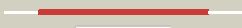
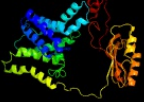











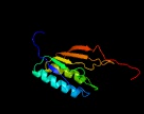



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2262c (-)_2534480_2535562
Date	Mon Aug 5 13:25:40 BST 2019
Unique Job ID	d004172d13c0d884

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5n6mA_	 Alignment		100.0	24	PDB header: membrane protein Chain: A: PDB Molecule: apolipoprotein n-acyltransferase; PDBTitle: structure of the membrane integral lipoprotein n-acyltransferase lnt2 from p. aeruginosa
2	c5vrhA_	 Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: apolipoprotein n-acyltransferase; PDBTitle: apolipoprotein n-acyltransferase c387s active site mutant
3	c2w1vA_	 Alignment		99.7	18	PDB header: hydrolase Chain: A: PDB Molecule: nitrilase homolog 2; PDBTitle: crystal structure of mouse nitrilase-2 at 1.4a resolution
4	dluf5a_	 Alignment		99.7	19	Fold: Carbon-nitrogen hydrolase Superfamily: Carbon-nitrogen hydrolase Family: Carbamilase
5	c2e11B_	 Alignment		99.7	22	PDB header: hydrolase Chain: B: PDB Molecule: hydrolase; PDBTitle: the crystal structure of xc1258 from xanthomonas campestris: a cn-2 hydrolase superfamily protein with an arsenic adduct in the active3 site
6	c5khaA_	 Alignment		99.7	21	PDB header: ligase Chain: A: PDB Molecule: glutamine-dependent nad+ synthetase; PDBTitle: structure of glutamine-dependent nad+ synthetase from acinetobacter2 baumannii in complex with adenosine diphosphate (adp)
7	dl1emsa2	 Alignment		99.7	12	Fold: Carbon-nitrogen hydrolase Superfamily: Carbon-nitrogen hydrolase Family: Nitrilase
8	c5h8IM_	 Alignment		99.7	24	PDB header: hydrolase Chain: M: PDB Molecule: n-carbamoylputrescine amidohydrolase; PDBTitle: crystal structure of medicago truncatula n-carbamoylputrescine2 amidohydrolase (mtcpa) c158s mutant in complex with putrescine
9	c1emsB_	 Alignment		99.7	13	PDB header: antitumor protein Chain: B: PDB Molecule: nit-fragile histidine triad fusion protein; PDBTitle: crystal structure of the c. elegans nitfhit protein
10	c3hkxA_	 Alignment		99.7	22	PDB header: hydrolase Chain: A: PDB Molecule: amidase; PDBTitle: crystal structure analysis of an amidase from nesterenkonia sp.
11	dlj31a_	 Alignment		99.7	23	Fold: Carbon-nitrogen hydrolase Superfamily: Carbon-nitrogen hydrolase Family: Carbamilase

12	c3wuyA	Alignment		99.7	17	PDB header: hydrolase Chain: A; PDB Molecule: nitrilase; PDBTitle: crystal structure of nit6803
13	c5hyyA	Alignment		99.7	17	PDB header: hydrolase Chain: A; PDB Molecule: nta1p; PDBTitle: crystal structure of n-terminal amidase
14	c3dlaD	Alignment		99.6	24	PDB header: ligase Chain: D; PDB Molecule: glutamine-dependent nad(+) synthetase; PDBTitle: x-ray crystal structure of glutamine-dependent nad+ synthetase from2 mycobacterium tuberculosis bound to naad+ and don
15	c4hg3C	Alignment		99.6	18	PDB header: hydrolase Chain: C; PDB Molecule: probable hydrolase nit2; PDBTitle: structural insights into yeast nit2: wild-type yeast nit2 in complex2 with alpha-ketoglutarate
16	c2plqA	Alignment		99.6	23	PDB header: hydrolase Chain: A; PDB Molecule: aliphatic amidase; PDBTitle: crystal structure of the amidase from geobacillus pallidus rapc8
17	c2vhiG	Alignment		99.6	19	PDB header: hydrolase Chain: G; PDB Molecule: cg3027-pa; PDBTitle: crystal structure of a pyrimidine degrading enzyme from2 drosophila melanogaster
18	c6ftqA	Alignment		99.6	14	PDB header: hydrolase Chain: A; PDB Molecule: beta-ureidopropionase; PDBTitle: crystal structure of human beta-ureidopropionase (beta-alanine2 synthase) - mutant t299c
19	c4f4hA	Alignment		99.6	24	PDB header: ligase Chain: A; PDB Molecule: glutamine dependent nad+ synthetase; PDBTitle: crystal structure of a glutamine dependent nad+ synthetase from2 burkholderia thailandensis
20	c3ilvA	Alignment		99.6	12	PDB header: ligase Chain: A; PDB Molecule: glutamine-dependent nad(+) synthetase; PDBTitle: crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
21	d1f89a	Alignment	not modelled	99.6	21	Fold: Carbon-nitrogen hydrolase Superfamily: Carbon-nitrogen hydrolase Family: Nitrilase
22	c2vhhA	Alignment	not modelled	99.6	19	PDB header: hydrolase Chain: A; PDB Molecule: cg3027-pa; PDBTitle: crystal structure of a pyrimidine degrading enzyme from2 drosophila melanogaster
23	c3n05B	Alignment	not modelled	99.6	21	PDB header: ligase Chain: B; PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis
24	c6i00C	Alignment	not modelled	99.6	25	PDB header: hydrolase Chain: C; PDB Molecule: bifunctional nitrilase/nitrile hydratase nit4; PDBTitle: cryo-em informed directed evolution of nitrilase 4 leads to a change2 in quaternary structure.
25	c2e2kC	Alignment	not modelled	99.5	17	PDB header: hydrolase Chain: C; PDB Molecule: formamidase; PDBTitle: helicobacter pylori formamidase amif contains a fine-tuned cysteine-2 glutamate-lysine catalytic triad
26	c6mg6D	Alignment	not modelled	99.5	15	PDB header: hydrolase Chain: D; PDB Molecule: carbon-nitrogen hydrolase; PDBTitle: crystal structure of carbon-nitrogen hydrolase from helicobacter2 pylori g27
27	c4cyyA	Alignment	not modelled	99.5	20	PDB header: hydrolase Chain: A; PDB Molecule: pantetheinase; PDBTitle: the structure of vanin-1: defining the link between metabolic disease,2 oxidative stress and inflammation
28	d1ejia	Alignment	not modelled	63.8	26	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like PDB header: protein transport

29	c6ic4I_	Alignment	not modelled	61.5	15	Chain: I: PDB Molecule: abc transporter atp-binding protein; PDBTitle: cryo-em structure of the a. baumannii mla complex at 8.7 a resolution
30	c3n8hA_	Alignment	not modelled	59.6	14	PDB header: ligase Chain: A: PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of pantoate-beta-alanine ligase from francisella2 tularensis
31	c3gfoA_	Alignment	not modelled	59.4	11	PDB header: atp binding protein Chain: A: PDB Molecule: cobalt import atp-binding protein cbio 1; PDBTitle: structure of cbio1 from clostridium perfringens: part of the abc2 transporter complex cbionq.
32	d1g2912	Alignment	not modelled	58.7	9	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
33	c5y0tD_	Alignment	not modelled	56.8	11	PDB header: ligase Chain: D: PDB Molecule: thermotoga maritima tmcal; PDBTitle: crystal structure of thermotoga maritima tmcal bound with alpha-thio2 atp(form ii)
34	d1v43a3	Alignment	not modelled	53.7	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
35	c1vciaA_	Alignment	not modelled	53.0	12	PDB header: transport protein Chain: A: PDB Molecule: sugar-binding transport atp-binding protein; PDBTitle: crystal structure of the atp-binding cassette of multisugar2 transporter from pyrococcus horikoshii ot3 complexed with3 atp
36	c3uk2B_	Alignment	not modelled	50.7	16	PDB header: ligase Chain: B: PDB Molecule: pantothenate synthetase; PDBTitle: the structure of pantothenate synthetase from burkholderia2 thailandensis
37	c5b57D_	Alignment	not modelled	50.6	12	PDB header: metal transport Chain: D: PDB Molecule: hemin import atp-binding protein hmuu; PDBTitle: inward-facing conformation of abc heme importer bhuuv from2 burkholderia cenocepacia
38	d1v8fa_	Alignment	not modelled	47.9	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
39	c4mycC_	Alignment	not modelled	47.6	8	PDB header: transport protein Chain: C: PDB Molecule: iron-sulfur clusters transporter atm1, mitochondrial; PDBTitle: structure of the mitochondrial abc transporter, atm1
40	c2ejcA_	Alignment	not modelled	46.5	16	PDB header: ligase Chain: A: PDB Molecule: pantoate--beta-alanine ligase; PDBTitle: crystal structure of pantoate--beta-alanine ligase (panc)2 from thermotoga maritima
41	d2awna2	Alignment	not modelled	46.5	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
42	c5d95A_	Alignment	not modelled	46.1	17	PDB header: transferase Chain: A: PDB Molecule: aminotransferase class-iii; PDBTitle: structure of thermostable omega-transaminase
43	d1yexa1	Alignment	not modelled	45.4	16	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
44	c1q1bD_	Alignment	not modelled	45.2	11	PDB header: transport protein Chain: D: PDB Molecule: maltose/maltodextrin transport atp-binding protein malk; PDBTitle: crystal structure of e. coli malk in the nucleotide-free form
45	c4g1uD_	Alignment	not modelled	45.1	12	PDB header: transport protein/hydrolase Chain: D: PDB Molecule: hemin import atp-binding protein hmuu; PDBTitle: x-ray structure of the bacterial heme transporter hmuuv from yersinia2 pestis
46	c3wmeA_	Alignment	not modelled	44.6	14	PDB header: transport protein Chain: A: PDB Molecule: atp-binding cassette, sub-family b, member 1; PDBTitle: crystal structure of an inward-facing eukaryotic abc multidrug2 transporter
47	d3dhwc1	Alignment	not modelled	44.5	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
48	c4e77A_	Alignment	not modelled	44.5	19	PDB header: isomerase Chain: A: PDB Molecule: glutamate-1-semialdehyde 2,1-aminomutase; PDBTitle: 2.0a crystal structure of a glutamate-1-semialdehyde aminotransferase2 from yersinia pestis co92
49	c3mxtA_	Alignment	not modelled	44.1	20	PDB header: ligase Chain: A: PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of pantoate-beta-alanine ligase from campylobacter2 jejuni
50	d1oxkx2	Alignment	not modelled	43.6	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
51	c3l44A_	Alignment	not modelled	43.5	14	PDB header: isomerase Chain: A: PDB Molecule: glutamate-1-semialdehyde 2,1-aminomutase 1; PDBTitle: crystal structure of bacillus anthracis hemI-1, glutamate semialdehyde2 aminotransferase
52	c2yyzA_	Alignment	not modelled	43.3	13	PDB header: transport protein Chain: A: PDB Molecule: sugar abc transporter, atp-binding protein; PDBTitle: crystal structure of sugar abc transporter, atp-binding protein
53	c5y0nB_	Alignment	not modelled	42.0	13	PDB header: ligase Chain: B: PDB Molecule: upf0348 protein b4417_3650; PDBTitle: crystal structure of bacillus subtilis tmcal bound with atp (semet2 derivative)

54	c3bs8A_	Alignment	not modelled	40.3	11	PDB header: isomerase Chain: A: PDB Molecule: glutamate-1-semialdehyde 2,1-aminomutase; PDBTitle: crystal structure of glutamate 1-semialdehyde aminotransferase2 complexed with pyridoxamine-5'-phosphate from bacillus subtilis
55	c3n0A_	Alignment	not modelled	39.5	26	PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of serine hydroxymethyltransferase from2 campylobacter jejuni
56	c2cy8A_	Alignment	not modelled	38.7	17	PDB header: transferase Chain: A: PDB Molecule: d-phenylglycine aminotransferase; PDBTitle: crystal structure of d-phenylglycine aminotransferase (d-phgat) from2 pseudomonas strutzeri st-201
57	d1ihoA_	Alignment	not modelled	37.2	24	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
58	c2zsmA_	Alignment	not modelled	35.8	24	PDB header: isomerase Chain: A: PDB Molecule: glutamate-1-semialdehyde 2,1-aminomutase; PDBTitle: crystal structure of glutamate-1-semialdehyde 2,1-2 aminomutase from aeropyrum pernix, hexagonal form
59	c4mkiB_	Alignment	not modelled	35.2	12	PDB header: hydrolase Chain: B: PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: cobalt transporter atp-binding subunit
60	d1jj7a_	Alignment	not modelled	35.1	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
61	c4fwiB_	Alignment	not modelled	34.6	13	PDB header: transport protein Chain: B: PDB Molecule: abc-type dipeptide/oligopeptide/nickel transport system, PDBTitle: crystal structure of the nucleotide-binding domain of a dipeptide abc2 transporter
62	c1oxtB_	Alignment	not modelled	33.3	21	PDB header: transport protein Chain: B: PDB Molecule: abc transporter, atp binding protein; PDBTitle: crystal structure of glcv, the abc-atpase of the glucose abc2 transporter from sulfolobus solfataricus
63	d1l2ta_	Alignment	not modelled	33.2	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
64	c2a7vA_	Alignment	not modelled	33.1	28	PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: human mitochondrial serine hydroxymethyltransferase 2
65	d2a7va1	Alignment	not modelled	33.1	28	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
66	c2it1B_	Alignment	not modelled	32.8	13	PDB header: transport protein Chain: B: PDB Molecule: 362aa long hypothetical maltose/maltodextrin PDBTitle: structure of ph0203 protein from pyrococcus horikoshii
67	c4hzuB_	Alignment	not modelled	31.7	13	PDB header: hydrolase, transport protein Chain: B: PDB Molecule: energy-coupling factor transporter atp-binding protein ecfa PDBTitle: structure of a bacterial energy-coupling factor transporter
68	c3i4jC_	Alignment	not modelled	31.6	8	PDB header: transferase Chain: C: PDB Molecule: aminotransferase, class iii; PDBTitle: crystal structure of aminotransferase, class iii from deinococcus2 radiodurans
69	c1z47B_	Alignment	not modelled	31.1	8	PDB header: ligand binding protein Chain: B: PDB Molecule: putative abc-transporter atp-binding protein; PDBTitle: structure of the atpase subunit cysa of the putative sulfate atp-2 binding cassette (abc) transporter from alicyclobacillus3 acidocaldarius
70	c3dodA_	Alignment	not modelled	30.3	12	PDB header: transferase Chain: A: PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate aminotransferase; PDBTitle: crystal structure of plp bound 7,8-diaminopelargonic acid synthase in2 bacillus subtilis
71	d2gsaa_	Alignment	not modelled	28.8	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
72	c6iz9B_	Alignment	not modelled	28.2	15	PDB header: transferase Chain: B: PDB Molecule: beta-transaminase; PDBTitle: crystal structure of the apo form of a beta-transaminase from2 mesorhizobium sp. strain luk
73	c5ochH_	Alignment	not modelled	27.9	17	PDB header: hydrolase Chain: H: PDB Molecule: atp-binding cassette sub-family b member 8, mitochondrial; PDBTitle: the crystal structure of human abcb8 in an outward-facing state
74	c4uoxB_	Alignment	not modelled	27.9	11	PDB header: transferase Chain: B: PDB Molecule: putrescine aminotransferase; PDBTitle: crystal structure of ygig in complex with pyridoxal-5'-phosphate2 and putrescine
75	c2ei9A_	Alignment	not modelled	27.7	22	PDB header: gene regulation Chain: A: PDB Molecule: non-ltr retrotransposon r1bmks orf2 protein; PDBTitle: crystal structure of r1bm endonuclease domain
76	c4hziA_	Alignment	not modelled	27.6	22	PDB header: transport protein Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: crystal structure of the leptospira interrogans atpase subunit of an2 orphan abc transporter
77	c5u1dA_	Alignment	not modelled	27.5	10	PDB header: transport protein Chain: A: PDB Molecule: antigen peptide transporter 1; PDBTitle: cryo-em structure of the human tap atp-binding cassette transporter

78	c3d31B_	Alignment	not modelled	27.3	10	PDB header: transport protein Chain: B: PDB Molecule: sulfate/molybdate abc transporter, atp-binding protein; PDBTitle: modbc from methanosarcina acetivorans
79	c5viuB_	Alignment	not modelled	27.1	17	PDB header: transferase Chain: B: PDB Molecule: acetylornithine aminotransferase; PDBTitle: crystal structure of acetylornithine aminotransferase from2 elizabethkingia anophelis
80	c4yerB_	Alignment	not modelled	27.0	8	PDB header: hydrolase Chain: B: PDB Molecule: abc transporter atp-binding protein; PDBTitle: crystal structure of an abc transporter atp-binding protein (tm_1403)2 from thermotoga maritima msb8 at 2.35 a resolution
81	c5do7B_	Alignment	not modelled	26.6	14	PDB header: transport protein Chain: B: PDB Molecule: atp-binding cassette sub-family g member 8; PDBTitle: crystal structure of the human sterol transporter abcg5/abcg8
82	c6cd1A_	Alignment	not modelled	26.5	30	PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of medicago truncatula serine2 hydroxymethyltransferase 3 (mtshmt3), complexes with reaction3 intermediates
83	c2d62A_	Alignment	not modelled	25.5	12	PDB header: sugar binding protein Chain: A: PDB Molecule: multiple sugar-binding transport atp-binding PDBTitle: crystal structure of multiple sugar binding transport atp-2 binding protein
84	c2ordA_	Alignment	not modelled	24.7	8	PDB header: transferase Chain: A: PDB Molecule: acetylornithine aminotransferase; PDBTitle: crystal structure of acetylornithine aminotransferase (ec 2.6.1.11)2 (acoat) (tm1785) from thermotoga maritima at 1.40 a resolution
85	c3lv2A_	Alignment	not modelled	24.5	24	PDB header: transferase Chain: A: PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate aminotransferase; PDBTitle: crystal structure of mycobacterium tuberculosis 7,8-diaminopelargonic2 acid synthase in complex with substrate analog sinefungin
86	d2pmka1	Alignment	not modelled	24.3	9	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
87	c2olkD_	Alignment	not modelled	23.6	13	PDB header: hydrolase Chain: D: PDB Molecule: amino acid abc transporter; PDBTitle: abc protein artp in complex with adp-beta-s
88	c3fvqB_	Alignment	not modelled	23.6	8	PDB header: hydrolase Chain: B: PDB Molecule: fe(3+) ions import atp-binding protein fbpc; PDBTitle: crystal structure of the nucleotide binding domain fbpc complexed with2 atp
89	c3dhwC_	Alignment	not modelled	23.6	13	PDB header: membrane protein/hydrolase Chain: C: PDB Molecule: methionine import atp-binding protein metni; PDBTitle: crystal structure of methionine importer metni
90	c2ykyB_	Alignment	not modelled	23.3	15	PDB header: transferase Chain: B: PDB Molecule: beta-transaminase; PDBTitle: structural determinants of the beta-selectivity of a bacterial2 aminotransferase
91	d2cfba1	Alignment	not modelled	23.2	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
92	c2nq2C_	Alignment	not modelled	23.1	18	PDB header: metal transport Chain: C: PDB Molecule: hypothetical abc transporter atp-binding protein PDBTitle: an inward-facing conformation of a putative metal-chelate2 type abc transporter.
93	c4tqvO_	Alignment	not modelled	22.8	10	PDB header: transport protein Chain: O: PDB Molecule: algs; PDBTitle: crystal structure of a bacterial abc transporter involved in the2 import of the acidic polysaccharide alginate
94	d3d31a2	Alignment	not modelled	22.4	10	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
95	d1bj4a_	Alignment	not modelled	22.0	24	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
96	d1rv3a_	Alignment	not modelled	21.9	24	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
97	c3jcuO_	Alignment	not modelled	21.1	21	PDB header: membrane protein Chain: O: PDB Molecule: oxygen-evolving enhancer protein 1, chloroplastic; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
98	c5f15A_	Alignment	not modelled	21.1	12	PDB header: transferase Chain: A: PDB Molecule: 4-amino-4-deoxy-l-arabinose (l-ara4n) transferase; PDBTitle: crystal structure of arnt from cupriavidus metallidurans bound to2 undecaprenyl phosphate
99	c5g4iA_	Alignment	not modelled	20.9	11	PDB header: transferase Chain: A: PDB Molecule: phosphorylase; PDBTitle: plp-dependent phosphorylase a1rdf1 from arthrobacter aureescens tc1