switch-like
92	c3ie5A	Alignment	not modelled	6.1	18 PDB header: plant protein, biosynthetic protein Chain: A: PDB Molecule: phenolic oxidative coupling protein hyp-1; PDBTitle: crystal structure of hyp-1 protein from hypericum perforatum2 (st john's wort) involved in hypericin biosynthesis
93	d3bgsa1	Alignment	not modelled	6.1	12 Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
94	d1e09a	Alignment	not modelled	6.1	15 Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
95	c3hv0A	Alignment	not modelled	6.1	31 PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: tryptophanyl-trna synthetase from cryptosporidium parvum
96	c1w8xP	Alignment	not modelled	6.0	29 PDB header: virus Chain: P: PDB Molecule: protein p16; PDBTitle: structural analysis of prd1
97	d1fm4a	Alignment	not modelled	6.0	8 Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
98	d1vla2	Alignment	not modelled	6.0	8 Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: NeuB-like
99	d1u94a1	Alignment	not modelled	5.9	11 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)