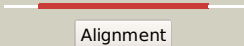

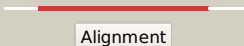

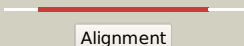







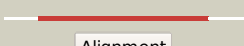











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2363_(amiA2)_2644330_2645784
Date	Mon Aug 5 13:25:51 BST 2019
Unique Job ID	9ca3113a720b1134

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6diiH_	 Alignment		100.0	29	PDB header: hydrolase Chain: H: PDB Molecule: fatty acid amide hydrolase; PDBTitle: structure of arabidopsis fatty acid amide hydrolase in complex with2 methyl linolenyl fluorophosphonate
2	d2f2aa1	 Alignment		100.0	28	Fold: Amidase signature (AS) enzymes Superfamily: Amidase signature (AS) enzymes Family: Amidase signature (AS) enzymes
3	c4wj3A_	 Alignment		100.0	36	PDB header: ligase/rna Chain: A: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit a; PDBTitle: crystal structure of the asparagine transamidosome from pseudomonas2 aeruginosa
4	c4gysA_	 Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: allophanate hydrolase; PDBTitle: granulibacter bethesdensis allophanate hydrolase co-crystallized with2 malonate
5	c4cp8C_	 Alignment		100.0	29	PDB header: hydrolase Chain: C: PDB Molecule: allophanate hydrolase; PDBTitle: structure of the amidase domain of allophanate hydrolase2 from pseudomonas sp strain adp
6	c3a2qA_	 Alignment		100.0	31	PDB header: hydrolase Chain: A: PDB Molecule: 6-aminohexanoate-cyclic-dimer hydrolase; PDBTitle: structure of 6-aminohexanoate cyclic dimer hydrolase complexed with2 substrate
7	c3h0rP_	 Alignment		100.0	30	PDB header: ligase Chain: P: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit a; PDBTitle: structure of trna-dependent amidotransferase gatcab from2 aquifex aeolicus
8	c3kfuE_	 Alignment		100.0	30	PDB header: ligase/rna Chain: E: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit a; PDBTitle: crystal structure of the transamidosome
9	d1m22a_	 Alignment		100.0	29	Fold: Amidase signature (AS) enzymes Superfamily: Amidase signature (AS) enzymes Family: Amidase signature (AS) enzymes
10	c5h6sB_	 Alignment		100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: amidase; PDBTitle: crystal structure of hydrazidase s179a mutant complexed with a2 substrate
11	c6c6gA_	 Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: biuret hydrolase; PDBTitle: an unexpected vestigial protein complex reveals the evolutionary2 origins of an s-triazine catabolic enzyme. inhibitor bound complex.

12	c2dc0A_	Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: probable amidase; PDBTitle: crystal structure of amidase
13	c5h6tB_	Alignment		100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: amidase; PDBTitle: crystal structure of hydrazidase from microbacterium sp. strain hm58-2
14	c4vj6A_	Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: aryl acylamidase; PDBTitle: the crystal structure of a bacterial aryl acylamidase belonging to the2 amidase signature (as) enzymes family
15	d1mt5a_	Alignment		100.0	27	Fold: Amidase signature (AS) enzymes Superfamily: Amidase signature (AS) enzymes Family: Amidase signature (AS) enzymes
16	c2vyaB_	Alignment		100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: fatty-acid amide hydrolase 1; PDBTitle: crystal structure of fatty acid amide hydrolase conjugated2 with the drug-like inhibitor pf-750
17	d2gi3a1	Alignment		100.0	28	Fold: Amidase signature (AS) enzymes Superfamily: Amidase signature (AS) enzymes Family: Amidase signature (AS) enzymes
18	c4issA_	Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: allophanate hydrolase; PDBTitle: semet-substituted kluyveromyces lactis allophanate hydrolase
19	c5i8iD_	Alignment		100.0	25	PDB header: hydrolase Chain: D: PDB Molecule: urea amidolyase; PDBTitle: crystal structure of the k. lactis urea amidolyase
20	c3a1iA_	Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: amidase; PDBTitle: crystal structure of rhodococcus sp. n-771 amidase complexed2 with benzamide
21	d1locka_	Alignment	not modelled	100.0	28	Fold: Amidase signature (AS) enzymes Superfamily: Amidase signature (AS) enzymes Family: Amidase signature (AS) enzymes
22	c5ewqC_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: C: PDB Molecule: amidase; PDBTitle: the crystal structure of an amidase family protein from bacillus2 anthracis str. ames
23	c4n0hA_	Alignment	not modelled	100.0	23	PDB header: ligase Chain: A: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit a, PDBTitle: crystal structure of s. cerevisiae mitochondrial gatfab
24	c5y6iB_	Alignment	not modelled	54.0	20	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator kdgr; PDBTitle: crystal structure of pseudomonas aeruginosa hmgr
25	d1h1js_	Alignment	not modelled	53.8	18	Fold: LEM/SAP HeH motif Superfamily: SAP domain Family: SAP domain
26	c5tjA_	Alignment	not modelled	44.2	23	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, iclr family; PDBTitle: crystal structure of iclr transcriptional regulator from2 alicyclobacillus acidocaldarius
27	c4m1eC_	Alignment	not modelled	43.8	28	PDB header: transferase Chain: C: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of purine nucleoside phosphorylase i from2 planctomyces limnophilus dsm 3776, nysgrc target 029364.
28	c2kvuA_	Alignment	not modelled	43.6	9	PDB header: transcription regulator Chain: A: PDB Molecule: mkI/myocardin-like protein 1; PDBTitle: solution nmr structure of sap domain of mkI/myocardin-like2 protein 1 from h.sapiens, northeast structural genomics3 consortium target target hr4547e

29	d1k75a_	Alignment	not modelled	42.6	16	Fold: ALDH-like Superfamily: ALDH-like Family: L-histidinol dehydrogenase HisD
30	c4lnaA_	Alignment	not modelled	38.0	25	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of purine nucleoside phosphorylase i from spirosoa2 linguale dsm 74, nysgrc target 029362
31	c3r4kD_	Alignment	not modelled	35.0	20	PDB header: dna binding protein Chain: D: PDB Molecule: transcriptional regulator, iclr family; PDBTitle: crystal structure of a putative iclr transcriptional regulator2 (tm1040_3717) from silicibacter sp. tm1040 at 2.46 a resolution
32	c4nsnC_	Alignment	not modelled	32.8	13	PDB header: transferase Chain: C: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of purine nucleoside phosphorylase from2 porphyromonas gingivalis atcc 33277, nysgrc target 030972,3 orthorhombic symmetry
33	d2o9aa1	Alignment	not modelled	32.0	22	Fold: Profilin-like Superfamily: GAF domain-like Family: IcLR ligand-binding domain-like
34	c4I5cE_	Alignment	not modelled	31.8	22	PDB header: transferase Chain: E: PDB Molecule: s-methyl-5'-thioadenosine phosphorylase; PDBTitle: methylthioadenosine phosphorylase from schistosoma mansoni in complex2 with adenine in space group p212121
35	c1ysqA_	Alignment	not modelled	30.3	25	PDB header: gene regulation Chain: A: PDB Molecule: hth-type transcriptional regulator yiaj; PDBTitle: the crystal structure of transcriptional regulator yaij
36	c3mq0A_	Alignment	not modelled	29.7	23	PDB header: transcription repressor Chain: A: PDB Molecule: transcriptional repressor of the blcabc operon; PDBTitle: crystal structure of agobacterium tumefaciens repressor blcr
37	c2g7uB_	Alignment	not modelled	29.4	27	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: 2.3 a structure of putative catechol degradative operon regulator from2 rhodococcus sp. rha1
38	c5xoeA_	Alignment	not modelled	28.6	14	PDB header: transferase Chain: A: PDB Molecule: atp-dependent 6-phosphofructokinase; PDBTitle: crystal structure of the apo staphylococcus aureus phosphofructokinase
39	c6an0A_	Alignment	not modelled	27.9	9	PDB header: oxidoreductase Chain: A: PDB Molecule: histidinol dehydrogenase; PDBTitle: crystal structure of histidinol dehydrogenase from elizabethkingia2 anophelis
40	c2do1A_	Alignment	not modelled	24.6	9	PDB header: gene regulation Chain: A: PDB Molecule: nuclear protein hcc-1; PDBTitle: solution structure of the sap domain of human nuclear2 protein hcc-1
41	d1zrja1	Alignment	not modelled	24.2	14	Fold: LEM/SAP HeH motif Superfamily: SAP domain Family: SAP domain
42	c1yspA_	Alignment	not modelled	24.1	41	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator kdgr; PDBTitle: crystal structure of the c-terminal domain of e. coli transcriptional2 regulator kdgr.
43	d1tf1a_	Alignment	not modelled	23.5	18	Fold: Profilin-like Superfamily: GAF domain-like Family: IcLR ligand-binding domain-like
44	c1zrjA_	Alignment	not modelled	21.9	14	PDB header: dna binding protein Chain: A: PDB Molecule: e1b-55kda-associated protein 5 isoform c; PDBTitle: solution structure of the sap domain of human e1b-55kda-2 associated protein 5 isoform c
45	d2dloa2	Alignment	not modelled	21.6	50	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
46	c4uc0A_	Alignment	not modelled	21.1	20	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of a purine nucleoside phosphorylase (psi-nysgrc-2 029736) from agrobacterium vitis
47	c2higA_	Alignment	not modelled	19.9	14	PDB header: transferase Chain: A: PDB Molecule: 6-phospho-1-fructokinase; PDBTitle: crystal structure of phosphofructokinase apoenzyme from trypanosoma2 brucei.
48	c3k2qA_	Alignment	not modelled	19.7	14	PDB header: transferase Chain: A: PDB Molecule: pyrophosphate-dependent phosphofructokinase; PDBTitle: crystal structure of pyrophosphate-dependent2 phosphofructokinase from marinobacter aquaeolei, northeast3 structural genomics consortium target mqr88
49	c2na9A_	Alignment	not modelled	18.6	13	PDB header: signaling protein Chain: A: PDB Molecule: cytokine receptor common subunit beta; PDBTitle: transmembrane structure of the p441a mutant of the cytokine receptor2 common subunit beta
50	c3p0jD_	Alignment	not modelled	18.6	17	PDB header: ligase Chain: D: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: leishmania major tyrosyl-trna synthetase in complex with tyrosinol,2 triclinic crystal form 1
51	c2na8A_	Alignment	not modelled	18.1	13	PDB header: membrane protein Chain: A: PDB Molecule: cytokine receptor common subunit beta; PDBTitle: transmembrane structure of the cytokine receptor common subunit beta
52	c3ilvA_	Alignment	not modelled	18.0	17	PDB header: ligase Chain: A: PDB Molecule: glutamine-dependent nad(+) synthetase; PDBTitle: crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
53	c4g07A_	Alignment	not modelled	17.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: histidinol dehydrogenase; PDBTitle: the crystal structure of the c366s mutant of hdh from brucella suis

54	c4g4sP_	Alignment	not modelled	17.7	20	PDB header: hydrolase/chaperone Chain: P: PDB Molecule: proteasome assembly chaperone 2; PDBTitle: structure of proteasome-pba1-pba2 complex
55	d4pfka_	Alignment	not modelled	14.9	16	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
56	d2do1a1	Alignment	not modelled	14.7	9	Fold: LEM/SAP HeH motif Superfamily: SAP domain Family: SAP domain
57	c3izbF_	Alignment	not modelled	13.9	22	PDB header: ribosome Chain: F: PDB Molecule: 40s ribosomal protein rps5 (s7p); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
58	c4gicB_	Alignment	not modelled	13.8	13	PDB header: oxidoreductase Chain: B: PDB Molecule: histidinol dehydrogenase; PDBTitle: crystal structure of a putative histidinol dehydrogenase (target psi-2 014034) from methylococcus capsulatus
59	c2ia2D_	Alignment	not modelled	13.2	20	PDB header: transcription Chain: D: PDB Molecule: putative transcriptional regulator; PDBTitle: the crystal structure of a putative transcriptional regulator rha061952 from rhodococcus sp. rha1
60	c5ifkC_	Alignment	not modelled	12.9	28	PDB header: transferase Chain: C: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: purine nucleoside phosphorylase
61	c1zxA_	Alignment	not modelled	12.8	15	PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase; PDBTitle: the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
62	c1mkmA_	Alignment	not modelled	12.3	34	PDB header: transcription Chain: A: PDB Molecule: iclr transcriptional regulator; PDBTitle: crystal structure of the thermotoga maritima iclr
63	c1x4pA_	Alignment	not modelled	12.0	15	PDB header: rna binding protein Chain: A: PDB Molecule: putative splicing factor, arginine/serine-rich PDBTitle: solution structure of surp domain in sfrs14 protei
64	c5ikjB_	Alignment	not modelled	11.1	15	PDB header: transcription Chain: B: PDB Molecule: cryptic loci regulator protein 1; PDBTitle: structure of clr2 bound to the clr1 c-terminus
65	c2o0yB_	Alignment	not modelled	10.9	23	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator rha1_ro069532 (iclr-family) from rhodococcus sp.
66	c6g69N_	Alignment	not modelled	10.9	18	PDB header: de novo protein Chain: N: PDB Molecule: cc-type2-il-sg-l17e; PDBTitle: crystal structure of a parallel seven-helix coiled coil cc-type2-il-2 sg-l17e
67	c3d3oA_	Alignment	not modelled	10.5	21	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcriptional regulator, iclr family; PDBTitle: crystal structure of the effector domain of the putative2 transcriptional regulator iclr from acinetobacter sp. adp1
68	c3hgkE_	Alignment	not modelled	10.4	19	PDB header: transferase Chain: E: PDB Molecule: effector protein hopab2; PDBTitle: crystal structure of effect protein avrptob complexed with2 kinase pto
69	c4qmkB_	Alignment	not modelled	10.4	47	PDB header: toxin Chain: B: PDB Molecule: type iii secretion system effector protein exou; PDBTitle: crystal structure of type iii effector protein exou (exou)
70	c3dlaD_	Alignment	not modelled	10.2	29	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
71	d1x4pa1	Alignment	not modelled	10.2	15	Fold: Surp module (SWAP domain) Superfamily: Surp module (SWAP domain) Family: Surp module (SWAP domain)
72	d1h5wa_	Alignment	not modelled	9.9	11	Fold: Upper collar protein gp10 (connector protein) Superfamily: Upper collar protein gp10 (connector protein) Family: Upper collar protein gp10 (connector protein)
73	c1ijgE_	Alignment	not modelled	9.5	11	PDB header: viral protein Chain: E: PDB Molecule: upper collar protein; PDBTitle: structure of the bacteriophage phi29 head-tail connector2 protein
74	c1vbiA_	Alignment	not modelled	9.3	23	PDB header: oxidoreductase Chain: A: PDB Molecule: type 2 malate/lactate dehydrogenase; PDBTitle: crystal structure of type 2 malate/lactate dehydrogenase from thermus2 thermophilus hb8
75	d1ulza2	Alignment	not modelled	9.1	18	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
76	d2h5na1	Alignment	not modelled	9.1	33	Fold: TerB-like Superfamily: TerB-like Family: PG1108-like
77	c2vvdA_	Alignment	not modelled	9.0	44	PDB header: viral protein Chain: A: PDB Molecule: spike protein p1; PDBTitle: crystal structure of the receptor binding domain of the2 spike protein p1 from bacteriophage pm2
78	d2j9ga2	Alignment	not modelled	8.8	9	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
79	c6g69K_	Alignment	not modelled	8.6	18	PDB header: de novo protein Chain: K: PDB Molecule: cc-type2-il-sg-l17e; PDBTitle: crystal structure of a parallel seven-helix coiled coil cc-type2-il-2 sg-l17e

80	c6g69M_	Alignment	not modelled	8.6	18	PDB header: de novo protein Chain: M: PDB Molecule: cc-type2-il-sg-l17e; PDBTitle: crystal structure of a parallel seven-helix coiled coil cc-type2-il-2 sg-l17e
81	c6g69B_	Alignment	not modelled	8.6	18	PDB header: de novo protein Chain: B: PDB Molecule: cc-type2-il-sg-l17e; PDBTitle: crystal structure of a parallel seven-helix coiled coil cc-type2-il-2 sg-l17e
82	c6g69G_	Alignment	not modelled	8.6	18	PDB header: de novo protein Chain: G: PDB Molecule: cc-type2-il-sg-l17e; PDBTitle: crystal structure of a parallel seven-helix coiled coil cc-type2-il-2 sg-l17e
83	c6g69J_	Alignment	not modelled	8.6	18	PDB header: de novo protein Chain: J: PDB Molecule: cc-type2-il-sg-l17e; PDBTitle: crystal structure of a parallel seven-helix coiled coil cc-type2-il-2 sg-l17e
84	c6g69A_	Alignment	not modelled	8.6	18	PDB header: de novo protein Chain: A: PDB Molecule: cc-type2-il-sg-l17e; PDBTitle: crystal structure of a parallel seven-helix coiled coil cc-type2-il-2 sg-l17e
85	c6g69F_	Alignment	not modelled	8.6	18	PDB header: de novo protein Chain: F: PDB Molecule: cc-type2-il-sg-l17e; PDBTitle: crystal structure of a parallel seven-helix coiled coil cc-type2-il-2 sg-l17e
86	c6g69D_	Alignment	not modelled	8.6	18	PDB header: de novo protein Chain: D: PDB Molecule: cc-type2-il-sg-l17e; PDBTitle: crystal structure of a parallel seven-helix coiled coil cc-type2-il-2 sg-l17e
87	c6g69I_	Alignment	not modelled	8.6	18	PDB header: de novo protein Chain: I: PDB Molecule: cc-type2-il-sg-l17e; PDBTitle: crystal structure of a parallel seven-helix coiled coil cc-type2-il-2 sg-l17e
88	c6g69E_	Alignment	not modelled	8.6	18	PDB header: de novo protein Chain: E: PDB Molecule: cc-type2-il-sg-l17e; PDBTitle: crystal structure of a parallel seven-helix coiled coil cc-type2-il-2 sg-l17e
89	c6g69L_	Alignment	not modelled	8.6	18	PDB header: de novo protein Chain: L: PDB Molecule: cc-type2-il-sg-l17e; PDBTitle: crystal structure of a parallel seven-helix coiled coil cc-type2-il-2 sg-l17e
90	c6g69C_	Alignment	not modelled	8.6	18	PDB header: de novo protein Chain: C: PDB Molecule: cc-type2-il-sg-l17e; PDBTitle: crystal structure of a parallel seven-helix coiled coil cc-type2-il-2 sg-l17e
91	c6g69H_	Alignment	not modelled	8.6	18	PDB header: de novo protein Chain: H: PDB Molecule: cc-type2-il-sg-l17e; PDBTitle: crystal structure of a parallel seven-helix coiled coil cc-type2-il-2 sg-l17e
92	c2z5il_	Alignment	not modelled	8.5	26	PDB header: contractile protein Chain: I: PDB Molecule: tropomyosin alpha-1 chain and general control protein gcn4; PDBTitle: crystal structure of the head-to-tail junction of tropomyosin
93	d1w53a_	Alignment	not modelled	8.4	12	Fold: KaiA/RbsU domain Superfamily: KaiA/RbsU domain Family: Phosphoserine phosphatase RsbU, N-terminal domain
94	d1zhva2	Alignment	not modelled	8.3	25	Fold: Ferredoxin-like Superfamily: ACT-like Family: Atu0741-like
95	c4glfA_	Alignment	not modelled	8.2	25	PDB header: transferase Chain: A: PDB Molecule: rsfp; PDBTitle: crystal structure of methylthioadenosine phosphorylase sourced from an2 antarctic soil metagenomic library
96	c1wtjB_	Alignment	not modelled	8.1	26	PDB header: oxidoreductase Chain: B: PDB Molecule: ureidoglycolate dehydrogenase; PDBTitle: crystal structure of delta1-piperideine-2-carboxylate2 reductase from pseudomonas syringae pvar.tomato
97	c1yr3A_	Alignment	not modelled	8.1	20	PDB header: transferase Chain: A: PDB Molecule: xanthosine phosphorylase; PDBTitle: escherichia coli purine nucleoside phosphorylase ii, the product of2 the xapa gene
98	c3mjdA_	Alignment	not modelled	8.1	18	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: 1.9 angstrom crystal structure of orotate phosphoribosyltransferase2 (pyre) francisella tularensis.
99	d1pfka_	Alignment	not modelled	8.0	17	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase