



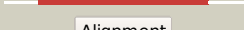

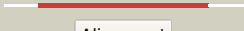






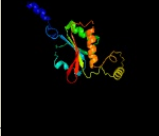


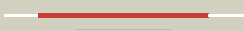







Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1284 (-) _1437330_1437821
Date	Wed Jul 31 22:05:37 BST 2019
Unique Job ID	3ba0cd8daa5885c2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ylkA_	 Alignment		100.0	100	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein rv1284/mt1322; PDBTitle: crystal structure of rv1284 from mycobacterium tuberculosis in complex2 with thiocyanate
2	c3lasA_	 Alignment		100.0	39	PDB header: lyase Chain: A: PDB Molecule: putative carbonic anhydrase; PDBTitle: crystal structure of carbonic anhydrase from streptococcus mutans to2 1.4 angstrom resolution
3	c3vrkA_	 Alignment		100.0	51	PDB header: hydrolase Chain: A: PDB Molecule: carbonyl sulfide hydrolase; PDBTitle: crystal structure of thiobacillus thioparus thi115 carbonyl sulfide2 hydrolase / thiocyanate complex
4	c5ztpB_	 Alignment		100.0	42	PDB header: lyase Chain: B: PDB Molecule: carbonic anhydrase; PDBTitle: carbonic anhydrase from glaciozyma antarctica
5	c3tenD_	 Alignment		100.0	34	PDB header: hydrolase Chain: D: PDB Molecule: cs2 hydrolase; PDBTitle: holo form of carbon disulfide hydrolase
6	d1ddza1	 Alignment		100.0	22	Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab
7	d1g5ca_	 Alignment		100.0	33	Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab
8	c5cxkG_	 Alignment		100.0	21	PDB header: lyase Chain: G: PDB Molecule: carbonic anhydrase; PDBTitle: crystal structure of beta carbonic anhydrase from vibrio cholerae
9	c2a8cE_	 Alignment		100.0	21	PDB header: lyase Chain: E: PDB Molecule: carbonic anhydrase 2; PDBTitle: haemophilus influenzae beta-carbonic anhydrase
10	c2w3nA_	 Alignment		100.0	19	PDB header: lyase Chain: A: PDB Molecule: carbonic anhydrase 2; PDBTitle: structure and inhibition of the co2-sensing carbonic anhydrase can22 from the pathogenic fungus cryptococcus neoformans
11	d1ekja_	 Alignment		100.0	22	Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab

12	c4o1jB_	Alignment		100.0	22	PDB header: lyase Chain: B: PDB Molecule: carbonic anhydrase; PDBTitle: crystal structures of two tetrameric beta-carbonic anhydrases from the2 filamentous ascomycete sordaria macrospora.
13	c3ucoB_	Alignment		100.0	20	PDB header: lyase/lyase inhibitor Chain: B: PDB Molecule: carbonic anhydrase; PDBTitle: coccomyxa beta-carbonic anhydrase in complex with iodide
14	d1ddza2	Alignment		100.0	20	Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab
15	c2a5vB_	Alignment		100.0	18	PDB header: lyase Chain: B: PDB Molecule: carbonic anhydrase (carbonate dehydratase) (carbonic PDBTitle: crystal structure of m. tuberculosis beta carbonic anhydrase, rv3588c,2 tetrameric form
16	d1i6pa_	Alignment		100.0	18	Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab
17	c5swcE_	Alignment		100.0	17	PDB header: lyase Chain: E: PDB Molecule: carbonic anhydrase; PDBTitle: the structure of the beta-carbonic anhydrase ccaa
18	c3eyxB_	Alignment		100.0	26	PDB header: lyase Chain: B: PDB Molecule: carbonic anhydrase; PDBTitle: crystal structure of carbonic anhydrase nce103 from2 saccharomyces cerevisiae
19	c4o1kA_	Alignment		100.0	21	PDB header: lyase Chain: A: PDB Molecule: carbonic anhydrase; PDBTitle: crystal structures of two tetrameric beta-carbonic anhydrases from the2 filamentous ascomycete sordaria macrospora.
20	c4rxyA_	Alignment		100.0	21	PDB header: lyase Chain: A: PDB Molecule: carbonic anhydrase; PDBTitle: crystal structure of the beta carbonic anhydrase psca3 isolated from2 pseudomonas aeruginosa
21	c1ddzA_	Alignment	not modelled	100.0	22	PDB header: lyase Chain: A: PDB Molecule: carbonic anhydrase; PDBTitle: x-ray structure of a beta-carbonic anhydrase from the red2 alga, porphyridium purpureum r-1
22	c6gwuB_	Alignment	not modelled	100.0	26	PDB header: lyase Chain: B: PDB Molecule: carbonic anhydrase; PDBTitle: carbonic anhydrase cance103p from candida albicans
23	c3hu5B_	Alignment	not modelled	38.4	12	PDB header: hydrolase Chain: B: PDB Molecule: isochorismatase family protein; PDBTitle: crystal structure of isochorismatase family protein from desulfovibrio2 vulgaris subsp. vulgaris str. hildenborough
24	d1z01a1	Alignment	not modelled	37.1	53	Fold: ISP domain Superfamily: ISP domain Family: Ring hydroxylating alpha subunit ISP domain
25	c3d89A_	Alignment	not modelled	32.8	25	PDB header: electron transport Chain: A: PDB Molecule: rieske domain-containing protein; PDBTitle: crystal structure of a soluble rieske ferredoxin from mus musculus
26	d2de6a1	Alignment	not modelled	32.4	13	Fold: ISP domain Superfamily: ISP domain Family: Ring hydroxylating alpha subunit ISP domain
27	d1fqta_	Alignment	not modelled	32.0	38	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
28	c3o93A_	Alignment	not modelled	31.2	18	PDB header: hydrolase Chain: A: PDB Molecule: nicotinamidase; PDBTitle: high resolution crystal structures of streptococcus pneumoniae2 nicotinamidase with trapped intermediates provide insights into3 catalytic mechanism and inhibition by aldehydes
29	c2de7E_	Alignment	not modelled	31.2	38	PDB header: oxidoreductase Chain: E: PDB Molecule: ferredoxin component of carbazole;

29	c2ue7L	Alignment	not modelled	31.2	30	PDBTitle: the substrate-bound complex between oxygenase and2 ferredoxin in carbazole 1,9a-dioxygenase PDB header: hydrolase
30	c3mcwA	Alignment	not modelled	30.8	13	Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of an a putative hydrolase of the isochorismatase2 family (cv_1320) from chromobacterium violaceum atcc 12472 at 1.06 a3 resolution
31	c3tb4A	Alignment	not modelled	29.4	18	PDB header: hydrolase Chain: A: PDB Molecule: vibriobactin-specific isochorismatase; PDBTitle: crystal structure of the isc domain of vibb
32	d1x9ga	Alignment	not modelled	28.8	11	Fold: Isochorismatase-like hydrolases Superfamily: Isochorismatase-like hydrolases Family: Isochorismatase-like hydrolases
33	c2hwkA	Alignment	not modelled	28.0	26	PDB header: hydrolase Chain: A: PDB Molecule: helicase nsp2; PDBTitle: crystal structure of venezuelan equine encephalitis alphavirus nsp22 protease domain
34	c1z01D	Alignment	not modelled	27.9	53	PDB header: oxidoreductase Chain: D: PDB Molecule: 2-oxo-1,2-dihydroquinoline 8-monoxygenase, oxygenase PDBTitle: 2-oxoquinoline 8-monoxygenase component: active site modulation by2 rieske-[2fe-2s] center oxidation/reduction
35	c3gceA	Alignment	not modelled	27.1	38	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin component of carbazole 1,9a- PDBTitle: ferredoxin of carbazole 1,9a-dioxygenase from nocardiooides2 aromaticivorans ic177
36	d2jo6a1	Alignment	not modelled	27.0	17	Fold: ISP domain Superfamily: ISP domain Family: NirD-like
37	d1nbaa	Alignment	not modelled	26.4	11	Fold: Isochorismatase-like hydrolases Superfamily: Isochorismatase-like hydrolases Family: Isochorismatase-like hydrolases
38	c3ot4F	Alignment	not modelled	26.2	18	PDB header: hydrolase Chain: F: PDB Molecule: putative isochorismatase; PDBTitle: structure and catalytic mechanism of bordetella bronchiseptica nicf
39	c2fq1A	Alignment	not modelled	25.9	16	PDB header: hydrolase Chain: A: PDB Molecule: isochorismatase; PDBTitle: crystal structure of the two-domain non-ribosomal peptide synthetase2 entb containing isochorismate lyase and aryl-carrier protein domains
40	c3vr1B	Alignment	not modelled	24.8	24	PDB header: translation Chain: B: PDB Molecule: peptide chain release factor 3; PDBTitle: crystal structure analysis of the translation factor rf3
41	c2de7B	Alignment	not modelled	24.5	13	PDB header: oxidoreductase Chain: B: PDB Molecule: terminal oxygenase component of carbazole; PDBTitle: the substrate-bound complex between oxygenase and2 ferredoxin in carbazole 1,9a-dioxygenase
42	d1j2ra	Alignment	not modelled	24.4	18	Fold: Isochorismatase-like hydrolases Superfamily: Isochorismatase-like hydrolases Family: Isochorismatase-like hydrolases
43	c3i8sC	Alignment	not modelled	24.1	27	PDB header: transport protein Chain: C: PDB Molecule: ferrous iron transport protein b; PDBTitle: structure of the cytosolic domain of e. coli feob, nucleotide-free2 form
44	c3gkqB	Alignment	not modelled	23.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: terminal oxygenase component of carbazole 1,9a-dioxygenase; PDBTitle: terminal oxygenase of carbazole 1,9a-dioxygenase from novosphingobium2 sp. ka1
45	c5cwsF	Alignment	not modelled	23.0	36	PDB header: protein transport Chain: F: PDB Molecule: nucleoporin nic96; PDBTitle: crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
46	c5cwsL	Alignment	not modelled	23.0	36	PDB header: protein transport Chain: L: PDB Molecule: nucleoporin nic96; PDBTitle: crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
47	c5ghrA	Alignment	not modelled	22.9	18	PDB header: dna binding protein/replication Chain: A: PDB Molecule: ssdna-specific exonuclease; PDBTitle: dna replication protein
48	d1nrjb	Alignment	not modelled	22.3	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
49	c2qpzA	Alignment	not modelled	21.0	46	PDB header: metal binding protein Chain: A: PDB Molecule: naphthalene 1,2-dioxygenase system ferredoxin PDBTitle: naphthalene 1,2-dioxygenase rieske ferredoxin
50	c2i7fB	Alignment	not modelled	20.9	55	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin component of dioxygenase; PDBTitle: sphingomonas yanoikuyae b1 ferredoxin
51	d3c0da1	Alignment	not modelled	20.4	18	Fold: ISP domain Superfamily: ISP domain Family: NirD-like
52	c3w5iB	Alignment	not modelled	19.7	33	PDB header: metal transport Chain: B: PDB Molecule: ferrous iron transport protein b; PDBTitle: crystal structure of nfeob from gallionella capsiferriformans
53	d1n0ua2	Alignment	not modelled	19.5	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
						Fold: ISP domain

54	d2jzaa1	Alignment	not modelled	19.5	18	Superfamily: ISP domain Family: NirD-like
55	c5ghrC	Alignment	not modelled	19.4	18	PDB header: dna binding protein/replication Chain: C: PDB Molecule: ssdna-specific exonuclease; PDBTitle: dna replication protein
56	c3j25A	Alignment	not modelled	19.3	28	PDB header: translation Chain: A: PDB Molecule: tetracycline resistance protein tetm; PDBTitle: structural basis for tetm-mediated tetracycline resistance
57	d1vm9a	Alignment	not modelled	19.2	27	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
58	c3degC	Alignment	not modelled	19.0	29	PDB header: ribosome Chain: C: PDB Molecule: gtp-binding protein lepa; PDBTitle: complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmppnp
59	c4aivA	Alignment	not modelled	18.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: probable nitrite reductase [nad(p)h] small subunit nirD; PDBTitle: crystal structure of putative nadh-dependent nitrite reductase small2 subunit from mycobacterium tuberculosis
60	c3oqpA	Alignment	not modelled	18.6	10	PDB header: hydrolase Chain: A: PDB Molecule: putative isochorismatase; PDBTitle: crystal structure of a putative isochorismatase (bxe_a0706) from2 burkholderia xenovorans lb400 at 1.22 a resolution
61	c3oqpB	Alignment	not modelled	18.5	10	PDB header: hydrolase Chain: B: PDB Molecule: putative isochorismatase; PDBTitle: crystal structure of a putative isochorismatase (bxe_a0706) from2 burkholderia xenovorans lb400 at 1.22 a resolution
62	d2fh5b1	Alignment	not modelled	18.4	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
63	c5zn8B	Alignment	not modelled	18.4	13	PDB header: metal binding protein Chain: B: PDB Molecule: isochorismatase; PDBTitle: crystal structure of nicotinamidase pnca from bacillus subtilis
64	c3irvA	Alignment	not modelled	17.9	18	PDB header: hydrolase Chain: A: PDB Molecule: cysteine hydrolase; PDBTitle: crystal structure of cysteine hydrolase pspsh_2384 from pseudomonas2 syringae pv. phaseolicola 1448a
65	d1a3xa3	Alignment	not modelled	17.8	14	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
66	c2qu8A	Alignment	not modelled	17.8	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative nucleolar gtp-binding protein 1; PDBTitle: crystal structure of putative nucleolar gtp-binding protein 1 pff0625w2 from plasmodium falciparum
67	c3ibyA	Alignment	not modelled	17.6	25	PDB header: transport protein Chain: A: PDB Molecule: ferrous iron transport protein b; PDBTitle: structure of cytosolic domain of I. pneumophila feob
68	c2r2cA	Alignment	not modelled	17.5	31	PDB header: membrane protein Chain: A: PDB Molecule: 28 kda outer membrane protein omp28; PDBTitle: crystal structure of a domain of the outer membrane lipoprotein omp282 from porphyromonas gingivalis
69	d1rkba	Alignment	not modelled	17.2	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
70	c3hb7G	Alignment	not modelled	16.8	16	PDB header: hydrolase Chain: G: PDB Molecule: isochorismatase hydrolase; PDBTitle: the crystal structure of an isochorismatase-like hydrolase from2 alkaliphilus metalliredigens to 2.3a
71	d1zo0a1	Alignment	not modelled	16.7	14	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: Ornithine decarboxylase antizyme-like
72	c1d2eA	Alignment	not modelled	16.7	27	PDB header: rna binding protein Chain: A: PDB Molecule: elongation factor tu (ef-tu); PDBTitle: crystal structure of mitochondrial ef-tu in complex with gdp
73	c3zjcC	Alignment	not modelled	16.3	40	PDB header: hydrolase Chain: C: PDB Molecule: gtpase imap family member 7; PDBTitle: crystal structure of gmppnp-bound human gimap7 I100q variant
74	c3k53B	Alignment	not modelled	15.8	15	PDB header: metal transport Chain: B: PDB Molecule: ferrous iron transport protein b; PDBTitle: crystal structure of nfeob from p. furiosus
75	c6cl4A	Alignment	not modelled	15.6	12	PDB header: hydrolase Chain: A: PDB Molecule: lipase c12; PDBTitle: lipc12 - lipase from metagenomics
76	c2h5eB	Alignment	not modelled	15.6	26	PDB header: translation Chain: B: PDB Molecule: peptide chain release factor rf-3; PDBTitle: crystal structure of e.coli polypeptide release factor rf3
77	c4zciA	Alignment	not modelled	15.6	28	PDB header: gtp-binding protein Chain: A: PDB Molecule: gtp-binding protein tya/bipa; PDBTitle: crystal structure of escherichia coli gtpase bipa/tya
78	c2qagC	Alignment	not modelled	15.6	9	PDB header: cell cycle, structural protein Chain: C: PDB Molecule: septin-7; PDBTitle: crystal structure of human septin trimer 2/6/7
79	d1r5ba3	Alignment	not modelled	15.3	36	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
						PDB header: hydrolase

80	c5jkjA_	Alignment	not modelled	15.2	13	Chain: A: PDB Molecule: esterase e22; PDBTitle: crystal structure of esterase e22 I374d mutant
81	d1s0ua3	Alignment	not modelled	15.1	36	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
82	c4proD_	Alignment	not modelled	14.8	6	PDB header: serine protease Chain: D: PDB Molecule: alpha-lytic protease; PDBTitle: alpha-lytic protease complexed with pro region
83	c1mj1A_	Alignment	not modelled	14.8	27	PDB header: ribosome Chain: A: PDB Molecule: elongation factor tu; PDBTitle: fitting the ternary complex of ef-tu/trna/gtp and ribosomal proteins2 into a 13 a cryo-em map of the coli 70s ribosome
84	c4hi2B_	Alignment	not modelled	14.6	24	PDB header: hydrolase Chain: B: PDB Molecule: acylphosphatase; PDBTitle: crystal structure of an acylphosphatase protein cage
85	c4b62A_	Alignment	not modelled	14.6	18	PDB header: membrane protein Chain: A: PDB Molecule: tss11; PDBTitle: the structure of the cell wall anchor of the t6ss from pseudomonas2 aeruginosa
86	c2bvnB_	Alignment	not modelled	14.6	27	PDB header: elongation factor Chain: B: PDB Molecule: elongation factor tu; PDBTitle: e. coli ef-tu:gdpnp in complex with the antibiotic enacyloxin iia
87	c6azoC_	Alignment	not modelled	14.4	21	PDB header: hydrolase Chain: C: PDB Molecule: putative amidase; PDBTitle: structural and biochemical characterization of a non-canonical biuret2 hydrolase (biuh) from the cyanuric acid catabolism pathway of3 rhizobium leguminosorum bv. viciae 3841
88	c3t5dC_	Alignment	not modelled	14.3	9	PDB header: signaling protein Chain: C: PDB Molecule: septin-7; PDBTitle: crystal structure of septin 7 in complex with gdp
89	d1efca3	Alignment	not modelled	14.0	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
90	d2bmoa1	Alignment	not modelled	14.0	29	Fold: ISP domain Superfamily: ISP domain Family: Ring hydroxylating alpha subunit ISP domain
91	d2ih2a2	Alignment	not modelled	13.9	17	Fold: DNA methylase specificity domain Superfamily: DNA methylase specificity domain Family: TaqI C-terminal domain-like
92	c5gleA_	Alignment	not modelled	13.8	9	PDB header: lyase Chain: A: PDB Molecule: ischorismate lyase; PDBTitle: the structure of vibrio anguillarum775 angb-icl
93	c4aayH_	Alignment	not modelled	13.7	33	PDB header: oxidoreductase Chain: H: PDB Molecule: arob; PDBTitle: crystal structure of the arsenite oxidase protein complex2 from rhizobium species strain nt-26
94	d1e8ca1	Alignment	not modelled	13.6	29	Fold: MurF and HprK N-domain-like Superfamily: MurE/MurF N-terminal domain Family: MurE/MurF N-terminal domain
95	c5f56A_	Alignment	not modelled	13.6	18	PDB header: dna binding protein/dna Chain: A: PDB Molecule: single-stranded-dna-specific exonuclease; PDBTitle: structure of recj complexed with dna and ssb-ct
96	c3p27A_	Alignment	not modelled	13.6	36	PDB header: signaling protein Chain: A: PDB Molecule: elongation factor 1 alpha-like protein; PDBTitle: crystal structure of s. cerevisiae hbs1 protein (gdp-bound form), a2 translational gtpase involved in rna quality control pathways and3 interacting with dom34/pelota
97	c2zxrA_	Alignment	not modelled	13.2	29	PDB header: hydrolase Chain: A: PDB Molecule: single-stranded dna specific exonuclease recj; PDBTitle: crystal structure of recj in complex with mg2+ from thermus2 thermophilus hb8
98	d2gp4a1	Alignment	not modelled	13.2	14	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/IlvD-like Family: IlvD/EDD C-terminal domain-like
99	d1apsa_	Alignment	not modelled	13.1	18	Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: Acylphosphatase-like