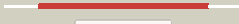



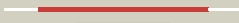
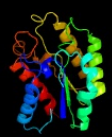


















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2418c (-)_2716405_2717148
Date	Wed Aug 7 12:50:04 BST 2019
Unique Job ID	43ee4d7e14842cae

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6iqbA_	 Alignment		99.2	18	PDB header: hydrolase Chain: A: PDB Molecule: sgnh-hydrolase family esterase; PDBTitle: esterase aline4 mutant-s13a
2	c3dciB_	 Alignment		99.1	17	PDB header: hydrolase Chain: B: PDB Molecule: arylesterase; PDBTitle: the structure of a putative arylesterase from agrobacterium2 tumefaciens str. c58
3	d1yzfa1	 Alignment		99.1	17	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: TAP-like
4	c4rshB_	 Alignment		99.0	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: lipolytic protein g-d-s-l family; PDBTitle: structure of a putative lipolytic protein of g-d-s-l family from2 desulfitobacterium hafniense dcb-2
5	c5hoeB_	 Alignment		99.0	22	PDB header: hydrolase Chain: B: PDB Molecule: hydrolase; PDBTitle: crystal structrue of est24, a carbohydrate acetylerase from2 sinorhizobium meliloti
6	c2o14A_	 Alignment		98.9	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yxim; PDBTitle: x-ray crystal structure of protein yxim_bacsu from bacillus subtilis.2 northeast structural genomics consortium target sr595
7	d2o14a2	 Alignment		98.9	15	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: YxiM C-terminal domain-like
8	c3milA_	 Alignment		98.8	17	PDB header: hydrolase Chain: A: PDB Molecule: isoamyl acetate-hydrolyzing esterase; PDBTitle: crystal structure of isoamyl acetate-hydrolyzing esterase from2 saccharomyces cerevisiae
9	c4tx1C_	 Alignment		98.8	18	PDB header: hydrolase Chain: C: PDB Molecule: esterase; PDBTitle: the crystal structure of carbohydrate acetylerase family member2 from sinorhizobium meliloti
10	c4lhsA_	 Alignment		98.8	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative gdsl-like lipase (bacova_00914) from2 bacteroides ovatus atcc 8483 at 1.40 a resolution
11	c4q7qA_	 Alignment		98.8	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lipolytic protein g-d-s-l family; PDBTitle: the crystal structure of a possible lipase from chitinophaga pinensis2 dsm 2588

12	d1k7ca_	Alignment		98.7	18	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: Rhamnogalacturonan acetylsterase
13	c2q0qC_	Alignment		98.7	22	PDB header: hydrolase Chain: C: PDB Molecule: aryl esterase; PDBTitle: structure of the native m. smegmatis aryl esterase
14	c4h08A_	Alignment		98.7	17	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of a putative hydrolase (bt3161) from bacteroides2 thetaiotaomicron vpi-5482 at 1.80 a resolution
15	c2waaA_	Alignment		98.7	21	PDB header: hydrolase Chain: A: PDB Molecule: xylan esterase, putative, axe2c; PDBTitle: structure of a family two carbohydrate esterase from2 cellvibrio japonicus
16	c2waoA_	Alignment		98.7	16	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase e; PDBTitle: structure of a family two carbohydrate esterase from clostridium2 thermocellum in complex with cellohexaose
17	c3bzwA_	Alignment		98.5	18	PDB header: hydrolase Chain: A: PDB Molecule: putative lipase; PDBTitle: crystal structure of a putative lipase from bacteroides2 thetaiotaomicron
18	d3bzwA1	Alignment		98.5	18	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: BT2961-like
19	c3hp4A_	Alignment		98.5	17	PDB header: hydrolase Chain: A: PDB Molecule: gdsI-esterase; PDBTitle: crystal structure of psychrotrophic esterase esta from2 pseudoalteromonas sp. 643a inhibited by monoethylphosphonate
20	c4hyqA_	Alignment		98.5	17	PDB header: hydrolase Chain: A: PDB Molecule: phospholipase a1; PDBTitle: crystal structure of phospholipase a1 from streptomyces albidoflavus2 na297
21	c4xvhA_	Alignment	not modelled	98.4	19	PDB header: hydrolase Chain: A: PDB Molecule: carbohydrate esterase family 2 (ce2); PDBTitle: crystal structure of a corynascus thermopiles (myceliophthora2 fergusii) carbohydrate esterase family 2 (ce2) enzyme plus3 carbohydrate binding domain (cbd)
22	c4rw0B_	Alignment	not modelled	98.4	15	PDB header: hydrolase Chain: B: PDB Molecule: lipolytic protein g-d-s-l family; PDBTitle: crystal structure of a member of the lipolytic protein g-d-s-l family2 from veillonella parvula dsm 2008
23	c4m8kA_	Alignment	not modelled	98.4	15	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein, gdsI-like lipase/acylhydrolase family PDBTitle: crystal structure of a putative gdsI-like lipase (bacuni_00748) from2 bacteroides uniformis atcc 8492 at 1.90 a resolution
24	d1jrla_	Alignment	not modelled	98.3	21	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: TAP-like
25	c4jhlA_	Alignment	not modelled	98.3	17	PDB header: hydrolase Chain: A: PDB Molecule: acetyl xylan esterase; PDBTitle: crystal structure of of axe2, an acetylxylan esterase from geobacillus2 stearothermophilus
26	c5jd3A_	Alignment	not modelled	98.3	22	PDB header: hydrolase Chain: A: PDB Molecule: lae5; PDBTitle: crystal structure of lae5, an alpha/beta hydrolase enzyme from the2 metagenome of lake arreo, spain
27	c4nrdA_	Alignment	not modelled	98.3	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative gdsI-like lipase (bacova_04955) from2 bacteroides ovatus atcc 8483 at 2.10 a resolution
						PDB header: hydrolase

28	c4q9aA	Alignment	not modelled	98.3	15	Chain: A: PDB Molecule: tat pathway signal sequence domain protein; PDBTitle: crystal structure of a putative gdsI-like lipase (parmer_00689) from <i>Parabacteroides merdae</i> atcc 43184 at 2.86 a resolution
29	c5ma1A	Alignment	not modelled	98.2	16	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of extracellular lipase from <i>Streptomyces rimosus</i> at2.1.7a resolution
30	c2w9xA	Alignment	not modelled	98.2	16	PDB header: hydrolase Chain: A: PDB Molecule: putative acetyl xylan esterase; PDBTitle: the active site of a carbohydrate esterase displays 2 divergent 3 catalytic and non-catalytic binding functions
31	c6iq8B	Alignment	not modelled	98.2	17	PDB header: hydrolase Chain: B: PDB Molecule: carboxylesterase; PDBTitle: esterase crme10 mutant-d178a
32	c3dc7B	Alignment	not modelled	98.2	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative uncharacterized protein lp_3323; PDBTitle: crystal structure of the protein q88sr8 from <i>Lactobacillus plantarum</i> .2 northeast structural genomics consortium target lpr109.
33	d3dc7a1	Alignment	not modelled	98.1	18	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: BT2961-like
34	d1esca	Alignment	not modelled	98.1	20	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: Esterase
35	c6njcB	Alignment	not modelled	98.0	12	PDB header: hydrolase Chain: B: PDB Molecule: sialate o-acylesterase; PDBTitle: crystal structure of the sialate o-acylesterase from <i>Bacteroides vulgatus</i>
36	c4iyjA	Alignment	not modelled	98.0	21	PDB header: hydrolase Chain: A: PDB Molecule: gdsI-like protein; PDBTitle: crystal structure of a putative acylhydrolase (bacuni_03406) from <i>Bacteroides uniformis</i> atcc 8492 at 1.37 a resolution
37	c3p94A	Alignment	not modelled	98.0	18	PDB header: hydrolase Chain: A: PDB Molecule: gdsI-like lipase; PDBTitle: crystal structure of a gdsI-like lipase (bdi_0976) from <i>Parabacteroides distasonis</i> atcc 8503 at 1.93 a resolution
38	d1es9a	Alignment	not modelled	98.0	13	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: Acetylhydrolase
39	c4jggB	Alignment	not modelled	98.0	19	PDB header: hydrolase Chain: B: PDB Molecule: esterase tesa; PDBTitle: crystal structure of tesa
40	c4s1pA	Alignment	not modelled	98.0	16	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: shel_16390 protein, a putative sgnh hydrolase from <i>Slackia2 heliotrinireducens</i>
41	d1vjga	Alignment	not modelled	97.9	17	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: Hypothetical protein alr1529
42	c4devE	Alignment	not modelled	97.9	19	PDB header: hydrolase Chain: E: PDB Molecule: acetyl-xylan esterase est2a; PDBTitle: an acetyl xylan esterase (est2a) from the rumen bacterium <i>Butyrivibrio2 proteoclasticus</i> .
43	c5ufyA	Alignment	not modelled	97.9	17	PDB header: transferase Chain: A: PDB Molecule: acyltransferase; PDBTitle: structure of streptococcus pneumoniae peptidoglycan o-2 acetyltransferase a (oata) c-terminal catalytic domain
44	c4c1bC	Alignment	not modelled	97.9	15	PDB header: hydrolase Chain: C: PDB Molecule: orf1-encoded protein; PDBTitle: esterase domain of the zfl2-1 orf1 protein from the zebrafish zfl2-12 retrotransposon
45	c4k40B	Alignment	not modelled	97.8	17	PDB header: hydrolase Chain: B: PDB Molecule: gdsI-like lipase/acylhydrolase family protein; PDBTitle: peptidoglycan o-acylesterase in action, 0 min
46	d1fxwf	Alignment	not modelled	97.6	12	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: Acetylhydrolase
47	c3rjtA	Alignment	not modelled	97.5	16	PDB header: hydrolase Chain: A: PDB Molecule: lipolytic protein g-d-s-l family; PDBTitle: crystal structure of lipolytic protein g-d-s-l family from <i>Alicyclobacillus acidocaldarius</i> subsp. <i>acidocaldarius</i> dsm 446
48	c4hf7A	Alignment	not modelled	97.1	13	PDB header: hydrolase Chain: A: PDB Molecule: putative acylhydrolase; PDBTitle: crystal structure of a gdsI-like lipase (bt0569) from <i>Bacteroides2 thetaiotaomicron</i> vpi-5482 at 1.77 a resolution
49	c2vptA	Alignment	not modelled	96.9	20	PDB header: hydrolase Chain: A: PDB Molecule: lipolytic enzyme; PDBTitle: clostridium thermocellum family 3 carbohydrate esterase
50	d2hsja1	Alignment	not modelled	96.8	17	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: Acetylhydrolase
51	c3x0hA	Alignment	not modelled	96.5	18	PDB header: hydrolase Chain: A: PDB Molecule: carbohydrate esterase 1; PDBTitle: crystal structure of a carbohydrate esterase family 1 from <i>Talaromyces2 cellulolyticus</i>
52	c5xtuA	Alignment	not modelled	83.0	28	PDB header: hydrolase Chain: A: PDB Molecule: gdsI-family esterase; PDBTitle: crystal structure of gdsI esterase of photobacterium sp. j15
53	c6jl1A	Alignment	not modelled	81.1	16	PDB header: hydrolase Chain: A: PDB Molecule: thermolabile hemolysin; PDBTitle: crystal structure of vvp1pa g389d from <i>Vibrio vulnificus</i>

54	c4o8vA_	Alignment	not modelled	49.7	13	PDB header: transferase Chain: A; PDB Molecule: alginate biosynthesis protein algj; PDBTitle: o-acetyltransferase domain of pseudomonas putida algj
55	d1p90a_	Alignment	not modelled	47.9	18	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: Nitrogenase accessory factor
56	d1qt1a_	Alignment	not modelled	40.7	17	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
57	c1ahuB_	Alignment	not modelled	39.4	19	PDB header: flavoenzyme Chain: B; PDB Molecule: vanillyl-alcohol oxidase; PDBTitle: structure of the octameric flavoenzyme vanillyl-alcohol2 oxidase in complex with p-cresol
58	d1xima_	Alignment	not modelled	34.1	16	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
59	c6pfxB_	Alignment	not modelled	33.1	14	PDB header: transferase Chain: B; PDB Molecule: d-alanyl transferase dltD; PDBTitle: d-alanyl transferase dltD from enterococcus faecium
60	d2c42a3	Alignment	not modelled	27.5	30	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Pyruvate-ferredoxin oxidoreductase, PFOR, domain II
61	d1lk0a_	Alignment	not modelled	25.3	53	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Short-chain cytokines
62	c4kncA_	Alignment	not modelled	24.6	15	PDB header: sugar binding protein Chain: A; PDB Molecule: alginate biosynthesis protein algx; PDBTitle: structural and functional characterization of pseudomonas aeruginosa2 algx
63	c6o93A_	Alignment	not modelled	24.2	14	PDB header: transferase Chain: A; PDB Molecule: d-alanyl transferase dltD; PDBTitle: d-alanyl transferase dltD from enterococcus faecalis
64	c3wfpB_	Alignment	not modelled	22.7	13	PDB header: transferase Chain: B; PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme (apo form 2)
65	c3wfpA_	Alignment	not modelled	20.2	13	PDB header: transferase Chain: A; PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme (apo form 2)
66	c4i14B_	Alignment	not modelled	18.6	15	PDB header: hydrolase, lyase Chain: B; PDB Molecule: riboflavin biosynthesis protein ribba; PDBTitle: crystal structure of mtb-riba2 (rv1415)
67	d1muwa_	Alignment	not modelled	16.6	14	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
68	d1zpdA1	Alignment	not modelled	16.6	17	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
69	c2kngA_	Alignment	not modelled	14.8	26	PDB header: dna binding protein Chain: A; PDB Molecule: protein lsr2; PDBTitle: solution structure of c-domain of lsr2
70	d1mioa_	Alignment	not modelled	13.8	11	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
71	d1bxca_	Alignment	not modelled	13.0	15	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
72	d1zmba1	Alignment	not modelled	12.5	23	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: Putative acetylxyylan esterase-like
73	c3mioA_	Alignment	not modelled	11.9	15	PDB header: lyase Chain: A; PDB Molecule: 3,4-dihydroxy-2-butanone 4-phosphate synthase; PDBTitle: crystal structure of 3,4-dihydroxy-2-butanone 4-phosphate synthase2 domain from mycobacterium tuberculosis at ph 6.00
74	d2apja1	Alignment	not modelled	11.3	21	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: Putative acetylxyylan esterase-like
75	d2glia5	Alignment	not modelled	11.1	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
76	c3gyxA_	Alignment	not modelled	11.0	45	PDB header: oxidoreductase Chain: A; PDB Molecule: adenylsulfate reductase; PDBTitle: crystal structure of adenylsulfate reductase from2 desulfovibrio gigas
77	c3bmaC_	Alignment	not modelled	10.6	17	PDB header: ligase Chain: C; PDB Molecule: d-alanyl-lipoteichoic acid synthetase; PDBTitle: crystal structure of d-alanyl-lipoteichoic acid synthetase from2 streptococcus pneumoniae r6
78	c3wfrF_	Alignment	not modelled	10.6	13	PDB header: transferase/rna Chain: F; PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 2
79	d1sq4a_	Alignment	not modelled	10.4	64	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Ylba-like
80	d1e8ga2	Alignment	not modelled	9.9	16	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain

81	c5ii0A_	Alignment	not modelled	9.4	36	PDB header: rna binding protein Chain: A: PDB Molecule: mettl3; PDBTitle: crystal structural of the mettl3-mettl14 complex for n6-adenosine2 methylation
82	c2fjaC_	Alignment	not modelled	9.4	50	PDB header: oxidoreductase Chain: C: PDB Molecule: adenylylsulfate reductase, subunit a; PDBTitle: adenosine 5'-phosphosulfate reductase in complex with substrate
83	c2bw2A_	Alignment	not modelled	9.0	24	PDB header: signaling protein Chain: A: PDB Molecule: bypass of forespore c; PDBTitle: bofc from bacillus subtilis
84	c5a29A_	Alignment	not modelled	9.0	39	PDB header: lyase Chain: A: PDB Molecule: exopolysaccharuronate lyase; PDBTitle: family 2 pectate lyase from vibrio vulnificus
85	c4o6gA_	Alignment	not modelled	8.5	18	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: rv3902c from m. tuberculosis
86	c3anyB_	Alignment	not modelled	8.3	37	PDB header: lyase Chain: B: PDB Molecule: ethanolamine ammonia-lyase light chain; PDBTitle: crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with cn-cbl and (r)-2-amino-1-propanol
87	c3absD_	Alignment	not modelled	8.3	37	PDB header: lyase Chain: D: PDB Molecule: ethanolamine ammonia-lyase light chain; PDBTitle: crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with adeninylpentylcobalamin and ethanolamine
88	d2b0ja2	Alignment	not modelled	8.3	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
89	d3bi1a3	Alignment	not modelled	8.1	22	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: FolH catalytic domain-like
90	c3wfrH_	Alignment	not modelled	8.1	14	PDB header: transferase/rna Chain: H: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 2
91	d1chua2	Alignment	not modelled	7.8	47	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
92	d1w4xa2	Alignment	not modelled	7.3	33	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
93	c3kdvB_	Alignment	not modelled	7.3	60	PDB header: dna binding protein Chain: B: PDB Molecule: dna damage response b protein; PDBTitle: crystal structure of dna damage response b (ddrb) from deinococcus2 geothermalis
94	c3l8mA_	Alignment	not modelled	7.1	26	PDB header: transferase Chain: A: PDB Molecule: probable thiamine pyrophosphokinase; PDBTitle: crystal structure of a probable thiamine pyrophosphokinase2 from staphylococcus saprophyticus subsp. saprophyticus.3 northeast structural genomics consortium target id syr86
95	d1nbaa_	Alignment	not modelled	6.8	26	Fold: Isochorismatase-like hydrolases Superfamily: Isochorismatase-like hydrolases Family: Isochorismatase-like hydrolases
96	c2p0yA_	Alignment	not modelled	6.8	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein lp_0780; PDBTitle: crystal structure of q88yi3_lacpl from lactobacillus plantarum.2 northeast structural genomics consortium target lpr6
97	c3vr8E_	Alignment	not modelled	6.7	33	PDB header: oxidoreductase Chain: E: PDB Molecule: flavoprotein subunit of complex ii; PDBTitle: mitochondrial rholoquinol-fumarate reductase from the parasitic2 nematode ascaris suum
98	c5teyB_	Alignment	not modelled	6.6	50	PDB header: transferase Chain: B: PDB Molecule: n6-adenosine-methyltransferase subunit mettl14; PDBTitle: human mettl3-mettl14 complex
99	c6hhnA_	Alignment	not modelled	6.4	24	PDB header: isomerase Chain: A: PDB Molecule: l-rhamnose mutarotase; PDBTitle: crystal structure of l-rhamnose mutarotase fa22100 from formosa2 agariphila