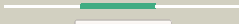
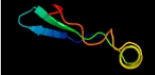
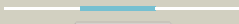
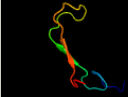
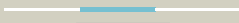
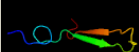

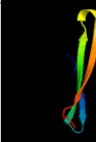



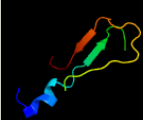
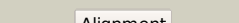
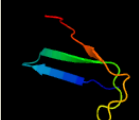

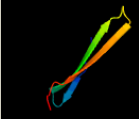

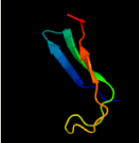
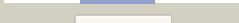
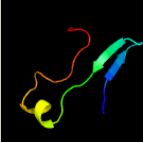

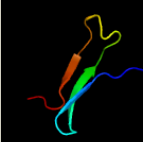
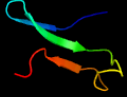


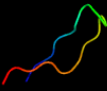
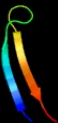

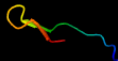

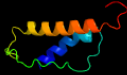


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1948c_(-)_2198721_2199071
Date	Mon Aug 5 13:25:04 BST 2019
Unique Job ID	791c469caa151ead

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2g9ha2	 Alignment		48.6	34	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
2	d1iaka2	 Alignment		31.5	34	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
3	d2p24a2	 Alignment		30.7	31	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
4	d1es0a2	 Alignment		30.2	34	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
5	d1p5dx3	 Alignment		30.0	18	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
6	d2b59b2	 Alignment		29.3	30	Fold: Prealbumin-like Superfamily: Carboxypeptidase regulatory domain-like Family: Pre-dockerin domain
7	d1uvqa2	 Alignment		29.1	38	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
8	d1s9va2	 Alignment		28.5	41	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
9	d1fnga2	 Alignment		28.4	28	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
10	d1klua2	 Alignment		28.4	34	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
11	d1muja2	 Alignment		26.8	34	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain

12	d1jk8a2	Alignment		23.9	31	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
13	c3d7aB_	Alignment		22.8	27	PDB header: unknown function Chain: B; PDB Molecule: upf0201 protein ph1010; PDBTitle: crystal structure of duf54 family protein ph1010 from2 hyperthermophilic archaea pyrococcus horikoshii ot3
14	d2dira1	Alignment		16.9	19	Fold: THUMP domain Superfamily: THUMP domain-like Family: Minimal THUMP
15	c2konA_	Alignment		16.4	50	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: nmr solution structure of cv_2116 from chromobacterium2 violaceum. northeast structural genomics consortium target3 cvt4(1-82)
16	c6hzbB_	Alignment		14.6	27	PDB header: transferase Chain: B; PDB Molecule: phosphoribulokinase; PDBTitle: crystal structure of redox-inhibited phosphoribulokinase from2 synechococcus sp. (strain pcc 6301)
17	c1ym0B_	Alignment		14.5	50	PDB header: hydrolase Chain: B; PDB Molecule: fibrinolytic enzyme component b; PDBTitle: crystal structure of earthworm fibrinolytic enzyme component b: a2 novel, glycosylated two-chained trypsin
18	c3tdqB_	Alignment		12.5	30	PDB header: cell adhesion Chain: B; PDB Molecule: pily2 protein; PDBTitle: crystal structure of a fimbrial biogenesis protein pily22 (pily2_pa4555) from pseudomonas aeruginosa pao1 at 2.10 a resolution
19	c3c9gB_	Alignment		12.3	20	PDB header: nucleotide binding protein Chain: B; PDB Molecule: upf0200/upf0201 protein af_1395; PDBTitle: crystal structure of uncharacterized upf0201 protein af_135
20	c1vraB_	Alignment		10.4	25	PDB header: transferase Chain: B; PDB Molecule: arginine biosynthesis bifunctional protein argj; PDBTitle: crystal structure of arginine biosynthesis bifunctional protein argj2 (10175521) from bacillus halodurans at 2.00 a resolution
21	d2e9xd2	Alignment	not modelled	10.1	42	Fold: GINS/PriA/YqbF domain Superfamily: PriA/YqbF domain Family: SLD5 C-terminal domain-like
22	c3jc5A_	Alignment	not modelled	9.4	28	PDB header: hydrolase Chain: A; PDB Molecule: dna replication complex gins protein psf1; PDBTitle: structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
23	d1wjka_	Alignment	not modelled	8.7	33	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
24	c3rgiA_	Alignment	not modelled	7.5	27	PDB header: transferase Chain: A; PDB Molecule: disd protein; PDBTitle: trans-acting transferase from disorazole synthase
25	c5d4pA_	Alignment	not modelled	7.3	12	PDB header: signaling protein Chain: A; PDB Molecule: putative nitrogen regulatory protein p-ii glnb; PDBTitle: structure of cpil bound to adp and bicarbonate, from thiomonas2 intermedia k12
26	c2hwf4_	Alignment	not modelled	7.2	31	PDB header: virus Chain: 4; PDB Molecule: human rhinovirus 1a coat protein (subunit vp4); PDBTitle: a comparison of the anti-rhinoviral drug binding pocket in hrv14 and2 hrv1a
27	c2hwe4_	Alignment	not modelled	7.2	31	PDB header: virus Chain: 4; PDB Molecule: human rhinovirus 1a coat protein (subunit vp4); PDBTitle: a comparison of the anti-rhinoviral drug binding pocket in hrv14 and2 hrv1a
						PDB header: virus Chain: 4; PDB Molecule: human rhinovirus 1a coat protein (subunit

28	c2hwd4	Alignment	not modelled	7.2	31	vp4); PDBTitle: a comparison of the anti-rhinoviral drug binding pocket in hrv14 and2 hrv1a
29	c1r1a4	Alignment	not modelled	7.2	31	PDB header: virus Chain: 4: PDB Molecule: human rhinovirus 1a coat protein (subunit vp4); PDBTitle: crystal structure of human rhinovirus serotype 1a (hrv1a)
30	c4u39J	Alignment	not modelled	7.0	38	PDB header: cell cycle Chain: J: PDB Molecule: cell division factor; PDBTitle: crystal structure of ftsz:mciz complex from bacillus subtilis
31	c4u39L	Alignment	not modelled	6.8	38	PDB header: cell cycle Chain: L: PDB Molecule: cell division factor; PDBTitle: crystal structure of ftsz:mciz complex from bacillus subtilis
32	c2gqcA	Alignment	not modelled	6.7	30	PDB header: hydrolase Chain: A: PDB Molecule: rhomboid intramembrane protease; PDBTitle: solution structure of the n-terminal domain of rhomboid intramembrane2 protease from p. aeruginosa
33	d3cx5c1	Alignment	not modelled	6.7	43	Fold: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
34	c2wskA	Alignment	not modelled	6.5	25	PDB header: hydrolase Chain: A: PDB Molecule: glycogen debranching enzyme; PDBTitle: crystal structure of glycogen debranching enzyme glgx from2 escherichia coli k-12
35	c2jrwA	Alignment	not modelled	6.4	80	PDB header: immune system Chain: A: PDB Molecule: cyclic extended pep.1; PDBTitle: solution structure of cyclic extended pep1(cyc.ext.pep.1)2 for autoimmune myasthenia gravis
36	c2l6tA	Alignment	not modelled	6.3	50	PDB header: antiviral protein Chain: A: PDB Molecule: vir-576; PDBTitle: efficacy of an hiv-1 entry inhibitor targeting the gp41 fusion peptide
37	c2l6sA	Alignment	not modelled	6.3	50	PDB header: antiviral protein Chain: A: PDB Molecule: vir-576; PDBTitle: efficacy of an hiv-1 entry inhibitor targeting the gp41 fusion peptide
38	d2qn6b1	Alignment	not modelled	6.3	15	Fold: Ferredoxin-like Superfamily: eIF-2-alpha, C-terminal domain Family: eIF-2-alpha, C-terminal domain
39	d1ppjc1	Alignment	not modelled	6.2	71	Fold: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
40	c2vopA	Alignment	not modelled	6.0	45	PDB header: rna-binding protein Chain: A: PDB Molecule: lupus la protein; PDBTitle: crystal structure of n-terminal domains of human la protein2 complexed with rna oligomer auuuu
41	d1x64a2	Alignment	not modelled	5.7	14	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
42	d1hvxal	Alignment	not modelled	5.7	18	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
43	c3c04A	Alignment	not modelled	5.7	18	PDB header: isomerase Chain: A: PDB Molecule: phosphomannomutase/phosphoglucomutase; PDBTitle: structure of the p368g mutant of pmm/pgm from p. aeruginosa
44	c1bf2A	Alignment	not modelled	5.5	31	PDB header: hydrolase Chain: A: PDB Molecule: isoamylase; PDBTitle: structure of pseudomonas isoamylase
45	d1zh5a1	Alignment	not modelled	5.5	45	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: La domain
46	c3it4B	Alignment	not modelled	5.4	23	PDB header: transferase Chain: B: PDB Molecule: arginine biosynthesis bifunctional protein argj PDBTitle: the crystal structure of ornithine acetyltransferase from2 mycobacterium tuberculosis (rv1653) at 1.7 a
47	c1unyA	Alignment	not modelled	5.4	64	PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces2 of four helix bundles
48	d1e43a1	Alignment	not modelled	5.4	24	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
49	d1x62a1	Alignment	not modelled	5.3	43	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
50	d1tzpa	Alignment	not modelled	5.2	32	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: MepA-like