

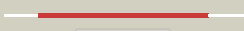






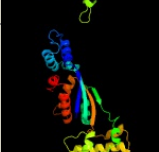
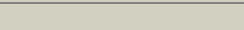
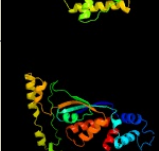

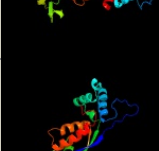

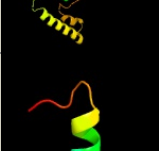

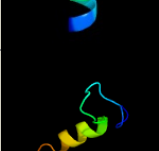
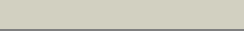
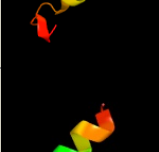

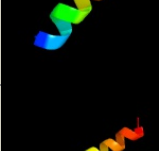
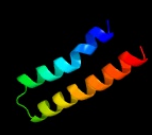

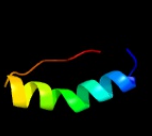




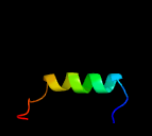



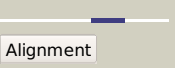
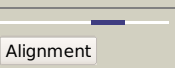
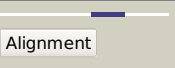
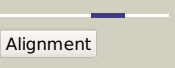
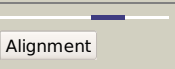
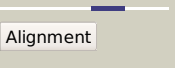
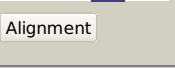
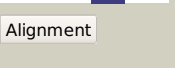
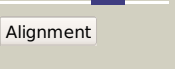
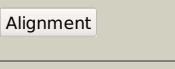
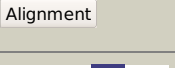
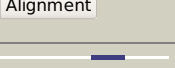
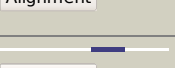

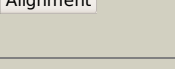
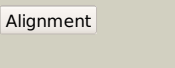
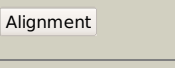
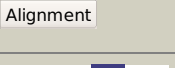
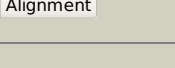
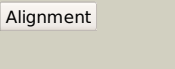
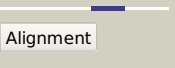
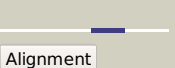

Phyre2

Email: mdejesus@rockefeller.edu
 Description: RVBD2754c_(thyX)_3067203_3067955
 Date: Wed Aug 7 12:50:41 BST 2019
 Unique Job ID: 8040a5899badc9bf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2af6G_	 Alignment		100.0	98	PDB header: transferase Chain: G: PDB Molecule: thymidylate synthase thyx; PDBTitle: crystal structure of mycobacterium tuberculosis flavin dependent2 thymidylate synthase (mtb thyx) in the presence of co-factor fad and3 substrate analog 5-bromo-2'-deoxyuridine-5'-monophosphate (brdump)
2	c3fnnA_	 Alignment		100.0	64	PDB header: transferase Chain: A: PDB Molecule: thymidylate synthase thyx; PDBTitle: biochemical and structural analysis of an atypical thyx:2 corynebacterium glutamicum nchu 87078 depends on thya for3 thymidine biosynthesis
3	c6j61B_	 Alignment		100.0	24	PDB header: transferase Chain: B: PDB Molecule: flavin-dependent thymidylate synthase; PDBTitle: crystal structure of thymidylate synthase, thy1, from thermus2 thermophilus having an extra c terminal domain
4	d1o26a_	 Alignment		100.0	21	Fold: Thymidylate synthase-complementing protein Thy1 Superfamily: Thymidylate synthase-complementing protein Thy1 Family: Thymidylate synthase-complementing protein Thy1
5	c3ah5E_	 Alignment		100.0	25	PDB header: transferase Chain: E: PDB Molecule: thymidylate synthase thyx; PDBTitle: crystal structure of flavin dependent thymidylate synthase thyx from2 helicobacter pylori complexed with fad and dump
6	c4p5aB_	 Alignment		100.0	23	PDB header: transferase Chain: B: PDB Molecule: thymidylate synthase thyx; PDBTitle: crystal structure of a ump/dump methylase polb from streptomyces2 cacaoui bound with 5-br ump
7	c2cfaB_	 Alignment		100.0	31	PDB header: transferase Chain: B: PDB Molecule: thymidylate synthase; PDBTitle: structure of viral flavin-dependant thymidylate synthase thyx
8	c3cuxA_	 Alignment		25.2	35	PDB header: transferase Chain: A: PDB Molecule: malate synthase; PDBTitle: atomic resolution structures of escherichia coli and2 bacillis anthracis malate synthase a: comparison with3 isoform g and implications for structure based drug design
9	c5ydfA_	 Alignment		19.1	25	PDB header: transcription Chain: A: PDB Molecule: parafibromin; PDBTitle: crystal structure of a disease-related gene, hcdc73(1-100)
10	c3cuzA_	 Alignment		14.9	38	PDB header: transferase Chain: A: PDB Molecule: malate synthase a; PDBTitle: atomic resolution structures of escherichia coli and2 bacillis anthracis malate synthase a: comparison with3 isoform g and implications for structure based drug design
11	d2v7fa1	 Alignment		14.0	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Rps19E-like

12	c3mmiB_	Alignment		12.8	11	PDB header: motor protein Chain: B: PDB Molecule: myosin-4; PDBTitle: crystal structure of the globular tail of myo4p
13	c5vfbB_	Alignment		12.0	31	PDB header: transferase Chain: B: PDB Molecule: malate synthase g; PDBTitle: 1.36 angstrom resolution crystal structure of malate synthase g from2 pseudomonas aeruginosa in complex with glycolic acid.
14	d1nb5i_	Alignment		11.2	21	Fold: Cystatin-like Superfamily: Cystatin/monellin Family: Cystatins
15	c4i1oD_	Alignment		10.5	16	PDB header: protein transport/hydrolase Chain: D: PDB Molecule: lepB; PDBTitle: crystal structure of the legionella pneumophila gap domain of lepB in2 complex with rab1b bound to gdp and bef3
16	c3j21a_	Alignment		10.5	9	PDB header: ribosome Chain: A: PDB Molecule: 50s ribosomal protein l1p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
17	c3mlqD_	Alignment		9.8	35	PDB header: transferase/transcription Chain: D: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: crystal structure of the thermus thermophilus transcription-repair2 coupling factor rna polymerase interacting domain with the thermus3 aquaticus rna polymerase beta1 domain
18	c5tpjA_	Alignment		9.5	32	PDB header: de novo protein Chain: A: PDB Molecule: denovo ntf2; PDBTitle: crystal structure of a de novo designed protein with curved beta-sheet
19	c5gyqA_	Alignment		9.2	17	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein; PDBTitle: putative receptor-binding domain of bat-derived coronavirus hku9 spike2 protein
20	d2np3a1	Alignment		8.8	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
21	d1vqox1	Alignment	not modelled	8.8	25	Fold: Ribosomal protein L31e Superfamily: Ribosomal protein L31e Family: Ribosomal protein L31e
22	d1d1da1	Alignment	not modelled	7.5	19	Fold: Acyl carrier protein-like Superfamily: Retrovirus capsid dimerization domain-like Family: Retrovirus capsid protein C-terminal domain
23	c5lphA_	Alignment	not modelled	7.4	19	PDB header: cell cycle Chain: A: PDB Molecule: centrosomal protein of 104 kda; PDBTitle: structure of the tog domain of human cep104
24	c2xalA_	Alignment	not modelled	7.4	30	PDB header: transferase Chain: A: PDB Molecule: inositol-pentakisphosphate 2-kinase; PDBTitle: lead derivative of inositol 1,3,4,5,6-pentakisphosphate 2-kinase from2 a. thaliana in complex with adp and ip6.
25	c5vbnE_	Alignment	not modelled	7.4	21	PDB header: transferase Chain: E: PDB Molecule: dna polymerase epsilon subunit 2; PDBTitle: crystal structure of human dna polymerase epsilon b-subunit in complex2 with c-terminal domain of catalytic subunit
26	c2n28A_	Alignment	not modelled	7.3	11	PDB header: viral protein Chain: A: PDB Molecule: protein vpu; PDBTitle: solid-state nmr structure of vpu
27	c3pp5A_	Alignment	not modelled	7.0	11	PDB header: structural protein Chain: A: PDB Molecule: brk1; PDBTitle: high-resolution structure of the trimeric scar/wave complex precursor2 brk1
28	c1yy1S_	Alignment	not modelled	7.0	30	PDB header: viral protein/immune system Chain: S: PDB Molecule: cd4m33, scorpion-toxin mimic of cd4; PDBTitle: crystal structure of cd4m33, a scorpion-toxin mimic of cd4, in complex2 with hiv-1 yu2 gp120 envelope glycoprotein and anti-hiv-1 antibody3 17b

29	c1yyIM		Alignment	not modelled	7.0	30	PDB header: viral protein/immune system Chain: M: PDB Molecule: cd4m33, scorpion-toxin mimic of cd4; PDBTitle: crystal structure of cd4m33, a scorpion-toxin mimic of cd4, in complex2 with hiv-1 yu2 gp120 envelope glycoprotein and anti-hiv-1 antibody3 17b
30	c4r4ns		Alignment	not modelled	6.9	30	PDB header: viral protein/immune system/inhibitor Chain: S: PDB Molecule: hiv-1 gp120; PDBTitle: crystal structure of the anti-hiv-1 antibody 2.2c in complex with hiv-2 1 93ug037 gp120
31	c4r4ni		Alignment	not modelled	6.9	30	PDB header: viral protein/immune system/inhibitor Chain: I: PDB Molecule: hiv-1 gp120; PDBTitle: crystal structure of the anti-hiv-1 antibody 2.2c in complex with hiv-2 1 93ug037 gp120
32	c5w4IM		Alignment	not modelled	6.9	30	PDB header: viral protein/immune system Chain: M: PDB Molecule: cd4 mimetic peptide m48u1; PDBTitle: crystal structure of the non-neutralizing and adcc-potent c11-like2 antibody n12-i3 in complex with hiv-1 clade a/e gp120, the cd43 mimetic m48u1, and the antibody n5-i5.
33	c4ka2R		Alignment	not modelled	6.9	30	PDB header: viral protein/inhibitor Chain: R: PDB Molecule: m48u12; PDBTitle: crystal structure of cd4-mimetic miniprotein m48u12 in complex with2 hiv-1 yu2 gp120
34	c4r4na		Alignment	not modelled	6.9	30	PDB header: viral protein/immune system/inhibitor Chain: A: PDB Molecule: hiv-1 gp120; PDBTitle: crystal structure of the anti-hiv-1 antibody 2.2c in complex with hiv-2 1 93ug037 gp120
35	c4r4nb		Alignment	not modelled	6.9	30	PDB header: viral protein/immune system/inhibitor Chain: B: PDB Molecule: hiv-1 gp120; PDBTitle: crystal structure of the anti-hiv-1 antibody 2.2c in complex with hiv-2 1 93ug037 gp120
36	c5kjrN		Alignment	not modelled	6.9	30	PDB header: viral protein/immune system/inhibitor Chain: N: PDB Molecule: m48u1 cd4 mimetic peptide; PDBTitle: crystal structure of the adcc-potent antibody n60-i3 fab in complex2 with hiv-1 clade a/e gp120 w69a/s115w mutant and m48u1.
37	c4k0aR		Alignment	not modelled	6.9	30	PDB header: viral protein/inhibitor Chain: R: PDB Molecule: cd4-mimetic miniprotein m48u7; PDBTitle: crystal structure of cd4-mimetic miniprotein m48u7 in complex with2 hiv-1 yu2 gp120
38	c4r4nm		Alignment	not modelled	6.9	30	PDB header: viral protein/immune system/inhibitor Chain: M: PDB Molecule: hiv-1 gp120; PDBTitle: crystal structure of the anti-hiv-1 antibody 2.2c in complex with hiv-2 1 93ug037 gp120
39	c4jzzR		Alignment	not modelled	6.9	30	PDB header: viral protein/inhibitor Chain: R: PDB Molecule: cd4-mimetic miniprotein m48u1; PDBTitle: crystal structure of cd4-mimetic miniprotein m48u1 in complex with2 hiv-1 yu2 gp120 in c2221 space group
40	c4r4nv		Alignment	not modelled	6.9	30	PDB header: viral protein/immune system/inhibitor Chain: V: PDB Molecule: hiv-1 gp120; PDBTitle: crystal structure of the anti-hiv-1 antibody 2.2c in complex with hiv-2 1 93ug037 gp120
41	c4rfoN		Alignment	not modelled	6.9	30	PDB header: viral protein/immune system/inhibitor Chain: N: PDB Molecule: m48u1 cd4 mimetic peptide; PDBTitle: crystal structure of the adcc-potent antibody n60-i3 fab in complex2 with hiv-1 clade a/e gp120 and m48u1
42	c4jzwR		Alignment	not modelled	6.9	30	PDB header: viral protein/inhibitor Chain: R: PDB Molecule: cd4-mimetic miniprotein m48u1; PDBTitle: crystal structure of cd4-mimetic miniprotein m48u1 in complex with2 hiv-1 yu2 gp120 in p212121 space group
43	c4lajK		Alignment	not modelled	6.9	30	PDB header: viral protein/inhibitor Chain: K: PDB Molecule: cd4-mimetic miniprotein m48u1; PDBTitle: crystal structure of hiv-1 yu2 envelope gp120 glycoprotein in complex2 with cd4-mimetic miniprotein, m48u1, and llama single-domain, broadly3 neutralizing, co-receptor binding site antibody, jm4
44	c5uweN		Alignment	not modelled	6.9	30	PDB header: viral protein/immune system Chain: N: PDB Molecule: m48u1 cd4 mimetic peptide; PDBTitle: crystal structure of the adcc-potent, weakly neutralizing hiv env co-2 receptor binding site antibody n12-i2 fab in complex with hiv-1 clade3 a/e gp120 and m48u1
45	c4r4np		Alignment	not modelled	6.9	30	PDB header: viral protein/immune system/inhibitor Chain: P: PDB Molecule: hiv-1 gp120; PDBTitle: crystal structure of the anti-hiv-1 antibody 2.2c in complex with hiv-2 1 93ug037 gp120
46	c4r4ne		Alignment	not modelled	6.9	30	PDB header: viral protein/immune system/inhibitor Chain: E: PDB Molecule: hiv-1 gp120; PDBTitle: crystal structure of the anti-hiv-1 antibody 2.2c in complex with hiv-2 1 93ug037 gp120
47	c4r4fr		Alignment	not modelled	6.9	30	PDB header: viral protein/immune system/inhibitor Chain: R: PDB Molecule: m48u1 peptide; PDBTitle: crystal structure of non-neutralizing, a32-like antibody 2.2c in2 complex with hiv-1 yu2 gp120
48	c4lajC		Alignment	not modelled	6.9	30	PDB header: viral protein/inhibitor Chain: C: PDB Molecule: cd4-mimetic miniprotein m48u1; PDBTitle: crystal structure of hiv-1 yu2 envelope gp120 glycoprotein in complex2 with cd4-mimetic miniprotein, m48u1, and llama single-domain, broadly3 neutralizing, co-receptor binding site antibody, jm4
49	c5w4IN		Alignment	not modelled	6.9	30	PDB header: viral protein/immune system Chain: N: PDB Molecule: cd4 mimetic peptide m48u1; PDBTitle: crystal structure of the non-neutralizing and adcc-potent c11-like2 antibody n12-i3 in complex with hiv-1 clade a/e gp120, the cd43 mimetic m48u1, and the antibody n5-i5.
50	c4lajG		Alignment	not modelled	6.9	30	PDB header: viral protein/inhibitor Chain: G: PDB Molecule: cd4-mimetic miniprotein m48u1; PDBTitle: crystal structure of hiv-1 yu2 envelope gp120 glycoprotein in complex2 with cd4-mimetic miniprotein, m48u1, and llama single-domain, broadly3 neutralizing, co-receptor binding site antibody, jm4
51	c2i5yM		Alignment	not modelled	6.8	30	PDB header: viral protein/immune system Chain: M: PDB Molecule: cd4m47, scorpion-toxin mimic of cd4; PDBTitle: crystal structure of cd4m47, a scorpion-toxin mimic of cd4, in complex2 with hiv-1 yu2 gp120 envelope glycoprotein and

						anti-hiv-1 antibody3 17b PDB header: structural protein Chain: D: PDB Molecule: actin-related protein 2/3 complex subunit 2; PDBTitle: crystal structure of bovine arp2/3 complex
52	c2p9ID_	Alignment	not modelled	6.8	19	PDB header: ribosome Chain: D: PDB Molecule: ribosomal protein s4; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
53	c3bbnD_	Alignment	not modelled	6.7	21	PDB header: viral protein/immune system Chain: S: PDB Molecule: f23, scorpion-toxin mimic of cd4; PDBTitle: crystal structure of f23, a scorpion-toxin mimic of cd4, in complex2 with hiv-1 yu2 gp120 envelope glycoprotein and anti-hiv-1 antibody3 17b
54	c1yymS_	Alignment	not modelled	6.7	30	PDB header: viral protein/immune system Chain: M: PDB Molecule: f23, scorpion-toxin mimic of cd4; PDBTitle: crystal structure of f23, a scorpion-toxin mimic of cd4, in complex2 with hiv-1 yu2 gp120 envelope glycoprotein and anti-hiv-1 antibody3 17b
55	c1yymM_	Alignment	not modelled	6.7	30	PDB header: viral protein/immune system Chain: D: PDB Molecule: t-cell surface glycoprotein cd4 mimetic m48; PDBTitle: crystal structure of adcc-potent rhesus macaque antibody jr4 in2 complex with hiv-1 clade a/e gp120 and m48
56	c4rfnD_	Alignment	not modelled	6.7	30	PDB header: viral protein/immune system Chain: M: PDB Molecule: t-cell surface glycoprotein cd4 mimetic m48; PDBTitle: crystal structure of adcc-potent rhesus macaque antibody jr4 in2 complex with hiv-1 clade a/e gp120 and m48
57	c4rfnM_	Alignment	not modelled	6.7	30	PDB header: viral protein/immune system Chain: M: PDB Molecule: [phe23]m47, scorpion-toxin mimic of cd4; PDBTitle: crystal structure of [phe23]m47, a scorpion-toxin mimic of cd4, in2 complex with hiv-1 yu2 gp120 envelope glycoprotein and anti-hiv-13 antibody 17b
58	c2i60M_	Alignment	not modelled	6.6	30	PDB header: viral protein/immune system Chain: S: PDB Molecule: [phe23]m47, scorpion-toxin mimic of cd4; PDBTitle: crystal structure of [phe23]m47, a scorpion-toxin mimic of cd4, in2 complex with hiv-1 yu2 gp120 envelope glycoprotein and anti-hiv-13 antibody 17b
59	c2i60S_	Alignment	not modelled	6.6	30	PDB header: viral protein/immune system Chain: S: PDB Molecule: [phe23]m47, scorpion-toxin mimic of cd4; PDBTitle: crystal structure of [phe23]m47, a scorpion-toxin mimic of cd4, in2 complex with hiv-1 yu2 gp120 envelope glycoprotein and anti-hiv-13 antibody 17b
60	d1n8ia_	Alignment	not modelled	6.4	33	Fold: TIM beta/alpha-barrel Superfamily: Malate synthase G Family: Malate synthase G
61	c3udsA_	Alignment	not modelled	6.1	30	PDB header: transferase Chain: A: PDB Molecule: inositol-pentakisphosphate 2-kinase; PDBTitle: inositol 1,3,4,5,6-pentakisphosphate 2-kinase from a thaliana in2 complex with adp.
62	c3pf6C_	Alignment	not modelled	5.6	38	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein pp-luz7_gp033; PDBTitle: the structure of uncharacterized protein pp-luz7_gp033 from2 pseudomonas phage luz7.
63	d1k8kd2	Alignment	not modelled	5.2	19	Fold: Secretion chaperone-like Superfamily: Arp2/3 complex subunits Family: Arp2/3 complex subunits
64	c3izr_	Alignment	not modelled	5.2	20	PDB header: ribosome Chain: G: PDB Molecule: 60s ribosomal protein l6 (l6e); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome