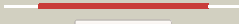



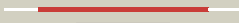














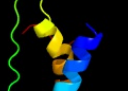




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2207_(cobT)_2471419_2472504
Date	Mon Aug 5 13:25:33 BST 2019
Unique Job ID	d5a984a7b3155d45

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1l5oa_	 Alignment		100.0	34	Fold: Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) Superfamily: Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) Family: Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
2	d1j33a_	 Alignment		100.0	50	Fold: Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) Superfamily: Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) Family: Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
3	c6b5fB_	 Alignment		100.0	35	PDB header: transferase Chain: B: PDB Molecule: nicotinate-nucleotide--dimethylbenzimidazole PDBTitle: crystal structure of nicotinate mononucleotide-5,6-2 dimethylbenzimidazole phosphoribosyltransferase cobt from yersinia3 enterocolitica
4	c4hdnA_	 Alignment		100.0	35	PDB header: transferase Chain: A: PDB Molecule: arsa; PDBTitle: crystal structure of arsa in the substrate-free state.
5	c4hdnB_	 Alignment		100.0	34	PDB header: transferase Chain: B: PDB Molecule: arsb; PDBTitle: crystal structure of arsa in the substrate-free state.
6	c3l0zC_	 Alignment		100.0	19	PDB header: transferase Chain: C: PDB Molecule: putative nicotinate-nucleotide-dimethylbenzimidazole PDBTitle: crystal structure of a putative nicotinate-nucleotide-2 dimethylbenzimidazole phosphoribosyltransferase from3 methanocaldococcus jannaschii dsm 2661
7	c3u4gA_	 Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: namn:dmb phosphoribosyltransferase; PDBTitle: the structure of cobt from pyrococcus horikoshii
8	c4fwvA_	 Alignment		87.4	16	PDB header: hydrolase Chain: A: PDB Molecule: ttc1975 peptidase; PDBTitle: crystal structure of the n-terminal domain of the lon-like protease2 mtalonc
9	d1htwa_	 Alignment		63.4	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: YjeE-like
10	c6fpeE_	 Alignment		48.2	17	PDB header: rna binding protein Chain: E: PDB Molecule: atpase yjee, predicted to have essential role in cell wall PDBTitle: bacterial protein complex
11	c6qell_	 Alignment		46.3	20	PDB header: replication Chain: L: PDB Molecule: dna replication protein dnac; PDBTitle: e. coli dnabc apo complex

12	c5c3cB_	Alignment		46.0	14	PDB header: protein binding Chain: B: PDB Molecule: cbbq/nirq/norq domain protein; PDBTitle: structural characterization of a newly identified component of alpha-2 carboxisomes: the aaa+ domain protein cso-cbbq
13	c2zktB_	Alignment		43.4	16	PDB header: isomerase Chain: B: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: structure of ph0037 protein from pyrococcus horikoshii
14	c5mvrA_	Alignment		41.6	24	PDB header: transferase Chain: A: PDB Molecule: trna threonylcarbamoyladenosine biosynthesis protein tsae; PDBTitle: crystal structure of bacillus subtilus ydib
15	c2c99A_	Alignment		38.5	11	PDB header: transcription regulation Chain: A: PDB Molecule: psp operon transcriptional activator; PDBTitle: structural basis of the nucleotide driven conformational2 changes in the aaa domain of transcription activator pspf
16	c4ww4A_	Alignment		35.9	24	PDB header: hydrolase Chain: A: PDB Molecule: rvub-like 1; PDBTitle: double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
17	c4gvgB_	Alignment		35.5	16	PDB header: hydrolase Chain: B: PDB Molecule: beta-hexosaminidase; PDBTitle: crystal structure of salmonella typhimurium family 3 glycoside2 hydrolase (nagz)
18	c2re2A_	Alignment		35.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein ta1041; PDBTitle: crystal structure of a putative iron-molybdenum cofactor (femo-co)2 dinitrogenase (ta1041m) from thermoplasma acidophilum dsm 1728 at3 1.30 a resolution
19	d1g41a_	Alignment		34.8	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
20	c5bq5A_	Alignment		33.6	18	PDB header: atp-binding protein Chain: A: PDB Molecule: insertion sequence is5376 putative atp-binding protein; PDBTitle: crystal structure of the istb aaa+ domain bound to adp-bef3
21	c3b5qB_	Alignment	not modelled	32.8	25	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
22	c3tqfA_	Alignment	not modelled	31.5	25	PDB header: transferase, hydrolase Chain: A: PDB Molecule: hpr(ser) kinase; PDBTitle: structure of the hpr(ser) kinase/phosphatase from coxiella burnetii
23	c6qi8E_	Alignment	not modelled	31.4	31	PDB header: chaperone Chain: E: PDB Molecule: rvub-like 2; PDBTitle: truncated human r2tp complex, structure 3 (adp-filled)
24	c5he8J_	Alignment	not modelled	29.5	18	PDB header: protein binding Chain: J: PDB Molecule: helicase loader; PDBTitle: bacterial initiation protein
25	c4uopB_	Alignment	not modelled	28.2	22	PDB header: transferase Chain: B: PDB Molecule: lipoteichoic acid primase; PDBTitle: crystal structure of the lipoteichoic acid synthase ltap from listeria2 monocytogenes
26	c5k4pA_	Alignment	not modelled	27.5	17	PDB header: transferase Chain: A: PDB Molecule: probable phosphatidylethanolamine transferase mcr-1; PDBTitle: catalytic domain of mcr-1 phosphoethanolamine transferase
27	c3ed4A_	Alignment	not modelled	27.1	19	PDB header: transferase Chain: A: PDB Molecule: arylsulfatase; PDBTitle: crystal structure of putative arylsulfatase from escherichia coli
28	c2c9oC_	Alignment	not modelled	27.0	24	PDB header: hydrolase Chain: C: PDB Molecule: rvub-like 1; PDBTitle: 3d structure of the human rvub-like helicase rvub1l
						Fold: P-loop containing nucleoside triphosphate hydrolases

29	d1g6oa_	Alignment	not modelled	26.9	19	Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
30	c3k6jA_	Alignment	not modelled	26.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: protein f01g10.3, confirmed by transcript evidence; PDBTitle: crystal structure of the dehydrogenase part of multifunctional enzyme 12 from c.elegans
31	d1kkma_	Alignment	not modelled	25.9	42	Fold: PEP carboxykinase-like Superfamily: PEP carboxykinase-like Family: HPr kinase HprK C-terminal domain
32	c6c02B_	Alignment	not modelled	25.8	14	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)
33	c4ug4H_	Alignment	not modelled	25.1	17	PDB header: hydrolase Chain: H: PDB Molecule: choline sulfatase; PDBTitle: crystal structure of a choline sulfatase from sinorhizobium2 melliloti
34	d2tpta2	Alignment	not modelled	25.0	21	Fold: Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain Family: Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
35	c2qmhK_	Alignment	not modelled	24.9	42	PDB header: transferase Chain: K: PDB Molecule: hpr kinase/phosphorylase; PDBTitle: structure of v267f mutant hprk/p
36	d1hdha_	Alignment	not modelled	24.8	14	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
37	c5gz4A_	Alignment	not modelled	24.8	14	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)
38	c1ojfF_	Alignment	not modelled	24.7	27	PDB header: response regulator Chain: F: PDB Molecule: transcriptional regulatory protein zrar; PDBTitle: crystal structure of a sigma54-activator suggests the mechanism for2 the conformational switch necessary for sigma54 binding
39	d1ko7a2	Alignment	not modelled	24.5	42	Fold: PEP carboxykinase-like Superfamily: PEP carboxykinase-like Family: HPr kinase HprK C-terminal domain
40	c4upiA_	Alignment	not modelled	23.9	19	PDB header: hydrolase Chain: A: PDB Molecule: sulfatase family protein; PDBTitle: dimeric sulfatase spas1 from silicibacter pomeroyi
41	c2qzuA_	Alignment	not modelled	23.8	19	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
42	c4uorK_	Alignment	not modelled	23.6	19	PDB header: transferase Chain: K: PDB Molecule: lipoteichoic acid synthase; PDBTitle: structure of lipoteichoic acid synthase ltas from listeria2 monocytogenes in complex with glycerol phosphate
43	c3rb8A_	Alignment	not modelled	23.5	9	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: structure of the phage tubulin phuz(semet)-gdp
44	c2w8dB_	Alignment	not modelled	23.3	17	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
45	c4uplC_	Alignment	not modelled	23.1	14	PDB header: hydrolase Chain: C: PDB Molecule: sulfatase family protein; PDBTitle: dimeric sulfatase spas2 from silicibacter pomeroyi
46	c5i5fA_	Alignment	not modelled	23.0	12	PDB header: membrane protein Chain: A: PDB Molecule: inner membrane protein yejm; PDBTitle: salmonella global domain 191
47	c6b8vA_	Alignment	not modelled	23.0	27	PDB header: transferase Chain: A: PDB Molecule: adenylsulfate kinase; PDBTitle: crystal structure of adenylyl-sulfate kinase from cryptococcus2 neoformans
48	c3lmaC_	Alignment	not modelled	22.8	23	PDB header: membrane protein Chain: C: PDB Molecule: stage v sporulation protein ad (spovad); PDBTitle: crystal structure of the stage v sporulation protein ad (spovad) from2 bacillus licheniformis. northeast structural genomics consortium3 target bir6.
49	c5u9zB_	Alignment	not modelled	22.5	47	PDB header: transferase Chain: B: PDB Molecule: phosphoglycerol transferase; PDBTitle: phosphoglycerol transferase gach from streptococcus pyogenes
50	c5fqIA_	Alignment	not modelled	22.5	22	PDB header: hydrolase Chain: A: PDB Molecule: iduronate-2-sulfatase; PDBTitle: insights into hunter syndrome from the structure of iduronate-2-2 sulfatase
51	c6a82A_	Alignment	not modelled	22.2	33	PDB header: transferase Chain: A: PDB Molecule: phosphoethanolamine transferase eptc; PDBTitle: crystal structure of the c-terminal periplasmic domain of eceptc from2 escherichia coli
52	c4fdiA_	Alignment	not modelled	22.1	11	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylgalactosamine-6-sulfatase; PDBTitle: the molecular basis of mucopolysaccharidosis iv a
						PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide

53	c4b56A	Alignment	not modelled	21.7	14	pyrophosphatase/phosphodiesterase family PDBTitle: structure of ectonucleotide pyrophosphatase-phosphodiesterase-12 (npp1)
54	d2fywa1	Alignment	not modelled	21.7	38	Fold: NIF3 (NGG1p interacting factor 3)-like Superfamily: NIF3 (NGG1p interacting factor 3)-like Family: NIF3 (NGG1p interacting factor 3)-like
55	d1l8qa2	Alignment	not modelled	21.6	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
56	c3co5B	Alignment	not modelled	21.3	19	PDB header: transcription regulator Chain: B: PDB Molecule: putative two-component system transcriptional response PDBTitle: crystal structure of sigma-54 interaction domain of putative2 transcriptional response regulator from neisseria gonorrhoeae
57	d1p49a	Alignment	not modelled	21.3	14	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
58	c3gh1A	Alignment	not modelled	21.0	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted nucleotide-binding protein; PDBTitle: crystal structure of predicted nucleotide-binding protein from vibrio2 cholerae
59	c3bq9A	Alignment	not modelled	21.0	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted rossmann fold nucleotide-binding domain- PDBTitle: crystal structure of predicted nucleotide-binding protein from2 idiomarina baltica os145
60	c3fdiA	Alignment	not modelled	20.8	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein from eubacterium2 ventriosum atcc 27560.
61	c5ep4A	Alignment	not modelled	20.7	22	PDB header: transcription Chain: A: PDB Molecule: putative repressor protein luxo; PDBTitle: structure, regulation, and inhibition of the quorum-sensing signal2 integrator luxo
62	c2gx8B	Alignment	not modelled	20.7	33	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: nif3-related protein; PDBTitle: the crystal structure of bacillus cereus protein related to nif3
63	c2vhiG	Alignment	not modelled	20.5	12	PDB header: hydrolase Chain: G: PDB Molecule: cg3027-pa; PDBTitle: crystal structure of a pyrimidine degrading enzyme from2 drosophila melanogaster
64	c5exsA	Alignment	not modelled	20.4	25	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator fleq; PDBTitle: aaa+ atpase fleq from pseudomonas aeruginosa bound to atp-gamma-s
65	c2gzaB	Alignment	not modelled	20.3	25	PDB header: hydrolase Chain: B: PDB Molecule: type iv secretion system protein virb11; PDBTitle: crystal structure of the virb11 atpase from the brucella suis type iv2 secretion system in complex with sulphate
66	c4ii7D	Alignment	not modelled	20.3	22	PDB header: hydrolase Chain: D: PDB Molecule: flai atpase; PDBTitle: archaeellum assembly atpase flai
67	d1fsua	Alignment	not modelled	20.2	17	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
68	c5tj3A	Alignment	not modelled	20.1	20	PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase pafa; PDBTitle: crystal structure of wild type alkaline phosphatase pafa to 1.7a2 resolution
69	c5a22A	Alignment	not modelled	19.9	21	PDB header: transferase Chain: A: PDB Molecule: vesicular stomatitis virus I polymerase; PDBTitle: structure of the I protein of vesicular stomatitis virus from electron2 cryomicroscopy
70	c2i09A	Alignment	not modelled	19.7	13	PDB header: isomerase Chain: A: PDB Molecule: phosphopentomutase; PDBTitle: crystal structure of putative phosphopentomutase from streptococcus2 mutans
71	c4fxsA	Alignment	not modelled	19.4	24	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae complexed2 with imp and mycophenolic acid
72	c2we7A	Alignment	not modelled	19.3	41	PDB header: oxidoreductase Chain: A: PDB Molecule: xanthine dehydrogenase; PDBTitle: crystal structure of mycobacterium tuberculosis rv0376c2 homologue from mycobacterium smegmatis
73	d1byia	Alignment	not modelled	18.8	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
74	c6b1vB	Alignment	not modelled	18.8	17	PDB header: hydrolase Chain: B: PDB Molecule: iota-carrageenan sulfatase; PDBTitle: crystal structure of ps i-cgsb c78s in complex with i-neocarratetraose
75	c2c9oA	Alignment	not modelled	18.6	24	PDB header: hydrolase Chain: A: PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1
76	c5gz5A	Alignment	not modelled	18.2	14	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
77	c6gfmA	Alignment	not modelled	18.2	15	PDB header: hydrolase Chain: A: PDB Molecule: pyrimidine/purine nucleotide 5'-monophosphate nucleosidase; PDBTitle: crystal structure of the escherichia coli nucleosidase ppnn (ppgpp-2 form)
						Fold: NIF3 (NGG1p interacting factor 3)-like

78	d2qx8a1	Alignment	not modelled	17.8	33	Superfamily: NIF3 (NGG1p interacting factor 3)-like Family: NIF3 (NGG1p interacting factor 3)-like
79	c5t4oA	Alignment	not modelled	17.4	18	PDB header: hydrolase Chain: A: PDB Molecule: atp synthase subunit alpha; PDBTitle: autoinhibited e. coli atp synthase state 1
80	c6blbA	Alignment	not modelled	17.4	22	PDB header: hydrolase Chain: A: PDB Molecule: holliday junction atp-dependent dna helicase ruvb; PDBTitle: 1.88 angstrom resolution crystal structure holliday junction atp-2 dependent dna helicase (ruvb) from pseudomonas aeruginosa in complex3 with adp
81	c3h5gA	Alignment	not modelled	17.0	26	PDB header: transferase Chain: A: PDB Molecule: pyrimidine-nucleoside phosphorylase; PDBTitle: crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
82	c2dsjA	Alignment	not modelled	17.0	16	PDB header: transferase Chain: A: PDB Molecule: pyrimidine-nucleoside (thymidine) phosphorylase; PDBTitle: crystal structure of project id tt0128 from thermus thermophilus hb8
83	c4fw9A	Alignment	not modelled	16.9	12	PDB header: hydrolase Chain: A: PDB Molecule: ttc1975 peptidase; PDBTitle: crystal structure of the lon-like protease mtalonc
84	d1knxa2	Alignment	not modelled	16.8	35	Fold: PEP carboxykinase-like Superfamily: PEP carboxykinase-like Family: HPr kinase HprK C-terminal domain
85	c1j6uA	Alignment	not modelled	16.8	15	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate-alanine ligase murc; PDBTitle: crystal structure of udp-n-acetylmuramate-alanine ligase murc (tm0231)2 from thermotoga maritima at 2.3 a resolution
86	c4uphA	Alignment	not modelled	16.7	14	PDB header: hydrolase Chain: A: PDB Molecule: sulfatase (sulfuric ester hydrolase) protein; PDBTitle: crystal structure of phosphonate monoester hydrolase of agrobacterium2 radiobacter
87	c4ga5H	Alignment	not modelled	16.4	16	PDB header: transferase Chain: H: PDB Molecule: putative thymidine phosphorylase; PDBTitle: crystal structure of amp phosphorylase c-terminal deletion mutant in2 the apo-form
88	c6hr5A	Alignment	not modelled	16.1	11	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
89	c2xrgA	Alignment	not modelled	16.1	25	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: crystal structure of autotaxin (enpp2) in complex with the2 ha155 boronic acid inhibitor
90	d1qvra2	Alignment	not modelled	15.8	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
91	c2xr9A	Alignment	not modelled	15.7	25	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: crystal structure of autotaxin (enpp2)
92	d1lauka	Alignment	not modelled	15.5	22	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
93	c1hqcB	Alignment	not modelled	15.3	24	PDB header: hydrolase Chain: B: PDB Molecule: ruvb; PDBTitle: structure of ruvb from thermus thermophilus hb8
94	c5f4hF	Alignment	not modelled	15.2	26	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
95	c3pfiB	Alignment	not modelled	15.0	18	PDB header: hydrolase Chain: B: PDB Molecule: holliday junction atp-dependent dna helicase ruvb; PDBTitle: 2.7 angstrom resolution crystal structure of a probable holliday2 junction dna helicase (ruvb) from campylobacter jejuni subsp. jejuni3 nctc 11168 in complex with adenosine-5'-diphosphate
96	d1ixsb2	Alignment	not modelled	15.0	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
97	c4xgcA	Alignment	not modelled	14.9	20	PDB header: dna binding protein Chain: A: PDB Molecule: origin recognition complex subunit 1; PDBTitle: crystal structure of the eukaryotic origin recognition complex
98	d1d2na	Alignment	not modelled	14.9	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
99	c1otpA	Alignment	not modelled	14.8	19	PDB header: phosphorylase Chain: A: PDB Molecule: thymidine phosphorylase; PDBTitle: structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase