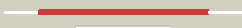



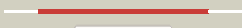



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2888c_amiC_3196874_3198295
Date	Thu Aug 8 16:20:04 BST 2019
Unique Job ID	fba73148335fd126

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3h0rP_	 Alignment		100.0	24	PDB header: ligase Chain: P; PDB Molecule: glutamyl-trna(gln) amidotransferase subunit a; PDBTitle: structure of trna-dependent amidotransferase gatcab from2 aquifex aeolicus
2	d2f2aa1	 Alignment		100.0	23	Fold: Amidase signature (AS) enzymes Superfamily: Amidase signature (AS) enzymes Family: Amidase signature (AS) enzymes
3	c4wj3A_	 Alignment		100.0	24	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	c6diiH_	 Alignment		100.0	23	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	c4gysA_	 Alignment		100.0	22	PDB header: hydrolase Chain: A; PDB Molecule: allophanate hydrolase; PDBTitle: granulibacter bethesdensis allophanate hydrolase co-crystallized with2 malonate
6	c3kfuE_	 Alignment		100.0	27	PDB header: ligase/rna Chain: E; PDB Molecule: glutamyl-trna(gln) amidotransferase subunit a; PDBTitle: crystal structure of the transamidosome
7	c3a2qA_	 Alignment		100.0	33	PDB header: hydrolase Chain: A; PDB Molecule: 6-aminohexanoate-cyclic-dimer hydrolase; PDBTitle: structure of 6-aminohexanoate cyclic dimer hydrolase complexed with2 substrate
8	d1mt5a_	 Alignment		100.0	23	Fold: Amidase signature (AS) enzymes Superfamily: Amidase signature (AS) enzymes Family: Amidase signature (AS) enzymes
9	c2vyaB_	 Alignment		100.0	24	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
10	c5h6sB_	 Alignment		100.0	22	PDB header: hydrolase Chain: B; PDB Molecule: amidase; PDBTitle: crystal structure of hydrazidase s179a mutant complexed with a2 substrate
11	c5h6tB_	 Alignment		100.0	22	PDB header: hydrolase Chain: B; PDB Molecule: amidase; PDBTitle: crystal structure of hydrazidase from microbacterium sp. strain hm58-2

12	c4cp8C_	Alignment		100.0	25	PDB header: hydrolase Chain: C: PDB Molecule: allophanate hydrolase; PDBTitle: structure of the amidase domain of allophanate hydrolase2 from pseudomonas sp strain adp
13	d1m22a_	Alignment		100.0	26	Fold: Amidase signature (AS) enzymes Superfamily: Amidase signature (AS) enzymes Family: Amidase signature (AS) enzymes
14	c6c6gA_	Alignment		100.0	27	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	c2dc0A_	Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: probable amidase; PDBTitle: crystal structure of amidase
16	c4yj6A_	Alignment		100.0	27	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
17	d2gi3a1	Alignment		100.0	24	Fold: Amidase signature (AS) enzymes Superfamily: Amidase signature (AS) enzymes Family: Amidase signature (AS) enzymes
18	d1locka	Alignment		100.0	24	Fold: Amidase signature (AS) enzymes Superfamily: Amidase signature (AS) enzymes Family: Amidase signature (AS) enzymes
19	c3a1iA_	Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: amidase; PDBTitle: crystal structure of rhodococcus sp. n-771 amidase complexed2 with benzamide
20	c4issA_	Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: allophanate hydrolase; PDBTitle: semet-substituted kluyveromyces lactis allophanate hydrolase
21	c5i8iD_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: D: PDB Molecule: urea amidolyase; PDBTitle: crystal structure of the k. lactis urea amidolyase
22	c5ewqC_	Alignment	not modelled	100.0	19	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	d1sknp_	Alignment	not modelled	37.6	3	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
25	c1ijgE_	Alignment	not modelled	32.0	13	PDB header: viral protein Chain: E: PDB Molecule: upper collar protein; PDBTitle: structure of the bacteriophage phi29 head-tail connector2 protein
26	c2lz1A_	Alignment	not modelled	30.7	17	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 hr35200
27	d1w53a_	Alignment	not modelled	29.1	9	Fold: KaiA/RbsU domain Superfamily: KaiA/RbsU domain Family: Phosphoserine phosphatase RsbU, N-terminal domain
28	c2kz5A_	Alignment	not modelled	29.0	10	PDB header: transcription Chain: A: PDB Molecule: transcription factor nf-e2 45 kda subunit; PDBTitle: solution nmr structure of transcription factor nf-e2 subunit's dna2 binding domain from homo sapiens, northeast

					structural genomics3 consortium target hr4653b
29	c3r4kD	Alignment	not modelled	27.6	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
30	c2zshA	Alignment	not modelled	27.2	17 PDB header: hormone receptor Chain: A: PDB Molecule: probable gibberellin receptor gid111; PDBTitle: structural basis of gibberellin(ga3)-induced della2 recognition by the gibberellin receptor
31	d1h5wa	Alignment	not modelled	26.6	15 Fold: Upper collar protein gp10 (connector protein) Superfamily: Upper collar protein gp10 (connector protein) Family: Upper collar protein gp10 (connector protein)
32	d1h1js	Alignment	not modelled	25.8	14 Fold: LEM/SAP HeH motif Superfamily: SAP domain Family: SAP domain
33	c1zrjA	Alignment	not modelled	24.8	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
34	c5tjA	Alignment	not modelled	24.7	16 PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, iclr family; PDBTitle: crystal structure of iclr transcriptional regulator from2 alicyclobacillus acidocaldarius
35	d2dloa2	Alignment	not modelled	24.5	20 Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
36	c2kvuA	Alignment	not modelled	24.3	13 PDB header: transcription regulator Chain: A: PDB Molecule: mkl/myocardin-like protein 1; PDBTitle: solution nmr structure of sap domain of mkl/myocardin-like2 protein 1 from h.sapiens, northeast structural genomics3 consortium target target hr4547e
37	c2do1A	Alignment	not modelled	22.2	17 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
38	d4pfka	Alignment	not modelled	22.0	19 Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
39	c5xoeA	Alignment	not modelled	20.4	20 PDB header: transferase Chain: A: PDB Molecule: atp-dependent 6-phosphofructokinase; PDBTitle: crystal structure of the apo staphylococcus aureus phosphofructokinase
40	c4m1eC	Alignment	not modelled	20.1	15 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.
41	d2do1a1	Alignment	not modelled	19.8	17 Fold: LEM/SAP HeH motif Superfamily: SAP domain Family: SAP domain
42	c4g4sP	Alignment	not modelled	19.5	20 PDB header: hydrolase/chaperone Chain: P: PDB Molecule: proteasome assembly chaperone 2; PDBTitle: structure of proteasome-pba1-pba2 complex
43	c1zxxA	Alignment	not modelled	19.3	20 PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase; PDBTitle: the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
44	d1zrja1	Alignment	not modelled	19.3	11 Fold: LEM/SAP HeH motif Superfamily: SAP domain Family: SAP domain
45	c4e94A	Alignment	not modelled	19.1	15 PDB header: hydrolase Chain: A: PDB Molecule: mccc family protein; PDBTitle: crystal structure of mccc-like protein from streptococcus pneumoniae
46	c2na9A	Alignment	not modelled	19.1	25 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
47	c2na8A	Alignment	not modelled	18.5	25 PDB header: membrane protein Chain: A: PDB Molecule: cytokine receptor common subunit beta; PDBTitle: transmembrane structure of the cytokine receptor common subunit beta
48	c4l5cE	Alignment	not modelled	18.4	13 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
49	c4lnaA	Alignment	not modelled	17.1	15 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
50	c5f1yA	Alignment	not modelled	16.6	15 PDB header: hydrolase Chain: A: PDB Molecule: mccc family protein; PDBTitle: crystal structure of ba3275, the member of s66 family of serine2 peptidases
51	c6iczX	Alignment	not modelled	16.1	29 PDB header: splicing Chain: X: PDB Molecule: prkr-interacting protein 1; PDBTitle: cryo-em structure of a human post-catalytic spliceosome (p complex) at2 3.0 angstrom
52	d1k1va	Alignment	not modelled	16.0	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
53	d1q7ra	Alignment	not modelled	15.9	14 Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
54	d1q23a	Alignment	not modelled	15.5	16 Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases

						Family: CAT-like
55	c4nsnC_	Alignment	not modelled	15.5	12	PDB header: transferase Chain: C: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of purine nucleoside phosphorylase from <i>Porphyromonas gingivalis</i> ATCC 33277, Nysgrc target 030972, 3 orthorhombic symmetry
56	c5y6iB_	Alignment	not modelled	15.3	20	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator kdgr; PDBTitle: crystal structure of <i>Pseudomonas aeruginosa</i> HmGr
57	c3ilvA_	Alignment	not modelled	15.1	10	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>
58	c4uc0A_	Alignment	not modelled	15.1	15	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>
59	c2obxH_	Alignment	not modelled	14.8	26	PDB header: transferase Chain: H: PDB Molecule: 6,7-dimethyl-8-ribityllumazine synthase 1; PDBTitle: lumazine synthase ribh2 from <i>Mesorhizobium loti</i> (gene ml17281, swiss-2 prot entry q986n2) complexed with inhibitor 5-nitro-6-(d-3-ribitylamino)-2,4(1h,3h) pyrimidinedione
60	c3d3oA_	Alignment	not modelled	14.2	26	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
61	c2hkeB_	Alignment	not modelled	13.9	26	PDB header: lyase Chain: B: PDB Molecule: diphosphomevalonate decarboxylase, putative; PDBTitle: mevalonate diphosphate decarboxylase from <i>Trypanosoma brucei</i>
62	c2kveA_	Alignment	not modelled	13.8	12	PDB header: hormone Chain: A: PDB Molecule: mesencephalic astrocyte-derived neurotrophic factor; PDBTitle: c-terminal domain of mesencephalic astrocyte-derived neurotrophic2 factor (manf)
63	c4e5sC_	Alignment	not modelled	13.7	23	PDB header: hydrolase Chain: C: PDB Molecule: mcclike protein (ba_5613); PDBTitle: crystal structure of mcclike protein (ba_5613) from <i>Bacillus anthracis</i> str. ames
64	c3zyqA_	Alignment	not modelled	13.6	14	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 Å resolution
65	d1v8ba2	Alignment	not modelled	13.2	6	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: S-adenosylhomocystein hydrolase
66	c2iv3B_	Alignment	not modelled	13.1	34	PDB header: transferase Chain: B: PDB Molecule: glycosyltransferase; PDBTitle: crystal structure of avigt4, a glycosyltransferase involved2 in avilamycin biosynthesis
67	d1ggaa2	Alignment	not modelled	12.7	20	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
68	c1dvpA_	Alignment	not modelled	12.5	13	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
69	c2vvdA_	Alignment	not modelled	12.0	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
70	c6gngB_	Alignment	not modelled	11.6	23	PDB header: transferase Chain: B: PDB Molecule: granule-bound starch synthase; PDBTitle: granule bound starch synthase i from <i>Cyanophora paradoxa</i> bound to2 acarbose and adp
71	d2auna2	Alignment	not modelled	11.6	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: LD-carboxypeptidase A N-terminal domain-like
72	c6njyB_	Alignment	not modelled	11.6	28	PDB header: rna binding protein Chain: B: PDB Molecule: type iv crispr associated cas6 rna endonuclease; PDBTitle: type iv crispr associated rna endonuclease cas6 - apo form
73	c2wnsB_	Alignment	not modelled	11.1	10	PDB header: transferase Chain: B: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: human orotate phosphoribosyltransferase (optase) domain of2 uridine 5'-monophosphate synthase (umps) in complex with3 its substrate orotidine 5'-monophosphate (omp)
74	d1pfka_	Alignment	not modelled	10.6	19	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
75	d3claa_	Alignment	not modelled	10.6	17	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
76	d1c41a_	Alignment	not modelled	10.4	15	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
77	d2b4ro2	Alignment	not modelled	10.3	13	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like

78	d2g82a2	Alignment	not modelled	10.1	16	Fold: Fwde/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
79	c2j6yB_	Alignment	not modelled	10.0	9	PDB header: hydrolase Chain: B: PDB Molecule: phosphoserine phosphatase rsbu; PDBTitle: structural and functional characterisation of partner switching2 regulating the environmental stress response in bacillus subtilis
80	c3nm3D_	Alignment	not modelled	9.9	12	PDB header: transferase Chain: D: PDB Molecule: thiamine biosynthetic bifunctional enzyme; PDBTitle: the crystal structure of candida glabrata th16, a bifunctional enzyme2 involved in thiamin biosynthesis of eukaryotes
81	c2g7uB_	Alignment	not modelled	9.8	29	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
82	d2h5na1	Alignment	not modelled	9.7	20	Fold: TerB-like Superfamily: TerB-like Family: PG1108-like
83	c3tlgB_	Alignment	not modelled	9.7	14	PDB header: hydrolase Chain: B: PDB Molecule: mccf; PDBTitle: microcin c7 self immunity protein mccf in the inactive mutant apo2 state
84	c2vveB_	Alignment	not modelled	9.7	44	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
85	d1li4a2	Alignment	not modelled	9.5	7	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: S-adenosylhomocystein hydrolase
86	c1uasA_	Alignment	not modelled	9.4	12	PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase; PDBTitle: crystal structure of rice alpha-galactosidase
87	c4gicB_	Alignment	not modelled	9.0	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
88	d2hi6a1	Alignment	not modelled	8.8	42	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/lvD-like Family: AF0055-like
89	c4gi5B_	Alignment	not modelled	8.6	20	PDB header: oxidoreductase Chain: B: PDB Molecule: quinone reductase; PDBTitle: crystal structure of a putative quinone reductase from klebsiella2 pneumoniae (target psi-013613)
90	c2w0cL_	Alignment	not modelled	8.3	44	PDB header: virus Chain: L: PDB Molecule: protein 2; PDBTitle: x-ray structure of the entire lipid-containing bacteriophage pm2
91	c5ulbA_	Alignment	not modelled	8.3	18	PDB header: sugar binding protein Chain: A: PDB Molecule: putative sugar abc transporter; PDBTitle: crystal structure of sugar abc transporter from yersinia2 enterocolitica subsp. enterocolitica 8081
92	c2i9dC_	Alignment	not modelled	8.1	11	PDB header: transferase Chain: C: PDB Molecule: chloramphenicol acetyltransferase; PDBTitle: chloramphenicol acetyltransferase
93	c3d7rB_	Alignment	not modelled	8.1	13	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of a putative esterase from staphylococcus aureus
94	c5ifkC_	Alignment	not modelled	8.1	17	PDB header: transferase Chain: C: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: purine nucleoside phosphorylase
95	c6aphA_	Alignment	not modelled	8.0	9	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of adenosylhomocysteinase from elizabethkingia2 anophelis nuhp1 in complex with nad and adenosine
96	d1uasa2	Alignment	not modelled	7.8	12	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
97	c3ndqA_	Alignment	not modelled	7.8	11	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor a protein 1; PDBTitle: structure of human tfiis domain ii
98	c3hgkE_	Alignment	not modelled	7.8	10	PDB header: transferase Chain: E: PDB Molecule: effector protein hopab2; PDBTitle: crystal structure of effect protein avrptob complexed with2 kinase pto
99	d1u1ha1	Alignment	not modelled	7.8	11	Fold: TIM beta/alpha-barrel Superfamily: UROD/MetE-like Family: Cobalamin-independent methionine synthase