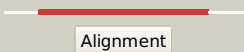

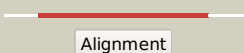

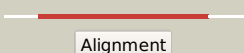

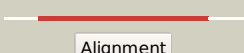





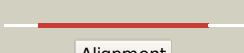

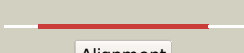




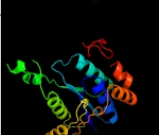
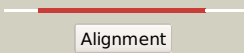



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2392_(cysH)_2686377_2687141
Date	Mon Aug 5 13:25:55 BST 2019
Unique Job ID	b45a82b33e3d24aa

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2oq2B_	 Alignment		100.0	29	PDB header: oxidoreductase Chain: B: PDB Molecule: phosphoadenosine phosphosulfate reductase; PDBTitle: crystal structure of yeast paps reductase with pap, a product complex
2	c2o8vA_	 Alignment		100.0	33	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoadenosine phosphosulfate reductase; PDBTitle: paps reductase in a covalent complex with thioredoxin c35a
3	c2goyC_	 Alignment		100.0	33	PDB header: oxidoreductase Chain: C: PDB Molecule: adenosine phosphosulfate reductase; PDBTitle: crystal structure of assimilatory adenosine 5'-2 phosphosulfate reductase with bound aps
4	c4bwwB_	 Alignment		100.0	31	PDB header: oxidoreductase Chain: B: PDB Molecule: phosphoadenosine-phosphosulphate reductase; PDBTitle: structure of adenosine 5-prime-phosphosulfate reductase apr-b from2 physcomitrella patens
5	d1sura_	 Alignment		100.0	31	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PAPS reductase-like
6	c3g59A_	 Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: fmn adenylyltransferase; PDBTitle: crystal structure of candida glabrata fmn adenylyltransferase in2 complex with atp
7	c2wsiA_	 Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: fad synthetase; PDBTitle: crystal structure of yeast fad synthetase (fad1) in complex2 with fad
8	c1zunA_	 Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: sulfate adenylyltransferase subunit 2; PDBTitle: crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
9	d1zuna1	 Alignment		100.0	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PAPS reductase-like
10	c3bl5E_	 Alignment		99.8	13	PDB header: hydrolase Chain: E: PDB Molecule: queuosine biosynthesis protein quec; PDBTitle: crystal structure of quec from bacillus subtilis: an enzyme2 involved in preq1 biosynthesis
11	c3vrhA_	 Alignment		99.7	17	PDB header: rna binding protein Chain: A: PDB Molecule: putative uncharacterized protein ph0300; PDBTitle: crystal structure of ph0300

12	c5ghaC_	Alignment		99.6	14	PDB header: transferase/transport protein Chain: C: PDB Molecule: sulfur transferase ttua; PDBTitle: sulfur transferase ttua in complex with sulfur carrier ttub
13	d1ni5a1	Alignment		99.6	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
14	d1wy5a1	Alignment		99.5	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
15	c3a2kB_	Alignment		99.5	9	PDB header: ligase/rna Chain: B: PDB Molecule: trna(ile)-lysine synthase; PDBTitle: crystal structure of tils complexed with trna
16	d1k92a1	Alignment		99.5	9	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
17	c1ni5A_	Alignment		99.5	12	PDB header: cell cycle Chain: A: PDB Molecule: putative cell cycle protein mesj; PDBTitle: structure of the mesj pp-atpase from escherichia coli
18	c2dplA_	Alignment		99.4	16	PDB header: ligase Chain: A: PDB Molecule: gmp synthase [glutamine-hydrolyzing] subunit b; PDBTitle: crystal structure of the gmp synthase from pyrococcus horikoshii ot3
19	c2e21A_	Alignment		99.4	13	PDB header: ligase Chain: A: PDB Molecule: trna(ile)-lysine synthase; PDBTitle: crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
20	d1j20a1	Alignment		99.4	9	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
21	d1gpma1	Alignment	not modelled	99.4	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
22	c5udwB_	Alignment	not modelled	99.3	12	PDB header: transferase Chain: B: PDB Molecule: lactate racemization operon protein lare; PDBTitle: lare, a sulfur transferase involved in synthesis of the cofactor for2 lactate racemase, in complex with nickel
23	c2e18B_	Alignment	not modelled	99.3	11	PDB header: ligase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of project ph0182 from pyrococcus horikoshii ot3
24	d1vl2a1	Alignment	not modelled	99.3	11	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
25	c2ywcC_	Alignment	not modelled	99.2	18	PDB header: ligase Chain: C: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
26	c3p52B_	Alignment	not modelled	99.2	7	PDB header: ligase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: nh3-dependent nad synthetase from campylobacter jejuni subsp. jejuni2 nctc 11168 in complex with the nitrate ion
27	c3fiuD_	Alignment	not modelled	99.1	10	PDB header: ligase Chain: D: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nmN synthetase from francisella tularensis
28	d2c5sa1	Alignment	not modelled	99.1	10	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Thil-like
						PDB header: transferase

29	c3k32D	Alignment	not modelled	99.1	10	Chain: D: PDB Molecule: uncharacterized protein mj0690; PDBTitle: the crystal structure of predicted subunit of trna methyltransferase2 from methanocaldococcus jannaschii dsm
30	c1vl2C	Alignment	not modelled	99.1	7	PDB header: ligase Chain: C: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of argininosuccinate synthase (tm1780) from2 thermotoga maritima at 1.65 a resolution
31	c3tqiB	Alignment	not modelled	99.1	15	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: structure of the gmp synthase (guaa) from coxiella burnetii
32	c2derA	Alignment	not modelled	99.0	11	PDB header: transferase/rna Chain: A: PDB Molecule: trna-specific 2-thiouridylase mnma; PDBTitle: cocrystal structure of an rna sulfuration enzyme mnma and2 trna-glu in the initial trna binding state
33	c2nz2A	Alignment	not modelled	99.0	11	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of human argininosuccinate synthase in complex with2 aspartate and citrulline
34	d2pg3a1	Alignment	not modelled	99.0	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
35	c1kh2D	Alignment	not modelled	99.0	11	PDB header: ligase Chain: D: PDB Molecule: argininosuccinate synthetase; PDBTitle: crystal structure of thermus thermophilus hb8 argininosuccinate2 synthetase in complex with atp
36	c1gpmD	Alignment	not modelled	98.9	17	PDB header: transferase (glutamine amidotransferase) Chain: D: PDB Molecule: gmp synthetase; PDBTitle: escherichia coli gmp synthetase complexed with amp and pyrophosphate
37	c1k97A	Alignment	not modelled	98.9	7	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
38	c2hmaA	Alignment	not modelled	98.9	16	PDB header: transferase Chain: A: PDB Molecule: probable trna (5-methylaminomethyl-2-thiouridylate)- PDBTitle: the crystal structure of trna (5-methylaminomethyl-2-thiouridylate)-2 methyltransferase trmu from streptococcus pneumoniae
39	c5tw7E	Alignment	not modelled	98.9	17	PDB header: ligase Chain: E: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of a gmp synthase (glutamine-hydrolyzing) from2 neisseria gonorrhoeae
40	d1xnga1	Alignment	not modelled	98.9	12	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
41	c2c5sA	Alignment	not modelled	98.9	12	PDB header: rna-binding protein Chain: A: PDB Molecule: probable thiamine biosynthesis protein thii; PDBTitle: crystal structure of bacillus anthracis thii, a trna-2 modifying enzyme containing the predicted rna-binding3 thump domain
42	c4kr7A	Alignment	not modelled	98.8	11	PDB header: transferase/rna Chain: A: PDB Molecule: probable trna sulfurtransferase; PDBTitle: crystal structure of a 4-thiouridine synthetase - rna complex with2 bound atp
43	c3uowB	Alignment	not modelled	98.8	12	PDB header: ligase Chain: B: PDB Molecule: gmp synthetase; PDBTitle: crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
44	c4nzpA	Alignment	not modelled	98.7	9	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: the crystal structure of argininosuccinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168
45	c2vxoB	Alignment	not modelled	98.6	13	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: human gmp synthetase in complex with xmp
46	c4xfdA	Alignment	not modelled	98.3	11	PDB header: ligase Chain: A: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of a nh(3)-dependent nad(+) synthetase from2 pseudomonas aeruginosa
47	c5hujB	Alignment	not modelled	98.3	12	PDB header: transferase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of nade from streptococcus pyogenes
48	c3dpiA	Alignment	not modelled	98.2	17	PDB header: ligase Chain: A: PDB Molecule: nad+ synthetase; PDBTitle: crystal structure of nad+ synthetase from burkholderia pseudomallei
49	d1kqpa	Alignment	not modelled	98.1	8	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
50	c4u7jB	Alignment	not modelled	97.9	12	PDB header: ligase Chain: B: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of argininosuccinate synthase from mycobacterium2 thermoresistibile
51	c3q4gA	Alignment	not modelled	97.9	9	PDB header: ligase Chain: A: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nad synthetase from vibrio cholerae
52	d1vbka1	Alignment	not modelled	97.9	9	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Thil-like
53	c5udtD	Alignment	not modelled	97.8	13	PDB header: transferase Chain: D: PDB Molecule: lactate racemization operon protein lare; PDBTitle: lare, a sulfur transferase involved in synthesis of the cofactor for2 lactate racemase, in complex with amp
54	c4n16C	Alignment	not modelled	97.6	11	PDB header: ligase Chain: C: PDB Molecule: nh(3)-dependent nad(+) synthetase;

54	c4q10C	Alignment	not modelled	97.0	11	PDBTitle: structure of nad+ synthetase from deinococcus radiodurans
55	d1ru8a	Alignment	not modelled	97.5	11	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
56	d1wxia1	Alignment	not modelled	97.4	11	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
57	c4f4hA	Alignment	not modelled	97.4	8	PDB header: ligase Chain: A: PDB Molecule: glutamine dependent nad+ synthetase; PDBTitle: crystal structure of a glutamine dependent nad+ synthetase from2 burkholderia thailandensis
58	c5khaA	Alignment	not modelled	97.1	10	PDB header: ligase Chain: A: PDB Molecule: glutamine-dependent nad+ synthetase; PDBTitle: structure of glutamine-dependent nad+ synthetase from acinetobacter2 baumannii in complex with adenosine diphosphate (adp)
59	c3n05B	Alignment	not modelled	97.0	10	PDB header: ligase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis
60	d2d13a1	Alignment	not modelled	96.8	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
61	d1jgta1	Alignment	not modelled	96.8	11	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
62	d1q15a1	Alignment	not modelled	96.6	10	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
63	c1ct9D	Alignment	not modelled	96.3	3	PDB header: ligase Chain: D: PDB Molecule: asparagine synthetase b; PDBTitle: crystal structure of asparagine synthetase b from2 escherichia coli
64	c1q15A	Alignment	not modelled	96.2	8	PDB header: biosynthetic protein Chain: A: PDB Molecule: carara; PDBTitle: carbapenam synthetase
65	c1m1zB	Alignment	not modelled	95.1	8	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactam synthetase; PDBTitle: beta-lactam synthetase apo enzyme
66	d1ct9a1	Alignment	not modelled	94.2	4	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
67	c1vbka	Alignment	not modelled	93.5	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ph1313; PDBTitle: crystal structure of ph1313 from pyrococcus horikoshii ot3
68	c3ilvA	Alignment	not modelled	78.1	11	PDB header: ligase Chain: A: PDB Molecule: glutamine-dependent nad(+) synthetase; PDBTitle: crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
69	c3bq7A	Alignment	not modelled	63.5	15	PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase delta; PDBTitle: sam domain of diacylglycerol kinase delta1 (e35g)
70	d1pk1c1	Alignment	not modelled	59.3	25	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
71	c3bs7A	Alignment	not modelled	57.5	15	PDB header: signaling protein Chain: A: PDB Molecule: protein aveugle; PDBTitle: crystal structure of the sterile alpha motif (sam) domain2 of hyphen/aveugle
72	c3ndnC	Alignment	not modelled	48.9	17	PDB header: lyase Chain: C: PDB Molecule: o-succinylhomoserine sulfhydrylase; PDBTitle: crystal structure of o-succinylhomoserine sulfhydrylase from2 mycobacterium tuberculosis covalently bound to pyridoxal-5-phosphate
73	c3nbmA	Alignment	not modelled	48.2	16	PDB header: transferase Chain: A: PDB Molecule: pts system, lactose-specific iibc components; PDBTitle: the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
74	c3l4eA	Alignment	not modelled	47.3	9	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized peptidase lmo0363; PDBTitle: 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
75	c3bs5A	Alignment	not modelled	47.1	22	PDB header: signaling protein/membrane protein Chain: A: PDB Molecule: protein aveugle; PDBTitle: crystal structure of hcnk2-sam/dhyp-sam complex
76	d2ctza1	Alignment	not modelled	45.4	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
77	d1wwva1	Alignment	not modelled	43.8	25	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
78	c1pk1A	Alignment	not modelled	43.6	25	PDB header: transcription repression Chain: A: PDB Molecule: polyhomoetic-proximal chromatin protein; PDBTitle: hetero sam domain structure of ph and scm.
79	c1v85A	Alignment	not modelled	43.0	17	PDB header: apoptosis Chain: A: PDB Molecule: similar to ring finger protein 36; PDBTitle: sterile alpha motif (sam) domain of mouse bifunctional2 apoptosis regulator
						PDB header: transcription repression

80	c1pk1B_	Alignment	not modelled	42.3	40	Chain: B: PDB Molecule: sex comb on midleg cg9495-pa; PDBTitle: hetero sam domain structure of ph and scm.
81	c5j8yC_	Alignment	not modelled	40.4	32	PDB header: nuclear protein Chain: C: PDB Molecule: polycomb protein sfmbt; PDBTitle: crystal structure of the scm-sam and sfmbt-sam heterodimer
82	c2d89A_	Alignment	not modelled	38.9	10	PDB header: structural protein, protein binding Chain: A: PDB Molecule: ehbp1 protein; PDBTitle: solution structure of the ch domain from human eh domain2 binding protein 1
83	d1kw4a_	Alignment	not modelled	38.9	25	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
84	c5i7wA_	Alignment	not modelled	37.8	17	PDB header: transferase Chain: A: PDB Molecule: cysteine synthase a; PDBTitle: crystal structure of a cysteine synthase from brucella suis
85	c2cb1A_	Alignment	not modelled	37.1	33	PDB header: lyase Chain: A: PDB Molecule: o-acetyl homoserine sulfhydrylase; PDBTitle: crystal structure of o-acetyl homoserine sulfhydrylase2 from thermus thermophilus hb8,oah2.
86	d1xx6a1	Alignment	not modelled	34.7	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Type II thymidine kinase
87	c2e8oA_	Alignment	not modelled	33.8	15	PDB header: signaling protein Chain: A: PDB Molecule: sam domain and hd domain-containing protein 1; PDBTitle: solution structure of the n-terminal sam-domain of the sam2 domain and hd domain containing protein 1 (dendritic cell-3 derived ifng-induced protein) (dcip) (monocyte protein 5)4 (mop-5)
88	d3bzka2	Alignment	not modelled	33.3	20	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Tex HhH-containing domain-like
89	c2ju2A_	Alignment	not modelled	31.9	6	PDB header: transferase Chain: A: PDB Molecule: erythronolide synthase; PDBTitle: minimized mean solution structure of the acyl carrier2 protein domain from module 2 of 6-deoxyerythronolide b3 synthase (debs)
90	c3ja7L_	Alignment	not modelled	30.2	23	PDB header: viral protein Chain: L: PDB Molecule: portal protein gp20; PDBTitle: cryo-em structure of the bacteriophage t4 portal protein assembly at2 near-atomic resolution
91	c2l5yA_	Alignment	not modelled	28.7	14	PDB header: signaling protein Chain: A: PDB Molecule: stromal interaction molecule 2; PDBTitle: nmr structure of calcium-loaded stim2 ef-sam.
92	c2afdA_	Alignment	not modelled	27.9	7	PDB header: ligand binding protein Chain: A: PDB Molecule: protein asl1650; PDBTitle: solution structure of asl1650, an acyl carrier protein from anaebaena2 sp. pcc 7120 with a variant phosphopantetheinylation-site sequence
93	d1pa7a_	Alignment	not modelled	27.9	17	Fold: CH domain-like Superfamily: Calponin-homology domain, CH-domain Family: Calponin-homology domain, CH-domain
94	c2k60A_	Alignment	not modelled	27.7	14	PDB header: signaling protein Chain: A: PDB Molecule: protein (stromal interaction molecule 1); PDBTitle: nmr structure of calcium-loaded stim1 ef-sam
95	c2dkzA_	Alignment	not modelled	27.2	11	PDB header: signaling protein Chain: A: PDB Molecule: hypothetical protein loc64762; PDBTitle: solution structure of the sam_pnt-domain of the2 hypothetical protein loc64762
96	d2f3na1	Alignment	not modelled	26.7	21	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
97	c3ecsD_	Alignment	not modelled	26.2	10	PDB header: translation Chain: D: PDB Molecule: translation initiation factor eif-2b subunit alpha; PDBTitle: crystal structure of human eif2b alpha
98	d1xpja_	Alignment	not modelled	25.9	15	Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein VC0232
99	c5kinD_	Alignment	not modelled	25.5	19	PDB header: lyase Chain: D: PDB Molecule: tryptophan synthase beta chain; PDBTitle: crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
100	d1r2aa_	Alignment	not modelled	25.0	27	Fold: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Superfamily: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Family: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
101	c2qq0B_	Alignment	not modelled	25.0	10	PDB header: transferase Chain: B: PDB Molecule: thymidine kinase; PDBTitle: thymidine kinase from thermotoga maritima in complex with2 thymidine + appnhp
102	c4uxjB_	Alignment	not modelled	24.4	14	PDB header: transferase Chain: B: PDB Molecule: thymidine kinase; PDBTitle: leishmania major thymidine kinase in complex with dttp
103	c4mwfC_	Alignment	not modelled	24.4	41	PDB header: immune system Chain: C: PDB Molecule: envelope glycoprotein e2; PDBTitle: structure of hepatitis c virus envelope glycoprotein e2 core bound to2 broadly neutralizing antibody ar3c
104	c2j87D_	Alignment	not modelled	24.3	18	PDB header: transferase Chain: D: PDB Molecule: thymidine kinase; PDBTitle: structure of vaccinia virus thymidine kinase in complex2 with dttp: insights for drug design PDB header: signaling protein Chain: A: PDB Molecule: nedd9 interactinq protein with calponin

105	c1wylA_	Alignment	not modelled	24.3	19	homology PDBTitle: solution structure of the ch domain of human nedd92 interacting protein with calponin homology and lim domains
106	d1v32a_	Alignment	not modelled	23.4	20	Fold: SWIB/MDM2 domain Superfamily: SWIB/MDM2 domain Family: SWIB/MDM2 domain
107	d2hwna1	Alignment	not modelled	22.9	27	Fold: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Superfamily: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Family: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
108	d1vp8a_	Alignment	not modelled	22.9	11	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: MTH1675-like
109	c1lkzB_	Alignment	not modelled	22.6	16	PDB header: isomerase Chain: B: PDB Molecule: ribose 5-phosphate isomerase a; PDBTitle: crystal structure of d-ribose-5-phosphate isomerase (rpiA) from2 escherichia coli.
110	d1uhra_	Alignment	not modelled	22.5	20	Fold: SWIB/MDM2 domain Superfamily: SWIB/MDM2 domain Family: SWIB/MDM2 domain
111	d1v31a_	Alignment	not modelled	22.5	10	Fold: SWIB/MDM2 domain Superfamily: SWIB/MDM2 domain Family: SWIB/MDM2 domain
112	d1sv0c_	Alignment	not modelled	21.8	29	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: Pointed domain
113	c3mk7B_	Alignment	not modelled	21.6	39	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome c oxidase, cbb3-type, subunit o; PDBTitle: the structure of cbb3 cytochrome oxidase
114	c3e2iA_	Alignment	not modelled	21.5	20	PDB header: transferase Chain: A: PDB Molecule: thymidine kinase; PDBTitle: crystal structure of thymidine kinase from s. aureus
115	c6hulB_	Alignment	not modelled	20.2	14	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase beta chain 1; PDBTitle: sulfolobus solfataricus tryptophan synthase ab complex
116	c3ferD_	Alignment	not modelled	20.2	15	PDB header: actin binding protein Chain: D: PDB Molecule: filamin-b; PDBTitle: crystal structure of n-terminal actin-binding domain from2 human filamin b (tandem ch-domains). northeast structural3 genomics consortium target hr5571a.
117	c6gcsY_	Alignment	not modelled	20.1	11	PDB header: oxidoreductase Chain: Y: PDB Molecule: nuym subunit; PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
118	d1uqva_	Alignment	not modelled	20.1	14	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain