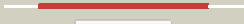



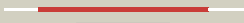



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3375_(amiD)_3788801_3790228
Date	Fri Aug 9 18:20:04 BST 2019
Unique Job ID	119fe5b4edf6b85b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6diiH_	 Alignment		100.0	26	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	30	Fold: Amidase signature (AS) enzymes Superfamily: Amidase signature (AS) enzymes Family: Amidase signature (AS) enzymes
3	c4wj3A_	 Alignment		100.0	35	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	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
5	c4gysA_	 Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: allophanate hydrolase; PDBTitle: granulibacter bethesdensis allophanate hydrolase co-crystallized with2 malonate
6	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
7	d1m22a_	 Alignment		100.0	30	Fold: Amidase signature (AS) enzymes Superfamily: Amidase signature (AS) enzymes Family: Amidase signature (AS) enzymes
8	c3a2qA_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: 6-aminohexanoate-cyclic-dimer hydrolase; PDBTitle: structure of 6-aminohexanoate cyclic dimer hydrolase complexed with2 substrate
9	c4cp8C_	 Alignment		100.0	27	PDB header: hydrolase Chain: C: PDB Molecule: allophanate hydrolase; PDBTitle: structure of the amidase domain of allophanate hydrolase2 from pseudomonas sp strain adp
10	c6c6gA_	 Alignment		100.0	31	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.
11	d1mt5a_	 Alignment		100.0	21	Fold: Amidase signature (AS) enzymes Superfamily: Amidase signature (AS) enzymes Family: Amidase signature (AS) enzymes

12	c5h6sB_	Alignment		100.0	25	PDB header: hydrolase Chain: B; PDB Molecule: amidase; PDBTitle: crystal structure of hydrazidase s179a mutant complexed with a2 substrate
13	c2vyaB_	Alignment		100.0	23	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
14	c5h6tB_	Alignment		100.0	25	PDB header: hydrolase Chain: B; PDB Molecule: amidase; PDBTitle: crystal structure of hydrazidase from microbacterium sp. strain hm58-2
15	c2dc0A_	Alignment		100.0	31	PDB header: hydrolase Chain: A; PDB Molecule: probable amidase; PDBTitle: crystal structure of amidase
16	c4yj6A_	Alignment		100.0	24	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	28	Fold: Amidase signature (AS) enzymes Superfamily: Amidase signature (AS) enzymes Family: Amidase signature (AS) enzymes
18	d1ocka_	Alignment		100.0	28	Fold: Amidase signature (AS) enzymes Superfamily: Amidase signature (AS) enzymes Family: Amidase signature (AS) enzymes
19	c3a1iA_	Alignment		100.0	28	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	22	PDB header: hydrolase Chain: A; PDB Molecule: allophanate hydrolase; PDBTitle: semet-substituted kluyveromyces lactis allophanate hydrolase
21	c5i8iD_	Alignment	not modelled	100.0	22	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	27	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	c2kvuA_	Alignment	not modelled	48.7	11	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
25	c2lz1A_	Alignment	not modelled	42.0	19	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
26	c5tjA_	Alignment	not modelled	33.7	16	PDB header: transcription Chain: A; PDB Molecule: transcriptional regulator, iclr family; PDBTitle: crystal structure of iclr transcriptional regulator from2 alicyclobacillus acidocaldarius
27	d1sknp_	Alignment	not modelled	31.4	17	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
28	d2f48a1	Alianment	not modelled	28.5	11	Fold: Phosphofructokinase Superfamily: Phosphofructokinase

					Family:Phosphofructokinase
29	d1y88a1	Alignment	not modelled	27.2	12 Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: Hypothetical protein AF1548, C-terminal domain
30	c3dahB	Alignment	not modelled	27.0	16 PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: 2.3 a crystal structure of ribose-phosphate pyrophosphokinase from2 burkholderia pseudomallei
31	d1us7b_	Alignment	not modelled	26.6	15 Fold: Hsp90 co-chaperone CDC37 Superfamily: Hsp90 co-chaperone CDC37 Family: Hsp90 co-chaperone CDC37
32	c1us7B_	Alignment	not modelled	26.6	15 PDB header: chaperone Chain: B: PDB Molecule: hsp90 co-chaperone cdc37; PDBTitle: complex of hsp90 and p50
33	c3r4kD_	Alignment	not modelled	25.2	17 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
34	d1q23a_	Alignment	not modelled	24.6	13 Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
35	c3k2qA_	Alignment	not modelled	23.4	13 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
36	d3claa_	Alignment	not modelled	22.3	11 Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like
37	c2kz5A_	Alignment	not modelled	20.9	24 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
38	c4g4sP_	Alignment	not modelled	20.4	27 PDB header: hydrolase/chaperone Chain: P: PDB Molecule: proteasome assembly chaperone 2; PDBTitle: structure of proteasome-pba1-pba2 complex
39	d2dloa2	Alignment	not modelled	19.5	31 Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
40	c1zrjA_	Alignment	not modelled	18.2	12 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
41	d1h1js_	Alignment	not modelled	18.1	22 Fold: LEM/SAP HeH motif Superfamily: SAP domain Family: SAP domain
42	c4m1eC_	Alignment	not modelled	17.8	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.
43	c2higA_	Alignment	not modelled	17.6	16 PDB header: transferase Chain: A: PDB Molecule: 6-phospho-1-fructokinase; PDBTitle: crystal structure of phosphofructokinase apoenzyme from trypanosoma2 brucei.
44	c6njyB_	Alignment	not modelled	16.6	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
45	c1vbiA_	Alignment	not modelled	16.4	22 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
46	c4lnaA_	Alignment	not modelled	15.9	22 PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of purine nucleoside phosphorylase i from spirosona2 linguale dsm 74, nysgrc target 029362
47	c2na9A_	Alignment	not modelled	15.8	38 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
48	c2na8A_	Alignment	not modelled	15.3	38 PDB header: membrane protein Chain: A: PDB Molecule: cytokine receptor common subunit beta; PDBTitle: transmembrane structure of the cytokine receptor common subunit beta
49	c2do1A_	Alignment	not modelled	15.0	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
50	c1wtjB_	Alignment	not modelled	14.9	19 PDB header: oxidoreductase Chain: B: PDB Molecule: ureidoglycolate dehydrogenase; PDBTitle: crystal structure of delta1-piperideine-2-carboxylate2 reductase from pseudomonas syringae pvar.tomato
51	c4l5cE_	Alignment	not modelled	14.0	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
52	c4uc0A_	Alignment	not modelled	13.9	17 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
53	c5xoeA_	Alignment	not modelled	13.1	10 PDB header: transferase Chain: A: PDB Molecule: atp-dependent 6-phosphofructokinase; PDBTitle: crystal structure of the apo staphylococcus aureus

						phosphofructokinase PDB header: transferase
54	c4nsnC_	Alignment	not modelled	12.9	15	Chain: C: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of purine nucleoside phosphorylase from 2 porphyromonas gingivalis atcc 33277, nysgrc target 030972,3 orthorhombic symmetry
55	d2o9aa1	Alignment	not modelled	12.8	13	Fold: Profilin-like Superfamily: GAF domain-like Family: lclR ligand-binding domain-like
56	d1zrja1	Alignment	not modelled	12.8	14	Fold: LEM/SAP HeH motif Superfamily: SAP domain Family: SAP domain
57	c2i9dC_	Alignment	not modelled	12.7	8	PDB header: transferase Chain: C: PDB Molecule: chloramphenicol acetyltransferase; PDBTitle: chloramphenicol acetyltransferase
58	c1v9nA_	Alignment	not modelled	12.6	22	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: structure of malate dehydrogenase from pyrococcus horikoshii ot3
59	d2do1a1	Alignment	not modelled	12.5	20	Fold: LEM/SAP HeH motif Superfamily: SAP domain Family: SAP domain
60	c3d3oA_	Alignment	not modelled	12.1	21	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 acinetobacter sp. adp1
61	c3obfA_	Alignment	not modelled	12.0	17	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
62	c6an0A_	Alignment	not modelled	12.0	9	PDB header: oxidoreductase Chain: A: PDB Molecule: histidinol dehydrogenase; PDBTitle: crystal structure of histidinol dehydrogenase from elizabethkingia2 anophelis
63	d1nxua_	Alignment	not modelled	11.9	14	Fold: L-sulfolactate dehydrogenase-like Superfamily: L-sulfolactate dehydrogenase-like Family: L-sulfolactate dehydrogenase-like
64	c1yspA_	Alignment	not modelled	11.6	30	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator kdgr; PDBTitle: crystal structure of the c-terminal domain of e. coli transcriptional2 regulator kdgr.
65	c2kqvA_	Alignment	not modelled	11.4	25	PDB header: viral protein Chain: A: PDB Molecule: non-structural protein 3; PDBTitle: sars coronavirus-unique domain (sud): three-domain molecular2 architecture in solution and rna binding. i: structure of the sud-m3 domain of sud-mc
66	c3uoeb_	Alignment	not modelled	11.2	19	PDB header: oxidoreductase Chain: B: PDB Molecule: dehydrogenase; PDBTitle: the crystal structure of dehydrogenase from sinorhizobium meliloti
67	c3mjda_	Alignment	not modelled	11.1	20	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: 1.9 angstrom crystal structure of orotate phosphoribosyltransferase2 (pyre) francisella tularensis.
68	d1xrha_	Alignment	not modelled	11.0	22	Fold: L-sulfolactate dehydrogenase-like Superfamily: L-sulfolactate dehydrogenase-like Family: L-sulfolactate dehydrogenase-like
69	d1k75a_	Alignment	not modelled	11.0	17	Fold: ALDH-like Superfamily: ALDH-like Family: L-histidinol dehydrogenase HisD
70	d4pfka_	Alignment	not modelled	10.8	7	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
71	d1rfma_	Alignment	not modelled	10.8	19	Fold: L-sulfolactate dehydrogenase-like Superfamily: L-sulfolactate dehydrogenase-like Family: L-sulfolactate dehydrogenase-like
72	c2g7uB_	Alignment	not modelled	10.6	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: 2.3 a structure of putative catechol degradative operon regulator from 2 rhodococcus sp. rha1
73	c3trsa_	Alignment	not modelled	10.4	42	PDB header: hydrolase Chain: A: PDB Molecule: aspergillopepsin-2 light chain; PDBTitle: the crystal structure of aspergilloglutamic peptidase from aspergillus2 niger
74	c2c4kD_	Alignment	not modelled	10.4	20	PDB header: regulatory protein Chain: D: PDB Molecule: phosphoribosyl pyrophosphate synthetase-associated protein PDBTitle: crystal structure of human phosphoribosylpyrophosphate synthetase-2 associated protein 39 (pap39)
75	c2jzfA_	Alignment	not modelled	10.3	25	PDB header: viral protein Chain: A: PDB Molecule: replicase polyprotein 1ab; PDBTitle: nmr conformer closest to the mean coordinates of the domain 513-651 of 2 the sars-cov nonstructural protein nsp3
76	d1o98a1	Alignment	not modelled	10.3	17	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
77	c3mq0A_	Alignment	not modelled	10.2	25	PDB header: transcription repressor Chain: A: PDB Molecule: transcriptional repressor of the blcabc operon; PDBTitle: crystal structure of agobacterium tumefaciens repressor blcr
						PDB header: transferase

78	c3o8oC	Alignment	not modelled	10.0	9	Chain: C; PDB Molecule: 6-phosphofructokinase subunit alpha; PDBTitle: structure of phosphofructokinase from saccharomyces cerevisiae
79	d1w53a	Alignment	not modelled	10.0	15	Fold: KaiA/RbsU domain Superfamily: KaiA/RbsU domain Family: Phosphoserine phosphatase RsbU, N-terminal domain
80	c4gicB	Alignment	not modelled	9.8	15	PDB header: oxidoreductase Chain: B; PDB Molecule: histidinol dehydrogenase; PDBTitle: crystal structure of a putative histidinol dehydrogenase (target psi-2 014034) from methylococcus capsulatus
81	c2hkeB	Alignment	not modelled	9.6	22	PDB header: lyase Chain: B; PDB Molecule: diphosphomevalonate decarboxylase, putative; PDBTitle: mevalonate diphosphate decarboxylase from trypanosoma brucei
82	c3dezA	Alignment	not modelled	9.5	17	PDB header: transferase Chain: A; PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: crystal structure of orotate phosphoribosyltransferase from streptococcus mutans
83	c3hgkE	Alignment	not modelled	9.5	20	PDB header: transferase Chain: E; PDB Molecule: effector protein hopab2; PDBTitle: crystal structure of effect protein avrptob complexed with 2 kinase pto
84	c4i2nC	Alignment	not modelled	9.5	11	PDB header: hydrolase Chain: C; PDB Molecule: intracellular protease/amidase; PDBTitle: crystal structure of 31kd heat shock protein, vchsp31 from vibrio cholerae
85	d1li4a2	Alignment	not modelled	9.4	20	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: S-adenosylhomocystein hydrolase
86	c4g07A	Alignment	not modelled	9.2	18	PDB header: oxidoreductase Chain: A; PDB Molecule: histidinol dehydrogenase; PDBTitle: the crystal structure of the c366s mutant of hdh from brucella suis
87	c2g8yB	Alignment	not modelled	9.2	27	PDB header: oxidoreductase Chain: B; PDB Molecule: malate/l-lactate dehydrogenases; PDBTitle: the structure of a putative malate/lactate dehydrogenase from e. coli.
88	d1dd4c	Alignment	not modelled	9.0	44	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
89	c6aphA	Alignment	not modelled	8.8	25	PDB header: hydrolase Chain: A; PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of adenosylhomocysteinase from elizabethkingia2 anophelis nuhp1 in complex with nad and adenosine
90	c3i0pA	Alignment	not modelled	8.6	27	PDB header: oxidoreductase Chain: A; PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of malate dehydrogenase from entamoeba histolytica
91	c5ifkC	Alignment	not modelled	8.6	25	PDB header: transferase Chain: C; PDB Molecule: purine nucleoside phosphorylase; PDBTitle: purine nucleoside phosphorylase
92	c2vvdA	Alignment	not modelled	7.9	56	PDB header: viral protein Chain: A; PDB Molecule: spike protein p1; PDBTitle: crystal structure of the receptor binding domain of the 2 spike protein p1 from bacteriophage pm2
93	c3s5pA	Alignment	not modelled	7.7	18	PDB header: isomerase Chain: A; PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: crystal structure of ribose-5-phosphate isomerase b rpib from giardia lamblia
94	c2h9aA	Alignment	not modelled	7.6	17	PDB header: oxidoreductase Chain: A; PDB Molecule: carbon monoxide dehydrogenase corrinoid/iron-sulfur PDBTitle: corrinoid iron-sulfur protein
95	c2rbca	Alignment	not modelled	7.5	15	PDB header: transferase Chain: A; PDB Molecule: sugar kinase; PDBTitle: crystal structure of a putative ribokinase from agrobacterium tumefaciens
96	c3ocrA	Alignment	not modelled	7.4	17	PDB header: lyase Chain: A; PDB Molecule: class ii aldolase/adducin domain protein; PDBTitle: crystal structure of aldolase ii superfamily protein from pseudomonas syringae
97	c3zxsB	Alignment	not modelled	7.3	13	PDB header: lyase Chain: B; PDB Molecule: cryptochrome b; PDBTitle: cryptochrome b from rhodobacter sphaeroides
98	c1z1sA	Alignment	not modelled	7.1	25	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein pa3332; PDBTitle: crystal structure of putative isomerase pa3332 from pseudomonas aeruginosa
99	c3ndqA	Alignment	not modelled	7.1	0	PDB header: transcription Chain: A; PDB Molecule: transcription elongation factor a protein 1; PDBTitle: structure of human tfiis domain ii