

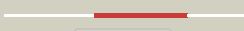








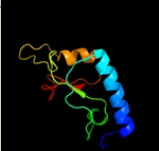





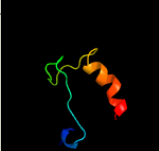

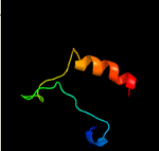










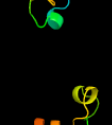


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1728c_(-) _1953871_1954641
Date	Fri Aug 2 13:30:33 BST 2019
Unique Job ID	fb6bb3be37d7afcd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1lbuu2	 Alignment		95.9	29	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: Muramoyl-pentapeptide carboxypeptidase
2	c4ox3A_	 Alignment		95.0	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		94.7	27	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	c4murA_	 Alignment		94.4	26	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 vanxyc d59s mutant
5	c4ox5A_	 Alignment		94.2	27	PDB header: hydrolase Chain: A: PDB Molecule: ldcb Id-carboxypeptidase; PDBTitle: structure of the ldcB Id-carboxypeptidase reveals the molecular basis2 of peptidoglycan recognition
6	c1lbuA_	 Alignment		94.1	22	PDB header: hydrolase Chain: A: PDB Molecule: muramoyl-pentapeptide carboxypeptidase; PDBTitle: hydrolase metallo (zn) dd-peptidase
7	d2vo9a1	 Alignment		93.2	23	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: VanY-like
8	c2vo9C_	 Alignment		91.2	22	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
9	c4jidA_	 Alignment		88.6	24	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
10	c4f78A_	 Alignment		87.7	22	PDB header: hydrolase Chain: A: PDB Molecule: d,d-dipeptidase/d,d-carboxypeptidase; PDBTitle: crystal structure of vancomycin resistance d,d-dipeptidase vanxyg
11	d1tzpa_	 Alignment		87.3	17	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: MepA-like

12	c5opzB_	Alignment		86.4	24	PDB header: hydrolase Chain: B: PDB Molecule: chix; PDBTitle: crystal structure of serratia marcescens l-ala d-glu endopeptidase2 chix
13	c2mxzA_	Alignment		82.6	24	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+)
14	d3d1ma1	Alignment		78.3	22	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: Hedgehog (development protein), N-terminal signaling domain
15	c3m1nB_	Alignment		61.5	22	PDB header: signaling protein Chain: B: PDB Molecule: sonic hedgehog protein; PDBTitle: crystal structure of human sonic hedgehog n-terminal domain
16	d2ibge1	Alignment		46.6	19	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: Hedgehog (development protein), N-terminal signaling domain
17	d1pbaa_	Alignment		38.6	7	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Pancreatic carboxypeptidase, activation domain
18	c3rcnA_	Alignment		29.7	15	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: crystal structure of beta-n-acetylhexosaminidase from arthrobacter2 aurescens
19	c5h4uB_	Alignment		26.6	45	PDB header: hydrolase Chain: B: PDB Molecule: endo-beta-1,4-glucanase; PDBTitle: crystal structure of cellulase from antarctic springtail, cryptopygus2 antarcticus
20	d1kwma2	Alignment		24.4	10	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Pancreatic carboxypeptidase, activation domain
21	d1nsaa2	Alignment	not modelled	22.8	7	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Pancreatic carboxypeptidase, activation domain
22	c2zhha_	Alignment	not modelled	19.2	23	PDB header: transcription Chain: A: PDB Molecule: redox-sensitive transcriptional activator soxr; PDBTitle: crystal structure of soxr
23	c6q63B_	Alignment	not modelled	15.7	15	PDB header: hydrolase Chain: B: PDB Molecule: beta-hexosaminidase; PDBTitle: bt0459
24	d1o6xa_	Alignment	not modelled	15.6	20	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Pancreatic carboxypeptidase, activation domain
25	d1ayea2	Alignment	not modelled	15.2	20	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Pancreatic carboxypeptidase, activation domain
26	c4i8oA_	Alignment	not modelled	13.5	12	PDB header: toxin Chain: A: PDB Molecule: toxin rnlA; PDBTitle: crystal structure of the toxin rnlA from escherichia coli
27	d1pyta_	Alignment	not modelled	13.5	23	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Pancreatic carboxypeptidase, activation domain
28	d1yloa2	Alignment	not modelled	13.4	19	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
29	c2fvaA_	Alignment	not modelled	13.0	12	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase;

29	c2lvqA	Alignment	not modelled	13.0	12	PDBTitle: crystal structure of endoglucanase (tm1049) from thermotoga maritima2 at 2.01 a resolution 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
30	c2k5kA	Alignment	not modelled	12.8	36	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
31	d2fhfa2	Alignment	not modelled	12.6	26	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Pancreatic carboxypeptidase, activation domain
32	d1pcaa1	Alignment	not modelled	12.2	27	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Pancreatic carboxypeptidase, activation domain
33	d1jqga2	Alignment	not modelled	11.7	20	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Pancreatic carboxypeptidase, activation domain
34	c5j4aA	Alignment	not modelled	11.6	16	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
35	d1l8fa	Alignment	not modelled	10.5	40	Fold: Double psi beta-barrel Superfamily: Barwin-like endoglucanases Family: Eng V-like
36	d2boaa2	Alignment	not modelled	9.3	16	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Pancreatic carboxypeptidase, activation domain
37	c3rpcD	Alignment	not modelled	9.1	40	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
38	c1qbaA	Alignment	not modelled	8.7	26	PDB header: glycosyl hydrolase Chain: A; PDB Molecule: chitobiase; PDBTitle: bacterial chitobiase, glycosyl hydrolase family 20
39	c9rubB	Alignment	not modelled	8.5	26	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
40	c6ezrA	Alignment	not modelled	8.5	21	PDB header: hydrolase Chain: A; PDB Molecule: beta-n-acetylglucosaminidase nag2; PDBTitle: crystal structure of gh20 exo beta-n-acetylglucosaminidase from vibrio2 harveyi
41	d1wiga2	Alignment	not modelled	8.3	38	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
42	d2cg7a1	Alignment	not modelled	8.3	63	Fold: Fnl-like domain Superfamily: Fnl-like domain Family: Fibronectin type I module
43	c5c5zA	Alignment	not modelled	8.0	30	PDB header: hydrolase Chain: A; PDB Molecule: glutamyl-trna amidotransferase; PDBTitle: crystal structure analysis of c4763, a uropathogenic e. coli-specific2 protein
44	c4jo0A	Alignment	not modelled	7.9	50	PDB header: oxidoreductase Chain: A; PDB Molecule: cmla; PDBTitle: crystal structure of cmla, a diiron beta-hydroxylase from streptomyces2 venezuelae
45	c4qn9A	Alignment	not modelled	7.7	50	PDB header: hydrolase Chain: A; PDB Molecule: n-acyl-phosphatidylethanolamine-hydrolyzing phospholipase PDBTitle: structure of human nape-pld
46	c4hlmD	Alignment	not modelled	7.6	45	PDB header: transferase Chain: D; PDB Molecule: tankyrase-2; PDBTitle: crystal structure of tankyrase 2 in complex with 3',4'-2 dihydroxyflavone
47	c6b4hB	Alignment	not modelled	7.6	40	PDB header: transport protein Chain: B; PDB Molecule: nucleoporin amo1; PDBTitle: crystal structure of chaetomium thermophilum gle1 ctd-nup42 gbm-ip62 complex
48	c2rkzD	Alignment	not modelled	7.5	63	PDB header: cell adhesion Chain: D; PDB Molecule: fibronectin; PDBTitle: crystal structure of the second and third fibronectin f1 modules in2 complex with a fragment of staphylococcus aureus fnbpa-1
49	d1r44a	Alignment	not modelled	7.4	24	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: VanX-like
50	c3k44D	Alignment	not modelled	7.3	50	PDB header: nucleic acid binding protein Chain: D; PDB Molecule: purine-rich binding protein-alpha, isoform b; PDBTitle: crystal structure of drosophila melanogaster pur-alpha
51	d1nowa1	Alignment	not modelled	6.9	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
52	c2fekA	Alignment	not modelled	6.6	33	PDB header: hydrolase Chain: A; PDB Molecule: low molecular weight protein-tyrosine- PDBTitle: structure of a protein tyrosine phosphatase
53	c5fgoA	Alignment	not modelled	6.3	40	PDB header: dna binding protein Chain: A; PDB Molecule: cg1507-pb, isoform b; PDBTitle: crystal structure of d. melanogaster pur-alpha repeat iii.
54	d1ug0a	Alignment	not modelled	6.2	6	Fold: Surp module (SWAP domain) Superfamily: Surp module (SWAP domain) Family: Surp module (SWAP domain)
55	c3qb8A	Alignment	not modelled	6.1	12	PDB header: transferase Chain: A; PDB Molecule: a654l protein; PDBTitle: paramecium chlorella bursaria virus1 putative orf a654l is

						a polyamine2 acetyltransferase
56	d2rkya2	Alignment	not modelled	6.1	63	Fold: Fnl-like domain Superfamily: Fnl-like domain Family: Fibronectin type I module
57	c2wyfF_	Alignment	not modelled	6.0	44	PDB header: hydrolase Chain: F: PDB Molecule: l-ascorbate-6-phosphate lactonase ulag; PDBTitle: apo structure of a metallo-b-lactamase
58	c2imuA_	Alignment	not modelled	5.8	44	PDB header: viral protein Chain: A: PDB Molecule: structural polyprotein (pp) p1; PDBTitle: nmr structure of pep46 from the infectious bursal disease2 virus (ibdv) in dodecylphosphocholin (dpc).
59	d1y1la_	Alignment	not modelled	5.8	63	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
60	d2rkya1	Alignment	not modelled	5.7	50	Fold: Fnl-like domain Superfamily: Fnl-like domain Family: Fibronectin type I module
61	c2rkyaA_	Alignment	not modelled	5.7	63	PDB header: cell adhesion Chain: A: PDB Molecule: fibronectin; PDBTitle: crystal structure of the fourth and fifth fibronectin f1 modules in2 complex with a fragment of staphylococcus aureus fnbpa-1
62	c2k89A_	Alignment	not modelled	5.7	40	PDB header: protein binding Chain: A: PDB Molecule: phospholipase a-2-activating protein; PDBTitle: solution structure of a novel ubiquitin-binding domain from2 human plaa (pfuc, gly76-pro77 cis isomer)
63	c5i8iD_	Alignment	not modelled	5.5	27	PDB header: hydrolase Chain: D: PDB Molecule: urea amidolyase; PDBTitle: crystal structure of the k. lactis urea amidolyase
64	c4lrqC_	Alignment	not modelled	5.5	56	PDB header: hydrolase Chain: C: PDB Molecule: phosphotyrosine protein phosphatase; PDBTitle: crystal structure of a low molecular weight phosphotyrosine2 phosphatase from vibrio choleraeo395
65	c3w36A_	Alignment	not modelled	5.4	30	PDB header: oxidoreductase Chain: A: PDB Molecule: naph1; PDBTitle: crystal structure of holo-type bacterial vanadium-dependent2 chloroperoxidase
66	c3pb6X_	Alignment	not modelled	5.4	12	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
67	c3bv6D_	Alignment	not modelled	5.3	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
68	d1t1lua1	Alignment	not modelled	5.1	26	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase