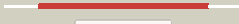



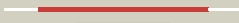



















Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3011c_gatA_3369960_3371444
 Date Thu Aug 8 16:20:18 BST 2019
 Unique Job ID 152e405b7f24d9a5















Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2f2aa1	 Alignment		100.0	47	Fold: Amidase signature (AS) enzymes Superfamily: Amidase signature (AS) enzymes Family: Amidase signature (AS) enzymes
2	c4wj3A	 Alignment		100.0	51	PDB header: ligase/rna Chain: A: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit a; PDBTitle: crystal structure of the asparagine transamidosome from pseudomonas2 aeruginosa
3	c3h0rP	 Alignment		100.0	47	PDB header: ligase Chain: P: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit a; PDBTitle: structure of trna-dependent amidotransferase gatcab from2 aquifex aeolicus
4	c6diiH	 Alignment		100.0	27	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
5	d1m22a	 Alignment		100.0	33	Fold: Amidase signature (AS) enzymes Superfamily: Amidase signature (AS) enzymes Family: Amidase signature (AS) enzymes
6	c3kfuE	 Alignment		100.0	49	PDB header: ligase/rna Chain: E: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit a; PDBTitle: crystal structure of the transamidosome
7	c4gysA	 Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: allophanate hydrolase; PDBTitle: granulibacter bethesdensis allophanate hydrolase co-crystallized with2 malonate
8	c2vyaB	 Alignment		100.0	21	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
9	d1mt5a	 Alignment		100.0	20	Fold: Amidase signature (AS) enzymes Superfamily: Amidase signature (AS) enzymes Family: Amidase signature (AS) enzymes
10	c4cp8C	 Alignment		100.0	28	PDB header: hydrolase Chain: C: PDB Molecule: allophanate hydrolase; PDBTitle: structure of the amidase domain of allophanate hydrolase2 from pseudomonas sp strain adp
11	c5h6sB	 Alignment		100.0	27	PDB header: hydrolase Chain: B: PDB Molecule: amidase; PDBTitle: crystal structure of hydrazidase s179a mutant complexed with a2 substrate

12	c5h6tB_	Alignment		100.0	27	PDB header: hydrolase Chain: B: PDB Molecule: amidase; PDBTitle: crystal structure of hydrazidase from microbacterium sp. strain hm58-2
13	c3a2qA_	Alignment		100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: 6-aminohexanoate-cyclic-dimer hydrolase; PDBTitle: structure of 6-aminohexanoate cyclic dimer hydrolase complexed with2 substrate
14	c6c6gA_	Alignment		100.0	35	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.
15	c4yj6A_	Alignment		100.0	29	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
16	c2dc0A_	Alignment		100.0	32	PDB header: hydrolase Chain: A: PDB Molecule: probable amidase; PDBTitle: crystal structure of amidase
17	c3a1iA_	Alignment		100.0	31	PDB header: hydrolase Chain: A: PDB Molecule: amidase; PDBTitle: crystal structure of rhodococcus sp. n-771 amidase complexed2 with benzamide
18	d2qi3a1	Alignment		100.0	45	Fold: Amidase signature (AS) enzymes Superfamily: Amidase signature (AS) enzymes Family: Amidase signature (AS) enzymes
19	d1locka_	Alignment		100.0	30	Fold: Amidase signature (AS) enzymes Superfamily: Amidase signature (AS) enzymes Family: Amidase signature (AS) enzymes
20	c4issA_	Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: allophanate hydrolase; PDBTitle: semet-substituted kluyveromyces lactis allophanate hydrolase
21	c5i8iD_	Alignment	not modelled	100.0	26	PDB header: hydrolase Chain: D: PDB Molecule: urea amidolyase; PDBTitle: crystal structure of the k. lactis urea amidolyase
22	c4n0hA_	Alignment	not modelled	100.0	32	PDB header: ligase Chain: A: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit a, PDBTitle: crystal structure of s. cerevisiae mitochondrial gatfab
23	c5ewqC_	Alignment	not modelled	100.0	27	PDB header: hydrolase Chain: C: PDB Molecule: amidase; PDBTitle: the crystal structure of an amidase family protein from bacillus2 anthracis str. ames
24	c4m1eC_	Alignment	not modelled	38.2	12	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.
25	d1y88a1	Alignment	not modelled	33.8	20	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: Hypothetical protein AF1548, C-terminal domain
26	c4lnaA_	Alignment	not modelled	33.3	20	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of purine nucleoside phosphorylase i from spirosuma2 linguale dsm 74, nysgrc target 029362
27	d1li4a2	Alignment	not modelled	32.2	19	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: S-adenosylhomocystein hydrolase
28	d1h5wa_	Alignment	not modelled	30.4	10	Fold: Upper collar protein gp10 (connector protein) Superfamily: Upper collar protein gp10 (connector protein) Family: Upper collar protein gp10 (connector protein)
						PDB header: transferase

29	c4nsnC_	Alignment	not modelled	30.3	15	Chain: C; PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of purine nucleoside phosphorylase from <i>2 porphyromonas gingivalis</i> atcc 33277, nysgrc target 030972,3 orthorhombic symmetry
30	c1ijgE_	Alignment	not modelled	30.0	10	PDB header: viral protein Chain: E; PDB Molecule: upper collar protein; PDBTitle: structure of the bacteriophage phi29 head-tail connector2 protein
31	c4l5cE_	Alignment	not modelled	29.2	16	PDB header: transferase Chain: E; PDB Molecule: s-methyl-5'-thioadenosine phosphorylase; PDBTitle: methylthioadenosine phosphorylase from <i>schistosoma mansoni</i> in complex2 with adenine in space group p212121
32	c4uc0A_	Alignment	not modelled	29.2	17	PDB header: transferase Chain: A; PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of a purine nucleoside phosphorylase (psi-nysgrc-2 029736) from <i>agrobacterium vitis</i>
33	c3o8oC_	Alignment	not modelled	26.2	7	PDB header: transferase Chain: C; PDB Molecule: 6-phosphofructokinase subunit alpha; PDBTitle: structure of phosphofructokinase from <i>saccharomyces cerevisiae</i>
34	d2dloa2	Alignment	not modelled	23.1	21	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
35	d1h1js_	Alignment	not modelled	22.1	11	Fold: LEM/SAP HeH motif Superfamily: SAP domain Family: SAP domain
36	d1jcb4	Alignment	not modelled	20.4	13	Fold: Ferredoxin-like Superfamily: Anticodon-binding domain of PheRS Family: Anticodon-binding domain of PheRS
37	c5ifkC_	Alignment	not modelled	20.2	20	PDB header: transferase Chain: C; PDB Molecule: purine nucleoside phosphorylase; PDBTitle: purine nucleoside phosphorylase
38	c3ilvA_	Alignment	not modelled	18.7	17	PDB header: ligase Chain: A; PDB Molecule: glutamine-dependent nad(+) synthetase; PDBTitle: crystal structure of a glutamine-dependent nad(+) synthetase2 from <i>cytophaga hutchinsonii</i>
39	c1us7B_	Alignment	not modelled	18.3	18	PDB header: chaperone Chain: B; PDB Molecule: hsp90 co-chaperone cdc37; PDBTitle: complex of hsp90 and p50
40	d1us7b_	Alignment	not modelled	18.3	18	Fold: Hsp90 co-chaperone CDC37 Superfamily: Hsp90 co-chaperone CDC37 Family: Hsp90 co-chaperone CDC37
41	c4g4sP_	Alignment	not modelled	18.2	13	PDB header: hydrolase/chaperone Chain: P; PDB Molecule: proteasome assembly chaperone 2; PDBTitle: structure of proteasome-pba1-pba2 complex
42	d1tf1a_	Alignment	not modelled	18.1	14	Fold: Profilin-like Superfamily: GAF domain-like Family: IcIR ligand-binding domain-like
43	c3d3oA_	Alignment	not modelled	17.5	16	PDB header: transcription regulator Chain: A; PDB Molecule: putative transcriptional regulator, icir family; PDBTitle: crystal structure of the effector domain of the putative2 transcriptional regulator iclr from <i>acinetobacter</i> sp. adp1
44	c5tjIA_	Alignment	not modelled	16.9	20	PDB header: transcription Chain: A; PDB Molecule: transcriptional regulator, iclr family; PDBTitle: crystal structure of icir transcriptional regulator from2 <i>alicyclobacillus acidocaldarius</i>
45	d1q23a_	Alignment	not modelled	16.7	5	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
46	c5y6iB_	Alignment	not modelled	16.6	25	PDB header: transcription Chain: B; PDB Molecule: transcriptional regulator kdgr; PDBTitle: crystal structure of <i>pseudomonas aeruginosa</i> hmgr
47	d3claa_	Alignment	not modelled	16.3	10	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
48	c2i9dC_	Alignment	not modelled	15.1	3	PDB header: transferase Chain: C; PDB Molecule: chloramphenicol acetyltransferase; PDBTitle: chloramphenicol acetyltransferase
49	d1ggaa2	Alignment	not modelled	14.6	27	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
50	c3obfA_	Alignment	not modelled	14.2	16	PDB header: transcription regulator Chain: A; PDB Molecule: putative transcriptional regulator, iclr family; PDBTitle: crystal structure of putative transcriptional regulator, iclr family;2 targeted domain 129...302
51	c2na9A_	Alignment	not modelled	13.7	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
52	c2na8A_	Alignment	not modelled	13.3	13	PDB header: membrane protein Chain: A; PDB Molecule: cytokine receptor common subunit beta; PDBTitle: transmembrane structure of the cytokine receptor common subunit beta
53	c3dahB_	Alignment	not modelled	13.0	16	PDB header: transferase Chain: B; PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: 2.3 a crystal structure of ribose-phosphate pyrophosphokinase from2 <i>burkholderia pseudomallei</i>
54	c3o8nA_	Alignment	not modelled	12.3	9	PDB header: transferase Chain: A; PDB Molecule: 6-phosphofructokinase, muscle type; PDBTitle: structure of phosphofructokinase from rabbit skeletal muscle

55	d2f48a1	Alignment	not modelled	11.5	13	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
56	d1i32a2	Alignment	not modelled	11.2	27	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
57	d1w53a_	Alignment	not modelled	11.1	12	Fold: KaiA/RbsU domain Superfamily: KaiA/RbsU domain Family: Phosphoserine phosphatase RsbU, N-terminal domain
58	c2kvuA_	Alignment	not modelled	11.0	8	PDB header: transcription regulator Chain: A: PDB Molecule: mk1/myocardin-like protein 1; PDBTitle: solution nmr structure of sap domain of mk1/myocardin-like2 protein 1 from h.sapiens, northeast structural genomics3 consortium target target hr4547e
59	c4qmkB_	Alignment	not modelled	10.8	41	PDB header: toxin Chain: B: PDB Molecule: type iii secretion system effector protein exou; PDBTitle: crystal structure of type iii effector protein exou (exou)
60	c2lz1A_	Alignment	not modelled	10.5	16	PDB header: transcription Chain: A: PDB Molecule: nuclear factor erythroid 2-related factor 2; PDBTitle: solution nmr structure of the dna-binding domain of human nf-e2-2 related factor 2, northeast structural genomics consortium (nesg)3 target hr3520o
61	d1zrja1	Alignment	not modelled	10.2	11	Fold: LEM/SAP HeH motif Superfamily: SAP domain Family: SAP domain
62	c4gjfA_	Alignment	not modelled	10.2	29	PDB header: transferase Chain: A: PDB Molecule: rsfp; PDBTitle: crystal structure of methylthioadenosine phosphorylase sourced from an2 antarctic soil metagenomic library
63	c3k2qA_	Alignment	not modelled	9.8	10	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
64	c4fqdA_	Alignment	not modelled	9.6	28	PDB header: transferase Chain: A: PDB Molecule: niko protein; PDBTitle: crystal structure of the enolpyruvyl transferase niko from2 streptomyces tendae
65	c3izbF_	Alignment	not modelled	9.3	16	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
66	c2vvdA_	Alignment	not modelled	9.1	67	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
67	c1ysqA_	Alignment	not modelled	9.1	16	PDB header: gene regulation Chain: A: PDB Molecule: hth-type transcriptional regulator yiaj; PDBTitle: the crystal structure of transcriptional regulator yaij
68	c6an0A_	Alignment	not modelled	8.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: histidinol dehydrogenase; PDBTitle: crystal structure of histidinol dehydrogenase from elizabethkingia2 anophelis
69	d1k3ta2	Alignment	not modelled	8.9	26	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
70	c4xfrB_	Alignment	not modelled	8.6	35	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a domain of unknown function (duf1537) from2 bordetella bronchiseptica (bb3215), target efi-511620, with bound3 citrate, domain swapped dimer, space group p6522
71	c3ke8A_	Alignment	not modelled	8.6	23	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; PDBTitle: crystal structure of isph:hmbpp-complex
72	c3urkA_	Alignment	not modelled	8.6	23	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; PDBTitle: isph in complex with propynyl diphosphate (1061)
73	d1sknp_	Alignment	not modelled	8.6	12	Fold: A DNA-binding domain in eukaryotic transcription factors Superfamily: A DNA-binding domain in eukaryotic transcription factors Family: A DNA-binding domain in eukaryotic transcription factors
74	c2akwB_	Alignment	not modelled	8.5	13	PDB header: ligase Chain: B: PDB Molecule: phenylalanyl-trna synthetase beta chain; PDBTitle: crystal structure of t.thermophilus phenylalanyl-trna synthetase2 complexed with p-cl-phenylalanine
75	c3b8if_	Alignment	not modelled	8.5	11	PDB header: lyase Chain: F: PDB Molecule: pa4872 oxaloacetate decarboxylase; PDBTitle: crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+.
76	d2g82a2	Alignment	not modelled	8.5	18	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
77	c5xoeA_	Alignment	not modelled	8.5	13	PDB header: transferase Chain: A: PDB Molecule: atp-dependent 6-phosphofructokinase; PDBTitle: crystal structure of the apo staphylococcus aureus phosphofructokinase
78	c4my4A_	Alignment	not modelled	8.4	12	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: crystal structure of phosphoglycerate mutase from staphylococcus2 aureus.

79	c3tu3B_	 Alignment	not modelled	8.3	50	PDB header: toxin/toxin chaperone Chain: B: PDB Molecule: exou; PDBTitle: 1.92 angstrom resolution crystal structure of the full-length spcu in2 complex with full-length exou from the type iii secretion system of3 pseudomonas aeruginosa
80	c1dvpA_	 Alignment	not modelled	8.3	12	PDB header: transferase Chain: A: PDB Molecule: hepatocyte growth factor-regulated tyrosine PDBTitle: crystal structure of the vhs and fyve tandem domains of hrs,2 a protein involved in membrane trafficking and signal3 transduction
81	c3dqqB_	 Alignment	not modelled	8.2	9	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative trna synthase; PDBTitle: the crystal structure of the putative trna synthase from salmonella2 typhimurium lt2
82	c3zyqA_	 Alignment	not modelled	8.2	3	PDB header: signaling Chain: A: PDB Molecule: hepatocyte growth factor-regulated tyrosine kinase PDBTitle: crystal structure of the tandem vhs and fyve domains of hepatocyte2 growth factor-regulated tyrosine kinase substrate (hgs-hrs) at 1.48 a3 resolution
83	d2do1a1	 Alignment	not modelled	8.2	11	Fold: LEM/SAP HeH motif Superfamily: SAP domain Family: SAP domain
84	c2do1A_	 Alignment	not modelled	8.2	11	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
85	d1hqsa_	 Alignment	not modelled	8.1	13	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
86	d1k75a_	 Alignment	not modelled	8.0	23	Fold: ALDH-like Superfamily: ALDH-like Family: L-histidinol dehydrogenase HisD
87	c1zrjA_	 Alignment	not modelled	7.9	11	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
88	d1qe5a_	 Alignment	not modelled	7.8	12	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
89	d1o98a1	 Alignment	not modelled	7.7	16	Fold: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain Superfamily: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain Family: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain
90	d1g2oa_	 Alignment	not modelled	7.6	14	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
91	c3dnfB_	 Alignment	not modelled	7.2	19	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; PDBTitle: structure of (e)-4-hydroxy-3-methyl-but-2-enyl diphosphate reductase,2 the terminal enzyme of the non-mevalonate pathway
92	c2vveB_	 Alignment	not modelled	7.1	67	PDB header: viral protein Chain: B: PDB Molecule: spike protein p1; PDBTitle: crystal structure of the stem and receptor binding domain2 of the spike protein p1 from bacteriophage pm2
93	c4au1A_	 Alignment	not modelled	7.1	11	PDB header: isomerase Chain: A: PDB Molecule: precorrin-8x methylmutase; PDBTitle: crystal structure of cobh (precorrin-8x methyl mutase)2 complexed with c5 desmethyl-hba
94	c3c5yD_	 Alignment	not modelled	7.0	16	PDB header: isomerase Chain: D: PDB Molecule: ribose/galactose isomerase; PDBTitle: crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution
95	c3opyG_	 Alignment	not modelled	7.0	12	PDB header: transferase Chain: G: PDB Molecule: 6-phosphofructo-1-kinase alpha-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
96	d2auna2	 Alignment	not modelled	7.0	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: LD-carboxypeptidase A N-terminal domain-like
97	d1gado2	 Alignment	not modelled	7.0	25	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
98	d1saza2	 Alignment	not modelled	6.9	23	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetokinase-like
99	d1ltkA_	 Alignment	not modelled	6.9	24	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase