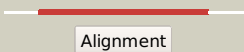

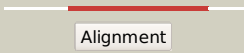



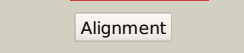



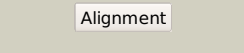

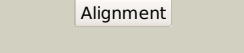



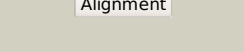
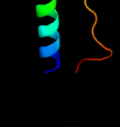
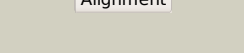

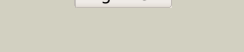
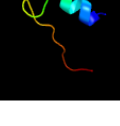


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3026c_(-)_3385174_3386088
Date	Thu Aug 8 16:20:19 BST 2019
Unique Job ID	fc941ea7ab800e01

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5kymA_</a>	 Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 1-acyl-sn-glycerol-3-phosphate acyltransferase; <b>PDBTitle:</b> crystal structure of the 1-acyl-sn-glycerophosphate (lpa)2 acyltransferase, plsc, from thermotoga maritima
2	<a href="#">c5f34A_</a>	 Alignment		99.3	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol mannoside acyltransferase; <b>PDBTitle:</b> crystal structure of membrane associated pata from mycobacterium2 smegmatis in complex with s-hexadecyl coenzyme a - p21 space group
3	<a href="#">c5knkB_</a>	 Alignment		99.0	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> lipid a biosynthesis lauroyl acyltransferase; <b>PDBTitle:</b> lipid a secondary acyltransferase lpxm from acinetobacter baumannii2 with catalytic residue substitution (e127a)
4	<a href="#">d1iuga_</a>	 Alignment		97.9	21	<b>Fold:</b> Glycerol-3-phosphate (1)-acyltransferase <b>Superfamily:</b> Glycerol-3-phosphate (1)-acyltransferase <b>Family:</b> Glycerol-3-phosphate (1)-acyltransferase
5	<a href="#">c5vrhA_</a>	 Alignment		78.5	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> apolipoprotein n-acyltransferase; <b>PDBTitle:</b> apolipoprotein n-acyltransferase c387s active site mutant
6	<a href="#">c4hg3C_</a>	 Alignment		49.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> probable hydrolase nit2; <b>PDBTitle:</b> structural insights into yeast nit2: wild-type yeast nit2 in complex2 with alpha-ketoglutarate
7	<a href="#">c4cyyA_</a>	 Alignment		43.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pantetheinase; <b>PDBTitle:</b> the structure of vanin-1: defining the link between metabolic disease,2 oxidative stress and inflammation
8	<a href="#">c2e11B_</a>	 Alignment		38.5	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hydrolase; <b>PDBTitle:</b> the crystal structure of xc1258 from xanthomonas campestris: a cn-2 hydrolase superfamily protein with an arsenic adduct in the active3 site
9	<a href="#">c3wuyA_</a>	 Alignment		36.3	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nitrilase; <b>PDBTitle:</b> crystal structure of nit6803
10	<a href="#">c3hkxA_</a>	 Alignment		33.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amidase; <b>PDBTitle:</b> crystal structure analysis of an amidase from nesterenkonia sp.
11	<a href="#">c4mxnB_</a>	 Alignment		30.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative glycosyl hydrolase (parmer_00599) from2 parabacteroides merdae atcc 43184 at 1.95 a resolution

12	<a href="#">c1emsB_</a>	Alignment		28.4	11	<b>PDB header:</b> antitumor protein <b>Chain:</b> B: <b>PDB Molecule:</b> nit-fragile histidine triad fusion protein; <b>PDBTitle:</b> crystal structure of the c. elegans nitfhit protein
13	<a href="#">c2vhhA_</a>	Alignment		27.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cg3027-pa; <b>PDBTitle:</b> crystal structure of a pyrimidine degrading enzyme from2 drosophila melanogaster
14	<a href="#">c1vj5B_</a>	Alignment		26.9	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 5' polynucleotide kinase-3' phosphatase catalytic domain; <b>PDBTitle:</b> molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
15	<a href="#">c6i00C_</a>	Alignment		26.3	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> bifunctional nitrilase/nitrile hydratase nit4; <b>PDBTitle:</b> cryo-em informed directed evolution of nitrilase 4 leads to a change2 in quaternary structure.
16	<a href="#">d1k7ja_</a>	Alignment		23.4	16	<b>Fold:</b> YrdC/RibB <b>Superfamily:</b> YrdC/RibB <b>Family:</b> YrdC-like
17	<a href="#">c3zvmA_</a>	Alignment		22.1	23	<b>PDB header:</b> hydrolase/transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional polynucleotide phosphatase/kinase; <b>PDBTitle:</b> the structural basis for substrate recognition by mammalian2 polynucleotide kinase 3' phosphatase
18	<a href="#">c6mg6D_</a>	Alignment		21.8	9	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> carbon-nitrogen hydrolase; <b>PDBTitle:</b> crystal structure of carbon-nitrogen hydrolase from helicobacter2 pylori g27
19	<a href="#">c6ftqA_</a>	Alignment		21.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-ureidopropionase; <b>PDBTitle:</b> crystal structure of human beta-ureidopropionase (beta-alanine2 synthase) - mutant t299c
20	<a href="#">d1uf5a_</a>	Alignment		20.8	14	<b>Fold:</b> Carbon-nitrogen hydrolase <b>Superfamily:</b> Carbon-nitrogen hydrolase <b>Family:</b> Carbamilase
21	<a href="#">d1emsa2</a>	Alignment	not modelled	19.1	14	<b>Fold:</b> Carbon-nitrogen hydrolase <b>Superfamily:</b> Carbon-nitrogen hydrolase <b>Family:</b> Nitrilase
22	<a href="#">c5uyvA_</a>	Alignment	not modelled	18.6	19	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic chelated iron-binding protein yfea; <b>PDBTitle:</b> yfea ancillary sites that do not co-load with site 2
23	<a href="#">c2vhiG_</a>	Alignment	not modelled	18.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> cg3027-pa; <b>PDBTitle:</b> crystal structure of a pyrimidine degrading enzyme from2 drosophila melanogaster
24	<a href="#">d1hrua_</a>	Alignment	not modelled	17.7	17	<b>Fold:</b> YrdC/RibB <b>Superfamily:</b> YrdC/RibB <b>Family:</b> YrdC-like
25	<a href="#">c2o1eB_</a>	Alignment	not modelled	17.6	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ycdh; <b>PDBTitle:</b> crystal structure of the metal-dependent lipoprotein ycdh2 from bacillus subtilis, northeast structural genomics3 target sr583
26	<a href="#">d1vj0a1</a>	Alignment	not modelled	16.7	27	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain
27	<a href="#">c3ilvA_</a>	Alignment	not modelled	16.3	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine-dependent nad(+) synthetase; <b>PDBTitle:</b> crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
28	<a href="#">c5khaA_</a>	Alignment	not modelled	15.3	8	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine-dependent nad+ synthetase; <b>PDBTitle:</b> structure of glutamine-dependent nad+ synthetase from acinetobacter2 baumannii in complex with adenosine diphosphate

						(adp)
29	<a href="#">c2w1vA_</a>	Alignment	not modelled	15.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nitrilase homolog 2; <b>PDBTitle:</b> crystal structure of mouse nitrilase-2 at 1.4a resolution
30	<a href="#">d1j31a_</a>	Alignment	not modelled	14.9	20	<b>Fold:</b> Carbon-nitrogen hydrolase <b>Superfamily:</b> Carbon-nitrogen hydrolase <b>Family:</b> Carbamilase
31	<a href="#">d1jcua_</a>	Alignment	not modelled	14.6	26	<b>Fold:</b> YrdC/RibB <b>Superfamily:</b> YrdC/RibB <b>Family:</b> YrdC-like
32	<a href="#">c5ixdB_</a>	Alignment	not modelled	14.1	19	<b>PDB header:</b> cytokine <b>Chain:</b> B: <b>PDB Molecule:</b> interferon lambda receptor 1; <b>PDBTitle:</b> structure of human jak1 ferm/sh2 in complex with ifn lambda receptor
33	<a href="#">c4makA_</a>	Alignment	not modelled	13.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> crispr-associated endoribonuclease cas2; <b>PDBTitle:</b> crystal structure of a putative ssrna endonuclease cas2, crispr2 adaptation protein from e.coli
34	<a href="#">c3hjtB_</a>	Alignment	not modelled	12.0	16	<b>PDB header:</b> cell adhesion, transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> lmb; <b>PDBTitle:</b> structure of laminin binding protein (lmb) of streptococcus agalactiae2 a bifunctional protein with adhesin and metal transporting activity
35	<a href="#">d1bg5a1</a>	Alignment	not modelled	12.0	11	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
36	<a href="#">c2ov3A_</a>	Alignment	not modelled	11.5	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic binding protein component of an abc type zinc <b>PDBTitle:</b> crystal structure of 138-173 znua deletion mutant plus zinc bound
37	<a href="#">d1f89a_</a>	Alignment	not modelled	11.4	14	<b>Fold:</b> Carbon-nitrogen hydrolase <b>Superfamily:</b> Carbon-nitrogen hydrolase <b>Family:</b> Nitrilase
38	<a href="#">d1pq4a_</a>	Alignment	not modelled	11.1	13	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> TroA-like
39	<a href="#">d1bhea_</a>	Alignment	not modelled	10.9	14	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> Pectin lyase-like <b>Family:</b> Galacturonase
40	<a href="#">c3zppA_</a>	Alignment	not modelled	10.4	30	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> cell wall surface anchor family protein; <b>PDBTitle:</b> structure of the streptococcus pneumoniae surface protein2 and adhesin pfba
41	<a href="#">c5h8IM_</a>	Alignment	not modelled	10.2	6	<b>PDB header:</b> hydrolase <b>Chain:</b> M: <b>PDB Molecule:</b> n-carbamoylputrescine amidohydrolase; <b>PDBTitle:</b> crystal structure of medicago truncatula n-carbamoylputrescine2 amidohydrolase (mtcpa) c158s mutant in complex with putrescine
42	<a href="#">c4cl2A_</a>	Alignment	not modelled	10.1	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic solute binding protein; <b>PDBTitle:</b> structure of periplasmic metal binding protein from candidatus2 liberibacter asiaticus
43	<a href="#">c4f4hA_</a>	Alignment	not modelled	9.9	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine dependent nad+ synthetase; <b>PDBTitle:</b> crystal structure of a glutamine dependent nad+ synthetase from2 burkholderia thailandensis
44	<a href="#">c3n05B_</a>	Alignment	not modelled	9.7	21	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> nh(3)-dependent nad(+) synthetase; <b>PDBTitle:</b> crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis
45	<a href="#">c2ogwB_</a>	Alignment	not modelled	9.3	16	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> high-affinity zinc uptake system protein znua <b>PDBTitle:</b> structure of abc type zinc transporter from e. coli
46	<a href="#">c3dlaD_</a>	Alignment	not modelled	8.9	24	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> glutamine-dependent nad(+) synthetase; <b>PDBTitle:</b> x-ray crystal structure of glutamine-dependent nad+ synthetase from2 mycobacterium tuberculosis bound to naad+ and don
47	<a href="#">c6f87C_</a>	Alignment	not modelled	8.8	35	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> threonylcarbamoyl-amp synthase; <b>PDBTitle:</b> crystal structure of p. abyssi sua5 complexed with l-threonine and ppi
48	<a href="#">c4c2IA_</a>	Alignment	not modelled	8.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-xylogalacturonan hydrolase a; <b>PDBTitle:</b> crystal structure of endo-xylogalacturonan hydrolase from aspergillus2 tubingensis
49	<a href="#">d1gnea1</a>	Alignment	not modelled	8.0	11	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
50	<a href="#">d1b8xa1</a>	Alignment	not modelled	8.0	11	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
51	<a href="#">d1y0na_</a>	Alignment	not modelled	7.8	25	<b>Fold:</b> YehU-like <b>Superfamily:</b> YehU-like <b>Family:</b> YehU-like
52	<a href="#">c2xc8B_</a>	Alignment	not modelled	7.5	50	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> gene 22 product; <b>PDBTitle:</b> crystal structure of the gene 22 product of the bacillus subtilis spp12 phage
53	<a href="#">c4as2D_</a>	Alignment	not modelled	7.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphorylcholine phosphatase; <b>PDBTitle:</b> pseudomonas aeruginosa phosphorylcholine phosphatase. monoclinic form <b>PDB header:</b> hydrolase

54	<a href="#">c3jurA_</a>	Alignment	not modelled	7.3	22	<b>Chain:</b> A: <b>PDB Molecule:</b> exo-poly-alpha-d-galacturonosidase; <b>PDBTitle:</b> the crystal structure of a hyperthermoactive exopolygalacturonase from <i>Thermotoga maritima</i>
55	<a href="#">c3eqnB_</a>	Alignment	not modelled	7.1	55	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glucan 1,3-beta-glucosidase; <b>PDBTitle:</b> crystal structure of beta-1,3-glucanase from <i>Phanerochaete2 chrysosporium (lam55a)</i>
56	<a href="#">c2eqaA_</a>	Alignment	not modelled	7.0	35	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein st1526; <b>PDBTitle:</b> crystal structure of the hypothetical sua5 protein from <i>Sulfolobus tokodaii</i>
57	<a href="#">d1g26a_</a>	Alignment	not modelled	7.0	50	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Granulin repeat <b>Family:</b> Granulin repeat
58	<a href="#">c4z42A_</a>	Alignment	not modelled	6.6	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> urease subunit gamma; <b>PDBTitle:</b> crystal structure of urease from <i>Yersinia enterocolitica</i>
59	<a href="#">d1k3ya1</a>	Alignment	not modelled	6.5	8	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
60	<a href="#">d1m5ha2</a>	Alignment	not modelled	6.5	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Formylmethanofuran:tetrahydromethanopterin formyltransferase <b>Family:</b> Formylmethanofuran:tetrahydromethanopterin formyltransferase
61	<a href="#">c5n6mA_</a>	Alignment	not modelled	6.0	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> apolipoprotein n-acyltransferase; <b>PDBTitle:</b> structure of the membrane integral lipoprotein n-acyltransferase Int2 from <i>P. aeruginosa</i>
62	<a href="#">c2ps3A_</a>	Alignment	not modelled	5.9	16	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> high-affinity zinc uptake system protein znua; <b>PDBTitle:</b> structure and metal binding properties of znua, a periplasmic zinc2 transporter from <i>Escherichia coli</i>
63	<a href="#">c4chmB_</a>	Alignment	not modelled	5.8	32	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> imc sub-compartment protein isp1; <b>PDBTitle:</b> structure of inner membrane complex (imc) sub-compartment protein 12 (isp1) from <i>Toxoplasma gondii</i>
64	<a href="#">d1rmga_</a>	Alignment	not modelled	5.7	14	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> Pectin lyase-like <b>Family:</b> Galacturonase
65	<a href="#">c2plqA_</a>	Alignment	not modelled	5.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aliphatic amidase; <b>PDBTitle:</b> crystal structure of the amidase from <i>Geobacillus pallidus</i> rapc8
66	<a href="#">c4furD_</a>	Alignment	not modelled	5.2	28	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> urease subunit gamma 2; <b>PDBTitle:</b> crystal structure of urease subunit gamma 2 from <i>Brucella melitensis2</i> biovar abortus 2308
67	<a href="#">d1u1ia1</a>	Alignment	not modelled	5.2	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain