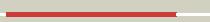
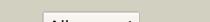
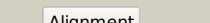
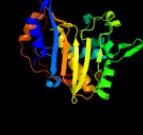
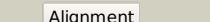
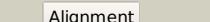
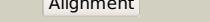
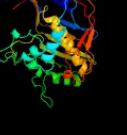


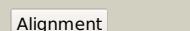
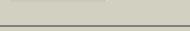
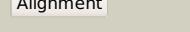
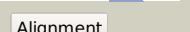
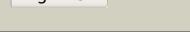
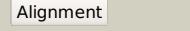
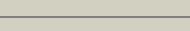
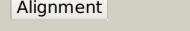
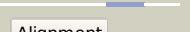
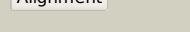
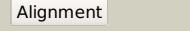
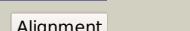
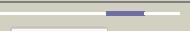
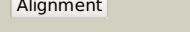
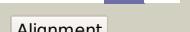
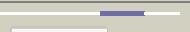
Phyre²

Email	mdejesus@rockefeller.edu
Description	RVBD2764c_(thyA)_3073690_3074481
Date	Wed Aug 7 12:50:42 BST 2019
Unique Job ID	798e61c333cd64c3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2oipE			100.0	48	PDB header: transferase, oxidoreductase Chain: E; PDB Molecule: chain a, crystal structure of dhfr; PDBTitle: crystal structure of the s290g active site mutant of ts-dhfr from2 cryptosporidium hominis
2	c4eckB			100.0	50	PDB header: transferase, oxidoreductase Chain: B; PDB Molecule: bifunctional dihydrofolate reductase-thymidylate synthase; PDBTitle: crystal structure of the toxoplasma gondii ts-dhfr
3	d1qzf2			100.0	49	Fold: Thymidylate synthase/dCMP hydroxymethylase Superfamily: Thymidylate synthase/dCMP hydroxymethylase Family: Thymidylate synthase/dCMP hydroxymethylase
4	d1j3kc			100.0	45	Fold: Thymidylate synthase/dCMP hydroxymethylase Superfamily: Thymidylate synthase/dCMP hydroxymethylase Family: Thymidylate synthase/dCMP hydroxymethylase
5	c3jsuA			100.0	45	PDB header: oxidoreductase, transferase Chain: A; PDB Molecule: dihydrofolate reductase-thymidylate synthase; PDBTitle: quadruple mutant(n51i+c59r+s108n+i164l) plasmodium falciparum2 dihydrofolate reductase-thymidylate synthase(pfdhfr-ts) complexed3 with qn254, nadph, and dump
6	c3qj7D			100.0	98	PDB header: transferase Chain: D; PDB Molecule: thymidylate synthase; PDBTitle: crystal structure of the mycobacterium tuberculosis thymidylate2 synthase (thyA) bound to dump
7	c3k2hA			100.0	50	PDB header: transferase Chain: A; PDB Molecule: dihydrofolate reductase/thymidylate synthase; PDBTitle: co-crystal structure of dihydrofolate reductase/thymidylate synthase2 from babesia bovis with dump, pemetrexed and nadp
8	d1tswa			100.0	61	Fold: Thymidylate synthase/dCMP hydroxymethylase Superfamily: Thymidylate synthase/dCMP hydroxymethylase Family: Thymidylate synthase/dCMP hydroxymethylase
9	d2g8oa1			100.0	66	Fold: Thymidylate synthase/dCMP hydroxymethylase Superfamily: Thymidylate synthase/dCMP hydroxymethylase Family: Thymidylate synthase/dCMP hydroxymethylase
10	c3clbA			100.0	49	PDB header: oxidoreductase, transferase Chain: A; PDB Molecule: dhfr-ts; PDBTitle: structure of bifunctional tcldhfr-ts in complex with tmq
11	d1hvya			100.0	54	Fold: Thymidylate synthase/dCMP hydroxymethylase Superfamily: Thymidylate synthase/dCMP hydroxymethylase Family: Thymidylate synthase/dCMP hydroxymethylase

12	d1seja2	Alignment		100.0	49	Fold: Thymidylate synthase/dCMP hydroxymethylase Superfamily: Thymidylate synthase/dCMP hydroxymethylase Family: Thymidylate synthase/dCMP hydroxymethylase
13	c4dq1A	Alignment		100.0	59	PDB header: transferase Chain: A: PDB Molecule: thymidylate synthase; PDBTitle: thymidylate synthase from staphylococcus aureus.
14	c2aaZG	Alignment		100.0	48	PDB header: transferase Chain: G: PDB Molecule: thymidylate synthase; PDBTitle: cryptococcus neoformans thymidylate synthase complexed with substrate2 and an antifolate
15	d1f28a	Alignment		100.0	48	Fold: Thymidylate synthase/dCMP hydroxymethylase Superfamily: Thymidylate synthase/dCMP hydroxymethylase Family: Thymidylate synthase/dCMP hydroxymethylase
16	c4iswB	Alignment		100.0	49	PDB header: transferase Chain: B: PDB Molecule: thymidylate synthase; PDBTitle: crystal structure of phosphorylated c.elegans thymidylate synthase in2 complex with dump
17	d2tsra	Alignment		100.0	53	Fold: Thymidylate synthase/dCMP hydroxymethylase Superfamily: Thymidylate synthase/dCMP hydroxymethylase Family: Thymidylate synthase/dCMP hydroxymethylase
18	d1bkpa	Alignment		100.0	37	Fold: Thymidylate synthase/dCMP hydroxymethylase Superfamily: Thymidylate synthase/dCMP hydroxymethylase Family: Thymidylate synthase/dCMP hydroxymethylase
19	c4g9uD	Alignment		100.0	51	PDB header: transferase Chain: D: PDB Molecule: thymidylate synthase; PDBTitle: crystal structure of trichinella spiralis thymidylate synthase2 complexed with dump
20	d1tisa	Alignment		100.0	50	Fold: Thymidylate synthase/dCMP hydroxymethylase Superfamily: Thymidylate synthase/dCMP hydroxymethylase Family: Thymidylate synthase/dCMP hydroxymethylase
21	c3v8hB	Alignment	not modelled	100.0	39	PDB header: transferase Chain: B: PDB Molecule: thymidylate synthase; PDBTitle: crystal structure of thymidylate synthase from burkholderia2 thailandensis
22	c6aujC	Alignment	not modelled	100.0	61	PDB header: transferase Chain: C: PDB Molecule: thymidylate synthase; PDBTitle: crystal structure of thymidylate synthase from elizabethkingia2 anophelis nuhp1
23	c1hw3A	Alignment	not modelled	100.0	54	PDB header: transferase Chain: A: PDB Molecule: thymidylate synthase; PDBTitle: structure of human thymidylate synthase suggests advantages of2 chemotherapy with noncompetitive inhibitors
24	c1hw4A	Alignment	not modelled	100.0	54	PDB header: transferase Chain: A: PDB Molecule: thymidylate synthase; PDBTitle: structure of thymidylate synthase suggests advantages of chemotherapy2 with noncompetitive inhibitors
25	c3ix6B	Alignment	not modelled	100.0	63	PDB header: transferase Chain: B: PDB Molecule: thymidylate synthase; PDBTitle: crystal structure of thymidylate synthase thya from brucella2 melitensis
26	c3kgbA	Alignment	not modelled	100.0	51	PDB header: transferase Chain: A: PDB Molecule: thymidylate synthase 1/2; PDBTitle: crystal structure of thymidylate synthase 1/2 from encephalitozoon2 cuniculi at 2.2 a resolution
27	c3egyX	Alignment	not modelled	100.0	55	PDB header: transferase Chain: X: PDB Molecule: thymidylate synthase; PDBTitle: crystal structure of human thymidylate synthase a191k with loop 181-2 197 stabilized in the inactive conformation
28	c5b6dB	Alignment	not modelled	100.0	23	PDB header: transferase Chain: B: PDB Molecule: cmp 5-hydroxymethylase; PDBTitle: crystal structure of cytidine monophosphate hydroxymethylase mila with2 cmp

29	d1b5ea		Alignment	not modelled	100.0	24	Fold: Thymidylate synthase/dCMP hydroxymethylase Superfamily: Thymidylate synthase/dCMP hydroxymethylase Family: Thymidylate synthase/dCMP hydroxymethylase
30	c2vsvB		Alignment	not modelled	45.7	16	PDB header: protein binding Chain: B: PDB Molecule: rphophilin-2; PDBTitle: crystal structure of the pdz domain of human rphophilin-2
31	c1w9qB		Alignment	not modelled	30.4	14	PDB header: cell adhesion Chain: B: PDB Molecule: syntenin 1; PDBTitle: crystal structure of the pdz tandem of human syntenin in complex with tneaf peptide
32	d1ueza		Alignment	not modelled	30.4	22	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
33	c3khfA		Alignment	not modelled	27.1	22	PDB header: transferase Chain: A: PDB Molecule: microtubule-associated serine/threonine-protein kinase 3; PDBTitle: the crystal structure of the pdz domain of human microtubule2 associated serine/threonine kinase 3 (mast3)
34	c6irdC		Alignment	not modelled	25.6	19	PDB header: hydrolase/protein binding Chain: C: PDB Molecule: inad-like protein; PDBTitle: complex structure of inadl pdz89 and plcb4 c-terminal cc-pbm
35	c4rhoA		Alignment	not modelled	25.2	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein (bpsl2088) from2 burkholderia pseudomallei k96243 at 2.25 a resolution
36	c6nmgB		Alignment	not modelled	24.6	22	PDB header: signaling protein Chain: B: PDB Molecule: resistance to inhibitors of cholinesterase 8 homolog a (c. PDBTitle: crystal structure of rat ric-8a g alpha binding domain
37	d1vaea		Alignment	not modelled	24.4	18	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
38	c4ghwA		Alignment	not modelled	23.3	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative two-domain sugar hydrolase2 (baccac_02064) from bacteroides caccae atcc 43185 at 1.35 a3 resolution
39	c3diwB		Alignment	not modelled	21.4	24	PDB header: signaling protein/cell adhesion Chain: B: PDB Molecule: tax1-binding protein 3; PDBTitle: c-terminal beta-catenin bound tip-1 structure
40	c2kv8A		Alignment	not modelled	21.3	15	PDB header: signaling protein Chain: A: PDB Molecule: regulator of g-protein signaling 12; PDBTitle: solution structure offrgs12 pdz domain
41	c2q3gA		Alignment	not modelled	19.7	20	PDB header: structural genomics Chain: A: PDB Molecule: pdz and lim domain protein 7; PDBTitle: structure of the pdz domain of human pdlim7 bound to a c-2 terminal extension from human beta-tropomyosin
42	d1fc6a3		Alignment	not modelled	19.6	23	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: Tail specific protease PDZ domain
43	c6jdpA		Alignment	not modelled	19.3	25	PDB header: antitoxin Chain: A: PDB Molecule: imm52 family protein; PDBTitle: the imm52 family protein tsit (pa3908) from pseudomonas aeruginosa
44	d1w9ea1		Alignment	not modelled	19.2	11	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
45	c4rgwB		Alignment	not modelled	18.5	28	PDB header: transferase/transcription Chain: B: PDB Molecule: transcription initiation factor tfiid subunit 7; PDBTitle: crystal structure of a taf1-taf7 complex in human transcription factor2 iid
46	c3o46A		Alignment	not modelled	17.9	15	PDB header: protein binding Chain: A: PDB Molecule: maguk p55 subfamily member 7; PDBTitle: crystal structure of the pdz domain of mpp7
47	d2byga1		Alignment	not modelled	17.4	18	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
48	d1y7na1		Alignment	not modelled	17.2	22	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
49	c3j39I		Alignment	not modelled	17.0	19	PDB header: ribosome Chain: I: PDB Molecule: 60s ribosomal protein l10; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
50	c3shub		Alignment	not modelled	16.5	28	PDB header: cell adhesion Chain: B: PDB Molecule: tight junction protein zo-1; PDBTitle: crystal structure of zo-1 pdz3
51	c2eeiA		Alignment	not modelled	15.8	17	PDB header: metal binding protein Chain: A: PDB Molecule: pdz domain-containing protein 1; PDBTitle: solution structure of second pdz domain of pdz domain2 containing protein 1
52	d1wi4a1		Alignment	not modelled	14.6	13	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
53	c2jikB		Alignment	not modelled	14.6	16	PDB header: membrane protein Chain: B: PDB Molecule: synaptjanin-2 binding protein; PDBTitle: crystal structure of pdz domain of synaptjanin-2 binding2 protein
54	d1nowa1		Alignment	not modelled	14.5	29	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
							Fold: PDZ domain-like

55	d1ihja	Alignment	not modelled	14.2	19	Superfamily: PDZ domain-like Family: PDZ domain
56	c3qgID	Alignment	not modelled	13.5	19	PDB header: protein binding Chain: D: PDB Molecule: sorting nexin-27; PDBTitle: crystal structure of pdz domain of sorting nexin 27 (snx27) in complex2 with the eseskv peptide corresponding to the c-terminal tail of girk3
57	d1jt6a1	Alignment	not modelled	13.1	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
58	c2gzvA	Alignment	not modelled	13.1	19	PDB header: signaling protein Chain: A: PDB Molecule: prkca-binding protein; PDBTitle: the crystal structure of the pdz domain of human pick1
59	d2o7ta1	Alignment	not modelled	12.8	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
60	c2ejyA	Alignment	not modelled	12.7	20	PDB header: membrane protein Chain: A: PDB Molecule: 55 kda erythrocyte membrane protein; PDBTitle: solution structure of the p55 pdz t85c domain complexed2 with the glycophorin c f127c peptide
61	c5oarB	Alignment	not modelled	12.7	13	PDB header: hydrolase Chain: B: PDB Molecule: beta-hexosaminidase; PDBTitle: crystal structure of native beta-n-acetylhexosaminidase isolated from2 aspergillus oryzae
62	c2z17A	Alignment	not modelled	12.7	19	PDB header: protein binding Chain: A: PDB Molecule: pleckstrin homology sec7 and coiled-coil domains- PDBTitle: crystal sturcture of pdz domain from human pleckstrin2 homology, sec7
63	c1u3bA	Alignment	not modelled	12.6	22	PDB header: protein transport Chain: A: PDB Molecule: amyloid beta a4 precursor protein-binding, PDBTitle: auto-inhibition mechanism of x11s/mints family scaffold2 proteins revealed by the closed conformation of the tandem3 pdz domains
64	c3l4fD	Alignment	not modelled	12.5	22	PDB header: signaling protein/protein binding Chain: D: PDB Molecule: sh3 and multiple ankyrin repeat domains protein 1; PDBTitle: crystal structure of betapix coiled-coil domain and shank pdz complex
65	c2v90E	Alignment	not modelled	12.3	14	PDB header: protein binding Chain: E: PDB Molecule: pdz domain-containing protein 3; PDBTitle: crystal structure of the 3rd pdz domain of intestine- and kidney-2 enriched pdz domain ikepp (pdz3)
66	c6gbeA	Alignment	not modelled	12.3	22	PDB header: protein binding Chain: A: PDB Molecule: tyrosine-protein phosphatase non-receptor type 13; PDBTitle: murine protein tyrosine phosphatase ptpn13 pdz3 domain-prk2 peptide2 complex
67	d1r6ja	Alignment	not modelled	12.0	22	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
68	c1r6jA	Alignment	not modelled	12.0	22	PDB header: membrane protein Chain: A: PDB Molecule: syntenin 1; PDBTitle: ultrahigh resolution crystal structure of syntenin pdz2
69	c1nteA	Alignment	not modelled	12.0	22	PDB header: signaling protein Chain: A: PDB Molecule: syntenin 1; PDBTitle: crystal structure analysis of the second pdz domain of syntenin
70	c2eehA	Alignment	not modelled	11.8	24	PDB header: metal binding protein Chain: A: PDB Molecule: pdz domain-containing protein 7; PDBTitle: solution structure of first pdz domain of pdz domain2 containing protein 7
71	c3zf7K	Alignment	not modelled	11.5	13	PDB header: ribosome Chain: K: PDB Molecule: 60s ribosomal protein l10, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
72	c2dm8A	Alignment	not modelled	11.3	25	PDB header: protein binding Chain: A: PDB Molecule: inad-like protein; PDBTitle: solution structure of the eighth pdz domain of human inad-2 like protein
73	d2fcfa1	Alignment	not modelled	11.2	24	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
74	d1uita	Alignment	not modelled	11.2	24	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
75	d1q3oa	Alignment	not modelled	10.6	22	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
76	c5yf4A	Alignment	not modelled	10.6	21	PDB header: protein binding Chain: A: PDB Molecule: mob-like protein phocein; PDBTitle: a kinase complex mst4-mob4
77	c2fneB	Alignment	not modelled	10.6	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: multiple pdz domain protein; PDBTitle: the crystal structure of the 13th pdz domain of mpdz
78	d1jakal	Alignment	not modelled	10.5	23	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
79	d1wifa	Alignment	not modelled	10.3	19	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
80	d2f5ya1	Alignment	not modelled	10.3	14	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain

81	c4lqqB_		Alignment	not modelled	10.3	29	PDB header: transferase/transferase activator Chain: B: PDB Molecule: cbk1 kinase activator protein mob2; PDBTitle: crystal structure of the cbk1(t743e)-mob2 kinase-coactivator complex2 in crystal form b
82	d1u3ba2		Alignment	not modelled	10.2	22	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
83	d1pi1a_		Alignment	not modelled	10.2	38	Fold: Bromodomain-like Superfamily: Mob1/phocean Family: Mob1/phocean
84	d1t2ma1		Alignment	not modelled	10.2	16	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
85	c3rcnA_		Alignment	not modelled	10.2	16	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: crystal structure of beta-n-acetylhexosaminidase from arthrobacter2 aurescens
86	c2ka9A_		Alignment	not modelled	9.9	20	PDB header: cell adhesion Chain: A: PDB Molecule: disks large homolog 4; PDBTitle: solution structure of psd-95 pdz12 complexed with cypin2 peptide
87	d1p1da2		Alignment	not modelled	9.9	15	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
88	c2yuyA_		Alignment	not modelled	9.8	22	PDB header: signaling protein Chain: A: PDB Molecule: rho gtpase activating protein 21; PDBTitle: solution structure of pdz domain of rho gtpase activating2 protein 21
89	c3qikA_		Alignment	not modelled	9.6	25	PDB header: hydrolase regulator Chain: A: PDB Molecule: phosphatidylinositol 3,4,5-trisphosphate-dependent rac PDBTitle: crystal structure of the first pdz domain of prex1
90	c4a8al_		Alignment	not modelled	9.6	32	PDB header: hydrolase/hydrolase Chain: I: PDB Molecule: periplasmic ph-dependent serine endoprotease degq; PDBTitle: asymmetric cryo-em reconstruction of e. coli degq 12-mer in complex2 with lysozyme
91	c2d92A_		Alignment	not modelled	9.5	18	PDB header: protein binding Chain: A: PDB Molecule: inad-like protein; PDBTitle: solution structure of the fifth pdz domain of inad-like2 protein
92	c1m04A_		Alignment	not modelled	9.4	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: mutant streptomyces plicatus beta-hexosaminidase (d313n) in complex2 with product (glcnac)
93	d1whaa_		Alignment	not modelled	9.3	19	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
94	d2gjxa1		Alignment	not modelled	9.0	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
95	c1obyA_		Alignment	not modelled	8.9	22	PDB header: cell adhesion Chain: A: PDB Molecule: syntenin 1; PDBTitle: crystal structure of the complex of pdz2 of syntenin with a syndecan-42 peptide.
96	c4tkzA_		Alignment	not modelled	8.9	58	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein gbs1890; PDBTitle: crystal structure of phosphotransferase system component eiia from2 streptococcus agalactiae
97	c2hjnA_		Alignment	not modelled	8.9	31	PDB header: cell cycle Chain: A: PDB Molecule: maintenance of ploidy protein mob1; PDBTitle: structural and functional analysis of saccharomyces2 cerevisiae mob1
98	c6ezrA_		Alignment	not modelled	8.7	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylglucosaminidase nag2; PDBTitle: crystal structure of gh20 exo beta-n-acetylglucosaminidase from vibrio2 harveyi
99	c1u39A_		Alignment	not modelled	8.7	22	PDB header: protein transport Chain: A: PDB Molecule: amyloid beta a4 precursor protein-binding PDBTitle: auto-inhibition mechanism of x11s/mints family scaffold2 proteins revealed by the closed conformation of the tandem3 pdz domains