

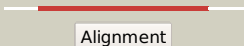

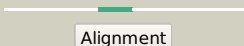
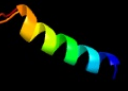


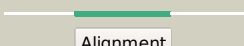
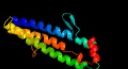
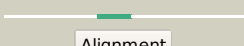

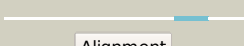


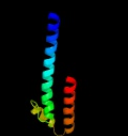








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3626c_(-)_4065030_4066082
Date	Fri Aug 9 18:20:31 BST 2019
Unique Job ID	ba1a9a231c8eca3a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cmnA_	 Alignment		100.0	33	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of a putative hydrolase with a novel fold2 from chloroflexus aurantiacus
2	d3cmna1	 Alignment		100.0	33	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Caur0242-like
3	c4jiuA_	 Alignment		49.3	17	PDB header: hydrolase Chain: A: PDB Molecule: proabylysin; PDBTitle: crystal structure of the metallopeptidase zymogen of pyrococcus abyssi2 abylysin
4	d1nkzb_	 Alignment		46.1	38	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
5	c4clvB_	 Alignment		41.8	11	PDB header: metal binding protein Chain: B: PDB Molecule: nickel-cobalt-cadmium resistance protein nccx; PDBTitle: crystal structure of dodecylphosphocholine-solubilized nccx2 from cupriavidus metallidurans 31a
6	c4jixB_	 Alignment		41.7	27	PDB header: hydrolase Chain: B: PDB Molecule: projannalysin; PDBTitle: crystal structure of the metallopeptidase zymogen of2 methanocaldococcus jannaschii jannalysin
7	c3u1dA_	 Alignment		33.1	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the structure of a protein with a gntr superfamily winged-helix-turn-2 helix domain from halomicrobium mukohataei.
8	c3cqxD_	 Alignment		26.5	15	PDB header: chaperone Chain: D: PDB Molecule: bag family molecular chaperone regulator 2; PDBTitle: chaperone complex
9	c5xbvA_	 Alignment		26.2	13	PDB header: hydrolase Chain: A: PDB Molecule: wss1p; PDBTitle: crystal structure of wss1 mutant from saccharomyces cerevisiae
10	c4b24A_	 Alignment		23.2	16	PDB header: hydrolase/dna Chain: A: PDB Molecule: probable dna-3-methyladenine glycosylase 2; PDBTitle: unprecedented sculpting of dna at abasic sites by dna glycosylase2 homolog mag2
11	c5ldeB_	 Alignment		21.2	20	PDB header: viral protein Chain: B: PDB Molecule: immunoglobulin g-binding protein g,viral flice protein; PDBTitle: crystal structure of a vfliip-ikkgamma stapled peptide dimer

12	d1a2za_	Alignment		21.0	12	Fold: Phosphorylase/hydrolase-like Superfamily: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) Family: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
13	d2cwl1_	Alignment		20.6	5	Fold: Ferritin-like Superfamily: Ferritin-like Family: Manganese catalase (T-catalase)
14	d1iofa_	Alignment		20.4	11	Fold: Phosphorylase/hydrolase-like Superfamily: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) Family: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
15	c5z5mB_	Alignment		19.1	9	PDB header: lyase Chain: B: PDB Molecule: predicted protein; PDBTitle: crystal structure of (s)-allantoin synthase
16	c3zdoC_	Alignment		18.5	40	PDB header: viral protein Chain: C: PDB Molecule: phosphoprotein; PDBTitle: tetramerization domain of measles virus phosphoprotein
17	d1e3oc2	Alignment		18.1	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
18	c6et5u_	Alignment		14.8	25	PDB header: photosynthesis Chain: U: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
19	c5mtwD_	Alignment		14.8	16	PDB header: chaperone Chain: D: PDB Molecule: secb-like chaperone rv1957; PDBTitle: mycobacterium tuberculosis rv1957 secb-like chaperone in complex with2 a chad peptide from rv1956 higa1 antitoxin
20	c1mqrA_	Alignment		14.8	26	PDB header: hydrolase Chain: A: PDB Molecule: alpha-d-glucuronidase; PDBTitle: the crystal structure of alpha-d-glucuronidase (e386q) from bacillus2 stearothermophilus t-6
21	c6h56A_	Alignment	not modelled	14.7	20	PDB header: metal binding protein Chain: A: PDB Molecule: effector domain of pseudomonas aeruginosa vgrg2b; PDBTitle: effector domain of pseudomonas aeruginosa vgrg2b
22	d1l8na1	Alignment	not modelled	14.6	26	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: alpha-D-glucuronidase/Hyaluronidase catalytic domain
23	c4yk3B_	Alignment	not modelled	14.1	15	PDB header: protein binding Chain: B: PDB Molecule: bepe protein; PDBTitle: crystal structure of the bid domain of bepe from bartonella henselae
24	d1au7a2	Alignment	not modelled	13.6	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
25	c3giuA_	Alignment	not modelled	12.3	16	PDB header: hydrolase Chain: A: PDB Molecule: pyrrolidone-carboxylate peptidase; PDBTitle: 1.25 angstrom crystal structure of pyrrolidone-carboxylate peptidase2 (pcp) from staphylococcus aureus
26	c3qzcA_	Alignment	not modelled	11.4	10	PDB header: signaling protein Chain: A: PDB Molecule: periplasmic protein cpxp; PDBTitle: structure of the periplasmic stress response protein cpxp
27	d1jo5a_	Alignment	not modelled	11.3	23	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
28	c3igeA_	Alignment	not modelled	10.5	14	PDB header: viral protein Chain: A: PDB Molecule: soc small outer capsid protein; PDBTitle: small outer capsid protein (soc) from bacteriophage rb69
29	d1ngka_	Alignment	not modelled	10.1	11	Fold: Globin-like Superfamily: Globin-like Family: Truncated hemoglobin

30	d1lmla_	Alignment	not modelled	10.0	26	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Leishmanalysis
31	d1jkva_	Alignment	not modelled	9.9	28	Fold: Ferritin-like Superfamily: Ferritin-like Family: Manganese catalase (T-catalase)
32	d1llib_	Alignment	not modelled	9.2	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
33	d1lmb3_	Alignment	not modelled	8.7	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
34	d1oqya2	Alignment	not modelled	8.6	21	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
35	c2kvrA_	Alignment	not modelled	8.0	20	PDB header: protein binding Chain: A; PDB Molecule: ubiquitin carboxyl-terminal hydrolase 7; PDBTitle: solution nmr structure of human ubiquitin specific protease usp7 ubl2 domain (residues 537-664). nesg target hr4395c/sgc-toronto
36	c6mdxA_	Alignment	not modelled	8.0	30	PDB header: dna binding protein/dna Chain: A; PDB Molecule: spirt-like domain-containing protein spartan; PDBTitle: mechanism of protease dependent dpc repair
37	c6nu9A_	Alignment	not modelled	8.0	21	PDB header: viral protein Chain: A; PDB Molecule: zinc-binding non-structural protein; PDBTitle: crystal structure of a zinc-binding non-structural protein from the2 hepatitis e virus
38	c2ewtA_	Alignment	not modelled	7.9	14	PDB header: dna binding protein Chain: A; PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of the dna-binding domain of bidd
39	c5tf3A_	Alignment	not modelled	7.7	21	PDB header: oxidoreductase Chain: A; PDB Molecule: putative membrane protein; PDBTitle: crystal structure of protein of unknown function ypo2564 from yersinia2 pestis
40	c5vf30_	Alignment	not modelled	7.6	10	PDB header: virus Chain: O; PDB Molecule: small outer capsid protein; PDBTitle: bacteriophage t4 isometric capsid
41	c3epvB_	Alignment	not modelled	7.5	11	PDB header: metal binding protein Chain: B; PDB Molecule: nickel and cobalt resistance protein cnrr; PDBTitle: x-ray structure of the metal-sensor cnrx in both the apo- and copper-2 bound forms
42	d2ce7a1	Alignment	not modelled	7.5	25	Fold: FtsH protease domain-like Superfamily: FtsH protease domain-like Family: FtsH protease domain-like
43	c6fqbE_	Alignment	not modelled	7.3	9	PDB header: ligase Chain: E; PDB Molecule: coobyric acid synthase; PDBTitle: murt/gatd peptidoglycan amidotransferase complex from streptococcus2 pneumoniae r6
44	c3ty8A_	Alignment	not modelled	7.3	9	PDB header: transferase Chain: A; PDB Molecule: polynucleotide 2',3'-cyclic phosphate phosphodiesterase / PDBTitle: crystal structure of c. thermocellum pnkp ligase domain apo form
45	c4gxhC_	Alignment	not modelled	7.3	13	PDB header: hydrolase Chain: C; PDB Molecule: pyrrolidone-carboxylate peptidase; PDBTitle: crystal structure of a pyrrolidone-carboxylate peptidase 1 (target id2 nysgrc-012831) from xenorhabdus bovienii ss-2004
46	c1pbyA_	Alignment	not modelled	7.1	12	PDB header: oxidoreductase Chain: A; PDB Molecule: quinoximoprotein amine dehydrogenase 60 kda subunit; PDBTitle: structure of the phenylhydrazine adduct of the quinoximoprotein amine2 dehydrogenase from paracoccus denitrificans at 1.7 a resolution
47	c4e6nC_	Alignment	not modelled	7.0	9	PDB header: protein binding Chain: C; PDB Molecule: metallophosphoesterase; PDBTitle: crystal structure of bacterial pnkp-c/hen1-n heterodimer
48	d1q1ra3	Alignment	not modelled	6.9	11	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: FAD/NAD-linked reductases, dimerisation (C-terminal) domain Family: FAD/NAD-linked reductases, dimerisation (C-terminal) domain
49	d2di4a1	Alignment	not modelled	6.9	19	Fold: FtsH protease domain-like Superfamily: FtsH protease domain-like Family: FtsH protease domain-like
50	c4ivvA_	Alignment	not modelled	6.9	15	PDB header: hydrolase Chain: A; PDB Molecule: autolysin; PDBTitle: catalytic amidase domain of the major autolysin lyta from2 streptococcus pneumoniae
51	c2di4B_	Alignment	not modelled	6.9	19	PDB header: hydrolase Chain: B; PDB Molecule: cell division protein ftsH homolog; PDBTitle: crystal structure of the ftsH protease domain
52	d1h41a1	Alignment	not modelled	6.9	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: alpha-D-glucuronidase/Hyaluronidase catalytic domain
53	c3o39A_	Alignment	not modelled	6.8	8	PDB header: chaperone Chain: A; PDB Molecule: periplasmic protein related to spheroblast formation; PDBTitle: crystal structure of spy
54	c2da4A_	Alignment	not modelled	6.5	21	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein dkfzp686k21156; PDBTitle: solution structure of the homeobox domain of the2 hypothetical protein, dkfzp686k21156
						PDB header: dna binding protein/dna

55	c5i44E_	Alignment	not modelled	6.4	26	Chain: E: PDB Molecule: chromosome-anchoring protein raca; PDBTitle: structure of raca-dna complex; p21 form
56	c4yk2B_	Alignment	not modelled	6.3	9	PDB header: protein binding Chain: B: PDB Molecule: bartonella effector protein (bep) substrate of virb t4ss; PDBTitle: crystal structure of the bid domain of bep9 from bartonella2 clarridgeiae
57	c2xsdC_	Alignment	not modelled	6.2	25	PDB header: transcription/dna Chain: C: PDB Molecule: pou domain, class 3, transcription factor 1; PDBTitle: crystal structure of the dimeric oct-6 (pou3f1) pou domain2 bound to palindromic more dna
58	c1gqkB_	Alignment	not modelled	6.1	21	PDB header: hydrolase Chain: B: PDB Molecule: alpha-d-glucuronidase; PDBTitle: structure of pseudomonas cellulosa alpha-d-glucuronidase complexed2 with glucuronic acid
59	d1y60a_	Alignment	not modelled	6.1	13	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Formaldehyde-activating enzyme, FAE
60	c3oeoD_	Alignment	not modelled	6.1	8	PDB header: signaling protein Chain: D: PDB Molecule: spheroplast protein y; PDBTitle: the crystal structure e. coli spy
61	c3f6wE_	Alignment	not modelled	6.1	17	PDB header: dna binding protein Chain: E: PDB Molecule: xre-family like protein; PDBTitle: xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
62	c2rn7A_	Alignment	not modelled	5.7	21	PDB header: unknown function Chain: A: PDB Molecule: is629 orfa; PDBTitle: nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125
63	c1l0oC_	Alignment	not modelled	5.7	27	PDB header: protein binding Chain: C: PDB Molecule: sigma factor; PDBTitle: crystal structure of the bacillus stearothermophilus anti-2 sigma factor spoiiab with the sporulation sigma factor3 sigmaf
64	d1l0oc_	Alignment	not modelled	5.7	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
65	d1c6vx_	Alignment	not modelled	5.7	31	Fold: SH3-like barrel Superfamily: DNA-binding domain of retroviral integrase Family: DNA-binding domain of retroviral integrase
66	c1c6vX_	Alignment	not modelled	5.7	31	PDB header: dna binding protein Chain: X: PDB Molecule: protein (siu89134); PDBTitle: siv integrase (catalytic domain + dna biding domain comprising2 residues 50-293) mutant with phe 185 replaced by his (f185h)
67	c4pdnA_	Alignment	not modelled	5.7	43	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of e. coli yfcm
68	d2hrca1	Alignment	not modelled	5.6	19	Fold: Chelatase-like Superfamily: Chelatase Family: Ferrochelatase
69	d1tjla1	Alignment	not modelled	5.3	13	Fold: Long alpha-hairpin Superfamily: DnaK suppressor protein DksA, alpha-hairpin domain Family: DnaK suppressor protein DksA, alpha-hairpin domain
70	c3b4rA_	Alignment	not modelled	5.3	50	PDB header: hydrolase Chain: A: PDB Molecule: putative zinc metalloprotease mj0392; PDBTitle: site-2 protease from methanocaldococcus jannaschii