



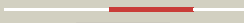























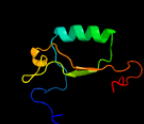

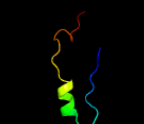


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0320 (-) _387888_388550
Date	Tue Jul 23 14:50:38 BST 2019
Unique Job ID	77498b2a7abc5136

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1lbuA2	 Alignment		96.9	29	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: Muramoyl-pentapeptide carboxypeptidase
2	c4ox3A_	 Alignment		96.2	15	PDB header: hydrolase Chain: A; PDB Molecule: putative carboxypeptidase yodj; PDBTitle: structure of the ldcB Id-carboxypeptidase reveals the molecular basis2 of peptidoglycan recognition
3	c5hnmC_	 Alignment		96.0	23	PDB header: hydrolase Chain: C; PDB Molecule: d-alanyl-d-alanine carboxypeptidase; PDBTitle: crystal structure of vancomycin resistance d,d-pentapeptidase vany2 e175a mutant from vanb-type resistance cassette in complex with3 zn(ii)
4	d2ibge1	 Alignment		95.9	20	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: Hedgehog (development protein), N-terminal signaling domain
5	d3d1ma1	 Alignment		95.6	25	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: Hedgehog (development protein), N-terminal signaling domain
6	c1lbuA_	 Alignment		95.6	22	PDB header: hydrolase Chain: A; PDB Molecule: muramoyl-pentapeptide carboxypeptidase; PDBTitle: hydrolase metallo (zn) dd-peptidase
7	c3m1nB_	 Alignment		95.4	25	PDB header: signaling protein Chain: B; PDB Molecule: sonic hedgehog protein; PDBTitle: crystal structure of human sonic hedgehog n-terminal domain
8	c4jidA_	 Alignment		95.3	20	PDB header: hydrolase Chain: A; PDB Molecule: d-alanyl-d-alanine carboxypeptidase family protein; PDBTitle: crystal structure of baldcb / vany-like I,d-carboxypeptidase zinc(ii)-2 free
9	c4murA_	 Alignment		95.0	24	PDB header: hydrolase Chain: A; PDB Molecule: d,d-dipeptidase/d,d-carboxypeptidase; PDBTitle: crystal structure of vancomycin resistance d,d-dipeptidase/d,d-2 pentapeptidase vanyxc d59s mutant
10	d2vo9a1	 Alignment		94.7	26	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: VanY-like
11	c4f78A_	 Alignment		94.5	19	PDB header: hydrolase Chain: A; PDB Molecule: d,d-dipeptidase/d,d-carboxypeptidase; PDBTitle: crystal structure of vancomycin resistance d,d-dipeptidase vanyg

12	c2vo9C_	Alignment		93.6	20	PDB header: hydrolase Chain: C: PDB Molecule: l-alanyl-d-glutamate peptidase; PDBTitle: crystal structure of the enzymatically active domain of the listeria2 monocytogenes bacteriophage 500 endolysin ply500
13	c4ox5A_	Alignment		93.1	23	PDB header: hydrolase Chain: A: PDB Molecule: ldcb ld-carboxypeptidase; PDBTitle: structure of the ldcb ld-carboxypeptidase reveals the molecular basis2 of peptidoglycan recognition
14	c2mxzA_	Alignment		92.9	18	PDB header: hydrolase Chain: A: PDB Molecule: l-alanyl-d-glutamate peptidase; PDBTitle: bacteriophage t5 l-alanyl-d-glutamate peptidase complex with zn2+2 (endo t5-zn2+)
15	d1tzpa_	Alignment		91.2	20	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: MepA-like
16	c5opzB_	Alignment		86.5	23	PDB header: hydrolase Chain: B: PDB Molecule: chix; PDBTitle: crystal structure of serratia marcescens l-ala d-glu endopeptidase2 chix
17	c9rubB_	Alignment		37.8	35	PDB header: lyase(carbon-carbon) Chain: B: PDB Molecule: ribulose-1,5-bisphosphate carboxylase; PDBTitle: crystal structure of activated ribulose-1,5-bisphosphate carboxylase2 complexed with its substrate, ribulose-1,5-bisphosphate
18	d1r44a_	Alignment		23.7	20	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: VanX-like
19	d1yloa2	Alignment		19.9	17	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
20	c4i8oA_	Alignment		19.2	20	PDB header: toxin Chain: A: PDB Molecule: toxin rnlA; PDBTitle: crystal structure of the toxin rnlA from escherichia coli
21	d2afwa1	Alignment	not modelled	19.1	19	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Glutaminyl-peptide cyclotransferase-like
22	d1pbaa_	Alignment	not modelled	18.7	15	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Pancreatic carboxypeptidase, activation domain
23	d1hl9a1	Alignment	not modelled	18.0	17	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: Putative alpha-L-fucosidase C-terminal domain
24	c2ojjB_	Alignment	not modelled	17.0	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of q7waf1_borpa from bordetella parapertussis.2 northeast structural genomics target bpr68.
25	c5j4aA_	Alignment	not modelled	16.7	34	PDB header: toxin Chain: A: PDB Molecule: trna nuclease cdia; PDBTitle: cdia-ct toxin from burkholderia pseudomallei e479 in complex with2 cognate cdii immunity protein
26	c2k5kA_	Alignment	not modelled	16.0	36	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein rhr2; PDBTitle: solution structure of rhr2 from rhodobacter sphaeroides.2 northeast structural genomics consortium
27	d1gk8a1	Alignment	not modelled	15.9	33	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
28	c2mw1A_	Alignment	not modelled	14.3	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lipocalin-like protein; PDBTitle: nmr structure of the protein np_809137.1 from bacteroides2 thetaiotaomicron
						PDB header: structural genomics, unknown function

29	c3dexA	Alignment	not modelled	13.9	16	Chain: A: PDB Molecule: sav_2001; PDBTitle: crystal structure of sav_2001 protein from streptomyces2 avermitilis, northeast structural genomics consortium3 target svr107.
30	d1ug0a	Alignment	not modelled	13.7	23	Fold: Surp module (SWAP domain) Superfamily: Surp module (SWAP domain) Family: Surp module (SWAP domain)
31	c3rcnA	Alignment	not modelled	13.6	17	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: crystal structure of beta-n-acetylhexosaminidase from arthrobacter2 aurescens
32	c2zhha	Alignment	not modelled	13.6	27	PDB header: transcription Chain: A: PDB Molecule: redox-sensitive transcriptional activator soxr; PDBTitle: crystal structure of soxr
33	d1gxha	Alignment	not modelled	11.9	32	Fold: Acyl carrier protein-like Superfamily: Colicin E immunity proteins Family: Colicin E immunity proteins
34	c2p0gB	Alignment	not modelled	11.7	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: selenoprotein w-related protein; PDBTitle: crystal structure of selenoprotein w-related protein from vibrio2 cholerae. northeast structural genomics target vcr75
35	c3nwrA	Alignment	not modelled	11.1	24	PDB header: lyase Chain: A: PDB Molecule: a rubisco-like protein; PDBTitle: crystal structure of a rubisco-like protein from burkholderia fungorum
36	d2fvga2	Alignment	not modelled	10.5	8	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
37	c1telA	Alignment	not modelled	10.3	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ribulose biphosphate carboxylase, large subunit; PDBTitle: crystal structure of a rubisco-like protein from chlorobium2 tepidum
38	d8ruca1	Alignment	not modelled	10.2	33	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
39	d1kwma2	Alignment	not modelled	9.8	17	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Pancreatic carboxypeptidase, activation domain
40	d1rbla1	Alignment	not modelled	9.6	29	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
41	d1geha1	Alignment	not modelled	9.5	26	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
42	d1ykwa1	Alignment	not modelled	9.1	24	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
43	c2qygC	Alignment	not modelled	9.0	19	PDB header: unknown function Chain: C: PDB Molecule: ribulose biphosphate carboxylase-like protein 2; PDBTitle: crystal structure of a rubisco-like protein rlp2 from rhodospseudomonas2 palustris
44	d2ga5a1	Alignment	not modelled	8.9	13	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Frataxin-like
45	d2fa8a1	Alignment	not modelled	8.8	20	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Selenoprotein W-related
46	d1svda1	Alignment	not modelled	8.8	29	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
47	c3pb6X	Alignment	not modelled	8.7	18	PDB header: transferase Chain: X: PDB Molecule: glutaminy-peptide cyclotransferase-like protein; PDBTitle: crystal structure of the catalytic domain of human golgi-resident2 glutaminy cyclase at ph 6.5
48	d1nsaa2	Alignment	not modelled	8.6	22	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Pancreatic carboxypeptidase, activation domain
49	c6mbcB	Alignment	not modelled	8.5	14	PDB header: apoptosis Chain: B: PDB Molecule: df4; PDBTitle: human bfl-1 in complex with the designed peptide df4
50	c2obkE	Alignment	not modelled	8.2	8	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: selt/selw/selh selenoprotein domain; PDBTitle: x-ray structure of the putative se binding protein from pseudomonas2 fluorescens. northeast structural genomics consortium target plr6.
51	d1wdda1	Alignment	not modelled	7.9	38	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
52	c1gehE	Alignment	not modelled	7.9	26	PDB header: lyase Chain: E: PDB Molecule: ribulose-1,5-bisphosphate carboxylase/oxygenase; PDBTitle: crystal structure of archaeal rubisco (ribulose 1,5-bisphosphate2 carboxylase/oxygenase)
53	d2d69a1	Alignment	not modelled	7.8	33	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
						PDB header: lyase (carbon-carbon) Chain: H: PDB Molecule: ribulose biphosphate

54	c1rcxH_	Alignment	not modelled	7.3	33	carboxylase/oxygenase; PDBTitle: non-activated spinach rubisco in complex with its substrate2 ribulose-1,5-bisphosphate
55	c3rpcD_	Alignment	not modelled	7.1	33	PDB header: hydrolase Chain: D: PDB Molecule: possible metal-dependent hydrolase; PDBTitle: the crystal structure of a possible metal-dependent hydrolase from2 veillonella parvula dsm 2008
56	c2wylF_	Alignment	not modelled	6.9	33	PDB header: hydrolase Chain: F: PDB Molecule: l-ascorbate-6-phosphate lactonase ulag; PDBTitle: apo structure of a metallo-b-lactamase
57	d2p8ia1	Alignment	not modelled	6.7	12	Fold: Ferredoxin-like Superfamily: DOPA-like Family: DOPA dioxygenase-like
58	c6fcoB_	Alignment	not modelled	6.6	19	PDB header: transport protein Chain: B: PDB Molecule: mitochondrial frataxin-like protein; PDBTitle: structural and functional characterisation of frataxin (fxn) like2 protein from chaetomium thermophilum
59	d1zdya1	Alignment	not modelled	6.5	15	Fold: Antiparallel beta/alpha barrel (PT-barrel) Superfamily: Prenyltransferase-like Family: Prenyltransferase-like
60	d1o6xa_	Alignment	not modelled	6.4	23	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Pancreatic carboxypeptidase, activation domain
61	c2d69B_	Alignment	not modelled	6.4	33	PDB header: lyase Chain: B: PDB Molecule: ribulose bisphosphate carboxylase; PDBTitle: crystal structure of the complex of sulfate ion and octameric2 ribulose-1,5-bisphosphate carboxylase/oxygenase (rubisco) from3 pyrococcus horikoshii ot3 (form-2 crystal)
62	c4chlA_	Alignment	not modelled	6.2	23	PDB header: oxidoreductase Chain: A: PDB Molecule: persulfide dioxygenase ethe1, mitochondrial; PDBTitle: human ethylmalonic encephalopathy protein 1 (hethel1)
63	c1hyhA_	Alignment	not modelled	6.1	23	PDB header: oxidoreductase (choh(d)-nad+(a)) Chain: A: PDB Molecule: l-2-hydroxyisocaproate dehydrogenase; PDBTitle: crystal structure of l-2-hydroxyisocaproate dehydrogenase from2 lactobacillus confusus at 2.2 angstroms resolution-an example of3 strong asymmetry between subunits
64	c4hf7A_	Alignment	not modelled	6.1	14	PDB header: hydrolase Chain: A: PDB Molecule: putative acylhydrolase; PDBTitle: crystal structure of a gdsI-like lipase (bt0569) from bacteroides2 thetaiotaomicron vpi-5482 at 1.77 a resolution
65	c3qfwB_	Alignment	not modelled	6.1	14	PDB header: lyase Chain: B: PDB Molecule: ribulose-1,5-bisphosphate carboxylase/oxygenase large PDBTitle: crystal structure of rubisco-like protein from rhodospseudomonas2 palustris
66	c4qn9A_	Alignment	not modelled	6.0	44	PDB header: hydrolase Chain: A: PDB Molecule: n-acyl-phosphatidylethanolamine-hydrolyzing phospholipase PDBTitle: structure of human nape-pld
67	c2ljkA_	Alignment	not modelled	5.9	20	PDB header: signaling protein Chain: A: PDB Molecule: protein c17orf37; PDBTitle: solution structure of the oncogenic-potential mien1 protein
68	c4z1bA_	Alignment	not modelled	5.8	14	PDB header: transferase Chain: A: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase; PDBTitle: structure of h204a mutant kdo8ps from h.pylori
69	c1rldB_	Alignment	not modelled	5.8	33	PDB header: lyase(carbon-carbon) Chain: B: PDB Molecule: ribulose 1,5 bisphosphate carboxylase/oxygenase (large PDBTitle: solid-state phase transition in the crystal structure of ribulose 1,5-2 biphosphate carboxylase(/slash)oxygenase
70	c4jo0A_	Alignment	not modelled	5.8	33	PDB header: oxidoreductase Chain: A: PDB Molecule: cmla; PDBTitle: crystal structure of cmla, a diiron beta-hydroxylase from streptomyces2 venezuelae
71	d2vlqa1	Alignment	not modelled	5.7	29	Fold: Acyl carrier protein-like Superfamily: Colicin E immunity proteins Family: Colicin E immunity proteins
72	c2qw5B_	Alignment	not modelled	5.6	12	PDB header: isomerase Chain: B: PDB Molecule: xylose isomerase-like tim barrel; PDBTitle: crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution
73	d1ayea2	Alignment	not modelled	5.6	23	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Pancreatic carboxypeptidase, activation domain
74	d1ej7I1	Alignment	not modelled	5.6	33	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
75	d2czra1	Alignment	not modelled	5.4	30	Fold: Restriction endonuclease-like Superfamily: TBP-interacting protein-like Family: TBP-interacting protein-like
76	d2fq1a1	Alignment	not modelled	5.4	13	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Frataxin-like
77	c3bv6D_	Alignment	not modelled	5.4	33	PDB header: hydrolase Chain: D: PDB Molecule: metal-dependent hydrolase; PDBTitle: crystal structure of uncharacterized metallo protein from vibrio2 cholerae with beta-lactamase like fold
78	c1qbaA_	Alignment	not modelled	5.2	33	PDB header: glycosyl hydrolase Chain: A: PDB Molecule: chitobiase; PDBTitle: bacterial chitobiase, glycosyl hydrolase family 20
						PDB header: hydrolase

79	c6q63B_	Alignment	not modelled	5.2	19	Chain: B: PDB Molecule: beta-hexosaminidase; PDBTitle: bt0459
80	d2boaa2	Alignment	not modelled	5.1	20	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Pancreatic carboxypeptidase, activation domain