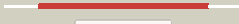



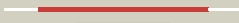




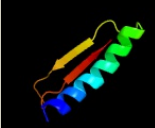





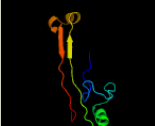





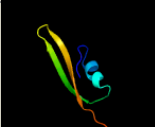






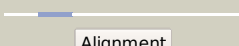

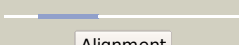

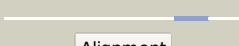


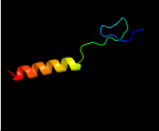

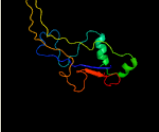

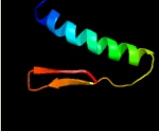


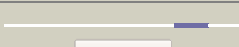







Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2315c (-)_2587297_2588814
Date	Mon Aug 5 13:25:46 BST 2019
Unique Job ID	8e8f8e370dde6cda

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5njaC_	 Alignment		100.0	21	PDB header: hydrolase Chain: C: PDB Molecule: metalloprotease tldd; PDBTitle: e. coli microcin-processing metalloprotease tldd/e with angiotensin2 analogue bound
2	d1vpba_	 Alignment		100.0	17	Fold: Putative modulator of DNA gyrase, PmbA/TldD Superfamily: Putative modulator of DNA gyrase, PmbA/TldD Family: Putative modulator of DNA gyrase, PmbA/TldD
3	c3qtdC_	 Alignment		100.0	17	PDB header: gene regulation Chain: C: PDB Molecule: pmba protein; PDBTitle: crystal structure of putative modulator of gyrase (pmba) from2 pseudomonas aeruginosa pao1
4	d1vl4a_	 Alignment		100.0	16	Fold: Putative modulator of DNA gyrase, PmbA/TldD Superfamily: Putative modulator of DNA gyrase, PmbA/TldD Family: Putative modulator of DNA gyrase, PmbA/TldD
5	c4b6cB_	 Alignment		47.8	23	PDB header: isomerase Chain: B: PDB Molecule: dna gyrase subunit b,dna gyrase subunit b,dna gyrase PDBTitle: structure of the m. smegmatis gyrb atpase domain in complex with an2 aminopyrazinamide
6	c4lhdB_	 Alignment		39.1	12	PDB header: oxidoreductase Chain: B: PDB Molecule: glycine dehydrogenase [decarboxylating]; PDBTitle: crystal structure of synechocystis sp. pcc 6803 glycine decarboxylase2 (p-protein), holo form with pyridoxal-5'-phosphate and glycine,3 closed flexible loop
7	d1s14a_	 Alignment		34.2	22	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
8	c1w7vD_	 Alignment		31.5	20	PDB header: hydrolase Chain: D: PDB Molecule: xaa-pro aminopeptidase; PDBTitle: znmg substituted aminopeptidase p from e. coli
9	c1bkna_	 Alignment		29.5	28	PDB header: dna repair Chain: A: PDB Molecule: mutI; PDBTitle: crystal structure of an n-terminal 40kd fragment of e. coli2 dna mismatch repair protein mutI
10	d1ydua1	 Alignment		27.6	10	Fold: At5g01610-like Superfamily: At5g01610-like Family: At5g01610-like
11	c3onrl_	 Alignment		27.4	14	PDB header: metal binding protein Chain: I: PDB Molecule: protein transport protein sece2; PDBTitle: crystal structure of the calcium chelating immunodominant antigen,2 calcium dodecin (rv0379),from mycobacterium tuberculosis with a novel3 calcium-binding site

12	c3g7bB_		Alignment		25.5	16	PDB header: isomerase/isomerase inhibitor Chain: B: PDB Molecule: dna gyrase subunit b; PDBTitle: staphylococcus aureus gyrase b co-complex with methyl ({5-[4-(4-2 hydroxypiperidin-1-yl)-2-phenyl-1,3-thiazol-5-yl]-1h-pyrazol-3-3 yl}methyl)carbamate inhibitor
13	c4k59A_		Alignment		25.3	26	PDB header: rna binding protein Chain: A: PDB Molecule: rna binding protein rsmf; PDBTitle: crystal structure of pseudomonas aeruginosa rsmf
14	c3zm7E_		Alignment		23.6	16	PDB header: isomerase Chain: E: PDB Molecule: dna gyrase subunit b; PDBTitle: crystal structure of the atpase region of mycobacterium2 tuberculosis gyrb with amppcp
15	c3qkbB_		Alignment		21.8	6	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein with unknown function which belongs to2 pfam duf74 family (pepe_0654) from pediococcus pentosaceus atcc 257453 at 2.73 a resolution
16	c3dx5A_		Alignment		21.6	10	PDB header: lyase Chain: A: PDB Molecule: uncharacterized protein asbf; PDBTitle: crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis
17	d1o12a1		Alignment		21.0	19	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA
18	d2pjuu1		Alignment		20.6	11	Fold: Chelatase-like Superfamily: PrpR receptor domain-like Family: PrpR receptor domain-like
19	c5k39A_		Alignment		20.2	13	PDB header: structural protein Chain: A: PDB Molecule: cellulosome anchoring protein cohesin region; PDBTitle: the type ii cohesin dockerin complex from clostridium thermocellum
20	c4emvA_		Alignment		17.0	16	PDB header: isomerase/isomerase inhibitor Chain: A: PDB Molecule: dna topoisomerase iv, b subunit; PDBTitle: crystal structure of a topoisomerase atp inhibitor
21	c1s16B_		Alignment	not modelled	16.5	20	PDB header: isomerase Chain: B: PDB Molecule: topoisomerase iv subunit b; PDBTitle: crystal structure of e. coli topoisomerase iv pare 43kda subunit2 complexed with adpnp
22	c5zfsA_		Alignment	not modelled	15.8	13	PDB header: isomerase Chain: A: PDB Molecule: d-allulose-3-epimerase; PDBTitle: crystal structure of arthrobacter globiformis m30 sugar epimerase2 which can produce d-allulose from d-fructose
23	c3gknA_		Alignment	not modelled	14.6	21	PDB header: oxidoreductase Chain: A: PDB Molecule: bacterioferritin comigratory protein; PDBTitle: insights into the alkyl peroxide reduction activity of xanthomonas2 campestris bacterioferritin comigratory protein from the trapped3 intermediate/ligand complex structures
24	c5j9bB_		Alignment	not modelled	14.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: peroxiredoxin asp f3; PDBTitle: crystal structure of peroxiredoxin asp f3
25	c2pjuD_		Alignment	not modelled	12.8	11	PDB header: transcription Chain: D: PDB Molecule: propionate catabolism operon regulatory protein; PDBTitle: crystal structure of propionate catabolism operon regulatory protein2 prpr
26	c4qlpB_		Alignment	not modelled	12.7	18	PDB header: hydrolase/protein binding Chain: B: PDB Molecule: alanine and proline rich protein, tuberculosis necrotizing PDBTitle: atomic structure of tuberculosis necrotizing toxin (tnt) complexed2 with its immunity factor ift
27	d1m1ha1		Alignment	not modelled	12.2	28	Fold: N-utilization substance G protein NusG, insert domain Superfamily: N-utilization substance G protein NusG, insert domain Family: N-utilization substance G protein NusG, insert domain
28	d1s16a2		Alignment	not modelled	11.8	19	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA

						<p>topoisomerase II/histidine kinase Family:DNA gyrase/MutL, N-terminal domain PDB header:oxidoreductase Chain: B: PDB Molecule:alkyl hydroperoxide reductase/ thiol specific antioxidant/ PDBTitle: crystal structure of an alkyl hyroperoxide reductase from burkholderia2 ambifaria</p>
29	c5enuB_	Alignment	not modelled	11.5	26	<p>PDB header:transferase Chain: A: PDB Molecule:protein (serratia marcescens aminoglycoside-3-n- PDBTitle: crystal structure of a gcn5-related n-acetyltransferase: serratia2 marescens aminoglycoside 3-n-acetyltransferase</p>
30	c1bo4A_	Alignment	not modelled	10.8	15	<p>Fold:Acyl-CoA N-acyltransferases (Nat) Superfamily:Acyl-CoA N-acyltransferases (Nat) Family:N-acetyl transferase, NAT</p>
31	d1bo4a_	Alignment	not modelled	10.8	15	<p>PDB header:oxidoreductase Chain: A: PDB Molecule:bacterioferritin comigratory protein; PDBTitle: crystal structure of xylella fastidiosa prqx c47s mutant</p>
32	c3ixrA_	Alignment	not modelled	10.6	18	<p>Fold:Dodecin subunit-like Superfamily:YbjQ-like Family:YbjQ-like</p>
33	d1vr4a1_	Alignment	not modelled	10.4	25	<p>PDB header:structural genomics, unknown function Chain: C: PDB Molecule:hypothetical protein s0862; PDBTitle: crystal structure of mcsg target apc27401 from shigella flexneri</p>
34	c1y2iC_	Alignment	not modelled	10.1	22	<p>Fold:Dodecin subunit-like Superfamily:YbjQ-like Family:YbjQ-like</p>
35	d1y2ia_	Alignment	not modelled	10.1	22	<p>PDB header:biosynthetic protein Chain: B: PDB Molecule:101015d; PDBTitle: the structure of [4+2] and [6+4] cyclase in the biosynthetic pathway2 of unidentified natural product</p>
36	c6a5hB_	Alignment	not modelled	10.1	8	<p>PDB header:transferase Chain: A: PDB Molecule:acetyltransferase, gnat family; PDBTitle: crystal structure of gnat family acetyltransferase staphylococcus2 aureus subsp. aureus usa300_tch1516</p>
37	c3t9yA_	Alignment	not modelled	10.1	10	<p>PDB header:biosynthetic protein Chain: A: PDB Molecule:phenazine biosynthesis protein phzb2 2; PDBTitle: crystal structure of a phenazine biosynthesis-related protein (phzb2)2 from pseudomonas aeruginosa at 1.90 a resolution</p>
38	c3ff0A_	Alignment	not modelled	9.1	9	<p>PDB header:proton transport Chain: O: PDB Molecule:nad(p)h-quinone oxidoreductase subunit o; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus</p>
39	c6humO_	Alignment	not modelled	9.1	18	<p>Fold:TBP-like Superfamily:Phosphoglucomutase, C-terminal domain Family:Phosphoglucomutase, C-terminal domain</p>
40	d1kfia4_	Alignment	not modelled	9.0	13	<p>PDB header:transferase Chain: A: PDB Molecule:rna polymerase sigma factor siga; PDBTitle: sigma1.1 domain of sigmaa from bacillus subtilis</p>
41	c5mwwA_	Alignment	not modelled	8.8	15	<p>PDB header:isomerase/dna Chain: B: PDB Molecule:dna topoisomerase 4 subunit b; PDBTitle: amp-pnp-stabilized atpase domain of topoisomerase iv from2 streptococcus pneumoniae, complex type i</p>
42	c5j5pB_	Alignment	not modelled	8.8	16	<p>PDB header:oxidoreductase Chain: A: PDB Molecule:isocitrate dehydrogenase; PDBTitle: thermal stability of isocitrate dehydrogenase from2 archaeoglobus fulgidus studied by crystal structure3 analysis and engineering of chimers</p>
43	c2iv0A_	Alignment	not modelled	8.6	9	<p>PDB header:oxidoreductase Chain: P: PDB Molecule:probable peroxiredoxin; PDBTitle: structure of peroxiredoxin from anaerobic hyperthermophilic archaeon2 pyrococcus horikoshii</p>
44	c3w6gP_	Alignment	not modelled	8.5	16	<p>PDB header:transcription Chain: A: PDB Molecule:trmb, a global transcription regulator; PDBTitle: the three-dimensional structure of trmb, a global transcriptional2 regulator of the hyperthermophilic archaeon pyrococcus furiosus in3 complex with sucrose</p>
45	c3qphA_	Alignment	not modelled	8.3	11	<p>PDB header:oxidoreductase Chain: A: PDB Molecule:probable thioredoxin; PDBTitle: structure of thioredoxin 2 from pseudomonas aeruginosa pao1 in its2 reduced form</p>
46	c2lrcA_	Alignment	not modelled	8.1	13	<p>PDB header:isomerase/isomerase inhibitor Chain: A: PDB Molecule:dna gyrase subunit b; PDBTitle: pyrrolopyrimidine inhibitors of dna gyrase b and topoisomerase iv,2 part i: structure guided discovery and optimization of dual targeting3 agents with potent, broad-spectrum enzymatic activity.</p>
47	c4geeA_	Alignment	not modelled	8.1	9	<p>PDB header:oxidoreductase Chain: A: PDB Molecule:thioredoxin; PDBTitle: crystal structure of thioredoxin from methanosarcina mazei</p>
48	c3hz4A_	Alignment	not modelled	8.0	9	<p>PDB header:transferase/rna Chain: A: PDB Molecule:rna-dependent rna polymerase; PDBTitle: crystal structure of rotavirus sa11 vp1/rna (ugugaacc) complex</p>
49	c2r7tA_	Alignment	not modelled	7.9	10	<p>PDB header:de novo protein Chain: A: PDB Molecule:de novo ntf2 with large cavity; PDBTitle: crystal structure of a de novo designed protein with curved beta-sheet</p>
50	c5u35A_	Alignment	not modelled	7.7	10	<p>PDB header:de novo protein Chain: A: PDB Molecule:de novo designed protein or459; PDBTitle: solution nmr structure of de novo designed protein, northeast2 structural genomics consortium (nesg) target or459</p>
51	c2mraA_	Alignment	not modelled	7.4	16	<p>PDB header:structural genomics, unknown function Chain: C: PDB Molecule:putative integron gene cassette protein; PDBTitle: structure from the mobile metagenome of cole harbour salt marsh:2 integron cassette protein hfx_cass1</p>
52	c3fuyC_	Alignment	not modelled	7.4	19	

53	c5e09A_	Alignment	not modelled	7.3	24	PDB header: hydrolase Chain: A: PDB Molecule: cellulase; PDBTitle: structural insight of a trimodular halophilic cellulase with a family2 46 carbohydrate-binding module
54	c1pyaD_	Alignment	not modelled	7.2	24	PDB header: carboxy-lyase Chain: D: PDB Molecule: pyruvoyl-dependent histidine decarboxylase (l-histidine PDBTitle: refined structure of the pyruvoyl-dependent histidine decarboxylase2 from lactobacillus 30a
55	c3oqtP_	Alignment	not modelled	7.0	22	PDB header: flavoprotein Chain: P: PDB Molecule: rv1498a protein; PDBTitle: crystal structure of rv1498a protein from mycobacterium tuberculosis
56	c4hymA_	Alignment	not modelled	6.6	13	PDB header: isomerase/isomerase inhibitor Chain: A: PDB Molecule: topoisomerase iv, subunit b; PDBTitle: pyrrolopyrimidine inhibitors of dna gyrase b and topoisomerase iv,2 part i: structure guided discovery and optimization of dual targeting3 agents with potent, broad-spectrum enzymatic activity.
57	c6feuj_	Alignment	not modelled	6.6	10	PDB header: oxidoreductase Chain: J: PDB Molecule: peroxiredoxin; PDBTitle: prxq2, a 1-cys peroxiredoxin of the thermo-acidophilic archaeon2 sulfobolus islandicus
58	c3jvnA_	Alignment	not modelled	6.2	14	PDB header: transferase Chain: A: PDB Molecule: acetyltransferase; PDBTitle: crystal structure of the acetyltransferase vf_1542 from vibrio2 fischeri, northeast structural genomics consortium target vfr136
59	c5it5B_	Alignment	not modelled	6.2	20	PDB header: transport protein Chain: B: PDB Molecule: atp binding motif-containing protein pilf; PDBTitle: thermus thermophilus pilb core atpase region
60	c6mspA_	Alignment	not modelled	6.2	17	PDB header: de novo protein Chain: A: PDB Molecule: de novo designed protein foldit3; PDBTitle: de novo designed protein foldit3
61	c3lggA_	Alignment	not modelled	6.1	10	PDB header: hydrolase Chain: A: PDB Molecule: adenosine deaminase cecr1; PDBTitle: crystal structure of human adenosine deaminase growth factor,2 adenosine deaminase type 2 (ada2) complexed with transition state3 analogue, coformycin
62	c5ovql_	Alignment	not modelled	6.1	13	PDB header: oxidoreductase Chain: L: PDB Molecule: peroxiredoxin; PDBTitle: crystal structure of the peroxiredoxin (ahpc2) from the2 hyperthermophilic bacteria aquifex aeolicus vf
63	c3f8hA_	Alignment	not modelled	6.0	19	PDB header: unknown function Chain: A: PDB Molecule: putative polyketide cyclase; PDBTitle: crystal structure of a putative polyketide cyclase (tm1040_3560) from2 silicibacter sp. tm1040 at 2.00 a resolution
64	d2fy6a1	Alignment	not modelled	5.9	10	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
65	d1m8ta_	Alignment	not modelled	5.8	21	Fold: Phospholipase A2, PLA2 Superfamily: Phospholipase A2, PLA2 Family: Vertebrate phospholipase A2
66	c1kijB_	Alignment	not modelled	5.7	16	PDB header: isomerase Chain: B: PDB Molecule: dna gyrase subunit b; PDBTitle: crystal structure of the 43k atpase domain of thermus thermophilus2 gyrase b in complex with novobiocin
67	d1gk8a2	Alignment	not modelled	5.7	13	Fold: Ferredoxin-like Superfamily: RuBisCO, large subunit, small (N-terminal) domain Family: Ribulose 1,5-bisphosphate carboxylase-oxygenase
68	d1tuha_	Alignment	not modelled	5.7	10	Fold: Cystatin-like Superfamily: NTF2-like Family: Hypothetical protein egc068 from a soil-derived mobile gene cassette
69	c1tuhA_	Alignment	not modelled	5.7	10	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein egc068; PDBTitle: structure of bal32a from a soil-derived mobile gene cassette
70	d1kija2	Alignment	not modelled	5.6	14	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
71	c5ykjA_	Alignment	not modelled	5.6	10	PDB header: transferase Chain: A: PDB Molecule: peroxiredoxin prx1, mitochondrial; PDBTitle: structural basis of the thiol resolving mechanism in yeast2 mitochondrial 1-cys peroxiredoxin via glutathione/thioredoxin systems
72	c3f7xA_	Alignment	not modelled	5.6	17	PDB header: unknown function Chain: A: PDB Molecule: putative polyketide cyclase; PDBTitle: crystal structure of a putative polyketide cyclase (pp0894) from2 pseudomonas putida kt2440 at 1.24 a resolution
73	d1dl6a_	Alignment	not modelled	5.6	17	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
74	c6r1eC_	Alignment	not modelled	5.6	19	PDB header: flavoprotein Chain: C: PDB Molecule: dodecin; PDBTitle: structure of dodecin from streptomyces coelicolor
75	c5x9yC_	Alignment	not modelled	5.4	17	PDB header: dna binding protein Chain: C: PDB Molecule: dna mismatch repair protein muti; PDBTitle: crystal structure of the atpase domain from bacterial mismatch repair2 endonuclease aquifex aeolicus mutl.
76	c4zquB_	Alignment	not modelled	5.4	8	PDB header: toxin Chain: B: PDB Molecule: cdii toxin; PDBTitle: cdia-ct/cdii toxin and immunity complex from yersinia2 pseudotuberculosis
77	d1luza_	Alignment	not modelled	5.4	14	Fold: OB-fold Superfamily: Nucleic acid-binding proteins

						Family: Cold shock DNA-binding domain-like
78	c5csaA_	Alignment	not modelled	5.4	10	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of domains bt-bccp-ac1-ac5 of yeast acetyl-coa2 carboxylase
79	d1ei1a2	Alignment	not modelled	5.4	15	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
80	c4kb3B_	Alignment	not modelled	5.4	23	PDB header: oxidoreductase Chain: B: PDB Molecule: peroxidoxin; PDBTitle: crystal structure of the mitochondrial peroxidoxin from leishmania2 braziliensis in the decameric form
81	d1u7ba2	Alignment	not modelled	5.4	3	Fold: DNA clamp Superfamily: DNA clamp Family: DNA polymerase processivity factor
82	c2w3gA_	Alignment	not modelled	5.3	15	PDB header: transferase Chain: A: PDB Molecule: two component sensor histidine kinase devs (gaf PDBTitle: air-oxidized structure of the first gaf domain of2 mycobacterium tuberculosis doss
83	c5tshF_	Alignment	not modelled	5.3	23	PDB header: atp-binding protein Chain: F: PDB Molecule: type iv pilus biogenesis atpase pilb; PDBTitle: pilb from geobacter metallireducens bound to amp-pnp
84	c4eo3A_	Alignment	not modelled	5.3	21	PDB header: oxidoreductase Chain: A: PDB Molecule: bacterioferritin comigratory protein/nadh dehydrogenase; PDBTitle: peroxidoxin nitroreductase fusion enzyme
85	c3zxqA_	Alignment	not modelled	5.3	17	PDB header: transferase Chain: A: PDB Molecule: hypoxia sensor histidine kinase response regulator dost; PDBTitle: crystal structure of the atp-binding domain of mycobacterium2 tuberculosis dost
86	d3ckma1	Alignment	not modelled	5.3	12	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
87	c5wzmA_	Alignment	not modelled	5.1	12	PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: group iie secretory phospholipase a2; PDBTitle: crystal structure of human secreted phospholipase a2 group iie
88	d1p7oa_	Alignment	not modelled	5.1	26	Fold: Phospholipase A2, PLA2 Superfamily: Phospholipase A2, PLA2 Family: Vertebrate phospholipase A2
89	c2i81B_	Alignment	not modelled	5.1	14	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-cys peroxidoxin; PDBTitle: crystal structure of plasmodium vivax 2-cys peroxidoxin,2 reduced