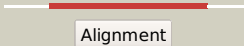

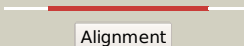

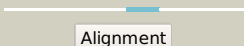
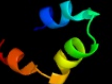
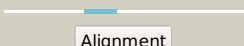

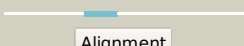

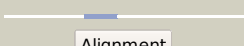

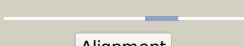
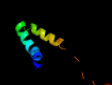









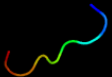




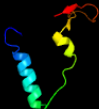




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3252c_alkB_3630735_3631985
 Date Thu Aug 8 16:20:45 BST 2019
 Unique Job ID 9b11e4ad0195cf27

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4zyoA_	 Alignment		98.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: acyl-coa desaturase; PDBTitle: crystal structure of human integral membrane stearyl-coa desaturase2 with substrate
2	c4ymkA_	 Alignment		98.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: acyl-coa desaturase 1; PDBTitle: crystal structure of stearyl-coenzyme a desaturase 1
3	c5lnkn_	 Alignment		37.3	25	PDB header: oxidoreductase Chain: N: PDB Molecule: mitochondrial complex i, nd2 subunit; PDBTitle: entire ovine respiratory complex i
4	c2i47A_	 Alignment		34.9	56	PDB header: hydrolase Chain: A: PDB Molecule: adam 17; PDBTitle: crystal structure of catalytic domain of tace with inhibitor
5	d2i47a1	 Alignment		32.9	56	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: TNF-alpha converting enzyme, TACE, catalytic domain
6	c3b8zB_	 Alignment		27.6	50	PDB header: hydrolase Chain: B: PDB Molecule: protein adams-5; PDBTitle: high resolution crystal structure of the catalytic domain of adams-52 (aggrecanase-2)
7	c4a01B_	 Alignment		26.2	14	PDB header: hydrolase Chain: B: PDB Molecule: proton pyrophosphatase; PDBTitle: crystal structure of the h-translocating pyrophosphatase
8	d1bswa_	 Alignment		25.3	67	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
9	d1r55a_	 Alignment		24.0	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
10	d1atla_	 Alignment		23.2	60	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
11	c4dd8B_	 Alignment		22.7	60	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: disintegrin and metalloproteinase domain-containing protein PDBTitle: adam-8 metalloproteinase domain with bound batimastat

12	c1yp1A_	Alignment		22.6	50	PDB header: hydrolase Chain: A: PDB Molecule: fij; PDBTitle: crystal structure of a non-hemorrhagic fibrin(ogen)olytic2 metalloproteinase from venom of agkistrodon acutus
13	c3cqbB_	Alignment		22.5	44	PDB header: hydrolase Chain: B: PDB Molecule: probable protease htpx homolog; PDBTitle: crystal structure of heat shock protein htpx domain from vibrio2 parahaemolyticus rimd 2210633
14	c2rjpC_	Alignment		22.3	40	PDB header: hydrolase Chain: C: PDB Molecule: adamts-4; PDBTitle: crystal structure of adamts4 with inhibitor bound
15	d1nda_	Alignment		22.2	56	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
16	c2erpA_	Alignment		22.0	70	PDB header: toxin Chain: A: PDB Molecule: vascular apoptosis-inducing protein 1; PDBTitle: crystal structure of vascular apoptosis-inducing protein-1(inhibitor-2 bound form)
17	d1wnia_	Alignment		21.1	40	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
18	d1x1na1	Alignment		20.9	25	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
19	c3k7nA_	Alignment		20.7	40	PDB header: hydrolase Chain: A: PDB Molecule: k-like; PDBTitle: structures of two elapid snake venom metalloproteases with2 distinct activities highlight the disulfide patterns in the3 d domain of adamalysin family proteins
20	d4aiga_	Alignment		20.7	56	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
21	c2dw1B_	Alignment	not modelled	20.4	60	PDB header: apoptosis, toxin Chain: B: PDB Molecule: catrocollastatin; PDBTitle: crystal structure of vap2 from crotalus atrox venom (form 2-2 crystal)
22	c2v4bB_	Alignment	not modelled	20.2	60	PDB header: hydrolase Chain: B: PDB Molecule: adamts-1; PDBTitle: crystal structure of human adamts-1 catalytic domain and cysteine-2 rich domain (apo-form)
23	c6be6D_	Alignment	not modelled	20.1	67	PDB header: membrane protein Chain: D: PDB Molecule: disintegrin and metalloproteinase domain-containing protein PDBTitle: adam10 extracellular domain
24	d1quaa_	Alignment	not modelled	19.8	56	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
25	d1kufa_	Alignment	not modelled	19.6	44	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
26	c2e3xA_	Alignment	not modelled	19.6	29	PDB header: hydrolase, blood clotting, toxin Chain: A: PDB Molecule: coagulation factor x-activating enzyme heavy chain; PDBTitle: crystal structure of russell's viper venom metalloproteinase
27	c3k7IA_	Alignment	not modelled	19.6	78	PDB header: hydrolase Chain: A: PDB Molecule: atragin; PDBTitle: structures of two elapid snake venom metalloproteases with2 distinct activities highlight the disulfide patterns in the3 d domain of adamalysin family proteins
28	c2rjqA_	Alignment	not modelled	19.4	50	PDB header: hydrolase Chain: A: PDB Molecule: adamts-5; PDBTitle: crystal structure of adamts5 with inhibitor bound

29	d1mxga1	Alignment	not modelled	17.3	33	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
30	c3g5cA	Alignment	not modelled	16.5	20	PDB header: membrane protein Chain: A: PDB Molecule: adam 22; PDBTitle: structural and biochemical studies on the ectodomain of human adam22
31	c2zfnA	Alignment	not modelled	16.2	17	PDB header: transferase Chain: A: PDB Molecule: regulator of ty1 transposition protein 109; PDBTitle: self-acetylation mediated histone h3 lysine 56 acetylation by rtt109
32	c2pmzW	Alignment	not modelled	15.5	21	PDB header: translation, transferase Chain: W: PDB Molecule: dna-directed rna polymerase subunit k; PDBTitle: archaeal rna polymerase from sulfolobus solfataricus
33	d1tz7a1	Alignment	not modelled	15.4	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
34	c6h9oB	Alignment	not modelled	14.6	50	PDB header: cell cycle Chain: B: PDB Molecule: cell division protein ftsb; PDBTitle: complex of the periplasmic domains of bacterial cell division proteins2 ftsq and ftsb
35	c6h9oD	Alignment	not modelled	14.6	50	PDB header: cell cycle Chain: D: PDB Molecule: cell division protein ftsb; PDBTitle: complex of the periplasmic domains of bacterial cell division proteins2 ftsq and ftsb
36	d1npca	Alignment	not modelled	14.2	38	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Thermolysin-like
37	c4ainB	Alignment	not modelled	14.2	9	PDB header: membrane protein Chain: B: PDB Molecule: glycine betaine transporter betp; PDBTitle: crystal structure of betp with asymmetric protomers.
38	c2j83B	Alignment	not modelled	13.7	50	PDB header: hydrolase Chain: B: PDB Molecule: ulilysin; PDBTitle: ulilysin metalloprotease in complex with batimastat.
39	c5mtzA	Alignment	not modelled	13.5	12	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease z; PDBTitle: crystal structure of a long form rnase z from yeast
40	d1eswa	Alignment	not modelled	13.2	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
41	d1u4ga	Alignment	not modelled	13.0	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Thermolysin-like
42	c3nqxA	Alignment	not modelled	12.9	50	PDB header: hydrolase Chain: A: PDB Molecule: secreted metalloprotease mcp02; PDBTitle: crystal structure of vibriolysin mcp-02 mature enzyme, a zinc2 metalloprotease from m4 family
43	d1bqqm	Alignment	not modelled	12.8	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
44	c4oojB	Alignment	not modelled	12.7	25	PDB header: unknown function Chain: B: PDB Molecule: sidc, interaptin; PDBTitle: crystal structure of the n-terminal domain of the legionella2 pneumophila protein sidc at 2.4a resolution
45	c3nqzB	Alignment	not modelled	12.6	50	PDB header: hydrolase Chain: B: PDB Molecule: secreted metalloprotease mcp02; PDBTitle: crystal structure of the autoprocessed vibriolysin mcp-02 with e369a2 mutation
46	c3d35A	Alignment	not modelled	12.6	17	PDB header: transferase Chain: A: PDB Molecule: regulator of ty1 transposition protein 109; PDBTitle: crystal structure of rtt109-ac-coa complex
47	c1yo4A	Alignment	not modelled	12.5	32	PDB header: viral protein Chain: A: PDB Molecule: hypothetical protein x4; PDBTitle: solution structure of the sars coronavirus orf 7a coded x42 protein
48	d1bqba	Alignment	not modelled	12.3	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Thermolysin-like
49	d1kjpA	Alignment	not modelled	12.3	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Thermolysin-like
50	c3dtkA	Alignment	not modelled	12.3	50	PDB header: gene regulation Chain: A: PDB Molecule: irre protein; PDBTitle: crystal structure of the irre protein, a central regulator2 of dna damage repair in deinococcaceae
51	c4il3B	Alignment	not modelled	12.0	22	PDB header: hydrolase Chain: B: PDB Molecule: ste24p; PDBTitle: crystal structure of s. mikatae ste24p
52	c4gerB	Alignment	not modelled	11.8	38	PDB header: hydrolase Chain: B: PDB Molecule: gentiyase metalloprotease; PDBTitle: crystal structure of gentiyase, the neutral metalloprotease of2 paenibacillus polymyxa
53	c2vqxA	Alignment	not modelled	11.8	25	PDB header: hydrolase Chain: A: PDB Molecule: metalloproteinase; PDBTitle: precursor of protealysin, metalloproteinase from serratia2 proteamaculans.
54	d1c7ka	Alignment	not modelled	11.7	75	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Zinc protease
55	d1cxva	Alignment	not modelled	11.6	63	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain

56	c6o38A	Alignment	not modelled	11.5	50	PDB header: sugar binding protein Chain: A: PDB Molecule: acinetobacter secreted protease cpaa; PDBTitle: structure of a chaperone-substrate complex
57	d1k4ta2	Alignment	not modelled	11.1	25	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Eukaryotic DNA topoisomerase I, catalytic core
58	d2ovxa1	Alignment	not modelled	10.8	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
59	c4nm7B_	Alignment	not modelled	10.7	22	PDB header: transferase/peptide Chain: B: PDB Molecule: axin-1; PDBTitle: crystal structure of gsk-3/axin complex bound to phosphorylated wnt2 receptor lrp6 e-motif
60	c4nm5B_	Alignment	not modelled	10.7	22	PDB header: transferase/peptide Chain: B: PDB Molecule: axin-1; PDBTitle: crystal structure of gsk-3/axin complex bound to phosphorylated wnt2 receptor lrp6 c-motif
61	c4nu1B_	Alignment	not modelled	10.7	22	PDB header: transferase/peptide Chain: B: PDB Molecule: axin-1; PDBTitle: crystal structure of a transition state mimic of the gsk-3/axin2 complex bound to phosphorylated n-terminal auto-inhibitory ps93 peptide
62	c4nm3B_	Alignment	not modelled	10.7	22	PDB header: transferase/peptide Chain: B: PDB Molecule: axin-1; PDBTitle: crystal structure of gsk-3/axin complex bound to phosphorylated n-2 terminal auto-inhibitory ps9 peptide
63	d1v54g_	Alignment	not modelled	10.6	33	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit VIa Family: Mitochondrial cytochrome c oxidase subunit VIa
64	c3cz7A_	Alignment	not modelled	10.5	17	PDB header: replication Chain: A: PDB Molecule: regulator of ty1 transposition protein 109; PDBTitle: molecular basis for the autoregulation of the protein acetyl2 transferase rtt109
65	d1rm8a_	Alignment	not modelled	10.4	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
66	c6h9nB_	Alignment	not modelled	10.2	50	PDB header: cell cycle Chain: B: PDB Molecule: cell division protein ftsb; PDBTitle: complex of the periplasmic domains of bacterial cell division proteins2 ftsq and ftsb
67	d1y93a1	Alignment	not modelled	10.1	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
68	c4k90A_	Alignment	not modelled	10.1	38	PDB header: hydrolase Chain: A: PDB Molecule: extracellular metalloproteinase mep; PDBTitle: extracellular metalloproteinase from aspergillus
69	d2a3qa1	Alignment	not modelled	10.1	11	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: MazG-like
70	c2q4pA_	Alignment	not modelled	10.1	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein rs21-c6; PDBTitle: ensemble refinement of the crystal structure of protein from mus2 musculus mm.29898
71	c3c37B_	Alignment	not modelled	10.0	50	PDB header: hydrolase Chain: B: PDB Molecule: peptidase, m48 family; PDBTitle: x-ray structure of the putative zn-dependent peptidase q74d82 at the2 resolution 1.7 a. northeast structural genomics consortium target3 gsr143a
72	d1q3aa_	Alignment	not modelled	9.9	63	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
73	d1i76a_	Alignment	not modelled	9.9	63	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
74	c3sksA_	Alignment	not modelled	9.9	50	PDB header: hydrolase Chain: A: PDB Molecule: putative oligoendopeptidase f; PDBTitle: crystal structure of a putative oligoendopeptidase f from bacillus2 anthracis str. ames
75	d1hova_	Alignment	not modelled	9.7	63	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
76	c4aw6B_	Alignment	not modelled	9.6	22	PDB header: hydrolase Chain: B: PDB Molecule: caax prenyl protease 1 homolog; PDBTitle: crystal structure of the human nuclear membrane zinc metalloprotease2 zmpste24 (face1)
77	c2h1ja_	Alignment	not modelled	9.6	44	PDB header: hydrolase Chain: A: PDB Molecule: oligoendopeptidase f; PDBTitle: 3.1 a x-ray structure of putative oligoendopeptidase f: crystals grown2 by microfluidic seeding
78	c3q66C_	Alignment	not modelled	9.6	17	PDB header: chaperone/transferase Chain: C: PDB Molecule: histone acetyltransferase rtt109; PDBTitle: structure of the vps75-rtt109 histone chaperone-lysine2 acetyltransferase complex (full-length proteins in space group p6122)
79	c2xs4A_	Alignment	not modelled	9.5	63	PDB header: hydrolase Chain: A: PDB Molecule: karilysin protease; PDBTitle: structure of karilysin catalytic mmp domain in complex with magnesium
80	d1hy7a_	Alignment	not modelled	9.4	63	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
81	d1hfca_	Alignment	not modelled	9.3	63	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain

82	c1twcF_	Alignment	not modelled	9.1	25	PDB header: transcription Chain: F: PDB Molecule: dna-directed rna polymerases i, ii, and iii 23 PDBTitle: rna polymerase ii complexed with gtp
83	d1qiba_	Alignment	not modelled	9.1	63	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
84	d1twff_	Alignment	not modelled	8.9	25	Fold: RPB6/omega subunit-like Superfamily: RPB6/omega subunit-like Family: RPB6
85	d1mmqa_	Alignment	not modelled	8.8	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
86	d1cgla_	Alignment	not modelled	8.8	63	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
87	c4jiuA_	Alignment	not modelled	8.7	38	PDB header: hydrolase Chain: A: PDB Molecule: proabylisin; PDBTitle: crystal structure of the metallopeptidase zymogen of pyrococcus abyssii2 abylysin
88	c5xswA_	Alignment	not modelled	8.7	19	PDB header: hydrolase Chain: A: PDB Molecule: chitinase; PDBTitle: crystal structure of an archaeal chitinase in the substrate-complex2 form (p63)
89	c5th6D_	Alignment	not modelled	8.6	63	PDB header: hydrolase/hydrolase inhibitor Chain: D: PDB Molecule: matrix metalloproteinase-9,matrix metalloproteinase-9; PDBTitle: structure determination of a potent, selective antibody inhibitor of 2 human mmp9 (apo mmp9)
90	d1fbla2	Alignment	not modelled	8.6	63	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
91	c2cltB_	Alignment	not modelled	8.3	50	PDB header: hydrolase Chain: B: PDB Molecule: interstitial collagenase; PDBTitle: crystal structure of the active form (full-length) of human2 fibroblast collagenase.
92	c3j01A_	Alignment	not modelled	8.3	17	PDB header: ribosome/ribosomal protein Chain: A: PDB Molecule: preprotein translocase secy subunit; PDBTitle: structure of the ribosome-secy complex in the membrane environment
93	c1dvaY_	Alignment	not modelled	8.3	50	PDB header: hydrolase/hydrolase inhibitor Chain: Y: PDB Molecule: peptide e-76; PDBTitle: crystal structure of the complex between the peptide exosite inhibitor2 e-76 and coagulation factor viia
94	c1dvaX_	Alignment	not modelled	8.3	50	PDB header: hydrolase/hydrolase inhibitor Chain: X: PDB Molecule: peptide e-76; PDBTitle: crystal structure of the complex between the peptide exosite inhibitor2 e-76 and coagulation factor viia
95	d1hv5a_	Alignment	not modelled	8.3	63	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
96	d1eaka2	Alignment	not modelled	8.2	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
97	d1rxwa1	Alignment	not modelled	8.2	23	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
98	c4jixB_	Alignment	not modelled	8.1	38	PDB header: hydrolase Chain: B: PDB Molecule: projannalysin; PDBTitle: crystal structure of the metallopeptidase zymogen of 2 methanocaldococcus jannaschii jannalysin
99	c3leuA_	Alignment	not modelled	8.0	28	PDB header: antibacterial peptide Chain: A: PDB Molecule: leucocin a; PDBTitle: high resolution 1h nmr study of leucocin a in2 dodecylphosphocholine micelles, 19 structures (1:40 ratio3 of leucocin a:dpc) (0.1% tfa)