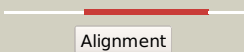

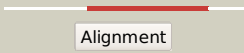



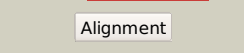



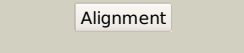

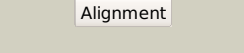



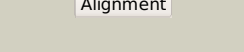

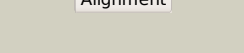

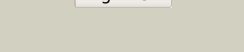












Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3207c_(-)_3583797_3584654
Date	Thu Aug 8 16:20:40 BST 2019
Unique Job ID	49c5432510e1c1b8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4g0dD_	 Alignment		98.0	17	PDB header: hydrolase Chain: D: PDB Molecule: collagenase 3; PDBTitle: human collagenase 3 (mmp-13) full form with peptides from pro-domain
2	d1hv5a_	 Alignment		97.9	18	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
3	d2ovxa1	 Alignment		97.9	16	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
4	c1slmA_	 Alignment		97.8	22	PDB header: hydrolase Chain: A: PDB Molecule: stromelysin-1; PDBTitle: crystal structure of fibroblast stromelysin-1: the c-truncated human2 proenzyme
5	d1y93a1	 Alignment		97.7	16	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
6	d1mmqa_	 Alignment		97.7	19	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
7	d1xuca1	 Alignment		97.7	17	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
8	d1hy7a_	 Alignment		97.7	20	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
9	d1hfca_	 Alignment		97.7	17	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
10	d1g9ka2	 Alignment		97.7	18	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Serralysin-like metalloprotease, catalytic (N-terminal) domain
11	d1sata2	 Alignment		97.7	18	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Serralysin-like metalloprotease, catalytic (N-terminal) domain

12	d1cxva_	Alignment		97.7	18	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
13	c2cltB_	Alignment		97.6	18	PDB header: hydrolase Chain: B: PDB Molecule: interstitial collagenase; PDBTitle: crystal structure of the active form (full-length) of human2 fibroblast collagenase.
14	d1hova_	Alignment		97.6	17	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
15	c3ba0A_	Alignment		97.6	17	PDB header: hydrolase Chain: A: PDB Molecule: macrophage metalloelastase; PDBTitle: crystal structure of full-length human mmp-12
16	d1cgl_a	Alignment		97.6	19	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
17	d1k7ia2	Alignment		97.6	15	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Serralysin-like metalloprotease, catalytic (N-terminal) domain
18	c2xs4A_	Alignment		97.6	14	PDB header: hydrolase Chain: A: PDB Molecule: karilysin protease; PDBTitle: structure of karilysin catalytic mmp domain in complex with magnesium
19	d1q3aa_	Alignment		97.6	21	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
20	c5th6D_	Alignment		97.6	19	PDB header: hydrolase/hydrolase inhibitor Chain: D: PDB Molecule: matrix metalloproteinase-9,matrix metalloproteinase-9; PDBTitle: structure determination of a potent, selective antibody inhibitor of2 human mmp9 (apo mmp9)
21	c2jsdA_	Alignment	not modelled	97.5	23	PDB header: hydrolase Chain: A: PDB Molecule: matrix metalloproteinase-20; PDBTitle: solution structure of mmp20 complexed with nngH
22	d1fbla2	Alignment	not modelled	97.5	17	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
23	d1qiba_	Alignment	not modelled	97.5	20	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
24	c2mzeA_	Alignment	not modelled	97.4	18	PDB header: hydrolase Chain: A: PDB Molecule: matrilysin; PDBTitle: nmr solution structure of the pro form of human matrilysin (prommp-7)
25	d1i76a_	Alignment	not modelled	97.4	17	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
26	c5czwA_	Alignment	not modelled	97.1	19	PDB header: hydrolase Chain: A: PDB Molecule: myroilysin; PDBTitle: crystal structure of myroilysin
27	c1su3A_	Alignment	not modelled	97.0	20	PDB header: hydrolase Chain: A: PDB Molecule: interstitial collagenase; PDBTitle: x-ray structure of human prommp-1: new insights into2 collagenase action
28	d1eaka2	Alignment	not modelled	97.0	21	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
29	d1kann2	Alignment	not modelled	97.0	19	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain

29	d1kappz	Alignment	not modelled	97.0	19	Family: Serralysin-like metalloprotease, catalytic (N-terminal) domain
30	d1rm8a	Alignment	not modelled	96.8	20	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
31	d1bqqm	Alignment	not modelled	96.7	18	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
32	c1satA	Alignment	not modelled	96.6	17	PDB header: hydrolase (serine protease) Chain: A: PDB Molecule: serratia protease; PDBTitle: crystal structure of the 50 kda metallo protease from s.2 marcescens
33	c1jiwP	Alignment	not modelled	96.3	17	PDB header: hydrolase/hyrolase inhibitor Chain: P: PDB Molecule: alkaline metalloproteinase; PDBTitle: crystal structure of the apr-aprin complex
34	c1om8A	Alignment	not modelled	95.3	19	PDB header: hydrolase Chain: A: PDB Molecule: serralysin; PDBTitle: crystal structure of a cold adapted alkaline protease from pseudomonas2 tac ii 18, co-crystallized with 10 mm edta
35	c3edhA	Alignment	not modelled	94.1	15	PDB header: hydrolase Chain: A: PDB Molecule: bone morphogenetic protein 1; PDBTitle: crystal structure of bone morphogenetic protein 1 protease2 domain in complex with partially bound dms0
36	c3vtgA	Alignment	not modelled	91.7	21	PDB header: hydrolase Chain: A: PDB Molecule: high choriolytic enzyme 1; PDBTitle: high choriolytic enzyme 1 (hce-1), a hatching enzyme zinc-protease2 from oryzias latipes (medaka fish)
37	d1nd1a	Alignment	not modelled	91.1	24	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
38	d1r55a	Alignment	not modelled	90.9	19	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
39	c2erpA	Alignment	not modelled	90.7	21	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)
40	c3k7nA	Alignment	not modelled	90.7	23	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
41	d1kufa	Alignment	not modelled	89.8	32	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
42	c1yp1A	Alignment	not modelled	89.8	28	PDB header: hydrolase Chain: A: PDB Molecule: ffii; PDBTitle: crystal structure of a non-hemorrhagic fibrin(ogen)olytic2 metalloproteinase from venom of agkistrodon acutus
43	d1atla	Alignment	not modelled	88.7	22	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
44	d4aiga	Alignment	not modelled	88.5	26	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
45	c3lqbA	Alignment	not modelled	88.1	41	PDB header: hydrolase Chain: A: PDB Molecule: loc792177 protein; PDBTitle: crystal structure of the hatching enzyme zhe1 from the zebrafish danio2 rerio
46	d2i47a1	Alignment	not modelled	88.1	33	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: TNF-alpha converting enzyme, TACE, catalytic domain
47	c2i47A	Alignment	not modelled	87.8	24	PDB header: hydrolase Chain: A: PDB Molecule: adam 17; PDBTitle: crystal structure of catalytic domain of tace with inhibitor
48	c4dd8B	Alignment	not modelled	87.3	17	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: disintegrin and metalloproteinase domain-containing protein PDBTitle: adam-8 metalloproteinase domain with bound batimastat
49	d1asta	Alignment	not modelled	87.1	53	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Astacin
50	c2e3xA	Alignment	not modelled	85.9	24	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
51	c3lq0A	Alignment	not modelled	85.9	40	PDB header: hydrolase Chain: A: PDB Molecule: prostacin; PDBTitle: zymogen structure of crayfish astacin metallopeptidase
52	c5zumB	Alignment	not modelled	85.7	13	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl-peptidase iii; PDBTitle: structure of dipeptidyl-peptidase iii from coralloccoccus sp. strain2 egb
53	d1bswa	Alignment	not modelled	85.7	32	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
54	c3b8zB	Alignment	not modelled	85.7	36	PDB header: hydrolase Chain: B: PDB Molecule: protein adams-5; PDBTitle: high resolution crystal structure of the catalytic domain of adams-52 (aggrecanase-2)
55	d1wnia	Alignment	not modelled	85.1	26	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like

56	c2j83B_	Alignment	not modelled	84.4	55	PDB header: hydrolase Chain: B: PDB Molecule: ulilysin; PDBTitle: ulilysin metalloprotease in complex with batimastat.
57	c1gxdA_	Alignment	not modelled	83.4	26	PDB header: hydrolase Chain: A: PDB Molecule: 72 kda type iv collagenase; PDBTitle: prommp-2/timp-2 complex
58	c2dw1B_	Alignment	not modelled	82.0	23	PDB header: apoptosis, toxin Chain: B: PDB Molecule: catrocollastatin; PDBTitle: crystal structure of vap2 from crotalus atrox venom (form 2-2 crystal)
59	c4gwmA_	Alignment	not modelled	81.5	35	PDB header: hydrolase Chain: A: PDB Molecule: meprin a subunit beta; PDBTitle: crystal structure of human promeprin beta
60	c6be6D_	Alignment	not modelled	81.5	29	PDB header: membrane protein Chain: D: PDB Molecule: disintegrin and metalloproteinase domain-containing protein PDBTitle: adam10 extracellular domain
61	c2rjqA_	Alignment	not modelled	81.2	35	PDB header: hydrolase Chain: A: PDB Molecule: adamts-5; PDBTitle: crystal structure of adamts5 with inhibitor bound
62	d1quaa_	Alignment	not modelled	81.2	24	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
63	c3g5cA_	Alignment	not modelled	79.3	20	PDB header: membrane protein Chain: A: PDB Molecule: adam 22; PDBTitle: structural and biochemical studies on the ectodomain of human adam22
64	c3k7IA_	Alignment	not modelled	79.3	19	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
65	c2v4bB_	Alignment	not modelled	78.3	29	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)
66	c4gwnA_	Alignment	not modelled	77.9	35	PDB header: hydrolase Chain: A: PDB Molecule: meprin a subunit beta; PDBTitle: crystal structure of human mature meprin beta
67	c3ujzA_	Alignment	not modelled	77.8	50	PDB header: hydrolase Chain: A: PDB Molecule: metalloprotease stce; PDBTitle: crystal structure of enterohemorrhagic e. coli stce
68	c1l6jA_	Alignment	not modelled	76.5	26	PDB header: hydrolase Chain: A: PDB Molecule: matrix metalloproteinase-9; PDBTitle: crystal structure of human matrix metalloproteinase mmp92 (gelatinase b).
69	c3lmcA_	Alignment	not modelled	76.3	24	PDB header: hydrolase Chain: A: PDB Molecule: peptidase, zinc-dependent; PDBTitle: crystal structure of zinc-dependent peptidase from methanocorpusculum2 labreanum (strain z), northeast structural genomics consortium target3 mur16
70	d1tvia_	Alignment	not modelled	75.8	18	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Predicted metal-dependent hydrolase
71	c3p24C_	Alignment	not modelled	75.1	33	PDB header: hydrolase Chain: C: PDB Molecule: bft-3; PDBTitle: structure of profragilysin-3 from bacteroides fragilis
72	c2rjpC_	Alignment	not modelled	71.3	24	PDB header: hydrolase Chain: C: PDB Molecule: adamts-4; PDBTitle: crystal structure of adamts4 with inhibitor bound
73	c1xaxA_	Alignment	not modelled	68.2	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical upf0054 protein hi0004; PDBTitle: nmr structure of hi0004, a putative essential gene product2 from haemophilus influenzae
74	c1eakA_	Alignment	not modelled	67.7	40	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: 72 kda type iv collagenase; PDBTitle: catalytic domain of prommp-2 e404q mutant
75	c6eomA_	Alignment	not modelled	64.9	20	PDB header: hydrolase Chain: A: PDB Molecule: mutt/nudix family protein; PDBTitle: structure of dpp iii from caldithrix abyssi
76	d1oz9a_	Alignment	not modelled	62.0	18	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Predicted metal-dependent hydrolase
77	c4on1B_	Alignment	not modelled	60.7	38	PDB header: hydrolase Chain: B: PDB Molecule: putative metalloprotease ii; PDBTitle: crystal structure of metalloproteinase-ii from bacteroides fragilis
78	c6o38A_	Alignment	not modelled	58.2	73	PDB header: sugar binding protein Chain: A: PDB Molecule: acinetobacter secreted protease cpaa; PDBTitle: structure of a chaperone-substrate complex
79	d1c7ka_	Alignment	not modelled	57.9	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Zinc protease
80	c3p1vB_	Alignment	not modelled	57.2	47	PDB header: hydrolase Chain: B: PDB Molecule: metallo-endopeptidase; PDBTitle: crystal structure of a metallo-endopeptidases (bacova_00663) from2 bacteroides ovatus at 1.93 a resolution
81	d1xm5a_	Alignment	not modelled	54.5	16	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Predicted metal-dependent hydrolase
						PDB header: hydrolase

82	c2xhqA	Alignment	not modelled	53.0	50	Chain: A: PDB Molecule: archaemetzincin; PDBTitle: crystal structure of archaemetzincin (amza) from archaeoglobus2 fulgidus at 1.45 a resolution
83	c2x7mA	Alignment	not modelled	50.6	50	PDB header: hydrolase Chain: A: PDB Molecule: archaemetzincin; PDBTitle: crystal structure of archaemetzincin (amza) from methanopyrus2 kandleri at 1.5 a resolution
84	c5yfcB	Alignment	not modelled	47.8	42	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl peptidase 3; PDBTitle: crystal structure of a new dpp iii family member
85	c4k90A	Alignment	not modelled	45.1	16	PDB header: hydrolase Chain: A: PDB Molecule: extracellular metalloproteinase mep; PDBTitle: extracellular metalloproteinase from aspergillus
86	d1lmla	Alignment	not modelled	44.5	35	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Leishmanolysin
87	c4yu5A	Alignment	not modelled	38.6	45	PDB header: hydrolase Chain: A: PDB Molecule: immune inhibitor a, metalloprotease; PDBTitle: crystal structure of selenomethionine variant of bacillus anthracis2 immune inhibitor a2 peptidase zymogen
88	c4gerB	Alignment	not modelled	36.9	40	PDB header: hydrolase Chain: B: PDB Molecule: gentlyase metalloprotease; PDBTitle: crystal structure of gentlyase, the neutral metalloprotease of2 paenibacillus polymyxa
89	d1npca	Alignment	not modelled	36.4	60	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Thermolysin-like
90	c2vqxA	Alignment	not modelled	35.6	30	PDB header: hydrolase Chain: A: PDB Molecule: metalloproteinase; PDBTitle: precursor of protealysin, metalloproteinase from serratia2 proteamaculans.
91	d1kjpA	Alignment	not modelled	35.0	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Thermolysin-like
92	c3nctC	Alignment	not modelled	34.5	30	PDB header: dna binding protein, chaperone Chain: C: PDB Molecule: protein psib; PDBTitle: x-ray crystal structure of the bacterial conjugation factor psib, a2 negative regulator of reca
93	d1bqba	Alignment	not modelled	32.0	40	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Thermolysin-like
94	c3cskA	Alignment	not modelled	31.8	33	PDB header: hydrolase Chain: A: PDB Molecule: probable dipeptidyl-peptidase 3; PDBTitle: structure of dpp iii from saccharomyces cerevisiae
95	c3dtkA	Alignment	not modelled	30.1	31	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
96	d1u4ga	Alignment	not modelled	29.9	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Thermolysin-like
97	c3ce2A	Alignment	not modelled	29.4	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative peptidase; PDBTitle: crystal structure of putative peptidase from chlamydomophila abortus
98	c3nqxA	Alignment	not modelled	28.0	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
99	c3nqxZ	Alignment	not modelled	27.3	50	PDB header: hydrolase Chain: B: PDB Molecule: secreted metalloprotease mcp02; PDBTitle: crystal structure of the autoprocessed vibriolysin mcp-02 with e369a2 mutation
100	c4l6tA	Alignment	not modelled	26.8	44	PDB header: hydrolase Chain: A: PDB Molecule: ecxa; PDBTitle: gm1 bound form of the ecx ab5 holotoxin
101	c2h1jA	Alignment	not modelled	25.8	40	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
102	c4xtrG	Alignment	not modelled	23.2	39	PDB header: hydrolase/transport protein Chain: G: PDB Molecule: pep12p; PDBTitle: structure of get3 bound to the transmembrane domain of pep12
103	d3e11a1	Alignment	not modelled	22.9	31	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: TTHA0227-like
104	c2di4B	Alignment	not modelled	22.9	33	PDB header: hydrolase Chain: B: PDB Molecule: cell division protein ftsh homolog; PDBTitle: crystal structure of the ftsh protease domain
105	c5na8B	Alignment	not modelled	22.7	29	PDB header: hydrolase Chain: B: PDB Molecule: putative dipeptidyl-peptidase iii; PDBTitle: structure of dpp iii from bacteroides thetaiotaomicron in closed form
106	d2di4a1	Alignment	not modelled	22.3	31	Fold: FtsH protease domain-like Superfamily: FtsH protease domain-like Family: FtsH protease domain-like
107	c3hq2A	Alignment	not modelled	22.1	55	PDB header: hydrolase Chain: A: PDB Molecule: bacillus subtilis m32 carboxypeptidase; PDBTitle: bsucp crystal structure