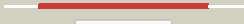



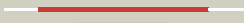



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0429c_(def)_517806_518399
Date	Tue Jul 23 14:50:50 BST 2019
Unique Job ID	edc4afb3f9802d33

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3e3uA_	 Alignment		100.0	100	PDB header: hydrolase Chain: A: PDB Molecule: peptide deformylase; PDBTitle: crystal structure of mycobacterium tuberculosis peptide2 deformylase in complex with inhibitor
2	c3ocaB_	 Alignment		100.0	31	PDB header: hydrolase Chain: B: PDB Molecule: peptide deformylase; PDBTitle: crystal structure of peptide deformylase from ehrlichia chaffeensis
3	c5j46A_	 Alignment		100.0	33	PDB header: hydrolase Chain: A: PDB Molecule: peptide deformylase; PDBTitle: crystal structure of a peptide deformylase from burkholderia2 multivorans
4	c3cpmA_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: peptide deformylase, chloroplast; PDBTitle: plant peptide deformylase pdf1b crystal structure
5	dlx1a_	 Alignment		100.0	37	Fold: Peptide deformylase Superfamily: Peptide deformylase Family: Peptide deformylase
6	dly6ha_	 Alignment		100.0	34	Fold: Peptide deformylase Superfamily: Peptide deformylase Family: Peptide deformylase
7	c2w3tA_	 Alignment		100.0	33	PDB header: hydrolase Chain: A: PDB Molecule: peptide deformylase; PDBTitle: chloro complex of the ni-form of e.coli deformylase
8	c2ew7A_	 Alignment		100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: peptide deformylase; PDBTitle: crystal structure of helicobacter pylori peptide deformylase
9	c3g5pB_	 Alignment		100.0	34	PDB header: hydrolase Chain: B: PDB Molecule: peptide deformylase, mitochondrial; PDBTitle: structure and activity of human mitochondrial peptide deformylase, a2 novel cancer target
10	dlxeoa1	 Alignment		100.0	33	Fold: Peptide deformylase Superfamily: Peptide deformylase Family: Peptide deformylase
11	clzy1B_	 Alignment		100.0	36	PDB header: hydrolase Chain: B: PDB Molecule: peptide deformylase, mitochondrial; PDBTitle: x-ray structure of peptide deformylase from arabidopsis2 thaliana (atpdf1a) in complex with met-ala-ser

12	c3qu1B_	Alignment		100.0	36	PDB header: hydrolase, metal binding protein Chain: B: PDB Molecule: peptide deformylase 2; PDBTitle: peptide deformylase from vibrio cholerae
13	c6cazA_	Alignment		100.0	40	PDB header: hydrolase Chain: A: PDB Molecule: peptide deformylase; PDBTitle: crystal structure of a peptide deformylase from legionella pneumophila
14	c4dr9C_	Alignment		100.0	35	PDB header: hydrolase/hydrolase inhibitor Chain: C: PDB Molecule: peptide deformylase; PDBTitle: crystal structure of a peptide deformylase from synechococcus2 elongatus in complex with actinonin
15	c5hgwA_	Alignment		100.0	35	PDB header: hydrolase Chain: A: PDB Molecule: peptide deformylase; PDBTitle: crystal structure of a peptide deformylase from burkholderia ambifaria
16	d1jyma_	Alignment		100.0	23	Fold: Peptide deformylase Superfamily: Peptide deformylase Family: Peptide deformylase
17	c4wx1B_	Alignment		100.0	33	PDB header: hydrolase Chain: B: PDB Molecule: peptide deformylase; PDBTitle: crystal structure of a peptide deformylase from haemophilus influenzae2 complex with actinonin
18	c3dldA_	Alignment		100.0	36	PDB header: hydrolase Chain: A: PDB Molecule: peptide deformylase; PDBTitle: crystal structure of peptide deformylase, xoo1075, from xanthomonas2 oryzae pv. oryzae kacc10331
19	d1rl4a_	Alignment		100.0	27	Fold: Peptide deformylase Superfamily: Peptide deformylase Family: Peptide deformylase
20	c3g6nA_	Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: peptide deformylase; PDBTitle: crystal structure of an epdf complex with met-ala-ser
21	d1lqya_	Alignment	not modelled	100.0	28	Fold: Peptide deformylase Superfamily: Peptide deformylase Family: Peptide deformylase
22	c1ws1A_	Alignment	not modelled	100.0	36	PDB header: hydrolase Chain: A: PDB Molecule: peptide deformylase 1; PDBTitle: structure analysis of peptide deformylase from bacillus2 cereus
23	d1lm4a_	Alignment	not modelled	100.0	21	Fold: Peptide deformylase Superfamily: Peptide deformylase Family: Peptide deformylase
24	d1v3ya_	Alignment	not modelled	100.0	41	Fold: Peptide deformylase Superfamily: Peptide deformylase Family: Peptide deformylase
25	d1lm6a_	Alignment	not modelled	100.0	24	Fold: Peptide deformylase Superfamily: Peptide deformylase Family: Peptide deformylase
26	c3uwaA_	Alignment	not modelled	100.0	31	PDB header: hydrolase Chain: A: PDB Molecule: riia-riib membrane-associated protein; PDBTitle: crystal structure of a probable peptide deformylase from synechococcus2 phage s-ssm7
27	d1lmea_	Alignment	not modelled	100.0	37	Fold: Peptide deformylase Superfamily: Peptide deformylase Family: Peptide deformylase
28	d2defa_	Alignment	not modelled	100.0	36	Fold: Peptide deformylase Superfamily: Peptide deformylase Family: Peptide deformylase
29	c3l87A_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: peptide deformylase;

29	c3b7A	Alignment	not modelled	100.0	29	PDBTitle: the crystal structure of smu.143c from streptococcus mutans ua159 PDB header: hydrolase
30	c5mtcA	Alignment	not modelled	100.0	39	Chain: A: PDB Molecule: putative uncharacterized protein orf60t; PDBTitle: crystal structure of pdf from the vibrio parahaemolyticus2 bacteriophage vp16t - crystal form i
31	d1quaa	Alignment	not modelled	36.2	44	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
32	c2kvzA	Alignment	not modelled	35.0	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ispse; PDBTitle: structure of residues 161-235 of putative peptidoglycan binding2 protein lmo0835 from listeria monocytogenes: target lmr64b of the3 northeast structural genomics consortium
33	d1wnia	Alignment	not modelled	31.2	40	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
34	d1nd1a	Alignment	not modelled	31.2	40	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
35	c1yp1A	Alignment	not modelled	31.1	47	PDB header: hydrolase Chain: A: PDB Molecule: fii; PDBTitle: crystal structure of a non-hemorrhagic fibrin(ogen)olytic2 metalloproteinase from venom of agkistrodon acutus
36	c5uebA	Alignment	not modelled	30.8	23	PDB header: unknown function Chain: A: PDB Molecule: negoa.19184.a; PDBTitle: novel crystal structure of a hypothetical protein from neisseria2 gonorrhoeae
37	d1bswa	Alignment	not modelled	30.4	44	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
38	d1r55a	Alignment	not modelled	29.6	40	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
39	d4aiga	Alignment	not modelled	28.8	47	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
40	d1wmha	Alignment	not modelled	27.3	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
41	c3k7nA	Alignment	not modelled	27.1	47	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
42	c3k7IA	Alignment	not modelled	26.3	40	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
43	d1atla	Alignment	not modelled	26.1	38	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
44	d1pqsa	Alignment	not modelled	25.9	11	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
45	d1kufa	Alignment	not modelled	25.2	40	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Reprolysin-like
46	c2dw1B	Alignment	not modelled	22.2	40	PDB header: apoptosis, toxin Chain: B: PDB Molecule: catrocollastatin; PDBTitle: crystal structure of vap2 from crotalus atrox venom (form 2-2 crystal)
47	c2erpA	Alignment	not modelled	21.7	47	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)
48	c2e3xA	Alignment	not modelled	20.9	33	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
49	d1ip9a	Alignment	not modelled	18.9	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
50	c1z5sD	Alignment	not modelled	18.7	40	PDB header: ligase Chain: D: PDB Molecule: ran-binding protein 2; PDBTitle: crystal structure of a complex between ubc9, sumo-1,2 rangap1 and nup358/ranbp2
51	c3b8zB	Alignment	not modelled	18.1	54	PDB header: hydrolase Chain: B: PDB Molecule: protein adams-5; PDBTitle: high resolution crystal structure of the catalytic domain of adams-52 (aggrecanase-2)
52	d2ap1a2	Alignment	not modelled	17.9	9	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
53	d1ytqa1	Alignment	not modelled	17.5	16	Fold: gamma-Crystallin-like Superfamily: gamma-Crystallin-like Family: Crystallins/Ca-binding development proteins
54	c4dd8B	Alignment	not modelled	17.3	40	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: disintegrin and metalloproteinase domain-containing protein PDBTitle: adam-8 metalloproteinase domain with bound batimastat PDB header: hydrolase

55	c2i47A_	Alignment	not modelled	16.7	33	Chain: A: PDB Molecule: adam 17; PDBTitle: crystal structure of catalytic domain of tace with inhibitor
56	d1q1oa_	Alignment	not modelled	16.7	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
57	c2kt7A_	Alignment	not modelled	16.0	28	PDB header: cell adhesion, membrane protein Chain: A: PDB Molecule: putative peptidoglycan bound protein (lpxtg) PDBTitle: solution nmr structure of mucin-binding domain of protein2 lmo0835 from listeria monocytogenes, northeast structural3 genomics consortium target lmr64a
58	c2rjpC_	Alignment	not modelled	15.5	31	PDB header: hydrolase Chain: C: PDB Molecule: adamts-4; PDBTitle: crystal structure of adamts4 with inhibitor bound
59	d2i47a1	Alignment	not modelled	14.8	33	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: TNF-alpha converting enzyme, TACE, catalytic domain
60	c5o9zN_	Alignment	not modelled	14.2	29	PDB header: splicing Chain: N: PDB Molecule: zinc finger matrin-type protein 2; PDBTitle: cryo-em structure of a pre-catalytic human spliceosome primed for2 activation (b complex)
61	d1c7ka_	Alignment	not modelled	14.0	58	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Zinc protease
62	d1cxva_	Alignment	not modelled	13.4	36	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
63	c4fd9B_	Alignment	not modelled	13.4	20	PDB header: structural protein Chain: B: PDB Molecule: beta/gamma crystallin domain-containing protein 3; PDBTitle: crystal structure of the third beta-gamma-crystallin domain of crybg32 (betagamma-crystallin domain-containing protein 3) from mus musculus
64	c3g5cA_	Alignment	not modelled	13.4	31	PDB header: membrane protein Chain: A: PDB Molecule: adam 22; PDBTitle: structural and biochemical studies on the ectodomain of human adam22
65	c5ttaB_	Alignment	not modelled	13.2	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative exported protein; PDBTitle: a 1.85a x-ray structure from peptoclostridium difficile 630 of a2 hypothetical protein
66	d1hv5a_	Alignment	not modelled	13.1	45	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
67	d1hova_	Alignment	not modelled	12.6	45	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
68	d2bkfa1	Alignment	not modelled	12.2	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
69	c1ytqA_	Alignment	not modelled	12.1	16	PDB header: structural protein Chain: A: PDB Molecule: beta crystallin b2; PDBTitle: structure of native human beta b2 crystallin
70	d1fbla2	Alignment	not modelled	11.7	45	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
71	d1xuca1	Alignment	not modelled	11.5	45	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
72	d1i76a_	Alignment	not modelled	11.2	45	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
73	d1qjba_	Alignment	not modelled	11.0	45	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
74	c5I20A_	Alignment	not modelled	10.9	25	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: clostripain-related protein; PDBTitle: crystal structure of a clostripain (bt_0727) from bacteroides2 thetaiotaomicron atcc 29148 in complex with peptide inhibitor btn-3 vltk-aomk
75	c6evuA_	Alignment	not modelled	10.7	22	PDB header: cell adhesion Chain: A: PDB Molecule: prgb; PDBTitle: adhesin domain of prgb from enterococcus faecalis
76	c6be6D_	Alignment	not modelled	10.5	33	PDB header: membrane protein Chain: D: PDB Molecule: disintegrin and metalloproteinase domain-containing protein PDBTitle: adam10 extracellular domain
77	c2xs4A_	Alignment	not modelled	10.5	55	PDB header: hydrolase Chain: A: PDB Molecule: karilysin protease; PDBTitle: structure of karilysin catalytic mmp domain in complex with magnesium
78	d1hy7a_	Alignment	not modelled	10.4	45	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
79	c3cqbB_	Alignment	not modelled	10.1	27	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
80	d1bqqm_	Alignment	not modelled	10.0	45	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain

81	c2x7mA	Alignment	not modelled	9.6	43	PDB header: hydrolase Chain: A: PDB Molecule: archaemetzincin; PDBTitle: crystal structure of archaemetzincin (amza) from methanopyrus2 kandleri at 1.5 a resolution
82	c3uinD	Alignment	not modelled	9.6	40	PDB header: ligase/isomerase/protein binding Chain: D: PDB Molecule: e3 sumo-protein ligase ranbp2; PDBTitle: complex between human rangap1-sumo2, ubc9 and the ir1 domain from2 ranbp2
83	d1rm8a	Alignment	not modelled	9.5	45	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
84	d2k5wa1	Alignment	not modelled	9.4	22	Fold: OB-fold Superfamily: BC4932-like Family: BC4932-like
85	c1zv8B	Alignment	not modelled	9.4	33	PDB header: viral protein Chain: B: PDB Molecule: e2 glycoprotein; PDBTitle: a structure-based mechanism of sars virus membrane fusion
86	d2ovxa1	Alignment	not modelled	9.2	36	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
87	d1y93a1	Alignment	not modelled	9.1	45	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
88	c4jztA	Alignment	not modelled	8.9	19	PDB header: hydrolase Chain: A: PDB Molecule: dgtp pyrophosphohydrolase; PDBTitle: crystal structure of the bacillus subtilis pyrophosphohydrolase bsrpph2 (e68a mutant) bound to gtp
89	c5j10A	Alignment	not modelled	8.9	32	PDB header: de novo protein Chain: A: PDB Molecule: peptide design 2l4hc2_24; PDBTitle: de novo design of protein homo-oligomers with modular hydrogen bond2 network-mediated specificity
90	c3nppA	Alignment	not modelled	8.6	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pfam duf1093 family protein; PDBTitle: crystal structure of a pfam duf1093 family protein (bsu39620) from2 bacillus subtilis at 2.15 a resolution
91	d1s1ga	Alignment	not modelled	8.6	14	Fold: POZ domain Superfamily: POZ domain Family: Tetramerization domain of potassium channels
92	c5a15A	Alignment	not modelled	8.6	20	PDB header: signaling protein Chain: A: PDB Molecule: btb/poz domain-containing protein kctd16; PDBTitle: crystal structure of the btb domain of human kctd16
93	c2wd6B	Alignment	not modelled	8.4	21	PDB header: cell adhesion Chain: B: PDB Molecule: agglutinin receptor; PDBTitle: crystal structure of the variable domain of the streptococcus gordonii2 surface protein sspp
94	d1wj6a	Alignment	not modelled	8.2	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
95	d1hnra	Alignment	not modelled	8.2	15	Fold: H-NS histone-like proteins Superfamily: H-NS histone-like proteins Family: H-NS histone-like proteins
96	c1o7dA	Alignment	not modelled	8.0	83	PDB header: hydrolase Chain: A: PDB Molecule: lysosomal alpha-mannosidase; PDBTitle: the structure of the bovine lysosomal a-mannosidase suggests a novel2 mechanism for low ph activation
97	d1eaka2	Alignment	not modelled	8.0	36	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
98	c2jsdA	Alignment	not modelled	7.9	45	PDB header: hydrolase Chain: A: PDB Molecule: matrix metalloproteinase-20; PDBTitle: solution structure of mmp20 complexed with nngh
99	c2mlwA	Alignment	not modelled	7.9	30	PDB header: toxin Chain: A: PDB Molecule: type-1ba cytolytic delta-endotoxin; PDBTitle: new cyt-like delta-endotoxins from dickeya dadantii - cyt protein