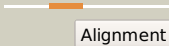

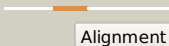

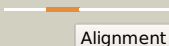



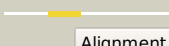
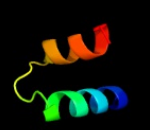
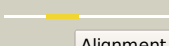

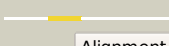






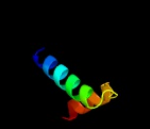

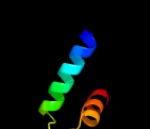





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1249c_(-)_1393200_1393988
Date	Wed Jul 31 22:05:34 BST 2019
Unique Job ID	441798dafb7b76b3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6bv7A_	 Alignment		86.9	15	PDB header: membrane protein Chain: A; PDB Molecule: sodium/calcium exchanger 1; PDBTitle: nmr structure of sodium/calcium exchanger 1 (ncx1) two-helix bundle2 (thb) domain
2	d1kxpd3	 Alignment		84.7	27	Fold: Serum albumin-like Superfamily: Serum albumin-like Family: Serum albumin-like
3	c2pmwB_	 Alignment		83.3	16	PDB header: hydrolase Chain: B; PDB Molecule: proprotein convertase subtilisin/kexin type 9; PDBTitle: the crystal structure of proprotein convertase subtilisin2 kexin type 9 (pcsk9)
4	c1s2nB_	 Alignment		82.0	20	PDB header: hydrolase Chain: B; PDB Molecule: extracellular subtilisin-like serine proteinase; PDBTitle: crystal structure of a cold adapted subtilisin-like serine proteinase
5	c4dztA_	 Alignment		79.2	20	PDB header: hydrolase/hydrolase inhibitor Chain: A; PDB Molecule: aqualysin-1; PDBTitle: aqualysin i: the crystal structure of a serine protease from an2 extreme thermophile, thermus aquaticus yt-1
6	c5yl7A_	 Alignment		78.2	25	PDB header: hydrolase Chain: A; PDB Molecule: pseudoalteromonas arctica pamc 21717; PDBTitle: proteases from pseudoalteromonas arctica pamc 21717 (pro21717)
7	c3f7oB_	 Alignment		75.9	10	PDB header: hydrolase Chain: B; PDB Molecule: serine protease; PDBTitle: crystal structure of cuticle-degrading protease from paecilomyces2 lilacinus (pl646)
8	c2b6nA_	 Alignment		75.8	27	PDB header: hydrolase Chain: A; PDB Molecule: proteinase k; PDBTitle: the 1.8 a crystal structure of a proteinase k like enzyme from a2 psychrotroph serratia species
9	c2w2qA_	 Alignment		75.6	15	PDB header: hydrolase/receptor Chain: A; PDB Molecule: proprotein convertase subtilisin/kexin type 9; PDBTitle: pcsk9-deltac d374h mutant bound to wt egf-a of ldlr
10	c5vlpA_	 Alignment		75.2	15	PDB header: hydrolase Chain: A; PDB Molecule: proprotein convertase subtilisin/kexin type 9; PDBTitle: pcsk9 complex with ldlr antagonist peptide and fab7g7
11	c4j94A_	 Alignment		73.3	16	PDB header: hydrolase Chain: A; PDB Molecule: membrane-anchored mycosin mycp1; PDBTitle: crystal structure of mycp1 from the esx-1 type vii secretion system

12	c4tr2A_	Alignment		72.3	22	PDB header: hydrolase Chain: A; PDB Molecule: subtilisin-like 1 serine protease; PDBTitle: crystal structure of pvsb1
13	c3bpsA_	Alignment		71.2	15	PDB header: hydrolase/lipid transport Chain: A; PDB Molecule: proprotein convertase subtilisin/kexin type 9; PDBTitle: pcsk9:egf-a complex
14	d1gnsa_	Alignment		70.6	19	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases
15	c5vllA_	Alignment		70.4	15	PDB header: hydrolase Chain: A; PDB Molecule: proprotein convertase subtilisin/kexin type 9; PDBTitle: short pcsk9 delta-p' complex with peptide pep3
16	c3vv3B_	Alignment		70.0	13	PDB header: hydrolase Chain: B; PDB Molecule: deseasin mcp-01; PDBTitle: crystal structure of deseasin mcp-01 from pseudoalteromonas sp. sm9913
17	d2ixta1	Alignment		69.7	18	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases
18	d1qcia_	Alignment		69.6	21	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases
19	c5z6oA_	Alignment		69.1	9	PDB header: hydrolase Chain: A; PDB Molecule: protease; PDBTitle: crystal structure of penicillium cyclopium protease
20	d1to2e_	Alignment		68.9	21	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases
21	c6paxA_	Alignment	not modelled	68.7	18	PDB header: gene regulation/dna Chain: A; PDB Molecule: homeobox protein pax-6; PDBTitle: crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
22	c2k27A_	Alignment	not modelled	67.9	15	PDB header: transcription regulator Chain: A; PDB Molecule: paired box protein pax-8; PDBTitle: solution structure of human pax8 paired box domain
23	c4mzdA_	Alignment	not modelled	67.6	13	PDB header: hydrolase Chain: A; PDB Molecule: nisin leader peptide-processing serine protease nisp; PDBTitle: high resolution crystal structure of the nisin leader peptidase nisp2 from lactococcus lactis
24	d1k78a2	Alignment	not modelled	67.1	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
25	c4kg7A_	Alignment	not modelled	65.9	16	PDB header: hydrolase Chain: A; PDB Molecule: peptidase s8 and s53, subtilisin, kexin, sedolisin; PDBTitle: structure of mycp3 protease from the type vii (esx-3) secretion2 system.
26	c3vtaB_	Alignment	not modelled	63.2	23	PDB header: hydrolase Chain: B; PDB Molecule: cucumisin; PDBTitle: crystal structure of cucumisin, a subtilisin-like endoprotease from2 cucumis melo l
27	c3hyiA_	Alignment	not modelled	59.9	27	PDB header: transcription regulator Chain: A; PDB Molecule: protein duf199/whia; PDBTitle: crystal structure of full-length duf199/whia from therratoga maritima
28	d1bh6a_	Alignment	not modelled	59.8	17	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases

29	c2iy9A_	Alignment	not modelled	58.9	12	PDB header: toxin Chain: A: PDB Molecule: suba; PDBTitle: crystal structure of the a-subunit of the ab5 toxin from e.2 coli
30	d6paxa2	Alignment	not modelled	58.5	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
31	d1pdnc_	Alignment	not modelled	57.5	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
32	d2ibaa1	Alignment	not modelled	55.9	12	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase)
33	d1r0re_	Alignment	not modelled	55.7	21	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases
34	c4lvnA_	Alignment	not modelled	54.6	19	PDB header: hydrolase/inhibitor/immune system Chain: A: PDB Molecule: subtilisin-like serine protease; PDBTitle: crystal structure of pfsb1-prodomain-nimp.m7 fab complex
35	d2fbqa2	Alignment	not modelled	50.7	19	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
36	c2oxaA_	Alignment	not modelled	50.5	22	PDB header: hydrolase Chain: A: PDB Molecule: extracellular serine protease; PDBTitle: crystal structure of serine protease of aeromonas sobria
37	c4r99B_	Alignment	not modelled	49.9	15	PDB header: hydrolase Chain: B: PDB Molecule: uricase; PDBTitle: crystal structure of a uricase from bacillus fastidious
38	d1j2ga1	Alignment	not modelled	48.4	10	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase)
39	c3zxyA_	Alignment	not modelled	48.0	17	PDB header: hydrolase Chain: A: PDB Molecule: subtilisin-like protein; PDBTitle: structure of s218a mutant of the protease domain of pata
40	c1p8jB_	Alignment	not modelled	47.9	12	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: furin precursor; PDBTitle: crystal structure of the proprotein convertase furin
41	d1v6ca_	Alignment	not modelled	45.6	19	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases
42	d1meeA_	Alignment	not modelled	45.4	24	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases
43	d1p8ja2	Alignment	not modelled	44.4	13	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases
44	c6a4mA_	Alignment	not modelled	42.6	12	PDB header: hydrolase Chain: A: PDB Molecule: uric acid degradation bifunctional protein pucl; PDBTitle: structure of urate oxidase from bacillus subtilis 168
45	c5m98H_	Alignment	not modelled	41.2	18	PDB header: oxidoreductase Chain: H: PDB Molecule: uricase; PDBTitle: crystal structure of urate oxidase from zebrafish
46	c3whiA_	Alignment	not modelled	41.0	22	PDB header: hydrolase Chain: A: PDB Molecule: subtilisin e; PDBTitle: crystal structure of unautoprocessed form of is1-inserted pro-2 subtilisin e
47	d2id4a2	Alignment	not modelled	40.1	17	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases
48	c1j2gC_	Alignment	not modelled	39.9	10	PDB header: oxidoreductase Chain: C: PDB Molecule: uricase; PDBTitle: crystal structure of urate oxidase from bacillus sp. tb-90 co-2 crystallized with 8-azaxanthine
49	d1wjta_	Alignment	not modelled	39.0	15	Fold: N-cbl like Superfamily: Conserved domain common to transcription factors TFIS, elongin A, CRSP70 Family: Conserved domain common to transcription factors TFIS, elongin A, CRSP70
50	c1r56H_	Alignment	not modelled	37.7	12	PDB header: oxidoreductase Chain: H: PDB Molecule: uricase; PDBTitle: uncomplexed urate oxidase from aspergillus flavus
51	c3zxxA_	Alignment	not modelled	36.6	17	PDB header: hydrolase Chain: A: PDB Molecule: subtilisin-like protein; PDBTitle: structure of self-cleaved protease domain of pata
52	d1r6va_	Alignment	not modelled	35.7	31	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases
53	c1r64A_	Alignment	not modelled	34.9	15	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: kexin; PDBTitle: the 2.2 a crystal structure of kex2 protease in complex with ac-arg-2 glu-lys-boroarg peptidyl boronic acid inhibitor
54	c2bf9A_	Alignment	not modelled	34.3	24	PDB header: hormone Chain: A: PDB Molecule: pancreatic hormone; PDBTitle: anisotropic refinement of avian (turkey) pancreatic polypeptide at 0.2 99 angstroms resolution.
55	c2x8jB_	Alignment	not modelled	31.9	21	PDB header: hydrolase Chain: B: PDB Molecule: intracellular subtilisin protease; PDBTitle: intracellular subtilisin precursor from b. clausii

56	c4aksA	Alignment	not modelled	30.6	6	PDB header: hydrolase Chain: A: PDB Molecule: thiazoline oxidase/subtilisin-like protease; PDBTitle: patg macrocyclase domain
57	c2dezA	Alignment	not modelled	30.0	29	PDB header: neuropeptide Chain: A: PDB Molecule: peptide yy; PDBTitle: structure of human pyy
58	d1eo0a	Alignment	not modelled	28.9	11	Fold: N-cbl like Superfamily: Conserved domain common to transcription factors TFIIIS, elongin A, CRSP70 Family: Conserved domain common to transcription factors TFIIIS, elongin A, CRSP70
59	c1tz5A	Alignment	not modelled	28.8	19	PDB header: hormone/growth factor Chain: A: PDB Molecule: chimera of pancreatic hormone and neuropeptide y; PDBTitle: [pnpy19-23]-hpp bound to dpc micelles
60	c3i74B	Alignment	not modelled	26.9	31	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: subtilisin-like protease; PDBTitle: crystal structure of the plant subtilisin-like protease sbt3 in2 complex with a chloromethylketone inhibitor
61	c1ronA	Alignment	not modelled	26.9	10	PDB header: neuropeptide Chain: A: PDB Molecule: neuropeptide y; PDBTitle: nmr solution structure of human neuropeptide y
62	c4wwxB	Alignment	not modelled	25.7	19	PDB header: hydrolase, ligase Chain: B: PDB Molecule: v(d)j recombination-activating protein 1; PDBTitle: crystal structure of the core rag1/2 recombinase
63	c2ph0A	Alignment	not modelled	24.6	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the q6d2t7_erwct protein from erwinia carotovora.2 nesg target ewr41.
64	c4wxmD	Alignment	not modelled	24.1	45	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator fleq; PDBTitle: fleq rec domain from pseudomonas aeruginosa pao1
65	c4r0gA	Alignment	not modelled	22.9	21	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of lpg0393 from legionella pneumophila
66	d1fdja	Alignment	not modelled	22.2	22	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
67	c4h6wB	Alignment	not modelled	18.6	14	PDB header: hydrolase Chain: B: PDB Molecule: n-terminal cyanobactin protease; PDBTitle: structure of prenylagaramide maturation protease paga
68	c6d79A	Alignment	not modelled	16.4	15	PDB header: transport protein Chain: A: PDB Molecule: sulfate transporter cysz; PDBTitle: structure of cysz, a sulfate permease from pseudomonas fragi
69	c3pxpA	Alignment	not modelled	16.1	21	PDB header: transcription regulator Chain: A: PDB Molecule: helix-turn-helix domain protein; PDBTitle: crystal structure of a pas and dna binding domain containing protein2 (caur_2278) from chloroflexus aurantiacus j-10-fl at 2.30 a3 resolution
70	c3wisA	Alignment	not modelled	15.5	24	PDB header: oxidoreductase Chain: A: PDB Molecule: putative dihydromethanopterin reductase (afpa); PDBTitle: crystal structure of burkholderia xenovorans dmrB in complex with fmn:2 a cubic protein cage for redox transfer
71	d1fbaa	Alignment	not modelled	15.0	24	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
72	c2oviA	Alignment	not modelled	14.4	5	PDB header: ligand binding protein, metal transport Chain: A: PDB Molecule: hypothetical protein chux; PDBTitle: structure of the heme binding protein chux
73	c3mmtC	Alignment	not modelled	14.4	29	PDB header: hydrolase Chain: C: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: crystal structure of fructose bisphosphate aldolase from bartonella2 henselae, bound to fructose bisphosphate
74	c2pc4B	Alignment	not modelled	14.1	16	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: crystal structure of fructose-bisphosphate aldolase from plasmodium2 falciparum in complex with trap-tail determined at 2.4 angstrom3 resolution
75	d1qo5b	Alignment	not modelled	13.9	24	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
76	c3lpcA	Alignment	not modelled	13.6	22	PDB header: hydrolase Chain: A: PDB Molecule: aprb2; PDBTitle: crystal structure of a subtilisin-like protease
77	c2z2yC	Alignment	not modelled	13.5	6	PDB header: hydrolase Chain: C: PDB Molecule: tk-subtilisin; PDBTitle: crystal structure of autoprocessed form of tk-subtilisin
78	c5ldwf	Alignment	not modelled	13.1	19	PDB header: oxidoreductase Chain: F: PDB Molecule: nahd dehydrogenase [ubiquinone] flavoprotein 1, PDBTitle: structure of mammalian respiratory complex i, class1
79	c5lc5f	Alignment	not modelled	13.1	19	PDB header: oxidoreductase Chain: F: PDB Molecule: nahd dehydrogenase [ubiquinone] flavoprotein 1, PDBTitle: structure of mammalian respiratory complex i, class2
80	c5exvD	Alignment	not modelled	12.7	35	PDB header: heme-binding protein Chain: D: PDB Molecule: hemin-degrading hems.chux domain protein; PDBTitle: crystal structure of heme binding protein hutx from vibrio cholerae
						PDB header: membrane protein

81	c4y0A_	Alignment	not modelled	12.6	25	Chain: A: PDB Molecule: putative membrane protein mmpl11; PDBTitle: mycobacterial membrane protein mmpl11d2
82	d2pwaa1	Alignment	not modelled	12.0	9	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases
83	d1zaia1	Alignment	not modelled	11.7	20	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
84	d2np3a2	Alignment	not modelled	11.7	22	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
85	d1vi7a1	Alignment	not modelled	11.4	47	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: YigZ N-terminal domain-like
86	c5m48A_	Alignment	not modelled	11.4	16	PDB header: transcription Chain: A: PDB Molecule: regulator of ty1 transposition protein 103; PDBTitle: coiled coil domain of rtt103p
87	c3onqB_	Alignment	not modelled	11.1	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: regulator of polyketide synthase expression; PDBTitle: crystal structure of regulator of polyketide synthase expression2 bad_0249 from bifidobacterium adolescentis
88	d1n5ua2	Alignment	not modelled	11.1	17	Fold: Serum albumin-like Superfamily: Serum albumin-like Family: Serum albumin-like
89	d2bxpa1	Alignment	not modelled	11.0	17	Fold: Serum albumin-like Superfamily: Serum albumin-like Family: Serum albumin-like
90	c2qs0A_	Alignment	not modelled	10.8	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: quinolinate synthetase a; PDBTitle: quinolinate synthase from pyrococcus furiosus
91	c1vi7A_	Alignment	not modelled	10.5	44	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yigz; PDBTitle: crystal structure of an hypothetical protein
92	c1fcua_	Alignment	not modelled	10.1	23	PDB header: hydrolase Chain: A: PDB Molecule: hyaluronoglucosaminidase; PDBTitle: crystal structure (trigonal) of bee venom hyaluronidase
93	c2pe4A_	Alignment	not modelled	10.1	19	PDB header: hydrolase Chain: A: PDB Molecule: hyaluronidase-1; PDBTitle: structure of human hyaluronidase 1, a hyaluronan hydrolyzing enzyme2 involved in tumor growth and angiogenesis
94	c3qfhE_	Alignment	not modelled	10.0	18	PDB header: hydrolase Chain: E: PDB Molecule: epidermin leader peptide processing serine protease epip; PDBTitle: 2.05 angstrom resolution crystal structure of epidermin leader peptide2 processing serine protease (epip) from staphylococcus aureus.
95	c6f9mA_	Alignment	not modelled	9.7	21	PDB header: hydrolase Chain: A: PDB Molecule: serine protease; PDBTitle: the lipy/f-motif in an intracellular subtilisin protease is involved2 in inhibition
96	c3n0uB_	Alignment	not modelled	9.5	18	PDB header: hydrolase, lyase Chain: B: PDB Molecule: probable n-glycosylase/dna lyase; PDBTitle: crystal structure of tm1821, the 8-oxoguanine dna glycosylase of2 thermotoga maritima
97	d1fcqa_	Alignment	not modelled	9.5	23	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Bee venom hyaluronidase
98	c6mwqB_	Alignment	not modelled	9.4	20	PDB header: lyase/fluorescent protein Chain: B: PDB Molecule: darpin, muscle-type aldolase chimeric fusion; PDBTitle: single particle cryoem structure of a darpin-aldolase platform in2 complex with gfp
99	c2kvcA_	Alignment	not modelled	9.4	30	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a