
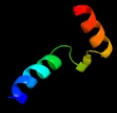
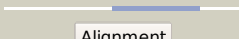

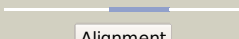
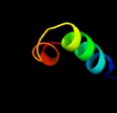







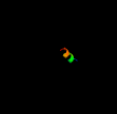





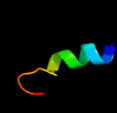

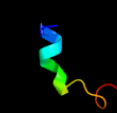











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1567c_(-)_1774866_1775150
Date	Fri Aug 2 13:30:15 BST 2019
Unique Job ID	2d3cda7de7b7ed2f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5o6vC_	 Alignment		37.6	33	PDB header: virus Chain: C: PDB Molecule: envelope protein; PDBTitle: the cryo-em structure of tick-borne encephalitis virus complexed with2 fab fragment of neutralizing antibody 19/1786
2	c4b03A_	 Alignment		28.3	15	PDB header: virus Chain: A: PDB Molecule: dengue virus 1 e protein; PDBTitle: 6a electron cryomicroscopy structure of immature dengue virus serotype2 1
3	c5n1qD_	 Alignment		27.8	52	PDB header: transferase Chain: D: PDB Molecule: methyl-coenzyme m reductase iii from methanothermococcus PDBTitle: methyl-coenzyme m reductase iii from methanothermococcus2 thermolithotrophicus at 1.9 a resolution
4	d1v4sa2	 Alignment		26.1	60	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
5	d1r3ba_	 Alignment		25.9	18	Fold: Bromodomain-like Superfamily: Mob1/phocein Family: Mob1/phocein
6	d1bg3a4	 Alignment		24.3	64	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
7	c3hm8D_	 Alignment		22.9	64	PDB header: transferase Chain: D: PDB Molecule: hexokinase-3; PDBTitle: crystal structure of the c-terminal hexokinase domain of human hk3
8	d1czan4	 Alignment		22.9	70	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
9	c5wvxA_	 Alignment		22.3	29	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: trypsin/chymotrypsin inhibitor; PDBTitle: crystal structure of bifunctional kunitz type trypsin /amylase2 inhibitor (amtin) from the tubers of aloccasia macrorrhiza
10	c5yf4A_	 Alignment		22.2	29	PDB header: protein binding Chain: A: PDB Molecule: mob-like protein phocein; PDBTitle: a kinase complex mst4-mob4
11	d1pi1a_	 Alignment		22.0	24	Fold: Bromodomain-like Superfamily: Mob1/phocein Family: Mob1/phocein

12	c2hjnA	Alignment		21.7	29	PDB header: cell cycle Chain: A; PDB Molecule: maintenance of ploidy protein mob1; PDBTitle: structural and functional analysis of saccharomyces2 cerevisiae mob1
13	c2kxaA	Alignment		21.6	42	PDB header: viral protein, immune system Chain: A; PDB Molecule: haemagglutinin ha2 chain peptide; PDBTitle: the hemagglutinin fusion peptide (h1 subtype) at ph 7.4
14	d1bg3a2	Alignment		21.6	70	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
15	d1czan2	Alignment		21.3	47	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
16	c6el1F	Alignment		20.7	21	PDB header: membrane protein Chain: F; PDB Molecule: yaxa; PDBTitle: yaxab pore complex
17	c1v4sA	Alignment		20.0	55	PDB header: transferase Chain: A; PDB Molecule: glucokinase isoform 2; PDBTitle: crystal structure of human glucokinase
18	d1ig8a2	Alignment		19.1	45	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
19	c2k27A	Alignment		17.0	36	PDB header: transcription regulator Chain: A; PDB Molecule: paired box protein pax-8; PDBTitle: solution structure of human pax8 paired box domain
20	c5zqtA	Alignment		16.9	55	PDB header: transferase Chain: A; PDB Molecule: hexokinase-6; PDBTitle: crystal structure of oryza sativa hexokinase 6
21	c2lbgA	Alignment	not modelled	16.7	45	PDB header: membrane protein Chain: A; PDB Molecule: major prion protein; PDBTitle: structure of the chr of the prion protein in dpc micelles
22	d1k78a2	Alignment	not modelled	15.3	35	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
23	c1ciiA	Alignment	not modelled	15.0	10	PDB header: transmembrane protein Chain: A; PDB Molecule: colicin ia; PDBTitle: colicin ia
24	c5wsnC	Alignment	not modelled	15.0	22	PDB header: virus Chain: C; PDB Molecule: e protein; PDBTitle: structure of japanese encephalitis virus
25	c1ig8A	Alignment	not modelled	14.5	45	PDB header: transferase Chain: A; PDB Molecule: hexokinase pii; PDBTitle: crystal structure of yeast hexokinase pii with the correct2 amino acid sequence
26	d1i8ya	Alignment	not modelled	14.3	44	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Granulin repeat Family: Granulin repeat
27	c1i8yA	Alignment	not modelled	14.3	44	PDB header: cytokine Chain: A; PDB Molecule: granulin-1; PDBTitle: semi-automatic structure determination of the cg1 3-302 peptide based on aria
28	d1bdqa2	Alignment	not modelled	14.3	56	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
29	d6paxa2	Alignment	not modelled	14.3	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like

						Family: Paired domain
30	c4ii0A_	Alignment	not modelled	14.3	38	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: cratabl; PDBTitle: crystal structure of cratabl, a trypsin inhibitor from crataeva tapia
31	c2w8mB_	Alignment	not modelled	14.0	63	PDB header: hydrolase Chain: B: PDB Molecule: orf d212; PDBTitle: structure of d212, a nuclease from a fusselovirus.
32	c4qs9A_	Alignment	not modelled	13.8	55	PDB header: transferase Chain: A: PDB Molecule: hexokinase-1; PDBTitle: arabidopsis hexokinase 1 (athxk1) mutant s177a structure in glucose-2 bound form
33	d3bx1c1	Alignment	not modelled	13.7	17	Fold: beta-Trefoil Superfamily: STI-like Family: Kunitz (STI) inhibitors
34	c6ijjK_	Alignment	not modelled	13.3	14	PDB header: membrane protein Chain: K: PDB Molecule: psak; PDBTitle: photosystem i of chlamydomonas reinhardtii
35	c1hkgA_	Alignment	not modelled	13.0	6	PDB header: transferase Chain: A: PDB Molecule: hexokinase a; PDBTitle: structural dynamics of yeast hexokinase during catalysis
36	c6c6lO_	Alignment	not modelled	12.9	21	PDB header: membrane protein Chain: O: PDB Molecule: v-type proton atpase subunit f; PDBTitle: yeast vacuolar atpase vo in lipid nanodisc
37	c4nl6C_	Alignment	not modelled	12.8	78	PDB header: splicing Chain: C: PDB Molecule: survival motor neuron protein; PDBTitle: structure of the full-length form of the protein smn found in healthy2 patients
38	c5dvhA_	Alignment	not modelled	12.6	18	PDB header: protease inhibitor Chain: A: PDB Molecule: pcpi-3; PDBTitle: structure of the kunitz-type cysteine protease inhibitor pcpi-3 from2 potato
39	c6nk6B_	Alignment	not modelled	12.4	38	PDB header: virus like particle/signaling protein Chain: B: PDB Molecule: e1 glycoprotein; PDBTitle: electron cryo-microscopy of chikungunya vlp in complex with mouse2 mxra8 receptor
40	c1r8oA_	Alignment	not modelled	11.7	29	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: kunitz trypsin inhibitor; PDBTitle: crystal structure of an unusual kunitz-type trypsin inhibitor from2 copaifera langsdorffii seeds
41	d1tiea_	Alignment	not modelled	11.6	30	Fold: beta-Trefoil Superfamily: STI-like Family: Kunitz (STI) inhibitors
42	c5ireA_	Alignment	not modelled	11.5	24	PDB header: virus Chain: A: PDB Molecule: e protein; PDBTitle: the cryo-em structure of zika virus
43	d2i1sa1	Alignment	not modelled	11.3	10	Fold: MM3350-like Superfamily: MM3350-like Family: MM3350-like
44	c5dssB_	Alignment	not modelled	11.2	29	PDB header: plant protein Chain: B: PDB Molecule: mp-4; PDBTitle: mp-4 contributes to snake venom neutralization by mucuna pruriens2 seeds through stimulation of cross-reactive antibodies
45	c2xfcD_	Alignment	not modelled	11.0	38	PDB header: virus Chain: D: PDB Molecule: e1 envelope glycoprotein; PDBTitle: the chikungunya e1 e2 envelope glycoprotein complex fit into2 the semliki forest virus cryo-em map
46	d1avwb_	Alignment	not modelled	10.9	15	Fold: beta-Trefoil Superfamily: STI-like Family: Kunitz (STI) inhibitors
47	c2yewB_	Alignment	not modelled	10.8	86	PDB header: virus Chain: B: PDB Molecule: e1 envelope glycoprotein; PDBTitle: modeling barmah forest virus structural proteins
48	d1m3va1	Alignment	not modelled	10.8	60	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
49	c5hpszB_	Alignment	not modelled	10.8	37	PDB header: chlorophyll binding protein Chain: B: PDB Molecule: water-soluble chlorophyll protein; PDBTitle: type ii water soluble chl binding proteins
50	c3izxE_	Alignment	not modelled	10.7	29	PDB header: virus Chain: E: PDB Molecule: viral structural protein 5; PDBTitle: 3.1 angstrom cryoem structure of cytoplasmic polyhedrosis virus
51	d1wbaa_	Alignment	not modelled	10.7	14	Fold: beta-Trefoil Superfamily: STI-like Family: Kunitz (STI) inhibitors
52	d1xqoa_	Alignment	not modelled	10.6	13	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: AgoG-like
53	c3n42F_	Alignment	not modelled	10.6	38	PDB header: viral protein Chain: F: PDB Molecule: e1 envelope glycoprotein; PDBTitle: crystal structures of the mature envelope glycoprotein complex (furin2 cleavage) of chikungunya virus.
54	c5yh4A_	Alignment	not modelled	10.6	38	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: miraculin-like protein; PDBTitle: miraculin-like protein from vitis vinifera
55	c2xfbF_	Alignment	not modelled	10.6	38	PDB header: virus Chain: F: PDB Molecule: e1 envelope glycoprotein; PDBTitle: the chikungunya e1 e2 envelope glycoprotein complex fit into2 the sindbis virus cryo-em map
						PDB header: virus

56	c1ld4O_	Alignment	not modelled	10.6	42	Chain: O: PDB Molecule: spike glycoprotein e1; PDBTitle: placement of the structural proteins in sindbis virus
57	d1hbna1	Alignment	not modelled	10.5	44	Fold: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain Superfamily: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain Family: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain
58	c1z8yE_	Alignment	not modelled	10.4	86	PDB header: virus Chain: E: PDB Molecule: spike glycoprotein e1; PDBTitle: mapping the e2 glycoprotein of alphaviruses
59	c3tc2C_	Alignment	not modelled	10.4	21	PDB header: hydrolase inhibitor Chain: C: PDB Molecule: kunitz-type proteinase inhibitor p1h5; PDBTitle: crystal structure of potato serine protease inhibitor.
60	d2alaa2	Alignment	not modelled	10.2	38	Fold: Viral glycoprotein, central and dimerisation domains Superfamily: Viral glycoprotein, central and dimerisation domains Family: Viral glycoprotein, central and dimerisation domains
61	c3lw5K_	Alignment	not modelled	10.2	27	PDB header: photosynthesis Chain: K: PDB Molecule: photosystem i reaction center subunit x psak; PDBTitle: improved model of plant photosystem i
62	c6fgnA_	Alignment	not modelled	10.1	35	PDB header: antitumor protein Chain: A: PDB Molecule: histone acetyltransferase p300,tumor protein 63; PDBTitle: solution structure of p300taz2-p63ta
63	c1qhaA_	Alignment	not modelled	9.5	70	PDB header: transferase Chain: A: PDB Molecule: protein (hexokinase); PDBTitle: human hexokinase type i complexed with atp analogue amp-pnp
64	c4j2yA_	Alignment	not modelled	9.5	29	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: trypsin inhibitor; PDBTitle: crystal structure of a plant trypsin inhibitor ecti in complex with2 bovine trypsin.
65	c3j0fG_	Alignment	not modelled	9.5	42	PDB header: virus Chain: G: PDB Molecule: e1 envelope glycoprotein; PDBTitle: sindbis virion
66	c3iirA_	Alignment	not modelled	9.5	37	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: trypsin inhibitor; PDBTitle: crystal structure of miraculin like protein from seeds of murraya2 koenigii
67	c2qn4B_	Alignment	not modelled	9.5	21	PDB header: hydrolase inhibitor Chain: B: PDB Molecule: alpha-amylase/subtilisin inhibitor; PDBTitle: structure and function study of rice bifunctional alpha-2 amylase/subtilisin inhibitor from oryza sativa
68	c2q2kA_	Alignment	not modelled	9.5	23	PDB header: dna binding protein/dna Chain: A: PDB Molecule: hypothetical protein; PDBTitle: structure of nucleic-acid binding protein
69	c1bdgA_	Alignment	not modelled	9.2	56	PDB header: hexokinase Chain: A: PDB Molecule: hexokinase; PDBTitle: hexokinase from schistosoma mansoni complexed with glucose
70	c2q2kB_	Alignment	not modelled	9.1	23	PDB header: dna binding protein/dna Chain: B: PDB Molecule: hypothetical protein; PDBTitle: structure of nucleic-acid binding protein
71	c1cirA_	Alignment	not modelled	9.0	60	PDB header: serine protease inhibitor Chain: A: PDB Molecule: chymotrypsin inhibitor 2; PDBTitle: complex of two fragments of ci2 [(1-40)(dot)(41-64)]
72	d1eyla_	Alignment	not modelled	8.9	31	Fold: beta-Trefoil Superfamily: STI-like Family: Kunitz (STI) inhibitors
73	d1s7ba_	Alignment	not modelled	8.9	23	Fold: Multidrug resistance efflux transporter EmrE Superfamily: Multidrug resistance efflux transporter EmrE Family: Multidrug resistance efflux transporter EmrE
74	c1hbuD_	Alignment	not modelled	8.9	41	PDB header: methanogenesis Chain: D: PDB Molecule: methyl-coenzyme m reductase i alpha subunit; PDBTitle: methyl-coenzyme m reductase in the mcr-red1-silent state in complex2 with coenzyme m
75	d1r8na_	Alignment	not modelled	8.7	29	Fold: beta-Trefoil Superfamily: STI-like Family: Kunitz (STI) inhibitors
76	c3s8jB_	Alignment	not modelled	8.7	29	PDB header: hydrolase inhibitor Chain: B: PDB Molecule: latex serine proteinase inhibitor; PDBTitle: crystal structure of a papaya latex serine protease inhibitor (ppi) at2 2.6a resolution
77	c2alaA_	Alignment	not modelled	8.6	38	PDB header: viral protein Chain: A: PDB Molecule: structural polyprotein (p130); PDBTitle: crystal structure of the semliki forest virus envelope protein e1 in2 its monomeric conformation.
78	d1p4ea2	Alignment	not modelled	8.6	22	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
79	c3d3sA_	Alignment	not modelled	8.6	15	PDB header: transferase Chain: A: PDB Molecule: l-2,4-diaminobutyric acid acetyltransferase; PDBTitle: crystal structure of l-2,4-diaminobutyric acid acetyltransferase from2 bordetella parapertussis
80	c4xb6D_	Alignment	not modelled	8.6	39	PDB header: transferase Chain: D: PDB Molecule: alpha-d-ribose 1-methylphosphonate 5-phosphate c-p lyase; PDBTitle: structure of the e. coli c-p lyase core complex
81	c1e6yA_	Alignment	not modelled	8.5	40	PDB header: oxidoreductase Chain: A: PDB Molecule: methyl-coenzyme m reductase subunit alpha; PDBTitle: methyl-coenzyme m reductase from methanosarcina

						barkeri
82	c6gy6O_	Alignment	not modelled	8.4	21	PDB header: toxin Chain: Q: PDB Molecule: xaxa; PDBTitle: xaxab pore complex from xenorhabdus nematophila
83	c6mx4J_	Alignment	not modelled	8.3	38	PDB header: virus Chain: J: PDB Molecule: e1; PDBTitle: cryoem structure of chimeric eastern equine encephalitis virus
84	d1j2oa1	Alignment	not modelled	8.3	60	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
85	c3muwE_	Alignment	not modelled	8.3	42	PDB header: virus Chain: E: PDB Molecule: structural polyprotein; PDBTitle: pseudo-atomic structure of the e2-e1 protein shell in sindbis virus
86	d1xg7a_	Alignment	not modelled	8.0	21	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: AgoG-like
87	c5hg1A_	Alignment	not modelled	8.0	70	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: hexokinase-2; PDBTitle: crystal structure of human hexokinase 2 with cmpd 1, a c-2-substituted2 glucosamine
88	c6igzK_	Alignment	not modelled	7.8	21	PDB header: plant protein Chain: K: PDB Molecule: psak; PDBTitle: structure of psi-lhci
89	c3j0cG_	Alignment	not modelled	7.6	42	PDB header: virus Chain: G: PDB Molecule: e1 envelope glycoprotein; PDBTitle: models of e1, e2 and cp of venezuelan equine encephalitis virus tc-832 strain restrained by a near atomic resolution cryo-em map
90	c1bctA_	Alignment	not modelled	7.6	57	PDB header: photoreceptor Chain: A: PDB Molecule: bacteriorhodopsin; PDBTitle: three-dimensional structure of proteolytic fragment 163-2312 of bacterioopsin determined from nuclear magnetic3 resonance data in solution
91	c3io2A_	Alignment	not modelled	7.4	35	PDB header: transferase Chain: A: PDB Molecule: histone acetyltransferase p300; PDBTitle: crystal structure of the taz2 domain of p300
92	c2dreA_	Alignment	not modelled	7.2	17	PDB header: plant protein Chain: A: PDB Molecule: water-soluble chlorophyll protein; PDBTitle: crystal structure of water-soluble chlorophyll protein from2 lepidium virginicum at 2.00 angstrom resolution
93	c2l3fA_	Alignment	not modelled	7.2	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of a putative uracil dna glycosylase from2 methanosarcina acetivorans, northeast structural genomics consortium3 target mvr76
94	c2go2A_	Alignment	not modelled	7.1	32	PDB header: protein binding Chain: A: PDB Molecule: kunitz-type serine protease inhibitor bbki; PDBTitle: crystal structure of bbki, a kunitz-type kallikrein inhibitor
95	c2aj6A_	Alignment	not modelled	7.0	24	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein mw0638; PDBTitle: crystal structure of a putative gnat family acetyltransferase (mw0638)2 from staphylococcus aureus subsp. aureus at 1.63 a resolution
96	c1p58C_	Alignment	not modelled	6.8	27	PDB header: virus Chain: C: PDB Molecule: major envelope protein e; PDBTitle: complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
97	d1rutx1	Alignment	not modelled	6.8	60	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
98	c4e72A_	Alignment	not modelled	6.7	36	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf3298 family protein (pa4972) from2 pseudomonas aeruginosa pao1 at 2.15 a resolution
99	c3iz3D_	Alignment	not modelled	6.6	32	PDB header: virus Chain: D: PDB Molecule: viral structural protein 5; PDBTitle: cryoem structure of cytoplasmic polyhedrosis virus