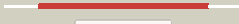



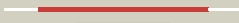

















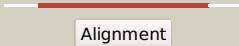

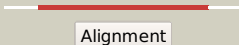
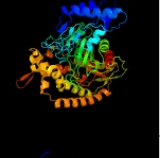
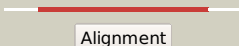
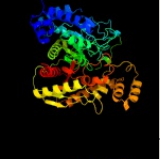

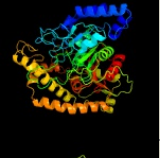
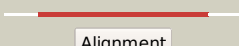
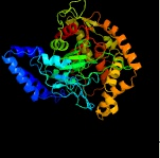
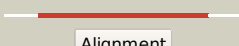

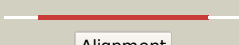
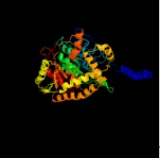

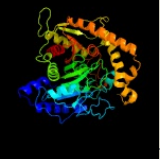



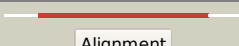

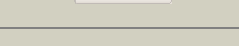

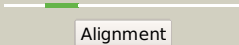
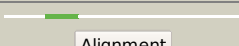
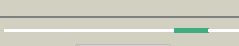


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3175 (-) _3542857_3544344
Date	Thu Aug 8 16:20:36 BST 2019
Unique Job ID	ed1082f69d63bf57

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2f2aa1</a>	 Alignment		100.0	25	<b>Fold:</b> Amidase signature (AS) enzymes <b>Superfamily:</b> Amidase signature (AS) enzymes <b>Family:</b> Amidase signature (AS) enzymes
2	<a href="#">c6diiH_</a>	 Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> fatty acid amide hydrolase; <b>PDBTitle:</b> structure of arabidopsis fatty acid amide hydrolase in complex with2 methyl linolenyl fluorophosphonate
3	<a href="#">c4wj3A_</a>	 Alignment		100.0	30	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna(gln) amidotransferase subunit a; <b>PDBTitle:</b> crystal structure of the asparagine transamidosome from pseudomonas2 aeruginosa
4	<a href="#">c3h0rP_</a>	 Alignment		100.0	27	<b>PDB header:</b> ligase <b>Chain:</b> P: <b>PDB Molecule:</b> glutamyl-trna(gln) amidotransferase subunit a; <b>PDBTitle:</b> structure of trna-dependent amidotransferase gatcab from2 aquifex aeolicus
5	<a href="#">c4yj6A_</a>	 Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aryl acylamidase; <b>PDBTitle:</b> the crystal structure of a bacterial aryl acylamidase belonging to the2 amidase signature (as) enzymes family
6	<a href="#">d1m22a_</a>	 Alignment		100.0	28	<b>Fold:</b> Amidase signature (AS) enzymes <b>Superfamily:</b> Amidase signature (AS) enzymes <b>Family:</b> Amidase signature (AS) enzymes
7	<a href="#">c3a2qA_</a>	 Alignment		100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-aminohexanoate-cyclic-dimer hydrolase; <b>PDBTitle:</b> structure of 6-aminohexanoate cyclic dimer hydrolase complexed with2 substrate
8	<a href="#">c4gysA_</a>	 Alignment		100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> allophanate hydrolase; <b>PDBTitle:</b> granulibacter bethesdensis allophanate hydrolase co-crystallized with2 malonate
9	<a href="#">c3kfuE_</a>	 Alignment		100.0	31	<b>PDB header:</b> ligase/rna <b>Chain:</b> E: <b>PDB Molecule:</b> glutamyl-trna(gln) amidotransferase subunit a; <b>PDBTitle:</b> crystal structure of the transamidosome
10	<a href="#">c5h6sB_</a>	 Alignment		100.0	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> amidase; <b>PDBTitle:</b> crystal structure of hydrazidase s179a mutant complexed with a2 substrate
11	<a href="#">c5h6tB_</a>	 Alignment		100.0	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> amidase; <b>PDBTitle:</b> crystal structure of hydrazidase from microbacterium sp. strain hm58-2

12	<a href="#">d1mt5a_</a>	 Alignment		100.0	23	<b>Fold:</b> Amidase signature (AS) enzymes <b>Superfamily:</b> Amidase signature (AS) enzymes <b>Family:</b> Amidase signature (AS) enzymes
13	<a href="#">c4cp8C_</a>	 Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> allophanate hydrolase; <b>PDBTitle:</b> structure of the amidase domain of allophanate hydrolase2 from pseudomonas sp strain adp
14	<a href="#">c2vyaB_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> fatty-acid amide hydrolase 1; <b>PDBTitle:</b> crystal structure of fatty acid amide hydrolase conjugated2 with the drug-like inhibitor pf-750
15	<a href="#">c6c6gA_</a>	 Alignment		100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> biuret hydrolase; <b>PDBTitle:</b> an unexpected vestigial protein complex reveals the evolutionary2 origins of an s-triazine catabolic enzyme. inhibitor bound complex.
16	<a href="#">c2dc0A_</a>	 Alignment		100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable amidase; <b>PDBTitle:</b> crystal structure of amidase
17	<a href="#">d2gi3a1</a>	 Alignment		100.0	25	<b>Fold:</b> Amidase signature (AS) enzymes <b>Superfamily:</b> Amidase signature (AS) enzymes <b>Family:</b> Amidase signature (AS) enzymes
18	<a href="#">c3a1iA_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amidase; <b>PDBTitle:</b> crystal structure of rhodococcus sp. n-771 amidase complexed2 with benzamide
19	<a href="#">d1locka_</a>	 Alignment		100.0	26	<b>Fold:</b> Amidase signature (AS) enzymes <b>Superfamily:</b> Amidase signature (AS) enzymes <b>Family:</b> Amidase signature (AS) enzymes
20	<a href="#">c4issA_</a>	 Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> allophanate hydrolase; <b>PDBTitle:</b> semet-substituted kluyveromyces lactis allophanate hydrolase
21	<a href="#">c5i8iD_</a>	 Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> urea amidolyase; <b>PDBTitle:</b> crystal structure of the k. lactis urea amidolyase
22	<a href="#">c5ewqC_</a>	 Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> amidase; <b>PDBTitle:</b> the crystal structure of an amidase family protein from bacillus2 anthracis str. ames
23	<a href="#">c4n0hA_</a>	 Alignment	not modelled	100.0	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna(gln) amidotransferase subunit a, <b>PDBTitle:</b> crystal structure of s. cerevisiae mitochondrial gatfab
24	<a href="#">c3r4kD_</a>	 Alignment	not modelled	56.5	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, iclr family; <b>PDBTitle:</b> crystal structure of a putative iclr transcriptional regulator2 (tm1040_3717) from silicibacter sp. tm1040 at 2.46 a resolution
25	<a href="#">d1h5wa_</a>	 Alignment	not modelled	50.7	15	<b>Fold:</b> Upper collar protein gp10 (connector protein) <b>Superfamily:</b> Upper collar protein gp10 (connector protein) <b>Family:</b> Upper collar protein gp10 (connector protein)
26	<a href="#">c1ijgE_</a>	 Alignment	not modelled	50.5	15	<b>PDB header:</b> viral protein <b>Chain:</b> E: <b>PDB Molecule:</b> upper collar protein; <b>PDBTitle:</b> structure of the bacteriophage phi29 head-tail connector2 protein
27	<a href="#">c5tjA_</a>	 Alignment	not modelled	44.7	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, iclr family; <b>PDBTitle:</b> crystal structure of iclr transcriptional regulator from2 alicyclobacillus acidocaldarius
28	<a href="#">c2kvuA_</a>	 Alignment	not modelled	37.2	7	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> mkl/myocardin-like protein 1; <b>PDBTitle:</b> solution nmr structure of sap domain of mkl/myocardin-like2 protein 1 from h.sapiens, northeast structural genomics3

						consortium target target hr4547e
29	<a href="#">c2do1A_</a>	Alignment	not modelled	35.6	12	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear protein hcc-1; <b>PDBTitle:</b> solution structure of the sap domain of human nuclear2 protein hcc-1
30	<a href="#">c3k2qA_</a>	Alignment	not modelled	35.6	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrophosphate-dependent phosphofructokinase; <b>PDBTitle:</b> crystal structure of pyrophosphate-dependent2 phosphofructokinase from marinobacter aquaeolei, northeast3 structural genomics consortium target mqr88
31	<a href="#">c2higA_</a>	Alignment	not modelled	34.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phospho-1-fructokinase; <b>PDBTitle:</b> crystal structure of phosphofructokinase apoenzyme from trypanosoma2 brucei.
32	<a href="#">d1k75a_</a>	Alignment	not modelled	27.1	20	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> L-histidinol dehydrogenase HisD
33	<a href="#">d1h1js_</a>	Alignment	not modelled	26.6	18	<b>Fold:</b> LEM/SAP HeH motif <b>Superfamily:</b> SAP domain <b>Family:</b> SAP domain
34	<a href="#">c6an0A_</a>	Alignment	not modelled	25.6	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> histidinol dehydrogenase; <b>PDBTitle:</b> crystal structure of histidinol dehydrogenase from elizabethkingia2 anophelis
35	<a href="#">c3obfA_</a>	Alignment	not modelled	23.7	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator, iclr family; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator, iclr family;2 targeted domain 129...302
36	<a href="#">c4m1eC_</a>	Alignment	not modelled	23.5	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> purine nucleoside phosphorylase; <b>PDBTitle:</b> crystal structure of purine nucleoside phosphorylase i from2 planctomyces limnophilus dsm 3776, nysgrc target 029364.
37	<a href="#">c4e94A_</a>	Alignment	not modelled	23.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mccc family protein; <b>PDBTitle:</b> crystal structure of mccc-like protein from streptococcus pneumoniae
38	<a href="#">c1zrjA_</a>	Alignment	not modelled	23.2	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> e1b-55kda-associated protein 5 isoform c; <b>PDBTitle:</b> solution structure of the sap domain of human e1b-55kda-2 associated protein 5 isoform c
39	<a href="#">c5xoeA_</a>	Alignment	not modelled	23.2	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent 6-phosphofructokinase; <b>PDBTitle:</b> crystal structure of the apo staphylococcus aureus phosphofructokinase
40	<a href="#">d2do1a1</a>	Alignment	not modelled	21.7	11	<b>Fold:</b> LEM/SAP HeH motif <b>Superfamily:</b> SAP domain <b>Family:</b> SAP domain
41	<a href="#">c1dvpA_</a>	Alignment	not modelled	21.7	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hepatocyte growth factor-regulated tyrosine <b>PDBTitle:</b> crystal structure of the vhs and fyve tandem domains of hrs,2 a protein involved in membrane trafficking and signal3 transduction
42	<a href="#">c3zyqA_</a>	Alignment	not modelled	21.0	7	<b>PDB header:</b> signaling <b>Chain:</b> A: <b>PDB Molecule:</b> hepatocyte growth factor-regulated tyrosine kinase <b>PDBTitle:</b> crystal structure of the tandem vhs and fyve domains of hepatocyte2 growth factor-regulated tyrosine kinase substrate (hgs-hrs) at 1.48 a3 resolution
43	<a href="#">d1zrja1</a>	Alignment	not modelled	20.6	14	<b>Fold:</b> LEM/SAP HeH motif <b>Superfamily:</b> SAP domain <b>Family:</b> SAP domain
44	<a href="#">c4lnaA_</a>	Alignment	not modelled	20.4	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> purine nucleoside phosphorylase; <b>PDBTitle:</b> crystal structure of purine nucleoside phosphorylase i from spirosona2 linguale dsm 74, nysgrc target 029362
45	<a href="#">c2c4kD_</a>	Alignment	not modelled	20.2	24	<b>PDB header:</b> regulatory protein <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoribosyl pyrophosphate synthetase-associated protein <b>PDBTitle:</b> crystal structure of human phosphoribosylpyrophosphate synthetase-2 associated protein 39 (pap39)
46	<a href="#">c2na9A_</a>	Alignment	not modelled	20.0	50	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytokine receptor common subunit beta; <b>PDBTitle:</b> transmembrane structure of the p441a mutant of the cytokine receptor2 common subunit beta
47	<a href="#">c4g4sP_</a>	Alignment	not modelled	19.8	27	<b>PDB header:</b> hydrolase/chaperone <b>Chain:</b> P: <b>PDB Molecule:</b> proteasome assembly chaperone 2; <b>PDBTitle:</b> structure of proteasome-pba1-pba2 complex
48	<a href="#">c4uc0A_</a>	Alignment	not modelled	19.4	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> purine nucleoside phosphorylase; <b>PDBTitle:</b> crystal structure of a purine nucleoside phosphorylase (psi-nysgrc-2 029736) from agrobacterium vitis
49	<a href="#">c2na8A_</a>	Alignment	not modelled	19.3	50	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytokine receptor common subunit beta; <b>PDBTitle:</b> transmembrane structure of the cytokine receptor common subunit beta
50	<a href="#">c4nsnC_</a>	Alignment	not modelled	18.6	10	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> purine nucleoside phosphorylase; <b>PDBTitle:</b> crystal structure of purine nucleoside phosphorylase from2 porphyromonas gingivalis atcc 33277, nysgrc target 030972,3 orthorhombic symmetry
51	<a href="#">d1w53a_</a>	Alignment	not modelled	18.2	12	<b>Fold:</b> KaiA/RbsU domain <b>Superfamily:</b> KaiA/RbsU domain <b>Family:</b> Phosphoserine phosphatase RsbU, N-terminal domain
52	<a href="#">c4g07A_</a>	Alignment	not modelled	18.2	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> histidinol dehydrogenase; <b>PDBTitle:</b> the crystal structure of the c366s mutant of hdh from

						brucella suis
53	<a href="#">c4l5cE_</a>	Alignment	not modelled	18.1	11	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> s-methyl-5'-thioadenosine phosphorylase; <b>PDBTitle:</b> methylthioadenosine phosphorylase from schistosoma mansoni in complex2 with adenine in space group p212121
54	<a href="#">d2f48a1</a>	Alignment	not modelled	16.8	20	<b>Fold:</b> Phosphofructokinase <b>Superfamily:</b> Phosphofructokinase <b>Family:</b> Phosphofructokinase
55	<a href="#">d3claa_</a>	Alignment	not modelled	16.7	7	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
56	<a href="#">d1li4a2</a>	Alignment	not modelled	16.7	25	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Formate/glycerate dehydrogenase catalytic domain-like <b>Family:</b> S-adenosylhomocystein hydrolase
57	<a href="#">d1saza2</a>	Alignment	not modelled	16.3	7	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Acetokinase-like
58	<a href="#">c4twbB_</a>	Alignment	not modelled	16.3	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ribose-phosphate pyrophosphokinase; <b>PDBTitle:</b> sulfolobus solfataricus ribose-phosphate pyrophosphokinase
59	<a href="#">c3p0jD_</a>	Alignment	not modelled	16.0	14	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> leishmania major tyrosyl-trna synthetase in complex with tyrosinol,2 triclinic crystal form 1
60	<a href="#">c2kveA_</a>	Alignment	not modelled	15.9	17	<b>PDB header:</b> hormone <b>Chain:</b> A: <b>PDB Molecule:</b> mesencephalic astrocyte-derived neurotrophic factor; <b>PDBTitle:</b> c-terminal domain of mesencephalic astrocyte-derived neurotrophic2 factor (manf)
61	<a href="#">c5f1yA_</a>	Alignment	not modelled	15.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mccc family protein; <b>PDBTitle:</b> crystal structure of ba3275, the member of s66 family of serine2 peptidases
62	<a href="#">d1y88a1</a>	Alignment	not modelled	15.7	11	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> Rad51 N-terminal domain-like <b>Family:</b> Hypothetical protein AF1548, C-terminal domain
63	<a href="#">c2iv3B_</a>	Alignment	not modelled	15.6	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyltransferase; <b>PDBTitle:</b> crystal structure of avigt4, a glycosyltransferase involved2 in avilamycin a biosynthesis
64	<a href="#">c4gicB_</a>	Alignment	not modelled	14.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> histidinol dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative histidinol dehydrogenase (target psi-2 014034) from methylococcus capsulatus
65	<a href="#">c3ilvA_</a>	Alignment	not modelled	14.9	13	<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
66	<a href="#">c4grdA_</a>	Alignment	not modelled	14.9	22	<b>PDB header:</b> lyase, isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase catalytic subunit; <b>PDBTitle:</b> crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from burkholderia cenocepacia j2315
67	<a href="#">d2dloa2</a>	Alignment	not modelled	14.9	56	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
68	<a href="#">d1q23a_</a>	Alignment	not modelled	14.8	17	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
69	<a href="#">d1zhva2</a>	Alignment	not modelled	14.7	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> Atu0741-like
70	<a href="#">c2kqvA_</a>	Alignment	not modelled	14.5	35	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> non-structural protein 3; <b>PDBTitle:</b> sars coronavirus-unique domain (sud): three-domain molecular2 architecture in solution and rna binding. i: structure of the sud-m3 domain of sud-mc
71	<a href="#">d1dvpa1</a>	Alignment	not modelled	14.4	9	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> ENTH/VHS domain <b>Family:</b> VHS domain
72	<a href="#">d4pfka_</a>	Alignment	not modelled	14.3	14	<b>Fold:</b> Phosphofructokinase <b>Superfamily:</b> Phosphofructokinase <b>Family:</b> Phosphofructokinase
73	<a href="#">c2lz1A_</a>	Alignment	not modelled	14.0	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear factor erythroid 2-related factor 2; <b>PDBTitle:</b> solution nmr structure of the dna-binding domain of human nf-e2-2 related factor 2, northeast structural genomics consortium (nesg)3 target hr3520o
74	<a href="#">c2vc6A_</a>	Alignment	not modelled	13.9	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> structure of mosa from s. melloti with pyruvate bound
75	<a href="#">d1ggaa2</a>	Alignment	not modelled	13.4	23	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
76	<a href="#">d1g99a2</a>	Alignment	not modelled	13.2	3	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Acetokinase-like
77	<a href="#">c2zfa_</a>	Alignment	not modelled	12.9	35	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> replicase polyprotein 1ab; <b>PDBTitle:</b> nmr conformer closest to the mean coordinates of the domain 513-651 of2 the sars-cov nonstructural protein nsp3
						<b>PDB header:</b> transferase

78	<a href="#">c2i9dC</a>	Alignment	not modelled	12.9	8	<b>Chain:</b> C; <b>PDB Molecule:</b> chloramphenicol acetyltransferase; <b>PDBTitle:</b> chloramphenicol acetyltransferase
79	<a href="#">d1tf1a</a>	Alignment	not modelled	12.8	20	<b>Fold:</b> Profilin-like <b>Superfamily:</b> GAF domain-like <b>Family:</b> lclR ligand-binding domain-like
80	<a href="#">c2jmkA</a>	Alignment	not modelled	12.7	17	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein ta0956; <b>PDBTitle:</b> solution structure of ta0956
81	<a href="#">c3dahB</a>	Alignment	not modelled	12.6	18	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> ribose-phosphate pyrophosphokinase; <b>PDBTitle:</b> 2.3 a crystal structure of ribose-phosphate pyrophosphokinase from2 burkholderia pseudomallei
82	<a href="#">d1sknp</a>	Alignment	not modelled	12.5	14	<b>Fold:</b> A DNA-binding domain in eukaryotic transcription factors <b>Superfamily:</b> A DNA-binding domain in eukaryotic transcription factors <b>Family:</b> A DNA-binding domain in eukaryotic transcription factors
83	<a href="#">c4qmkB</a>	Alignment	not modelled	12.5	41	<b>PDB header:</b> toxin <b>Chain:</b> B; <b>PDB Molecule:</b> type iii secretion system effector protein exou; <b>PDBTitle:</b> crystal structure of type iii effector protein exou (exou)
84	<a href="#">c2g7uB</a>	Alignment	not modelled	12.0	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> 2.3 a structure of putative catechol degradative operon regulator from2 rhodococcus sp. rha1
85	<a href="#">c6aphA</a>	Alignment	not modelled	11.9	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of adenosylhomocysteinase from elizabethkingia2 anophelis nuhp1 in complex with nad and adenosine
86	<a href="#">c5ifkC</a>	Alignment	not modelled	11.8	25	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> purine nucleoside phosphorylase; <b>PDBTitle:</b> purine nucleoside phosphorylase
87	<a href="#">c3mq0A</a>	Alignment	not modelled	11.7	25	<b>PDB header:</b> transcription repressor <b>Chain:</b> A; <b>PDB Molecule:</b> transcriptional repressor of the blcabc operon; <b>PDBTitle:</b> crystal structure of agobacterium tumefaciens repressor blcr
88	<a href="#">c3c5yD</a>	Alignment	not modelled	11.4	19	<b>PDB header:</b> isomerase <b>Chain:</b> D; <b>PDB Molecule:</b> ribose/galactose isomerase; <b>PDBTitle:</b> crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution
89	<a href="#">c2mfqB</a>	Alignment	not modelled	11.1	50	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> bdnf/nt-3 growth factors receptor; <b>PDBTitle:</b> nmr solution structures of frs2a ptb domain with neurotrophin receptor2 trkb
90	<a href="#">c1zxxA</a>	Alignment	not modelled	11.1	12	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 6-phosphofructokinase; <b>PDBTitle:</b> the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
91	<a href="#">c3p4iA</a>	Alignment	not modelled	10.9	7	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> acetate kinase; <b>PDBTitle:</b> crystal structure of acetate kinase from mycobacterium avium
92	<a href="#">c1wtjB</a>	Alignment	not modelled	10.8	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> ureidoglycolate dehydrogenase; <b>PDBTitle:</b> crystal structure of delta1-piperidine-2-carboxylate2 reductase from pseudomonas syringae pvar.tomato
93	<a href="#">c1vbiA</a>	Alignment	not modelled	10.7	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> type 2 malate/lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of type 2 malate/lactate dehydrogenase from thermus2 thermophilus hb8
94	<a href="#">c2hkeB</a>	Alignment	not modelled	10.6	30	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> diphosphomevalonate decarboxylase, putative; <b>PDBTitle:</b> mevalonate diphosphate decarboxylase from trypanosoma brucei
95	<a href="#">d2g82a2</a>	Alignment	not modelled	10.6	22	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
96	<a href="#">c3izbF</a>	Alignment	not modelled	10.6	16	<b>PDB header:</b> ribosome <b>Chain:</b> F; <b>PDB Molecule:</b> 40s ribosomal protein rps5 (s7p); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
97	<a href="#">c3dezA</a>	Alignment	not modelled	10.5	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> orotate phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of orotate phosphoribosyltransferase from2 streptococcus mutans
98	<a href="#">d1i27a</a>	Alignment	not modelled	10.5	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> C-terminal domain of the rap74 subunit of TFIIF
99	<a href="#">d1v8ba2</a>	Alignment	not modelled	10.1	25	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Formate/glycerate dehydrogenase catalytic domain-like <b>Family:</b> S-adenosylhomocystein hydrolase