

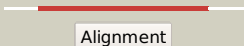

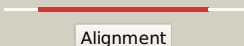
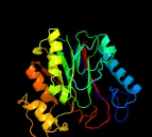





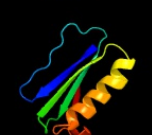
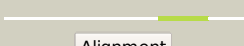




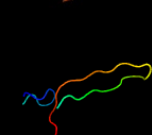

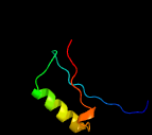






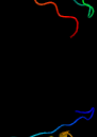



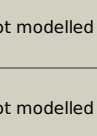


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2149c_(yfiH)_2407630_2408382
Date	Mon Aug 5 13:25:27 BST 2019
Unique Job ID	b483546c3df3fc9a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1t8ha_	 Alignment		100.0	34	Fold: CNF1/YfiH-like putative cysteine hydrolases Superfamily: CNF1/YfiH-like putative cysteine hydrolases Family: YfiH-like
2	d1xfja_	 Alignment		100.0	34	Fold: CNF1/YfiH-like putative cysteine hydrolases Superfamily: CNF1/YfiH-like putative cysteine hydrolases Family: YfiH-like
3	d1rv9a_	 Alignment		100.0	37	Fold: CNF1/YfiH-like putative cysteine hydrolases Superfamily: CNF1/YfiH-like putative cysteine hydrolases Family: YfiH-like
4	d1rw0a_	 Alignment		100.0	36	Fold: CNF1/YfiH-like putative cysteine hydrolases Superfamily: CNF1/YfiH-like putative cysteine hydrolases Family: YfiH-like
5	d1xafa_	 Alignment		100.0	37	Fold: CNF1/YfiH-like putative cysteine hydrolases Superfamily: CNF1/YfiH-like putative cysteine hydrolases Family: YfiH-like
6	d2f9zc1	 Alignment		91.5	28	Fold: CNF1/YfiH-like putative cysteine hydrolases Superfamily: CNF1/YfiH-like putative cysteine hydrolases Family: CheD-like
7	c3giwA_	 Alignment		62.3	13	PDB header: unknown function Chain: A: PDB Molecule: protein of unknown function duf574; PDBTitle: crystal structure of a duf574 family protein (sav_2177) from2 streptomyces avermitilis ma-4680 at 1.45 a resolution
8	c2qe6B_	 Alignment		60.8	17	PDB header: transferase Chain: B: PDB Molecule: uncharacterized protein tfu_2867; PDBTitle: crystal structure of a putative methyltransferase (tfu_2867) from2 thermobifida fusca yx at 1.95 a resolution
9	c4adoA_	 Alignment		45.3	14	PDB header: antibiotic resistance Chain: A: PDB Molecule: far1; PDBTitle: fusidic acid resistance protein fusb
10	c3by0B_	 Alignment		37.0	17	PDB header: ligand binding protein Chain: B: PDB Molecule: neutrophil gelatinase-associated lipocalin; PDBTitle: crystal structure of siderocalin (ngal, lipocalin 2) w79a-r81a2 complexed with ferric enterobactin
11	c2l5pA_	 Alignment		35.9	9	PDB header: transport protein Chain: A: PDB Molecule: lipocalin 12; PDBTitle: solution nmr structure of protein lipocalin 12 from rat epididymis

12	c1kjkA	Alignment		34.1	30	PDB header: viral protein Chain: A: PDB Molecule: integrase; PDBTitle: solution structure of the lambda integrase amino-terminal2 domain
13	c1jd7A	Alignment		33.3	15	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: crystal structure analysis of the mutant k300r of2 pseudoalteromonas haloplanctis alpha-amylase
14	d1z1ba1	Alignment		31.9	30	Fold: DNA-binding domain Superfamily: DNA-binding domain Family: lambda integrase N-terminal domain
15	c3sdsA	Alignment		31.2	23	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase, mitochondrial; PDBTitle: crystal structure of a mitochondrial ornithine carbamoyltransferase2 from coccidioides immitis
16	d1xkia	Alignment		30.1	16	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
17	d1x71a1	Alignment		26.9	17	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
18	c2pw0A	Alignment		24.8	29	PDB header: unknown function Chain: A: PDB Molecule: prpf methylaconitate isomerase; PDBTitle: crystal structure of trans-aconitate bound to methylaconitate2 isomerase prpf from shewanella oneidensis
19	c2xstA	Alignment		23.9	15	PDB header: transport protein Chain: A: PDB Molecule: lipocalin 15; PDBTitle: crystal structure of the human lipocalin 15
20	c3qkgA	Alignment		23.9	15	PDB header: immune system Chain: A: PDB Molecule: protein ambp; PDBTitle: crystal structure of alpha-1-microglobulin at 2.3 a resolution
21	c3ct4B	Alignment	not modelled	23.0	25	PDB header: transferase Chain: B: PDB Molecule: pts-dependent dihydroxyacetone kinase, dihydroxyacetone- PDBTitle: structure of dha-kinase subunit dhak from l. lactis
22	c2e4jA	Alignment	not modelled	22.8	16	PDB header: isomerase Chain: A: PDB Molecule: prostaglandin-h2 d-isomerase; PDBTitle: solution structure of mouse lipocalin-type prostaglandin d2 synthase
23	c5yq7C	Alignment	not modelled	21.3	27	PDB header: photosynthesis Chain: C: PDB Molecule: cytochrome subunit of photosynthetic reaction center; PDBTitle: cryo-em structure of the rc-lh core complex from roseiflexus2 castenholzii
24	c5nghA	Alignment	not modelled	21.3	9	PDB header: protein binding Chain: A: PDB Molecule: odorant binding protein 3; PDBTitle: structure of odorant binding protein 3 from giant panda (ailuropoda2 melanoleuca)
25	c6otvA	Alignment	not modelled	21.1	26	PDB header: isomerase Chain: A: PDB Molecule: putative isomerase ybhh; PDBTitle: crystal structure of putative isomerase ec2056
26	c6p3hB	Alignment	not modelled	20.5	34	PDB header: isomerase Chain: B: PDB Molecule: (4e)-oxalomesaconate delta-isomerase; PDBTitle: crystal structure of ligu(k66m) bound to substrate
27	d1yupa1	Alignment	not modelled	19.5	4	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
28	c3g7kD	Alignment	not modelled	19.4	29	PDB header: isomerase Chain: D: PDB Molecule: 3-methylitaconate isomerase; PDBTitle: crystal structure of methylitaconate-delta-isomerase

29	d1np7a2	Alignment	not modelled	17.8	16	Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain
30	d1yaca	Alignment	not modelled	17.2	18	Fold: Isochorismatase-like hydrolases Superfamily: Isochorismatase-like hydrolases Family: Isochorismatase-like hydrolases
31	d2h9fa1	Alignment	not modelled	16.6	26	Fold: Diaminopimelate epimerase-like Superfamily: Diaminopimelate epimerase-like Family: PA0793-like
32	c1h7bA	Alignment	not modelled	16.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: anaerobic ribonucleotide-triphosphate reductase large PDBTitle: structural basis for allosteric substrate specificity regulation in2 class iii ribonucleotide reductases, native nrdd
33	d1beba	Alignment	not modelled	15.9	4	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
34	d1wjpa2	Alignment	not modelled	15.7	27	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
35	c4wwxY	Alignment	not modelled	15.0	38	PDB header: hydrolase, ligase Chain: Y: PDB Molecule: v(d)j recombination-activating protein 2; PDBTitle: crystal structure of the core rag1/2 recombinase
36	c2k23A	Alignment	not modelled	14.4	15	PDB header: transport protein Chain: A: PDB Molecule: lipocalin 2; PDBTitle: solution structure analysis of the rlcn2
37	d2nvma1	Alignment	not modelled	13.9	21	Fold: Xisl-like Superfamily: Xisl-like Family: Xisl-like
38	c2r73C	Alignment	not modelled	13.3	9	PDB header: transport protein Chain: C: PDB Molecule: trichosurin; PDBTitle: crystal structure of the possum milk whey lipocalin2 trichosurin at ph 8.2
39	c2n4kA	Alignment	not modelled	12.9	50	PDB header: antimicrobial protein Chain: A: PDB Molecule: enterocin-hf; PDBTitle: solution structure of enterocin hf, an antilisterial bacteriocin2 produced by enterococcus faecium m3k31
40	d1eysc	Alignment	not modelled	12.8	18	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Photosynthetic reaction centre (cytochrome subunit)
41	c1eysC	Alignment	not modelled	12.8	18	PDB header: electron transport Chain: C: PDB Molecule: photosynthetic reaction center; PDBTitle: crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
42	c2wl8D	Alignment	not modelled	12.3	14	PDB header: protein transport Chain: D: PDB Molecule: peroxisomal biogenesis factor 19; PDBTitle: x-ray crystal structure of pex19p
43	c3bx6A	Alignment	not modelled	12.2	9	PDB header: signaling protein Chain: A: PDB Molecule: alpha-1-acid glycoprotein; PDBTitle: crystal structure of human alpha 1 acid glycoprotein
44	c5b5yA	Alignment	not modelled	12.1	10	PDB header: metal binding protein Chain: A: PDB Molecule: ptlcib4; PDBTitle: crystal structure of ptcib4, a homolog of the limiting co2-inducible2 protein lcib
45	c1c4gB	Alignment	not modelled	12.1	15	PDB header: transferase Chain: B: PDB Molecule: protein (alpha-d-glucose 1-phosphate phosphoglucomutase); PDBTitle: phosphoglucomutase vanadate based transition state analog complex
46	c5x7yB	Alignment	not modelled	11.9	13	PDB header: allergen Chain: B: PDB Molecule: lipocalin-can f 6 allergen; PDBTitle: crystal structure of the dog lipocalin allergen can f 6
47	d1ew3a	Alignment	not modelled	11.7	9	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
48	c6fezB	Alignment	not modelled	11.6	33	PDB header: viral protein Chain: B: PDB Molecule: serine protease domain; PDBTitle: ryegrass mottle virus protease domain
49	c1hynQ	Alignment	not modelled	11.6	32	PDB header: membrane protein Chain: Q: PDB Molecule: band 3 anion transport protein; PDBTitle: crystal structure of the cytoplasmic domain of human erythrocyte band-2 3 protein
50	c3grfA	Alignment	not modelled	11.6	16	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: x-ray structure of ornithine transcarbamoylase from giardia2 lamblia
51	d1hk8a	Alignment	not modelled	11.5	16	Fold: PFL-like glycy radical enzymes Superfamily: PFL-like glycy radical enzymes Family: Class III anaerobic ribonucleotide reductase NRDD subunit
52	c1hk8A	Alignment	not modelled	11.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: anaerobic ribonucleotide-triphosphate reductase; PDBTitle: structural basis for allosteric substrate specificity regulation in2 class iii ribonucleotide reductases: nrdd in complex with dgtp
53	c1bagA	Alignment	not modelled	11.2	9	PDB header: alpha-amylase Chain: A: PDB Molecule: alpha-1,4-glucon-4-gluconohydrolase; PDBTitle: alpha-amylase from bacillus subtilis complexed with2 maltopentaose
54	d2i5nc1	Alignment	not modelled	11.0	36	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Photosynthetic reaction centre (cytochrome subunit)

55	c2jblC_	Alignment	not modelled	11.0	36	PDB header: electron transport Chain: C: PDB Molecule: photosynthetic reaction center cytochrome c subunit; PDBTitle: photosynthetic reaction center from blastochloris viridis
56	d1hynp_	Alignment	not modelled	10.8	32	Fold: Phosphotransferase/anion transport protein Superfamily: Phosphotransferase/anion transport protein Family: Anion transport protein, cytoplasmic domain
57	c3cqrB_	Alignment	not modelled	10.7	9	PDB header: oxidoreductase Chain: B: PDB Molecule: violaxanthin de-epoxidase, chloroplast; PDBTitle: crystal structure of the lipocalin domain of violaxanthin de-epoxidase2 (vde) at pH5
58	d1eg7a_	Alignment	not modelled	10.6	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
59	c3lyvF_	Alignment	not modelled	10.5	50	PDB header: chaperone Chain: F: PDB Molecule: ribosome-associated factor y; PDBTitle: crystal structure of a domain of ribosome-associated factor y from2 streptococcus pyogenes serotype m6. northeast structural genomics3 consortium target id dr64a
60	d2ch5a2	Alignment	not modelled	10.3	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
61	c6rdu9_	Alignment	not modelled	9.9	17	PDB header: proton transport Chain: 9: PDB Molecule: asa-9: polytomella f-atp synthase associated subunit 9; PDBTitle: cryo-em structure of polytomella f-atp synthase, rotary substate 1e,2 monomer-masked refinement
62	c3jbxB_	Alignment	not modelled	9.7	33	PDB header: recombination/dna Chain: B: PDB Molecule: v(dj) recombination-activating protein 2; PDBTitle: cryo-electron microscopy structure of rag signal end complex (c22 symmetry)
63	d1duvg2	Alignment	not modelled	9.6	20	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
64	c3l4rA_	Alignment	not modelled	9.4	9	PDB header: allergen, lipid binding protein Chain: A: PDB Molecule: minor allergen can f 2; PDBTitle: crystal structure of the dog lipocalin allergen can f 2 and2 implications for cross-reactivity to the cat allergen fel d 4
65	c3do6B_	Alignment	not modelled	9.3	43	PDB header: ligase Chain: B: PDB Molecule: formate--tetrahydrofolate ligase; PDBTitle: crystal structure of putative formyltetrahydrofolate synthetase2 (tm1766) from thermotoga maritima at 1.85 a resolution
66	c2z8nB_	Alignment	not modelled	9.3	17	PDB header: lyase Chain: B: PDB Molecule: 27.5 kda virulence protein; PDBTitle: structural basis for the catalytic mechanism of phosphothreonine lyase
67	c2hfaA_	Alignment	not modelled	9.1	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: nmr structure of protein ne1680 from nitrosomonas europaea:2 northeast structural genomics consortium target net5
68	d2hfa1	Alignment	not modelled	9.1	14	Fold: NE1680-like Superfamily: NE1680-like Family: NE1680-like
69	d2nlva1	Alignment	not modelled	8.9	21	Fold: Xisl-like Superfamily: Xisl-like Family: Xisl-like
70	c4oh7B_	Alignment	not modelled	8.6	22	PDB header: transferase Chain: B: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from brucella2 melitensis
71	d1oi2a_	Alignment	not modelled	8.5	24	Fold: DAK1/DegV-like Superfamily: DAK1/DegV-like Family: DAK1
72	d1gm6a_	Alignment	not modelled	8.5	7	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
73	c2lf3A_	Alignment	not modelled	8.5	21	PDB header: signaling protein Chain: A: PDB Molecule: effector protein hopab3; PDBTitle: solution nmr structure of hoppel_281_385 from pseudomonas syringae2 pv. maculicola str. es4326, midwest center for structural genomics3 target apc40104.5 and northeast structural genomics consortium target4_pst2a
74	c4r0bA_	Alignment	not modelled	8.3	7	PDB header: lipid binding protein Chain: A: PDB Molecule: glycodelin; PDBTitle: structure of dimeric human glycodelin
75	d1jzua_	Alignment	not modelled	8.2	13	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
76	c4e5gB_	Alignment	not modelled	8.0	15	PDB header: viral protein, transcription Chain: B: PDB Molecule: polymerase protein pa; PDBTitle: crystal structure of avian influenza virus pan bound to compound 2
77	d1gd0a_	Alignment	not modelled	8.0	16	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
78	d2ddza1	Alignment	not modelled	7.9	11	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: PH0223-like
79	c3rlhA_	Alignment	not modelled	7.9	33	PDB header: hydrolase Chain: A: PDB Molecule: sphingomyelin phosphodiesterase d liscitox-alphaia1a; PDBTitle: crystal structure of a class ii phospholipase d from loxosceles2 intermedia venom

80	d1znda1	Alignment	not modelled	7.9	13	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
81	c3cjxE	Alignment	not modelled	7.6	15	PDB header: unknown function Chain: E: PDB Molecule: protein of unknown function with a cupin-like fold; PDBTitle: crystal structure of a protein of unknown function with a cupin-like2 fold (reut_b4571) from ralstonia eutropha jmp134 at 2.60 a resolution
82	c6n5uC	Alignment	not modelled	7.6	0	PDB header: metal binding protein Chain: C: PDB Molecule: protein sco1 homolog 1, mitochondrial; PDBTitle: crystal structure of arabidopsis thaliana scoi with copper bound
83	c3jr7A	Alignment	not modelled	7.2	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized egv family protein cog1307; PDBTitle: the crystal structure of the protein of degv family cog1307 with2 unknown function from ruminococcus gnavus atcc 29149
84	c5f6zD	Alignment	not modelled	7.2	11	PDB header: fluorescent protein Chain: D: PDB Molecule: sandercyanin fluorescent protein; PDBTitle: sandercyanin fluorescent protein purified from sander vitreus
85	c2qlcC	Alignment	not modelled	7.1	18	PDB header: dna binding protein Chain: C: PDB Molecule: dna repair protein radc homolog; PDBTitle: the crystal structure of dna repair protein radc from chlorobium2 tepidum t1s
86	d2p62a1	Alignment	not modelled	7.0	12	Fold: PH0156-like Superfamily: PH0156-like Family: PH0156-like
87	c3d7qB	Alignment	not modelled	7.0	11	PDB header: unknown function Chain: B: PDB Molecule: xisi protein-like; PDBTitle: crystal structure of a xisi-like protein (npun_ar114) from nostoc2 punctiforme pcc 73102 at 2.30 a resolution
88	c2yhbA	Alignment	not modelled	7.0	20	PDB header: rna binding protein Chain: A: PDB Molecule: post-transcriptional gene silencing protein qde-2; PDBTitle: crystal structure of the n. crassa qde-2 ago mid-piwi domains
89	c5a4jC	Alignment	not modelled	6.9	33	PDB header: ligase Chain: C: PDB Molecule: formate--tetrahydrofolate ligase; PDBTitle: crystal structure of fthfs1 from t. acetoydians re1
90	c2w37A	Alignment	not modelled	6.8	20	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase, catabolic; PDBTitle: crystal structure of the hexameric catabolic ornithine2 transcarbamylase from lactobacillus hilgardii
91	d1rvv1	Alignment	not modelled	6.6	18	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
92	c4oddB	Alignment	not modelled	6.6	12	PDB header: allergen Chain: B: PDB Molecule: lipocalin allergen; PDBTitle: crystal structure of a dog lipocalin allergen
93	c2yhaA	Alignment	not modelled	6.5	20	PDB header: rna binding protein Chain: A: PDB Molecule: post-transcriptional gene silencing protein qde-2; PDBTitle: crystal structure of the n. crassa qde-2 ago mid-piwi2 domains
94	c4ic5B	Alignment	not modelled	6.4	22	PDB header: hydrolase Chain: B: PDB Molecule: protease do-like 5, chloroplastic; PDBTitle: crystal structure of deg5
95	d1wkta	Alignment	not modelled	6.3	29	Fold: gamma-Crystallin-like Superfamily: gamma-Crystallin-like Family: Yeast killer toxin
96	d2nu7b1	Alignment	not modelled	6.3	9	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
97	c4fgpB	Alignment	not modelled	6.3	21	PDB header: hydrolase Chain: B: PDB Molecule: periplasmic protein; PDBTitle: legionella pneumophila lapg (egta-treated)
98	d1vlca	Alignment	not modelled	6.2	20	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
99	d1saza1	Alignment	not modelled	6.2	26	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetokinase-like