
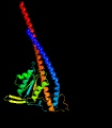
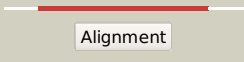

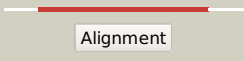
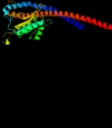
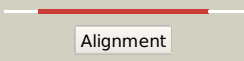
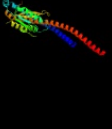
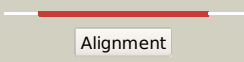

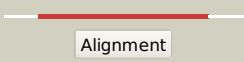

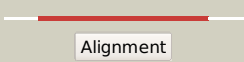

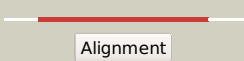

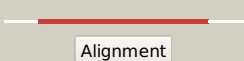

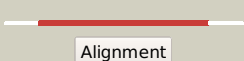
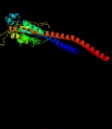
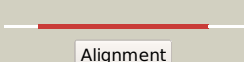

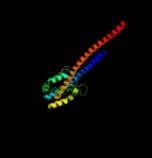
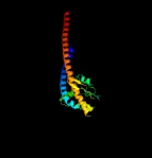

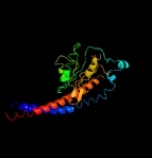
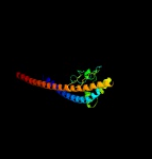
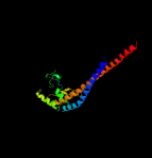
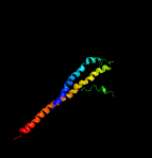
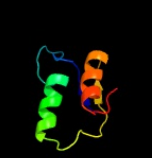



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1309_(atpG)_1464890_1465807
 Date Wed Jul 31 22:05:40 BST 2019
 Unique Job ID 5cf4a56db2a5ba84

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6fkig_	 Alignment		100.0	36	PDB header: membrane protein Chain: G; PDB Molecule: atp synthase subunit c, chloroplastic; PDBTitle: chloroplast f1fo conformation 3
2	c30aaO_	 Alignment		100.0	35	PDB header: hydrolase/transport protein Chain: O; PDB Molecule: atp synthase gamma chain; PDBTitle: structure of the e.coli f1-atp synthase inhibited by subunit epsilon
3	c6q45G_	 Alignment		100.0	35	PDB header: hydrolase Chain: G; PDB Molecule: atp synthase gamma chain; PDBTitle: f1-atpase from fusobacterium nucleatum
4	c5dn6G_	 Alignment		100.0	37	PDB header: hydrolase Chain: G; PDB Molecule: atp synthase gamma chain; PDBTitle: atp synthase from paracoccus denitrificans
5	c6re1S_	 Alignment		100.0	27	PDB header: proton transport Chain: S; PDB Molecule: atp synthase gamma chain, mitochondrial; PDBTitle: cryo-em structure of polytomella f-atp synthase, rotary substate 2a,2 focussed refinement of f1 head and rotor
6	c2w6hG_	 Alignment		100.0	31	PDB header: hydrolase Chain: G; PDB Molecule: atp synthase subunit gamma, mitochondrial; PDBTitle: low resolution structures of bovine mitochondrial f1-atpase during2 controlled dehydration: hydration state 4a.
7	c5lqxG_	 Alignment		100.0	30	PDB header: hydrolase Chain: G; PDB Molecule: atp synthase gamma subunit; PDBTitle: structure of f-atpase from pichia angusta, state3
8	c6f5dG_	 Alignment		100.0	21	PDB header: hydrolase Chain: G; PDB Molecule: atp synthase gamma subunit; PDBTitle: trypanosoma brucei f1-atpase
9	c2xokG_	 Alignment		100.0	27	PDB header: hydrolase Chain: G; PDB Molecule: atp synthase subunit gamma, mitochondrial; PDBTitle: refined structure of yeast f1c10 atpase complex to 3 a resolution
10	c4xd7G_	 Alignment		100.0	41	PDB header: hydrolase Chain: G; PDB Molecule: atp synthase gamma chain; PDBTitle: structure of thermophilic f1-atpase inhibited by epsilon subunit
11	c5zwlG_	 Alignment		100.0	35	PDB header: hydrolase Chain: G; PDB Molecule: atp synthase gamma chain; PDBTitle: crystal structure of the gamma - epsilon complex of photosynthetic2 cyanobacterial f1-atpase

12	c6focG_	Alignment		100.0	88	PDB header: hydrolase Chain: G; PDB Molecule: atp synthase gamma chain; PDBTitle: f1-atpase from mycobacterium smegmatis
13	d2jdjg1	Alignment		100.0	43	Fold: Pyruvate kinase C-terminal domain-like Superfamily: ATP synthase (F1-ATPase), gamma subunit Family: ATP synthase (F1-ATPase), gamma subunit
14	d1fs0g_	Alignment		100.0	33	Fold: Pyruvate kinase C-terminal domain-like Superfamily: ATP synthase (F1-ATPase), gamma subunit Family: ATP synthase (F1-ATPase), gamma subunit
15	c2qe7G_	Alignment		100.0	39	PDB header: hydrolase Chain: G; PDB Molecule: atp synthase subunit gamma; PDBTitle: crystal structure of the f1-atpase from the thermoalkaliphilic bacterium bacillus sp. ta2.a1
16	c2w6jG_	Alignment		100.0	45	PDB header: hydrolase Chain: G; PDB Molecule: atp synthase subunit gamma, mitochondrial; PDBTitle: low resolution structures of bovine mitochondrial f1-atpase during controlled dehydration: hydration state 5.
17	c3fksY_	Alignment		100.0	33	PDB header: hydrolase Chain: Y; PDB Molecule: atp synthase subunit gamma, mitochondrial; PDBTitle: yeast f1 atpase in the absence of bound nucleotides
18	d1mabg_	Alignment		100.0	44	Fold: Pyruvate kinase C-terminal domain-like Superfamily: ATP synthase (F1-ATPase), gamma subunit Family: ATP synthase (F1-ATPase), gamma subunit
19	c3re1B_	Alignment		68.0	19	PDB header: lyase Chain: B; PDB Molecule: uroporphyrinogen-iii synthetase; PDBTitle: crystal structure of uroporphyrinogen iii synthase from pseudomonas2 syringae pv. tomato dc3000
20	c4es6A_	Alignment		52.3	23	PDB header: lyase Chain: A; PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: crystal structure of hemd (pa5259) from pseudomonas aeruginosa (pao1)2 at 2.22 a resolution
21	c3k8vB_	Alignment	not modelled	50.8	19	PDB header: structural protein Chain: B; PDB Molecule: flagellin homolog; PDBTitle: crysatl structure of a bacterial cell-surface flagellin n20c20
22	d1wd7a_	Alignment	not modelled	49.3	14	Fold: HemD-like Superfamily: HemD-like Family: HemD-like
23	c3gitA_	Alignment	not modelled	45.0	21	PDB header: transferase Chain: A; PDB Molecule: carbon monoxide dehydrogenase/acetyl-coa synthase subunit PDBTitle: crystal structure of a truncated acetyl-coa synthase
24	d1ru3a_	Alignment	not modelled	44.8	23	Fold: Prismane protein-like Superfamily: Prismane protein-like Family: Acetyl-CoA synthase
25	d1oaoc_	Alignment	not modelled	41.2	21	Fold: Prismane protein-like Superfamily: Prismane protein-like Family: Acetyl-CoA synthase
26	c3d8tB_	Alignment	not modelled	35.1	14	PDB header: lyase Chain: B; PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: thermus thermophilus uroporphyrinogen iii synthase
27	c5vayF_	Alignment	not modelled	33.1	28	PDB header: apoptosis Chain: F; PDB Molecule: beclin-1; PDBTitle: bcl-2 complex with beclin 1 t108d bh3 domain
28	c5vayE_	Alignment	not modelled	33.1	28	PDB header: apoptosis Chain: E; PDB Molecule: beclin-1; PDBTitle: bcl-2 complex with beclin 1 t108d bh3 domain
29	c5vaxE_	Alignment	not modelled	33.1	28	PDB header: apoptosis Chain: E; PDB Molecule: beclin-1;

						PDBTitle: bcl-2 complex with beclin 1 bh3 domain
30	c6dcoD_	Alignment	not modelled	30.3	28	PDB header: apoptosis Chain: D: PDB Molecule: beclin-1; PDBTitle: bcl-xl complex with beclin 1 bh3 domain t108d
31	c5vb4D_	Alignment	not modelled	30.1	28	PDB header: apoptosis Chain: D: PDB Molecule: beclin-1; PDBTitle: bcl-xl complex with beclin 1 bh3 domain t108d
32	c5vaxG_	Alignment	not modelled	30.0	28	PDB header: apoptosis Chain: G: PDB Molecule: beclin-1; PDBTitle: bcl-2 complex with beclin 1 bh3 domain
33	c5vauF_	Alignment	not modelled	28.7	28	PDB header: apoptosis Chain: F: PDB Molecule: beclin-1; PDBTitle: bcl-2 complex with beclin 1 bh3 domain
34	d1qw2a_	Alignment	not modelled	27.9	23	Fold: Hypothetical protein Ta1206 Superfamily: Hypothetical protein Ta1206 Family: Hypothetical protein Ta1206
35	c6hr5A_	Alignment	not modelled	27.1	20	PDB header: hydrolase Chain: A: PDB Molecule: alpha-l-rhamnosidase/sulfatase (gh78); PDBTitle: structure of the s1_25 family sulfatase module of the rhamnosidase2 fa22250 from formosa agariphila
36	c2p1B_	Alignment	not modelled	26.3	28	PDB header: apoptosis Chain: B: PDB Molecule: beclin 1; PDBTitle: structure of the bcl-xl:beclin 1 complex
37	c2p1F_	Alignment	not modelled	26.3	28	PDB header: apoptosis Chain: F: PDB Molecule: beclin 1; PDBTitle: structure of the bcl-xl:beclin 1 complex
38	c2p1D_	Alignment	not modelled	26.3	28	PDB header: apoptosis Chain: D: PDB Molecule: beclin 1; PDBTitle: structure of the bcl-xl:beclin 1 complex
39	c2p1H_	Alignment	not modelled	26.3	28	PDB header: apoptosis Chain: H: PDB Molecule: beclin 1; PDBTitle: structure of the bcl-xl:beclin 1 complex
40	c5vauE_	Alignment	not modelled	25.0	28	PDB header: apoptosis Chain: E: PDB Molecule: beclin-1; PDBTitle: bcl-2 complex with beclin 1 bh3 domain
41	c5vaxF_	Alignment	not modelled	25.0	28	PDB header: apoptosis Chain: F: PDB Molecule: beclin-1; PDBTitle: bcl-2 complex with beclin 1 bh3 domain
42	c5vaxH_	Alignment	not modelled	25.0	28	PDB header: apoptosis Chain: H: PDB Molecule: beclin-1; PDBTitle: bcl-2 complex with beclin 1 bh3 domain
43	c3v47D_	Alignment	not modelled	24.0	23	PDB header: immune system Chain: D: PDB Molecule: flagellin; PDBTitle: crystal structure of the n-terminal fragment of zebrafish tir5 in2 complex with salmonella flagellin
44	d1sfea2	Alignment	not modelled	23.7	50	Fold: Ribonuclease H-like motif Superfamily: Methylated DNA-protein cysteine methyltransferase domain Family: Methylated DNA-protein cysteine methyltransferase domain
45	c2zktB_	Alignment	not modelled	22.2	18	PDB header: isomerase Chain: B: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: structure of ph0037 protein from pyrococcus horikoshii
46	c3dvuD_	Alignment	not modelled	21.8	28	PDB header: viral protein/apoptosis Chain: D: PDB Molecule: beclin-1; PDBTitle: crystal structure of the complex of murine gamma-herpesvirus 68 bcl-22 homolog m11 and the beclin 1 bh3 domain
47	c5gz5A_	Alignment	not modelled	21.5	15	PDB header: hydrolase Chain: A: PDB Molecule: snake venom phosphodiesterase (pde); PDBTitle: crystal structure of snake venom phosphodiesterase (pde) from taiwan2 cobra (naja atra atra) in complex with amp
48	c3m8yC_	Alignment	not modelled	21.3	23	PDB header: isomerase Chain: C: PDB Molecule: phosphopentomutase; PDBTitle: phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
49	c3lzcA_	Alignment	not modelled	21.1	23	PDB header: biosynthetic protein Chain: A: PDB Molecule: dph2; PDBTitle: crystal structure of dph2 from pyrococcus horikoshii
50	d2fefa1	Alignment	not modelled	20.0	42	Fold: Bromodomain-like Superfamily: PA2201 N-terminal domain-like Family: PA2201 N-terminal domain-like
51	c3dvuC_	Alignment	not modelled	19.8	28	PDB header: viral protein/apoptosis Chain: C: PDB Molecule: beclin-1; PDBTitle: crystal structure of the complex of murine gamma-herpesvirus 68 bcl-22 homolog m11 and the beclin 1 bh3 domain
52	d2pk8a1	Alignment	not modelled	18.9	31	Fold: Hypothetical protein PF0899 Superfamily: Hypothetical protein PF0899 Family: Hypothetical protein PF0899
53	c5gz4A_	Alignment	not modelled	18.8	15	PDB header: hydrolase Chain: A: PDB Molecule: snake venom phosphodiesterase (pde); PDBTitle: crystal structure of snake venom phosphodiesterase (pde) from taiwan2 cobra (naja atra atra)
54	c5i5fA_	Alignment	not modelled	18.8	12	PDB header: membrane protein Chain: A: PDB Molecule: inner membrane protein yejm; PDBTitle: salmonella global domain 191
55	c2kiIA_	Alignment	not modelled	18.6	14	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: nmr structure of the h103g mutant so2144 h-nox domain from2 shewanella oneidensis in the fe(ii)co ligation state
						PDB header: dna binding protein Chain: C: PDB Molecule: suppressor of hu sensitivity involved in

56	c5xynC_	Alignment	not modelled	17.9	17	recombination PDBTitle: the crystal structure of csm2-psy3-shu1-shu2 complex from budding2 yeast
57	d1o98a2	Alignment	not modelled	17.8	13	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain
58	c2qzuA_	Alignment	not modelled	17.5	10	PDB header: hydrolase Chain: A: PDB Molecule: putative sulfatase yidj; PDBTitle: crystal structure of the putative sulfatase yidj from bacteroides2 fragilis. northeast structural genomics consortium target bfr123
59	c4b56A_	Alignment	not modelled	16.7	17	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: structure of ectonucleotide pyrophosphatase-phosphodiesterase-12 (npp1)
60	c1pqrA_	Alignment	not modelled	16.4	71	PDB header: toxin Chain: A: PDB Molecule: alpha-a-conotoxin eiva; PDBTitle: solution conformation of alphaa-conotoxin eiva
61	d1lauka	Alignment	not modelled	15.9	15	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
62	d1q77a_	Alignment	not modelled	15.8	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
63	c3opyB_	Alignment	not modelled	15.8	16	PDB header: transferase Chain: B: PDB Molecule: 6-phosphofructo-1-kinase beta-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
64	c3opyH_	Alignment	not modelled	15.8	16	PDB header: transferase Chain: H: PDB Molecule: 6-phosphofructo-1-kinase beta-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
65	c6c02B_	Alignment	not modelled	15.6	7	PDB header: hydrolase Chain: B: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: human ectonucleotide pyrophosphatase / phosphodiesterase 3 (enpp3,2 npp3, cd203c, inactive (t205a), n594s, with alpha,beta-methylene-atp3 (ampcpp)
66	c2dq2D_	Alignment	not modelled	15.4	14	PDB header: protein binding Chain: D: PDB Molecule: apolipoprotein a-i binding protein; PDBTitle: crystal structure of mouse apolipoprotein a-i binding protein
67	c3q3qA_	Alignment	not modelled	15.3	13	PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase; PDBTitle: crystal structure of spap: an novel alkaline phosphatase from2 bacterium sphingomonas sp. strain bsar-1
68	c4fdiA_	Alignment	not modelled	15.1	19	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylgalactosamine-6-sulfatase; PDBTitle: the molecular basis of mucopolysaccharidosis iv a
69	c3ed4A_	Alignment	not modelled	14.7	33	PDB header: transferase Chain: A: PDB Molecule: arylsulfatase; PDBTitle: crystal structure of putative arylsulfatase from escherichia coli
70	d1fsua_	Alignment	not modelled	14.6	11	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
71	c4ug4H_	Alignment	not modelled	14.4	10	PDB header: hydrolase Chain: H: PDB Molecule: choline sulfatase; PDBTitle: crystal structure of a choline sulfatase from sinorhizobium2 melliloti
72	c3o3xA_	Alignment	not modelled	14.2	24	PDB header: viral protein Chain: A: PDB Molecule: gp41-5; PDBTitle: crystal structure of gp41-5, a single-chain 5-helix-bundle based on2 hiv gp41
73	c3b5qB_	Alignment	not modelled	13.7	12	PDB header: hydrolase Chain: B: PDB Molecule: putative sulfatase yidj; PDBTitle: crystal structure of a putative sulfatase (np_810509.1) from2 bacteroides thetaiotaomicron vpi-5482 at 2.40 a resolution
74	c2ponA_	Alignment	not modelled	13.0	28	PDB header: apoptosis inhibitor Chain: A: PDB Molecule: beclin-1; PDBTitle: solution structure of the bcl-xl/beclin-1 complex
75	c5jp6A_	Alignment	not modelled	12.3	22	PDB header: hydrolase Chain: A: PDB Molecule: putative polysaccharide deacetylase; PDBTitle: bdellovibrio bacteriovorus peptidoglycan deacetylase bd3279
76	d2gqfa1	Alignment	not modelled	12.2	57	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
77	d1kxpd3	Alignment	not modelled	12.2	26	Fold: Serum albumin-like Superfamily: Serum albumin-like Family: Serum albumin-like
78	c3lxqB_	Alignment	not modelled	12.1	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein vp1736; PDBTitle: the crystal structure of a protein in the alkaline phosphatase2 superfamily from vibrio parahaemolyticus to 1.95a
79	d1m2da_	Alignment	not modelled	12.0	24	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioredoxin-like 2Fe-2S ferredoxin
80	c2w8dB_	Alignment	not modelled	11.8	7	PDB header: transferase Chain: B: PDB Molecule: processed glycerol phosphate lipoteichoic acid synthase 2; PDBTitle: distinct and essential morphogenic functions for wall-and2 lipo-teichoic acids in bacillus subtilis
81	c2iucB_	Alignment	not modelled	11.8	17	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase;

81	c2iucB	Alignment	not modelled	11.8	17	PDBTitle: structure of alkaline phosphatase from the antarctic bacterium tab5 PDB header: hydrolase
82	c2xrgA	Alignment	not modelled	11.7	18	Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: crystal structure of autotaxin (enpp2) in complex with the2 ha155 boronic acid inhibitor
83	c5xhbA	Alignment	not modelled	11.7	45	PDB header: immune system Chain: A: PDB Molecule: nisin immunity protein; PDBTitle: crystal structure of the full length of nisi in a lipid free form, the2 nisin immunity protein, from lactococcus lactis
84	d1hdha	Alignment	not modelled	11.3	15	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
85	c4oydB	Alignment	not modelled	11.2	25	PDB header: viral protein/inhibitor Chain: B: PDB Molecule: computationally designed inhibitor; PDBTitle: crystal structure of a computationally designed inhibitor of an2 epstein-barr viral bcl-2 protein
86	d1p49a	Alignment	not modelled	11.1	14	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
87	c2m6rA	Alignment	not modelled	10.6	19	PDB header: electron transport Chain: A: PDB Molecule: flavodoxin; PDBTitle: apo_yqca
88	c3k8wA	Alignment	not modelled	10.4	20	PDB header: structural protein Chain: A: PDB Molecule: flagellin homolog; PDBTitle: crysatl structure of a bacterial cell-surface flagellin n20c45
89	c2xr9A	Alignment	not modelled	10.3	15	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: crystal structure of autotaxin (enpp2)
90	c3o8nA	Alignment	not modelled	10.1	15	PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase, muscle type; PDBTitle: structure of phosphofructokinase from rabbit skeletal muscle
91	d1v10a3	Alignment	not modelled	10.1	60	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
92	d2i09a1	Alignment	not modelled	10.1	18	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: DeoB catalytic domain-like
93	d1i5oa	Alignment	not modelled	10.0	18	Fold: Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) Superfamily: Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) Family: Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
94	c2jmKA	Alignment	not modelled	9.8	22	PDB header: protein binding Chain: A: PDB Molecule: hypothetical protein ta0956; PDBTitle: solution structure of ta0956
95	c1ihqA	Alignment	not modelled	9.7	31	PDB header: de novo protein Chain: A: PDB Molecule: chimeric peptide glytm1bzip: tropomyosin alpha PDBTitle: glytm1bzip: a chimeric peptide model of the n-terminus of a2 rat short alpha tropomyosin with the n-terminus encoded by3 exon 1b
96	c4uplC	Alignment	not modelled	9.6	14	PDB header: hydrolase Chain: C: PDB Molecule: sulfatase family protein; PDBTitle: dimeric sulfatase spas2 from silicibacter pomeroyi
97	c5fqIA	Alignment	not modelled	9.5	12	PDB header: hydrolase Chain: A: PDB Molecule: iduronate-2-sulfatase; PDBTitle: insights into hunter syndrome from the structure of iduronate-2-2 sulfatase
98	c3opyG	Alignment	not modelled	9.5	13	PDB header: transferase Chain: G: PDB Molecule: 6-phosphofructo-1-kinase alpha-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
99	d1j33a	Alignment	not modelled	9.4	21	Fold: Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) Superfamily: Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) Family: Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)