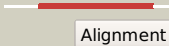

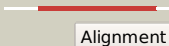

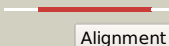







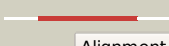











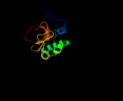








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1115_(-)_1240192_1240890
Date	Wed Jul 31 22:05:19 BST 2019
Unique Job ID	5deea439c2ae151e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2xivA_	 Alignment		99.9	21	PDB header: structural protein Chain: A: PDB Molecule: hypothetical invasion protein; PDBTitle: structure of rv1477, hypothetical invasion protein of mycobacterium2 tuberculosis
2	c6biqA_	 Alignment		99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: clan ca, family c40, nlp/p60 superfamily cysteine PDBTitle: structure of nlp2 from trichomonas vaginalis
3	c3pbIA_	 Alignment		99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: invasion protein; PDBTitle: structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution
4	c6b8cA_	 Alignment		99.9	28	PDB header: hydrolase Chain: A: PDB Molecule: nlp/p60; PDBTitle: crystal structure of nlp/p60 domain of peptidoglycan hydrolase saga
5	c2fg0B_	 Alignment		99.9	17	PDB header: hydrolase Chain: B: PDB Molecule: cog0791: cell wall-associated hydrolases (invasion- PDBTitle: crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (npun_r0659) from nostoc punctiforme pcc 73102 at 1.793 a resolution
6	c3gt2A_	 Alignment		99.9	21	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the p60 domain from m. avium paratuberculosis2 antigen map1272c
7	d2evra2	 Alignment		99.9	20	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: NlpC/P60
8	c4fdyA_	 Alignment		99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: similar to lipoprotein, nlp/p60 family; PDBTitle: crystal structure of a similar to lipoprotein, nlp/p60 family2 (sav0400) from staphylococcus aureus subsp. aureus mu50 at 2.23 a3 resolution
9	c3nfpB_	 Alignment		99.9	15	PDB header: hydrolase Chain: B: PDB Molecule: putative dipeptidyl-peptidase vi; PDBTitle: crystal structure of a putative dipeptidyl-peptidase vi (bacova_00612)2 from bacteroides ovatus at 1.72 a resolution
10	c3i86A_	 Alignment		99.9	22	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the p60 domain from m. avium subspecies2 paratuberculosis antigen map1204
11	c2k1gA_	 Alignment		99.9	16	PDB header: lipoprotein Chain: A: PDB Molecule: lipoprotein spr; PDBTitle: solution nmr structure of lipoprotein spr from escherichia coli k12.2 northeast structural genomics target er541-37-162

12	c4hpeA	Alignment		99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: putative cell wall hydrolase tn916-like,ctn1-orf17; PDBTitle: crystal structure of a putative cell wall hydrolase (cd630_03720) from2 clostridium difficile 630 at 2.38 a resolution
13	c3h41A	Alignment		99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: nlp/p60 family protein; PDBTitle: crystal structure of a nlp/p60 family protein (bce_2878) from2 bacillus cereus atcc 10987 at 1.79 a resolution
14	c4xcmB	Alignment		99.7	23	PDB header: hydrolase Chain: B: PDB Molecule: cell wall-binding endopeptidase-related protein; PDBTitle: crystal structure of the putative nlp/p60 d,l endopeptidase from t.2 thermophilus
15	c3m1uB	Alignment		99.5	17	PDB header: hydrolase Chain: B: PDB Molecule: putative gamma-d-glutamyl-l-diamino acid endopeptidase; PDBTitle: crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (dvu_0896) from desulfovibrio vulgaris hildenborough at3 1.75 a resolution
16	d2if6a1	Alignment		95.4	22	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Yiix-like
17	c2p1gA	Alignment		94.3	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative xylanase; PDBTitle: crystal structure of a putative xylanase from bacteroides fragilis
18	c5udmA	Alignment		93.1	21	PDB header: hydrolase Chain: A: PDB Molecule: phage-associated cell wall hydrolase; PDBTitle: phage-associated cell wall hydrolase plypy from streptococcus2 pyogenes, space group p6522
19	c2lktA	Alignment		88.3	28	PDB header: hydrolase Chain: A: PDB Molecule: retinoic acid receptor responder protein 3; PDBTitle: solution structure of n-terminal domain of human tig3 in 2 m urea
20	c2kyaA	Alignment		86.8	25	PDB header: hydrolase Chain: A: PDB Molecule: group xvi phospholipase a2; PDBTitle: solution structure of the h-rev107 n-terminal domain
21	c2im9A	Alignment	not modelled	86.7	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of protein lpg0564 from legionella pneumophila str.2 philadelphia 1, pfam duf1460
22	d2im9a1	Alignment	not modelled	86.7	28	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Lpg0564-like
23	c4h4jA	Alignment	not modelled	86.3	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a n-acetylmuramoyl-l-alanine amidase2 (bacuni_02947) from bacteroides uniformis atcc 8492 at 1.15 a3 resolution
24	c4pa5A	Alignment	not modelled	80.1	15	PDB header: transferase Chain: A: PDB Molecule: protein-glutamine gamma-glutamyltransferase; PDBTitle: tgl - a bacterial spore coat transglutaminase - cystamine complex
25	c3kw0D	Alignment	not modelled	76.2	23	PDB header: hydrolase Chain: D: PDB Molecule: cysteine peptidase; PDBTitle: crystal structure of cysteine peptidase (np_982244.1) from bacillus2 cereus atcc 10987 at 2.50 a resolution
26	c4f0wA	Alignment	not modelled	71.7	18	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of type effector tse1 c30a mutant from pseudomonas2 aeruginosa
27	c4f4mA	Alignment	not modelled	70.9	18	PDB header: hydrolase regulator Chain: A: PDB Molecule: papain peptidoglycan amidase effector tse1; PDBTitle: structure of the type vi peptidoglycan amidase effector tse1 (c30a)2 from pseudomonas aeruginosa
28	c2lrjA	Alignment	not modelled	69.2	25	PDB header: biosynthetic protein Chain: A: PDB Molecule: staphyloxanthin biosynthesis protein, putative;

						PDBTitle: nmr solution structure of staphyloxanthin biosynthesis protein
29	c2k3aA_	Alignment	not modelled	64.8	22	PDB header: hydrolase Chain: A: PDB Molecule: chap domain protein; PDBTitle: nmr solution structure of staphylococcus saprophyticus chap2 (cysteine, histidine-dependent amidohydrolases/peptidases)3 domain protein. northeast structural genomics consortium4 target syr11
30	c5t1qB_	Alignment	not modelled	61.7	22	PDB header: hydrolase Chain: B: PDB Molecule: n-acetylmuramoyl-l-alanine amidase domain-containing PDBTitle: 2.15 angstrom crystal structure of n-acetylmuramoyl-l-alanine amidase2 from staphylococcus aureus.
31	c4hzbA_	Alignment	not modelled	40.6	22	PDB header: hydrolase Chain: A: PDB Molecule: putative cytoplasmic protein; PDBTitle: crystal structure of the type vi semet effector-immunity complex tae3-2 tai3 from ralstonia pickettii
32	c4hfkB_	Alignment	not modelled	37.5	14	PDB header: hydrolase Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the type vi effector-immunity complex tae4-tai42 from enterobacter cloacae
33	c4olkB_	Alignment	not modelled	31.7	22	PDB header: hydrolase Chain: B: PDB Molecule: endolysin; PDBTitle: the chap domain of lysgh15
34	d1f35a_	Alignment	not modelled	19.2	17	Fold: Olfactory marker protein Superfamily: Olfactory marker protein Family: Olfactory marker protein
35	c6avaA_	Alignment	not modelled	13.0	36	PDB header: toxin Chain: A: PDB Molecule: insectotoxin-i1; PDBTitle: exploring cystine dense peptide space to open a unique molecular2 toolbox
36	c4b6iD_	Alignment	not modelled	12.6	17	PDB header: signaling protein Chain: D: PDB Molecule: sma2266; PDBTitle: crystal structure rap2b (sma2266) from serratia marcescens
37	c3cjcC_	Alignment	not modelled	10.0	27	PDB header: virus Chain: C: PDB Molecule: polyprotein; PDBTitle: structure of seneca valley virus-001
38	d1iyca_	Alignment	not modelled	6.5	44	Fold: Invertebrate chitin-binding proteins Superfamily: Invertebrate chitin-binding proteins Family: Antifungal peptide scarabaecin
39	c3zibD_	Alignment	not modelled	6.5	21	PDB header: protein binding Chain: D: PDB Molecule: rap2a sma2265; PDBTitle: rap2a protein (sma2265) from serratia marcescens
40	c2vpmB_	Alignment	not modelled	6.2	24	PDB header: ligase Chain: B: PDB Molecule: trypanothione synthetase; PDBTitle: trypanothione synthetase
41	d2io8a2	Alignment	not modelled	5.8	39	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: CHAP domain
42	c2ls1A_	Alignment	not modelled	5.7	56	PDB header: antimicrobial protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: structure of svuceucin, an antibacterial type i lasso peptide from2 streptomyces svuceus
43	c5fx8U_	Alignment	not modelled	5.7	45	PDB header: oxidoreductase Chain: U: PDB Molecule: zonadhesin; PDBTitle: complete structure of manganese lipoxygenase of gaeumannomyces2 graminis and partial structure of zonadhesin of komagataella3 pastoris