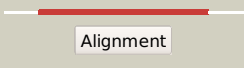

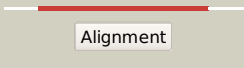

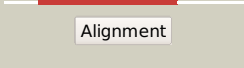

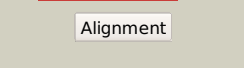

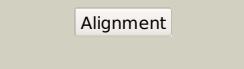
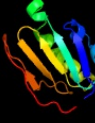
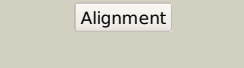

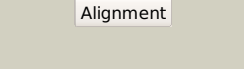

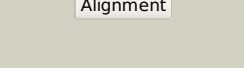

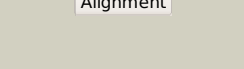

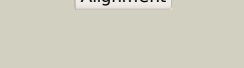

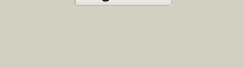



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2261c_(-)_2534052_2534474
Date	Mon Aug 5 13:25:40 BST 2019
Unique Job ID	fcf84f03eee8de14

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5vrhA_	 Alignment		100.0	21	PDB header: transferase Chain: A; PDB Molecule: apolipoprotein n-acyltransferase; PDBTitle: apolipoprotein n-acyltransferase c387s active site mutant
2	c5n6mA_	 Alignment		100.0	22	PDB header: membrane protein Chain: A; PDB Molecule: apolipoprotein n-acyltransferase; PDBTitle: structure of the membrane integral lipoprotein n-acyltransferase Int2 from p. aeruginosa
3	c5h8lM_	 Alignment		99.9	20	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
4	c2plqA_	 Alignment		99.9	25	PDB header: hydrolase Chain: A; PDB Molecule: aliphatic amidase; PDBTitle: crystal structure of the amidase from geobacillus pallidus rapc8
5	c2e2kC_	 Alignment		99.9	19	PDB header: hydrolase Chain: C; PDB Molecule: formamidase; PDBTitle: helicobacter pylori formamidase amif contains a fine-tuned cysteine-2 glutamate-lysine catalytic triad
6	c6i00C_	 Alignment		99.9	21	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.
7	d1uf5a_	 Alignment		99.9	13	Fold: Carbon-nitrogen hydrolase Superfamily: Carbon-nitrogen hydrolase Family: Carbamilase
8	c6mg6D_	 Alignment		99.9	20	PDB header: hydrolase Chain: D; PDB Molecule: carbon-nitrogen hydrolase; PDBTitle: crystal structure of carbon-nitrogen hydrolase from helicobacter2 pylori g27
9	c1emsB_	 Alignment		99.9	27	PDB header: antitumor protein Chain: B; PDB Molecule: nit-fragile histidine triad fusion protein; PDBTitle: crystal structure of the c. elegans nitfhit protein
10	c3wuyA_	 Alignment		99.9	18	PDB header: hydrolase Chain: A; PDB Molecule: nitrilase; PDBTitle: crystal structure of nit6803
11	c2vhhA_	 Alignment		99.9	20	PDB header: hydrolase Chain: A; PDB Molecule: cg3027-pa; PDBTitle: crystal structure of a pyrimidine degrading enzyme from2 drosophila melanogaster

12	d1f89a_	Alignment		99.8	27	Fold: Carbon-nitrogen hydrolase Superfamily: Carbon-nitrogen hydrolase Family: Nitrilase
13	c2w1vA_	Alignment		99.8	26	PDB header: hydrolase Chain: A: PDB Molecule: nitrilase homolog 2; PDBTitle: crystal structure of mouse nitrilase-2 at 1.4a resolution
14	c2vhiG_	Alignment		99.8	24	PDB header: hydrolase Chain: G: PDB Molecule: cg3027-pa; PDBTitle: crystal structure of a pyrimidine degrading enzyme from2 drosophila melanogaster
15	d1j31a_	Alignment		99.8	20	Fold: Carbon-nitrogen hydrolase Superfamily: Carbon-nitrogen hydrolase Family: Carbamilase
16	c4hg3C_	Alignment		99.8	25	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
17	c3hkxA_	Alignment		99.8	26	PDB header: hydrolase Chain: A: PDB Molecule: amidase; PDBTitle: crystal structure analysis of an amidase from nesterenkonia sp.
18	d1emsa2	Alignment		99.8	27	Fold: Carbon-nitrogen hydrolase Superfamily: Carbon-nitrogen hydrolase Family: Nitrilase
19	c5khaA_	Alignment		99.8	10	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)
20	c4f4hA_	Alignment		99.8	20	PDB header: ligase Chain: A: PDB Molecule: glutamine dependent nad+ synthetase; PDBTitle: crystal structure of a glutamine dependent nad+ synthetase from2 burkholderia thailandensis
21	c3n05B_	Alignment	not modelled	99.8	23	PDB header: ligase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis
22	c6ftqA_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-ureidopropionase; PDBTitle: crystal structure of human beta-ureidopropionase (beta-alanine2 synthase) - mutant t299c
23	c2e11B_	Alignment	not modelled	99.8	18	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
24	c3dlaD_	Alignment	not modelled	99.6	19	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
25	c4cyyA_	Alignment	not modelled	99.4	8	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
26	c3ilvA_	Alignment	not modelled	99.2	16	PDB header: ligase Chain: A: PDB Molecule: glutamine-dependent nad(+) synthetase; PDBTitle: crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
27	c5hyvA_	Alignment	not modelled	98.0	8	PDB header: hydrolase Chain: A: PDB Molecule: nta1p; PDBTitle: crystal structure of n-terminal amidase
28	d1sgva1	Alianment	not modelled	78.1	26	Fold: PUA domain-like Superfamily: PUA domain-like

					Family:PUA domain
29	d4pgaa_	Alignment	not modelled	65.2	13 Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
30	d1agxa_	Alignment	not modelled	63.6	13 Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
31	c4mwaA_	Alignment	not modelled	59.6	18 PDB header: oxidoreductase Chain: A; PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: 1.85 angstrom crystal structure of gcpe protein from bacillus2 anthracis
32	d1zq1a2	Alignment	not modelled	50.1	19 Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
33	c6bmaA_	Alignment	not modelled	48.4	17 PDB header: lyase Chain: A; PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: the crystal structure of indole-3-glycerol phosphate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
34	d2d6fa2	Alignment	not modelled	44.5	18 Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
35	c2wltA_	Alignment	not modelled	43.4	15 PDB header: hydrolase Chain: A; PDB Molecule: l-asparaginase; PDBTitle: the crystal structure of helicobacter pylori l-asparaginase at 1.4 a2 resolution
36	c4r8kC_	Alignment	not modelled	43.3	21 PDB header: hydrolase Chain: C; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the guinea pig l-asparaginase 1 catalytic domain
37	d1o7ja_	Alignment	not modelled	41.4	18 Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
38	c3tsmB_	Alignment	not modelled	40.1	28 PDB header: lyase Chain: B; PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of indole-3-glycerol phosphate synthase from2 brucella melitensis
39	c2d6fA_	Alignment	not modelled	37.8	16 PDB header: ligase/rna Chain: A; PDB Molecule: glutamyl-trna(gln) amidotransferase subunit d; PDBTitle: crystal structure of glu-trna(gln) amidotransferase in the2 complex with trna(gln)
40	d1nnsa_	Alignment	not modelled	37.7	11 Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
41	c2p2dA_	Alignment	not modelled	37.2	25 PDB header: transferase Chain: A; PDB Molecule: l-asparaginase i; PDBTitle: crystal structure and allosteric regulation of the cytoplasmic2 escherichia coli l-asparaginase i
42	c1zq1B_	Alignment	not modelled	36.3	19 PDB header: lyase Chain: B; PDB Molecule: glutamyl-trna(gln) amidotransferase subunit d; PDBTitle: structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi
43	c3qjaA_	Alignment	not modelled	35.6	17 PDB header: lyase Chain: A; PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
44	c4q0mA_	Alignment	not modelled	34.4	14 PDB header: hydrolase Chain: A; PDB Molecule: l-asparaginase; PDBTitle: crystal structure of pyrococcus furiosus l-asparaginase
45	c2nydB_	Alignment	not modelled	32.7	7 PDB header: unknown function Chain: B; PDB Molecule: upf0135 protein sa1388; PDBTitle: crystal structure of staphylococcus aureus hypothetical protein sa1388
46	c6eacC_	Alignment	not modelled	30.2	26 PDB header: transferase Chain: C; PDB Molecule: selo; PDBTitle: pseudomonas syringae selo
47	c3w6gP_	Alignment	not modelled	29.9	14 PDB header: oxidoreductase Chain: P; PDB Molecule: probable peroxiredoxin; PDBTitle: structure of peroxiredoxin from anaerobic hyperthermophilic archaon2 pyrococcus horikoshii
48	d2ocda1	Alignment	not modelled	29.6	19 Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
49	d1wsaa_	Alignment	not modelled	26.7	18 Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
50	c1wnfA_	Alignment	not modelled	26.3	16 PDB header: hydrolase Chain: A; PDB Molecule: l-asparaginase; PDBTitle: crystal structure of ph0066 from pyrococcus horikoshii
51	c4tziA_	Alignment	not modelled	23.9	13 PDB header: transferase Chain: A; PDB Molecule: tyrosine-protein kinase lyn; PDBTitle: structure of unliganded lyn sh2 domain
52	c5xxzB_	Alignment	not modelled	23.4	23 PDB header: lyase Chain: B; PDB Molecule: chemokine protease c; PDBTitle: crystal structure of a serine protease from streptococcus species
53	c4m4zA_	Alignment	not modelled	23.0	10 PDB header: signaling protein Chain: A; PDB Molecule: src-like-adaptor 2; PDBTitle: sh3 and sh2 domains of human src-like adaptor protein 2 (slap2)
54	d1nmpa_	Alignment	not modelled	22.7	13 Fold: NIF3 (NGG1p interacting factor 3)-like Superfamily: NIF3 (NGG1p interacting factor 3)-like

						Family:NIF3 (NGG1p interacting factor 3)-like
55	c1xf1A	Alignment	not modelled	22.5	19	PDB header: hydrolase Chain: A: PDB Molecule: c5a peptidase; PDBTitle: structure of c5a peptidase- a key virulence factor from2 streptococcus
56	c5ovqL	Alignment	not modelled	21.2	14	PDB header: oxidoreductase Chain: L: PDB Molecule: peroxiredoxin; PDBTitle: crystal structure of the peroxiredoxin (ahpc2) from the2 hyperthermophilic bacteria aquifex aeolicus vf
57	d1lkka	Alignment	not modelled	20.9	14	Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
58	d2zcta1	Alignment	not modelled	20.7	17	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
59	d1vc4a	Alignment	not modelled	19.9	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
60	d1cwea	Alignment	not modelled	19.6	18	Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
61	d1qcfa2	Alignment	not modelled	18.1	12	Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
62	c3o3cD	Alignment	not modelled	15.7	19	PDB header: transferase Chain: D: PDB Molecule: glycogen [starch] synthase isoform 2; PDBTitle: glycogen synthase basal state udp complex
63	d1a81a2	Alignment	not modelled	15.4	15	Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
64	c3eurA	Alignment	not modelled	15.3	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the c-terminal domain of uncharacterized protein2 from bacteroides fragilis nctc 9343
65	d1g83a2	Alignment	not modelled	15.2	11	Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
66	d2oq1a1	Alignment	not modelled	14.9	12	Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
67	d1f2fa	Alignment	not modelled	14.7	10	Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
68	d1i4na	Alignment	not modelled	14.6	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
69	c3llvA	Alignment	not modelled	14.2	17	PDB header: nad(p) binding protein Chain: A: PDB Molecule: exopolyphosphatase-related protein; PDBTitle: the crystal structure of the nad(p)-binding domain of an2 exopolyphosphatase-related protein from archaeoglobus fulgidus to3 1.7a
70	d1bkla	Alignment	not modelled	14.1	12	Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
71	d2iuba2	Alignment	not modelled	14.0	17	Fold: Transmembrane helix hairpin Superfamily: Magnesium transport protein CorA, transmembrane region Family: Magnesium transport protein CorA, transmembrane region
72	d1a81e2	Alignment	not modelled	13.3	15	Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
73	c3ew1A	Alignment	not modelled	13.3	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized conserved protein bf1870; PDBTitle: crystal structure of conserved protein bf1870 of unknown function from2 bacteroides fragilis
74	c5uswD	Alignment	not modelled	13.2	19	PDB header: transferase Chain: D: PDB Molecule: dihydropteroate synthase; PDBTitle: the crystal structure of 7,8-dihydropteroate synthase from vibrio2 fischeri es114
75	c2cdh1	Alignment	not modelled	12.9	18	PDB header: transferase Chain: 1: PDB Molecule: enoyl reductase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
76	d2b7ka1	Alignment	not modelled	12.7	15	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
77	c4dniA	Alignment	not modelled	12.7	16	PDB header: protein binding, rna binding protein Chain: A: PDB Molecule: fusion protein of rna-editing complex proteins mp42 and PDBTitle: structure of editosome protein
78	c4l6wA	Alignment	not modelled	12.2	17	PDB header: ligase Chain: A: PDB Molecule: probable propionyl-coa carboxylase beta chain 6; PDBTitle: carboxyltransferase subunit (accd6) of mycobacterium tuberculosis2 acetyl-coa carboxylase
79	d1o48a	Alignment	not modelled	11.9	11	Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
80	c4fo5A	Alignment	not modelled	11.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin-like protein; PDBTitle: crystal structure of a thioredoxin-like protein (bdi_1100)

					from2 parabacteroides distasonis atcc 8503 at 2.02 a resolution
81	c3elbA_	Alignment	not modelled	11.9	16 PDB header: transferase Chain: A: PDB Molecule: ethanolamine-phosphate cytidylyltransferase; PDBTitle: human ctp: phosphoethanolamine cytidylyltransferase in complex with2 cmp
82	d1ajza_	Alignment	not modelled	11.4	24 Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
83	c3cynC_	Alignment	not modelled	11.4	9 PDB header: oxidoreductase Chain: C: PDB Molecule: probable glutathione peroxidase 8; PDBTitle: the structure of human gpx8
84	c3arct_	Alignment	not modelled	11.1	26 PDB header: electron transport, photosynthesis Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
85	c4fyuB_	Alignment	not modelled	10.7	8 PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from wuchereria bancrofti at 2.02 angstrom
86	c4d77A_	Alignment	not modelled	10.7	38 PDB header: signaling protein Chain: A: PDB Molecule: gliomedin; PDBTitle: high-resolution structure of the extracellular olfactomedin2 domain from gliomedin
87	d1xcca_	Alignment	not modelled	10.5	11 Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
88	c2p31B_	Alignment	not modelled	10.4	5 PDB header: oxidoreductase Chain: B: PDB Molecule: glutathione peroxidase 7; PDBTitle: crystal structure of human glutathione peroxidase 7
89	c1a81E_	Alignment	not modelled	10.3	15 PDB header: complex (transferase/peptide) Chain: E: PDB Molecule: syk kinase; PDBTitle: crystal structure of the tandem sh2 domain of the syk kinase bound to2 a dually tyrosine-phosphorylated itam
90	c2y5sA_	Alignment	not modelled	10.0	20 PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
91	d1jfla1	Alignment	not modelled	9.9	13 Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
92	c5epfA_	Alignment	not modelled	9.8	23 PDB header: oxidoreductase Chain: A: PDB Molecule: peroxidoxin; PDBTitle: crystal structure of peroxidoxin bcpb from mycobacterium tuberculosis
93	c2f9iD_	Alignment	not modelled	9.7	20 PDB header: transferase Chain: D: PDB Molecule: acetyl-coenzyme a carboxylase carboxyl transferase subunit PDBTitle: crystal structure of the carboxyltransferase subunit of acc from2 staphylococcus aureus
94	d2gx8a1	Alignment	not modelled	9.5	13 Fold: NIF3 (NGG1p interacting factor 3)-like Superfamily: NIF3 (NGG1p interacting factor 3)-like Family: NIF3 (NGG1p interacting factor 3)-like
95	c6gk9C_	Alignment	not modelled	9.4	21 PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inhibited structure of impdh from pseudomonas aeruginosa
96	d1luia_	Alignment	not modelled	9.3	9 Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
97	c3tr9A_	Alignment	not modelled	9.3	26 PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: structure of a dihydropteroate synthase (folp) in complex with pteroiC2 acid from coxiella burnetii
98	d1blja_	Alignment	not modelled	9.1	18 Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
99	c4jr8A_	Alignment	not modelled	9.1	19 PDB header: proton transport Chain: A: PDB Molecule: cruxrhodopsin-3; PDBTitle: crystal structure of cruxrhodopsin-3 from haloarcula vallismortis at2 2.3 angstrom resolution