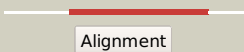

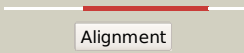

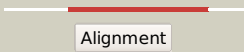

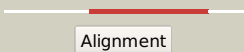

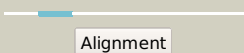

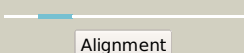



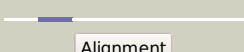

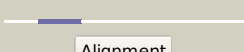

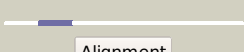

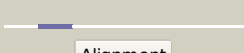



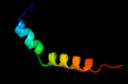



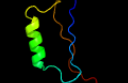

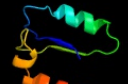


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0502 (-)_592794_593870
Date	Fri Jul 26 01:50:05 BST 2019
Unique Job ID	958b36ca72f9f435

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5kymA_	 Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: 1-acyl-sn-glycerol-3-phosphate acyltransferase; PDBTitle: crystal structure of the 1-acyl-sn-glycerophosphate (lpa)2 acyltransferase, plsc, from thermotoga maritima
2	c5f34A_	 Alignment		99.5	15	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol mannoside acyltransferase; PDBTitle: crystal structure of membrane associated pata from mycobacterium2 smegmatis in complex with s-hexadecyl coenzyme a - p21 space group
3	c5knkB_	 Alignment		99.3	15	PDB header: transferase Chain: B: PDB Molecule: lipid a biosynthesis lauroyl acyltransferase; PDBTitle: lipid a secondary acyltransferase lpxm from acinetobacter baumannii2 with catalytic residue substitution (e127a)
4	d1iuga_	 Alignment		98.5	16	Fold: Glycerol-3-phosphate (1)-acyltransferase Superfamily: Glycerol-3-phosphate (1)-acyltransferase Family: Glycerol-3-phosphate (1)-acyltransferase
5	c1jliA_	 Alignment		34.4	14	PDB header: hydrolase Chain: A: PDB Molecule: meta cleavage compound hydrolase; PDBTitle: crystal structure of a his-tagged serine hydrolase involved2 in the carbazole degradation (carc enzyme)
6	d1jlia_	 Alignment		34.4	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
7	c1emsB_	 Alignment		21.8	7	PDB header: antitumor protein Chain: B: PDB Molecule: nit-fragile histidine triad fusion protein; PDBTitle: crystal structure of the c. elegans nitfhit protein
8	c3bdiA_	 Alignment		17.6	16	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ta0194; PDBTitle: crystal structure of predicted cib-like hydrolase (np_393672.1) from2 thermoplasma acidophilum at 1.45 a resolution
9	d1q0ra_	 Alignment		17.1	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: AcIacinomycin methylesterase RdmC
10	c1wprA_	 Alignment		17.0	5	PDB header: signaling protein Chain: A: PDB Molecule: sigma factor sigb regulation protein rsbq; PDBTitle: crystal structure of rsbq inhibited by pmsf
11	c5d6oB_	 Alignment		15.9	7	PDB header: transferase Chain: B: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: orthorhombic crystal structure of an acetylester hydrolase from2 corynebacterium glutamicum

12	c4uhhA	Alignment		14.9	10	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural studies of a thermophilic esterase from2 thermogutta terrifontis (cacodylate complex)
13	c1u2eA	Alignment		14.9	13	PDB header: hydrolase Chain: A: PDB Molecule: 2-hydroxy-6-ketonona-2,4-dienedioic acid PDBTitle: crystal structure of the c-c bond hydrolase mhpc
14	c4wvrE	Alignment		14.6	29	PDB header: transport protein Chain: E: PDB Molecule: large proline-rich protein bag6; PDBTitle: crystal structure of bag6-ubl4a dimerization domain
15	c4psuA	Alignment		13.3	21	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase; PDBTitle: crystal structure of alpha/beta hydrolase from rhodopseudomonas2 palustris cga009
16	c2ockA	Alignment		13.1	9	PDB header: hydrolase Chain: A: PDB Molecule: valacyclovir hydrolase; PDBTitle: crystal structure of valacyclovir hydrolase d123n mutant
17	c4q3lC	Alignment		12.0	14	PDB header: hydrolase Chain: C: PDB Molecule: mgs-m2; PDBTitle: crystal structure of mgs-m2, an alpha/beta hydrolase enzyme from a2 medee basin deep-sea metagenome library
18	c3wrbB	Alignment		11.8	16	PDB header: oxidoreductase Chain: B: PDB Molecule: gallate dioxygenase; PDBTitle: crystal structure of the anaerobic h124f desb-gallate complex
19	c5nfgA	Alignment		11.8	16	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase belonging to alpha/beta hydrolase PDBTitle: novel epoxide hydrolases belonging to the alpha/beta hydrolases2 superfamily in metagenomes from hot environments
20	d1c4xa	Alignment		11.6	9	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
21	d2rhwa1	Alignment	not modelled	11.4	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
22	c5ltiA	Alignment	not modelled	11.2	30	PDB header: oxidoreductase Chain: A: PDB Molecule: heme dependent oxidative n-demethylase; PDBTitle: crystal structure of the alpha subunit of heme dependent oxidative n-2 demethylase (hodm) in complex with the dimethylamine substrate
23	c4imyl	Alignment	not modelled	10.9	36	PDB header: transferase Chain: I: PDB Molecule: af4/fmr2 family member 4; PDBTitle: the aff4 scaffold binds human p-tefb adjacent to hiv tat
24	c4imyG	Alignment	not modelled	10.9	36	PDB header: transferase Chain: G: PDB Molecule: af4/fmr2 family member 4; PDBTitle: the aff4 scaffold binds human p-tefb adjacent to hiv tat
25	c4lxgA	Alignment	not modelled	10.5	7	PDB header: hydrolase Chain: A: PDB Molecule: mcp hydrolase; PDBTitle: crystal structure of dxnb2, a carbon - carbon bond hydrolase from2 sphingomonas wittichii rw1
26	c4inzB	Alignment	not modelled	10.4	9	PDB header: hydrolase Chain: B: PDB Molecule: soluble epoxide hydrolase; PDBTitle: the crystal structure of m145a mutant of an epoxide hydrolase from2 bacillus megaterium
27	c4imyH	Alignment	not modelled	9.8	36	PDB header: transferase Chain: H: PDB Molecule: af4/fmr2 family member 4; PDBTitle: the aff4 scaffold binds human p-tefb adjacent to hiv tat
28	d1np7a2	Alignment	not modelled	9.7	22	Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain

29	d1m33a_	Alignment	not modelled	9.6	7	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Biotin biosynthesis protein BioH
30	c3kdaB_	Alignment	not modelled	9.4	10	PDB header: hydrolase Chain: B: PDB Molecule: cftr inhibitory factor (cif); PDBTitle: crystal structure of the cftr inhibitory factor cif with the h269a2 mutation
31	c3wibB_	Alignment	not modelled	9.4	9	PDB header: hydrolase Chain: B: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of y109w mutant haloalkane dehalogenase data from2 agrobacterium tumefaciens c58
32	c2zo7A_	Alignment	not modelled	8.9	13	PDB header: luminescent protein Chain: A: PDB Molecule: cyan/green-emitting gfp-like protein, kusabira-cyan mutant PDBTitle: crystal structure of a kusabira-cyan mutant (kcy-r1), a cyan/green-2 emitting gfp-like protein
33	c3dqzB_	Alignment	not modelled	8.6	5	PDB header: lyase Chain: B: PDB Molecule: alpha-hydroxynitrile lyase-like protein; PDBTitle: structure of the hydroxynitrile lyase from arabidopsis thaliana
34	d1b4ub_	Alignment	not modelled	8.6	9	Fold: Phosphorylase/hydrolase-like Superfamily: LigB-like Family: LigB-like
35	c4rncB_	Alignment	not modelled	8.4	14	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of an esterase rhest1 from rhodococcus sp. ecu1013
36	d2vata1	Alignment	not modelled	8.4	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
37	c5jd6A_	Alignment	not modelled	8.2	10	PDB header: hydrolase Chain: A: PDB Molecule: mgs-mche2; PDBTitle: crystal structure of mgs-mche2, an alpha/beta hydrolase enzyme from2 the metagenome of sediments from the lagoon of mar chica, morocco
38	d1va4a_	Alignment	not modelled	8.1	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
39	c5h3hB_	Alignment	not modelled	8.0	12	PDB header: hydrolase Chain: B: PDB Molecule: abhydrolase domain-containing protein; PDBTitle: esterase (eaest) from exiguobacterium antarcticum
40	d1bn7a_	Alignment	not modelled	7.9	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
41	c5z89A_	Alignment	not modelled	7.8	15	PDB header: hydrolase Chain: A: PDB Molecule: hyposensitive to light 7; PDBTitle: structural basis for specific inhibition of highly sensitive shhtl72 receptor
42	d1brta_	Alignment	not modelled	7.5	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
43	c3u1tA_	Alignment	not modelled	7.5	9	PDB header: hydrolase Chain: A: PDB Molecule: dmma haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase, dmma, of marine microbial origin
44	c3v3kB_	Alignment	not modelled	7.5	14	PDB header: hydrolase Chain: B: PDB Molecule: putative uncharacterized protein ecs1815; PDBTitle: human caspase 9 in complex with bacterial effector protein
45	c5egnB_	Alignment	not modelled	7.4	5	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: est816 as an n-acyl homoserine lactone degrading enzyme
46	c3i1iA_	Alignment	not modelled	7.2	12	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
47	c2vf2A_	Alignment	not modelled	7.2	13	PDB header: hydrolase Chain: A: PDB Molecule: 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate PDBTitle: x-ray crystal structure of hsd from mycobacterium2 tuberculosis
48	c3qvmA_	Alignment	not modelled	7.1	7	PDB header: hydrolase Chain: A: PDB Molecule: olei00960; PDBTitle: the structure of olei00960, a hydrolase from oleispira antarctica
49	c5frdA_	Alignment	not modelled	7.1	8	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase (est-2); PDBTitle: structure of a thermophilic esterase
50	d1weha_	Alignment	not modelled	7.0	16	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like
51	c5mxbB_	Alignment	not modelled	6.9	9	PDB header: hydrolase Chain: B: PDB Molecule: alpha/beta hydrolase; PDBTitle: haloalkane dehalogenase dmxa from marinobacter sp. elb17 possessing a2 unique catalytic residue
52	c3fsgC_	Alignment	not modelled	6.8	11	PDB header: hydrolase Chain: C: PDB Molecule: alpha/beta superfamily hydrolase; PDBTitle: crystal structure of alpha/beta superfamily hydrolase from oenococcus2 oeni psu-1
53	d1zd3a2	Alignment	not modelled	6.5	7	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
54	d1o8bb1	Alignment	not modelled	6.4	11	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain

55	c6ehrD_	Alignment	not modelled	6.4	35	PDB header: signaling protein Chain: D: PDB Molecule: ragulator complex protein lamtor4; PDBTitle: the crystal structure of the human lamtor-raga ctd-ragc ctd complex
56	c2xc8B_	Alignment	not modelled	6.4	36	PDB header: viral protein Chain: B: PDB Molecule: gene 22 product; PDBTitle: crystal structure of the gene 22 product of the bacillus subtilis spp12 phage
57	c3c0fB_	Alignment	not modelled	6.3	55	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein af_1514; PDBTitle: crystal structure of a novel non-pfam protein af1514 from archeoglobus2 fulgidus dsm 4304 solved by s-sad using a cr x-ray source
58	c3imkA_	Alignment	not modelled	6.2	22	PDB header: metal binding protein Chain: A: PDB Molecule: putative molybdenum carrier protein; PDBTitle: crystal structure of putative molybdenum carrier protein (yp_461806.1)2 from syntrophus aciditrophicus sb at 1.45 a resolution
59	c2zo6A_	Alignment	not modelled	6.2	13	PDB header: luminescent protein Chain: A: PDB Molecule: cyan-emitting gfp-like protein, kusabira-cyan (kcy); PDBTitle: crystal structure of kusabira-cyan (kcy), a cyan-emitting gfp-like2 protein
60	c1yzxB_	Alignment	not modelled	5.9	29	PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase kappa 1; PDBTitle: crystal structure of human kappa class glutathione transferase
61	c2j4dA_	Alignment	not modelled	5.8	16	PDB header: dna binding protein Chain: A: PDB Molecule: cryptochrome dash; PDBTitle: cryptochrome 3 from arabidopsis thaliana
62	d1vj0a1	Alignment	not modelled	5.8	17	Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain
63	c2kogA_	Alignment	not modelled	5.8	15	PDB header: membrane protein Chain: A: PDB Molecule: vesicle-associated membrane protein 2; PDBTitle: lipid-bound synaptobrevin solution nmr structure
64	d1azwa_	Alignment	not modelled	5.7	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
65	d1uk8a_	Alignment	not modelled	5.7	9	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
66	c1xtzA_	Alignment	not modelled	5.6	23	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase; PDBTitle: crystal structure of the s. cerevisiae d-ribose-5-phosphate isomerase:2 comparison with the archeal and bacterial enzymes
67	d1cr6a2	Alignment	not modelled	5.6	4	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
68	c4btgB_	Alignment	not modelled	5.6	13	PDB header: virus Chain: B: PDB Molecule: major inner protein p1; PDBTitle: coordinates of the bacteriophage phi6 capsid subunits (p1a and p1b)2 fitted into the cryoem reconstruction of the procapsid at 4.4 a3 resolution
69	c3a2nF_	Alignment	not modelled	5.5	9	PDB header: hydrolase Chain: F: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of dbja (wild type type ii p21)
70	c4x84C_	Alignment	not modelled	5.4	15	PDB header: isomerase Chain: C: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from pseudomonas2 aeruginosa
71	c2x49A_	Alignment	not modelled	5.4	24	PDB header: protein transport Chain: A: PDB Molecule: invasion protein inva; PDBTitle: crystal structure of the c-terminal domain of inva
72	c4cyjF_	Alignment	not modelled	5.4	11	PDB header: transferase Chain: F: PDB Molecule: pan2; PDBTitle: chaetomium thermophilum pan2:pan3 complex
73	c2vavL_	Alignment	not modelled	5.3	16	PDB header: transferase Chain: L: PDB Molecule: acetyl-coa--deacetylcephalosporin c acetyltransferase; PDBTitle: crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak)
74	d1hkha_	Alignment	not modelled	5.3	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
75	c6orbA_	Alignment	not modelled	5.3	13	PDB header: motor protein Chain: A: PDB Molecule: midasin; PDBTitle: full-length s. pombe mdn1 in the presence of atp and rbin-1