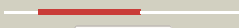










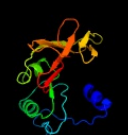










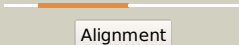
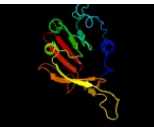

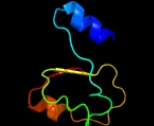
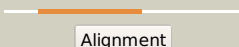



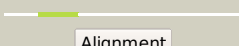

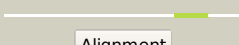

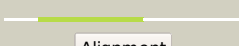


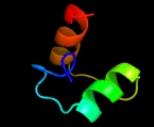


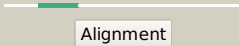
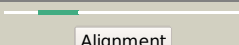
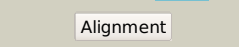

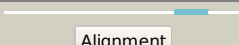

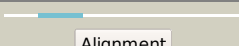

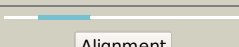


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3691 (- )_4132696_4133697
Date	Fri Aug 9 18:20:38 BST 2019
Unique Job ID	06a8ffe4d9f78982

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5fmrC_</a>	 Alignment		98.8	13	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> intraflagellar transport protein component ift52; <b>PDBTitle:</b> crift52 n-terminal domain
2	<a href="#">c5fmsA_</a>	 Alignment		98.6	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> intraflagellar transport protein 52 homolog; <b>PDBTitle:</b> mmift52 n-terminal domain
3	<a href="#">c5gslB_</a>	 Alignment		96.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 778aa long hypothetical beta-galactosidase; <b>PDBTitle:</b> glycoside hydrolase a
4	<a href="#">c6eznG_</a>	 Alignment		95.2	13	<b>PDB header:</b> membrane protein <b>Chain:</b> G: <b>PDB Molecule:</b> dolichyl-diphosphooligosaccharide--protein <b>PDBTitle:</b> cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
5	<a href="#">c5xb7E_</a>	 Alignment		95.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> gh42 alpha-l-arabinopyranosidase from bifidobacterium animalis subsp.2 lactis bl-04
6	<a href="#">d1kwga3</a>	 Alignment		94.9	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> A4 beta-galactosidase middle domain
7	<a href="#">d2qk3a1</a>	 Alignment		94.4	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> STM3548-like
8	<a href="#">c1kwgA_</a>	 Alignment		93.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> crystal structure of thermus thermophilus a4 beta-galactosidase
9	<a href="#">c5gsmB_</a>	 Alignment		92.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> exo-beta-d-glucosaminidase; <b>PDBTitle:</b> glycoside hydrolase b with product
10	<a href="#">c4uzsB_</a>	 Alignment		91.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> crystal structure of bifidobacterium bifidum beta-galactosidase
11	<a href="#">c4ojvA_</a>	 Alignment		89.7	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> 3d structure of the e323a catalytic mutant of gan42b, a gh42 beta-2 galactosidase from g. stearothermophilus

12	<a href="#">c4uozc_</a>	 Alignment		84.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> beta-(1,6)-galactosidase from bifidobacterium animalis subsp. lactis2 bl-04 nucleophile mutant e324a in complex with galactose
13	<a href="#">c5vymB_</a>	 Alignment		83.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-galactosidase bgab; <b>PDBTitle:</b> crystal structure of beta-galactosidase from bifidobacterium2 adolescentis
14	<a href="#">c3sozc_</a>	 Alignment		83.5	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> cytoplasmic protein stm1381; <b>PDBTitle:</b> cytoplasmic protein stm1381 from salmonella typhimurium lt2
15	<a href="#">d1x7da_</a>	 Alignment		69.7	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Ornithine cyclodeaminase-like
16	<a href="#">c4e5vA_</a>	 Alignment		66.6	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative thua-like protein; <b>PDBTitle:</b> crystal structure of a putative thua-like protein (parmer_02418) from2 parabacteroides merdae atcc 43184 at 1.75 a resolution
17	<a href="#">c2lv1j_</a>	 Alignment		66.1	20	<b>PDB header:</b> lyase <b>Chain:</b> J: <b>PDB Molecule:</b> cyanate hydratase; <b>PDBTitle:</b> site directed mutagenesis of key residues involved in the catalytic2 mechanism of cyanase
18	<a href="#">c5e9aB_</a>	 Alignment		64.2	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> crystal structure analysis of the cold-adamped beta-galactosidase from2 rahnella sp. r3
19	<a href="#">d1dwka1</a>	 Alignment		58.2	19	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Cyanase N-terminal domain
20	<a href="#">c3ttsD_</a>	 Alignment		46.6	11	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> crystal structure of beta-galactosidase from bacillus circulans sp.2 alkalophilus
21	<a href="#">d1j6ua1</a>	 Alignment	not modelled	45.0	19	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
22	<a href="#">d1p3da1</a>	 Alignment	not modelled	41.7	24	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
23	<a href="#">c3mkzU_</a>	 Alignment	not modelled	38.7	10	<b>PDB header:</b> dna-binding protein/dna <b>Chain:</b> U: <b>PDB Molecule:</b> protein sobp; <b>PDBTitle:</b> structure of sobp(155-272)-18mer complex, p21 form
24	<a href="#">c3mkyP_</a>	 Alignment	not modelled	36.9	10	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> P: <b>PDB Molecule:</b> protein sobp; <b>PDBTitle:</b> structure of sobp(155-323)-18mer dna complex, i23 form
25	<a href="#">c5uk3j_</a>	 Alignment	not modelled	35.7	14	<b>PDB header:</b> lyase <b>Chain:</b> J: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of cyanase from t. urticae
26	<a href="#">c1y9qA_</a>	 Alignment	not modelled	33.9	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, hth_3 family; <b>PDBTitle:</b> crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
27	<a href="#">c3rhtB_</a>	 Alignment	not modelled	33.2	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> (gatase1)-like protein; <b>PDBTitle:</b> crystal structure of type 1 glutamine amidotransferase (gatase1)-like2 protein from planctomyces limnophilus
28	<a href="#">c3smaD_</a>	 Alignment	not modelled	32.3	20	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> frbf; <b>PDBTitle:</b> a new n-acetyltransferase fold in the structure and mechanism of the2 phosphonate biosynthetic enzyme frbf
29	<a href="#">c6bc3A_</a>	 Alignment	not modelled	31.0	20	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> aac 3-vi protein; <b>PDBTitle:</b> cryo x-ray structure of sisomicin bound aac-via

30	<a href="#">c6b9tH_</a>	Alignment	not modelled	30.8	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> methyolphosphonate synthase; <b>PDBTitle:</b> crystal structure of mpns with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound
31	<a href="#">c6mn5A_</a>	Alignment	not modelled	30.6	18	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> aminoglycoside n(3)-acetyltransferase, aac(3)-iva; <b>PDBTitle:</b> crystal structure of aminoglycoside acetyltransferase aac(3)-iva,2 h154a mutant, in complex with gentamicin c1a
32	<a href="#">d2nyga1</a>	Alignment	not modelled	29.5	15	<b>Fold:</b> TTHA0583/YokD-like <b>Superfamily:</b> TTHA0583/YokD-like <b>Family:</b> Aminoglycoside 3-N-acetyltransferase-like
33	<a href="#">c6b9rD_</a>	Alignment	not modelled	29.4	39	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> hydroxyethylphosphonate dioxygenase; <b>PDBTitle:</b> streptomyces albus hepd with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound
34	<a href="#">d1t0ba_</a>	Alignment	not modelled	29.0	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> ThuA-like
35	<a href="#">c4jqsC_</a>	Alignment	not modelled	26.9	6	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a putative thua-like protein (bacuni_01602) from2 bacteroides uniformis atcc 8492 at 2.30 a resolution
36	<a href="#">c3e4fB_</a>	Alignment	not modelled	25.9	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminoglycoside n3-acetyltransferase; <b>PDBTitle:</b> crystal structure of ba2930- a putative aminoglycoside n3-2 acetyltransferase from bacillus anthracis
37	<a href="#">d1gr0a2</a>	Alignment	not modelled	25.3	25	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> Dihydrodipicolinate reductase-like
38	<a href="#">c6mb6A_</a>	Alignment	not modelled	25.2	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aac(3)-iiib protein; <b>PDBTitle:</b> aac-iiib binary with coash
39	<a href="#">c4mcxE_</a>	Alignment	not modelled	23.7	24	<b>PDB header:</b> toxin <b>Chain:</b> E: <b>PDB Molecule:</b> antidote protein; <b>PDBTitle:</b> p. vulgaris higa structure, crystal form 2
40	<a href="#">c1yi1A_</a>	Alignment	not modelled	23.3	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetolactate synthase; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana acetohydroxyacid synthase in2 complex with a sulfonylurea herbicide, tribenuron methyl
41	<a href="#">c5gziB_</a>	Alignment	not modelled	23.3	22	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> lysine cyclodeaminase; <b>PDBTitle:</b> cyclodeaminase_pa
42	<a href="#">c4mp6A_</a>	Alignment	not modelled	22.8	3	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative ornithine cyclodeaminase; <b>PDBTitle:</b> staphyloferrin b precursor biosynthetic enzyme sbnb bound to citrate2 and nad+
43	<a href="#">c3cecA_</a>	Alignment	not modelled	22.5	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative antidote protein of plasmid maintenance system; <b>PDBTitle:</b> crystal structure of a putative antidote protein of plasmid2 maintenance system (npun_f2943) from nostoc punctiforme pcc 73102 at3 1.60 a resolution
44	<a href="#">c3trbA_</a>	Alignment	not modelled	22.3	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> virulence-associated protein i; <b>PDBTitle:</b> structure of an addiction module antidote protein of a higa (higa)2 family from coxiella burnetii
45	<a href="#">c2bnoA_</a>	Alignment	not modelled	21.3	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxidase; <b>PDBTitle:</b> the structure of hydroxypropylphosphonic acid epoxidase from s.2 wedmorenis.
46	<a href="#">c6f8sA_</a>	Alignment	not modelled	21.3	19	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> xre family transcriptional regulator; <b>PDBTitle:</b> toxin-antitoxin complex grata
47	<a href="#">c8jdwA_</a>	Alignment	not modelled	19.6	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (l-arginine:glycine amidinotransferase); <b>PDBTitle:</b> crystal structure of human l-arginine:glycine amidinotransferase in2 complex with l-alanine
48	<a href="#">c1zzgB_</a>	Alignment	not modelled	19.4	21	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of hypothetical protein tt0462 from thermus2 thermophilus hb8
49	<a href="#">d1ybha2</a>	Alignment	not modelled	19.2	35	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase Pyr module
50	<a href="#">d2icta1</a>	Alignment	not modelled	18.8	19	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
51	<a href="#">c1jdwA_</a>	Alignment	not modelled	18.5	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> l-arginine\glycine amidinotransferase; <b>PDBTitle:</b> crystal structure and mechanism of l-arginine: glycine2 amidinotransferase: a mitochondrial enzyme involved in3 creatine biosynthesis
52	<a href="#">d1jdwA_</a>	Alignment	not modelled	18.5	27	<b>Fold:</b> Pentain, beta/alpha-propeller <b>Superfamily:</b> Pentain <b>Family:</b> Amidinotransferase
53	<a href="#">c5ht0B_</a>	Alignment	not modelled	17.3	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminoglycoside acetyltransferase hmb0005; <b>PDBTitle:</b> crystal structure of an antibiotic_nat family aminoglycoside2 acetyltransferase hmb0038 from an uncultured soil metagenomic sample3 in complex with coenzyme a <b>PDB header:</b> transferase

54	<a href="#">c2an1D_</a>	Alignment	not modelled	16.7	24	<b>Chain:</b> D: <b>PDB Molecule:</b> putative kinase; <b>PDBTitle:</b> structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
55	<a href="#">c1eysH_</a>	Alignment	not modelled	16.4	25	<b>PDB header:</b> electron transport <b>Chain:</b> H: <b>PDB Molecule:</b> photosynthetic reaction center; <b>PDBTitle:</b> crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
56	<a href="#">c5wpiB_</a>	Alignment	not modelled	16.0	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> hsva; <b>PDBTitle:</b> the virulence-associated protein hsva from the fire blight pathogen2 erwinia amylovora is a polyamine amidinotransferase
57	<a href="#">c5d50I_</a>	Alignment	not modelled	15.4	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> I: <b>PDB Molecule:</b> repressor; <b>PDBTitle:</b> crystal structure of rep-ant complex from salmonella-temperate phage
58	<a href="#">c1w8xP_</a>	Alignment	not modelled	14.7	14	<b>PDB header:</b> virus <b>Chain:</b> P: <b>PDB Molecule:</b> protein p16; <b>PDBTitle:</b> structural analysis of prd1
59	<a href="#">c2dg2D_</a>	Alignment	not modelled	14.6	20	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> apolipoprotein a-i binding protein; <b>PDBTitle:</b> crystal structure of mouse apolipoprotein a-i binding protein
60	<a href="#">c3mczB_</a>	Alignment	not modelled	14.3	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> the structure of an o-methyltransferase family protein from2 burkholderia thailandensis.
61	<a href="#">c3hdiA_</a>	Alignment	not modelled	13.5	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> probable ornithine cyclodeaminase; <b>PDBTitle:</b> the crystal structure of probable ornithine cyclodeaminase from2 bordetella pertussis tohama i
62	<a href="#">d1t6t1_</a>	Alignment	not modelled	13.1	15	<b>Fold:</b> Toprim domain <b>Superfamily:</b> Toprim domain <b>Family:</b> Toprim domain
63	<a href="#">c5emiA_</a>	Alignment	not modelled	12.9	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cell wall hydrolase/autolysin; <b>PDBTitle:</b> n-acetylmuramoyl-l-alanine amidase amic2 of nostoc punctiforme
64	<a href="#">c2n1pA_</a>	Alignment	not modelled	12.7	20	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> non-structural protein 5b, ns5b; <b>PDBTitle:</b> structure of the c-terminal membrane domain of hcv ns5b protein
65	<a href="#">c6ohiA_</a>	Alignment	not modelled	12.4	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> debraminase bmp8; <b>PDBTitle:</b> crystal structure of the debraminase bmp8 (apo)
66	<a href="#">d2ihta2</a>	Alignment	not modelled	12.4	47	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase Pyr module
67	<a href="#">c2lonA_</a>	Alignment	not modelled	12.4	17	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> hig1 domain family member 1b; <b>PDBTitle:</b> backbone structure of human membrane protein higd1b
68	<a href="#">c3kgkA_</a>	Alignment	not modelled	12.2	18	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> arsenical resistance operon trans-acting repressor arsd; <b>PDBTitle:</b> crystal structure of arsd
69	<a href="#">c2i99A_</a>	Alignment	not modelled	12.2	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mu-crystallin homolog; <b>PDBTitle:</b> crystal structure of human mu_crystallin at 2.6 angstrom
70	<a href="#">d1u1ia2</a>	Alignment	not modelled	11.8	30	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> Dihydrodipicolinate reductase-like
71	<a href="#">c3eagA_</a>	Alignment	not modelled	11.1	29	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-meso- <b>PDBTitle:</b> the crystal structure of udp-n-acetylmuramate:l-alanyl-gamma-d-2 glutamyl-meso-diaminopimelate ligase (mpl) from neisseria3 meningitides
72	<a href="#">d2ji7a2</a>	Alignment	not modelled	10.7	25	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase Pyr module
73	<a href="#">c6cauA_</a>	Alignment	not modelled	10.6	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate--l-alanine ligase; <b>PDBTitle:</b> udp-n-acetylmuramate--alanine ligase from acinetobacter baumannii2 ab5075-uw with amppnp
74	<a href="#">c2ebyA_</a>	Alignment	not modelled	10.5	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ybaq; <b>PDBTitle:</b> crystal structure of a hypothetical protein from e. coli
75	<a href="#">c4zp3O_</a>	Alignment	not modelled	10.5	33	<b>PDB header:</b> signaling protein <b>Chain:</b> O: <b>PDB Molecule:</b> a-kinase anchor protein 7 isoforms alpha and beta; <b>PDBTitle:</b> akap18:pka-riialpha structure reveals crucial anchor points for2 recognition of regulatory subunits of pka
76	<a href="#">c4zp3R_</a>	Alignment	not modelled	10.5	33	<b>PDB header:</b> signaling protein <b>Chain:</b> R: <b>PDB Molecule:</b> a-kinase anchor protein 7 isoforms alpha and beta; <b>PDBTitle:</b> akap18:pka-riialpha structure reveals crucial anchor points for2 recognition of regulatory subunits of pka
77	<a href="#">c4zp3Q_</a>	Alignment	not modelled	10.5	33	<b>PDB header:</b> signaling protein <b>Chain:</b> Q: <b>PDB Molecule:</b> a-kinase anchor protein 7 isoforms alpha and beta; <b>PDBTitle:</b> akap18:pka-riialpha structure reveals crucial anchor points for2 recognition of regulatory subunits of pka
78	<a href="#">c1upaC_</a>	Alignment	not modelled	10.2	44	<b>PDB header:</b> synthase <b>Chain:</b> C: <b>PDB Molecule:</b> carboxyethylarginine synthase; <b>PDBTitle:</b> carboxyethylarginine synthase from streptomyces2 clavuligerus (semet structure)
						<b>PDB header:</b> hydrolase

79	<a href="#">c4v0bA_</a>	Alignment	not modelled	10.1	25	<b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent zinc metalloprotease ftsh; <b>PDBTitle:</b> escherichia coli ftsh hexameric n-domain
80	<a href="#">d1vjpa2</a>	Alignment	not modelled	10.1	10	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> Dihydrodipicolinate reductase-like
81	<a href="#">d1p1ja2</a>	Alignment	not modelled	9.6	30	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> Dihydrodipicolinate reductase-like
82	<a href="#">c2l9uA_</a>	Alignment	not modelled	9.1	21	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbb-3; <b>PDBTitle:</b> spatial structure of dimeric erbb3 transmembrane domain
83	<a href="#">c2l9uB_</a>	Alignment	not modelled	9.1	21	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbb-3; <b>PDBTitle:</b> spatial structure of dimeric erbb3 transmembrane domain
84	<a href="#">c2f00A_</a>	Alignment	not modelled	9.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate--l-alanine ligase; <b>PDBTitle:</b> escherichia coli murc
85	<a href="#">c4binA_</a>	Alignment	not modelled	9.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylmuramoyl-l-alanine amidase amic; <b>PDBTitle:</b> crystal structure of the e. coli n-acetylmuramoyl-l-alanine amidase2 amic
86	<a href="#">c3eusB_</a>	Alignment	not modelled	8.6	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna-binding protein; <b>PDBTitle:</b> the crystal structure of the dna binding protein from silicibacter2 pomeroyi
87	<a href="#">c1ta9A_</a>	Alignment	not modelled	8.3	5	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol dehydrogenase; <b>PDBTitle:</b> crystal structure of glycerol dehydrogenase from schizosaccharomyces2 pombe
88	<a href="#">c2lowA_</a>	Alignment	not modelled	8.1	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> apelin receptor; <b>PDBTitle:</b> solution structure of ar55 in 50% hfip
89	<a href="#">d1rioa_</a>	Alignment	not modelled	8.0	17	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
90	<a href="#">c5zc2B_</a>	Alignment	not modelled	8.0	10	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> p-hydroxyphenylacetate 3-hydroxylase, reductase component; <b>PDBTitle:</b> acinetobacter baumannii p-hydroxyphenylacetate 3-hydroxylase (hpah),2 reductase component (c1)
91	<a href="#">d1vkoa2</a>	Alignment	not modelled	7.8	20	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> Dihydrodipicolinate reductase-like
92	<a href="#">c3ktbD_</a>	Alignment	not modelled	7.6	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> arsenical resistance operon trans-acting repressor; <b>PDBTitle:</b> crystal structure of arsenical resistance operon trans-acting2 repressor from bacteroides vulgatus atcc 8482
93	<a href="#">c2xgja_</a>	Alignment	not modelled	7.6	14	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase dob1; <b>PDBTitle:</b> structure of mtr4, a dexh helicase involved in nuclear rna2 processing and surveillance
94	<a href="#">d2jgra1</a>	Alignment	not modelled	7.5	20	<b>Fold:</b> NAD kinase/diacylglycerol kinase-like <b>Superfamily:</b> NAD kinase/diacylglycerol kinase-like <b>Family:</b> Diacylglycerol kinase-like
95	<a href="#">d1ozha2</a>	Alignment	not modelled	7.3	24	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase Pyr module
96	<a href="#">d1adra_</a>	Alignment	not modelled	7.2	13	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
97	<a href="#">c6iegA_</a>	Alignment	not modelled	6.9	21	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> exosome rna helicase mtr4; <b>PDBTitle:</b> crystal structure of human mtr4
98	<a href="#">d2ff4a2</a>	Alignment	not modelled	6.8	19	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> BTAD-like
99	<a href="#">c2lcoA_</a>	Alignment	not modelled	6.7	24	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> walp19-p8 peptide; <b>PDBTitle:</b> 1h and 15n assignments of walp19-p8 peptide in sds micelles