



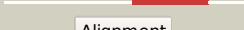







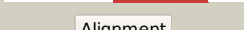

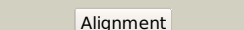

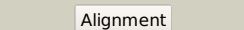

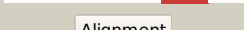

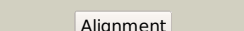









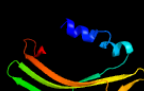


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1363c_(-)_1534613_1535398
Date	Wed Jul 31 22:05:46 BST 2019
Unique Job ID	40a905c391135e15

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5d9rA_</a>	 Alignment		97.4	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein accumulation and replication of chloroplasts 6, <b>PDBTitle:</b> crystal structure of a conserved domain in the intermembrane space2 region of the plastid division protein arc6
2	<a href="#">c5cnlA_</a>	 Alignment		97.2	8	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> icml-like; <b>PDBTitle:</b> crystal structure of an icml-like type iv secretion system protein2 (lpg0120) from legionella pneumophila subsp. pneumophila str.3 philadelphia 1 at 2.65 a resolution
3	<a href="#">c5u9oD_</a>	 Alignment		97.1	10	<b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> plastid division protein cdp1, chloroplastic, plastid <b>PDBTitle:</b> cocrystal structure of the intermembrane space region of the plastid2 division proteins parc6 and pdv1
4	<a href="#">c3a76B_</a>	 Alignment		97.1	10	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> gamma-hexachlorocyclohexane dehydrochlorinase; <b>PDBTitle:</b> the crystal structure of lina
5	<a href="#">d2ux0a1</a>	 Alignment		96.8	11	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
6	<a href="#">c3wz4F_</a>	 Alignment		96.8	15	<b>PDB header:</b> unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> doti; <b>PDBTitle:</b> structure of the periplasmic domain of doti (crystal form i)
7	<a href="#">d3d9ra1</a>	 Alignment		96.7	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> ECA1476-like
8	<a href="#">c4nhfF_</a>	 Alignment		96.3	12	<b>PDB header:</b> protein transport <b>Chain:</b> F: <b>PDB Molecule:</b> trwg protein; <b>PDBTitle:</b> crystal structure of the soluble domain of trwg type iv secretion2 machinery from bartonella grahamii
9	<a href="#">d3b8la1</a>	 Alignment		96.2	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
10	<a href="#">d3stda_</a>	 Alignment		96.2	9	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Scytalone dehydratase
11	<a href="#">d3ef8a1</a>	 Alignment		96.2	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like

12	<a href="#">d2cc3a1</a>	Alignment		96.1	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> VirB8-like
13	<a href="#">c5i97C</a>	Alignment		96.1	20	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> conjugal transfer protein; <b>PDBTitle:</b> structural analysis and inhibition of trae from the pkm101 type iv2 secretion system
14	<a href="#">c3wz3A</a>	Alignment		96.0	12	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> tram protein; <b>PDBTitle:</b> structure of a periplasmic fragment of tram
15	<a href="#">d3cu3a1</a>	Alignment		95.9	11	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
16	<a href="#">c3h51A</a>	Alignment		95.9	18	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> putative calcium/calmodulin dependent protein kinase ii <b>PDBTitle:</b> crystal structure of putative calcium/calmodulin dependent protein2 kinase ii association domain (np_636218.1) from xanthomonas3 campestris at 1.70 a resolution
17	<a href="#">d1hkxa</a>	Alignment		95.9	11	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
18	<a href="#">c4i4kB</a>	Alignment		95.9	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein sgcj; <b>PDBTitle:</b> streptomycetes globisporus c-1027 9-membered enediyne conserved protein2 sgc6
19	<a href="#">c3gzaA</a>	Alignment		95.7	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein with a ntf2-like fold; <b>PDBTitle:</b> crystal structure of an uncharacterized protein with a cystatin-like2 fold (cc_2572) from caulobacter vibrioides at 1.40 a resolution
20	<a href="#">d2rfra1</a>	Alignment		95.6	9	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
21	<a href="#">d1idpa</a>	Alignment	not modelled	95.5	9	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Scytalone dehydratase
22	<a href="#">c3robC</a>	Alignment	not modelled	95.4	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized conserved protein; <b>PDBTitle:</b> the crystal structure of a conserved protein from planctomyces2 limnophilus dsm 3776
23	<a href="#">d2f86b1</a>	Alignment	not modelled	95.3	6	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
24	<a href="#">d3ebya1</a>	Alignment	not modelled	94.9	9	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
25	<a href="#">c4ovmE</a>	Alignment	not modelled	94.7	10	<b>PDB header:</b> unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> uncharacterized protein sgcj; <b>PDBTitle:</b> crystal structure of sgcj protein from streptomycetes carzinostaticus
26	<a href="#">c5ig4A</a>	Alignment	not modelled	94.6	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> predicted protein; <b>PDBTitle:</b> crystal structure of n. vectensis camkii-a hub
27	<a href="#">d2rgqa1</a>	Alignment	not modelled	94.5	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rv3472-like
28	<a href="#">c4lehA</a>	Alignment	not modelled	94.5	10	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> bile acid 7-alpha dehydratase, baie; <b>PDBTitle:</b> crystal structure of a bile-acid 7-alpha dehydratase (closci_03134)2 from clostridium scindens atcc 35704 at 2.90 a resolution

29	<a href="#">c4gb5A_</a>	Alignment	not modelled	94.2	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of kfla4162 protein from kribbella flavida
30	<a href="#">d3b7ca1</a>	Alignment	not modelled	93.7	11	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SO0125-like
31	<a href="#">d2bhma1</a>	Alignment	not modelled	93.4	14	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> VirB8-like
32	<a href="#">d2chca1</a>	Alignment	not modelled	93.1	11	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rv3472-like
33	<a href="#">c2bhmE_</a>	Alignment	not modelled	93.1	14	<b>PDB header:</b> bacterial protein <b>Chain:</b> E: <b>PDB Molecule:</b> type iv secretion system protein virb8; <b>PDBTitle:</b> crystal structure of virb8 from brucella suis
34	<a href="#">c3f7sA_</a>	Alignment	not modelled	92.5	9	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized ntf2-like protein; <b>PDBTitle:</b> crystal structure of a ntf2-like protein of unknown function (pp_4556)2 from pseudomonas putida kt2440 at 2.11 a resolution
35	<a href="#">d2b1xb1</a>	Alignment	not modelled	92.4	15	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
36	<a href="#">c4meiA_</a>	Alignment	not modelled	91.1	12	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> virb8 protein; <b>PDBTitle:</b> crystal structure of a virb8 type iv secretion system machinery2 soluble domain from bartonella tribocorum
37	<a href="#">c3soyA_</a>	Alignment	not modelled	90.8	6	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> ntf2-like superfamily protein; <b>PDBTitle:</b> nuclear transport factor 2 (ntf2-like) superfamily protein from 2 salmonella enterica subsp. enterica serovar typhimurium str. lt2
38	<a href="#">c6of9G_</a>	Alignment	not modelled	90.4	13	<b>PDB header:</b> unknown function <b>Chain:</b> G: <b>PDB Molecule:</b> camkii hub; <b>PDBTitle:</b> structure of the chlamydamonas reinhardtii camkii hub homology domain
39	<a href="#">d3ejva1</a>	Alignment	not modelled	90.0	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BaiE/LinA-like
40	<a href="#">c2gbxF_</a>	Alignment	not modelled	88.7	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> biphenyl 2,3-dioxygenase beta subunit; <b>PDBTitle:</b> crystal structure of biphenyl 2,3-dioxygenase from sphingomonas2 yanoikuyae b1 bound to biphenyl
41	<a href="#">d3blza1</a>	Alignment	not modelled	88.5	8	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Sbal0622-like
42	<a href="#">d2r4ia1</a>	Alignment	not modelled	87.0	11	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> CHU142-like
43	<a href="#">c5ig5E_</a>	Alignment	not modelled	86.9	9	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> camkii-b hub; <b>PDBTitle:</b> crystal structure of n. vectensis camkii-b hub at ph 4.2
44	<a href="#">c4o3vA_</a>	Alignment	not modelled	86.6	16	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> virb8-like protein of type iv secretion system; <b>PDBTitle:</b> crystal structure of a virb8-like protein of type iv secretion system2 from rickettsia typhi
45	<a href="#">c3hx8A_</a>	Alignment	not modelled	85.7	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative ketosteroid isomerase; <b>PDBTitle:</b> crystal structure of putative ketosteroid isomerase (np_103587.1) from 2 mesorhizobium loti at 1.45 a resolution
46	<a href="#">c3bb9D_</a>	Alignment	not modelled	84.5	10	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> putative orphan protein; <b>PDBTitle:</b> crystal structure of a putative ketosteroid isomerase (sfri_1973) from 2 shewanella frigidimarina ncimb 400 at 1.80 a resolution
47	<a href="#">c3k7cC_</a>	Alignment	not modelled	83.8	17	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> putative ntf2-like transpeptidase; <b>PDBTitle:</b> crystal structure of putative ntf2-like transpeptidase (np_281412.1)2 from campylobacter jejuni at 2.00 a resolution
48	<a href="#">c5ig0A_</a>	Alignment	not modelled	83.4	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> camk/camk2 protein kinase; <b>PDBTitle:</b> crystal structure of s. rosetta camkii hub
49	<a href="#">c4hzbE_</a>	Alignment	not modelled	81.2	12	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> putative periplasmic protein; <b>PDBTitle:</b> crystal structure of the type vi semet effector-immunity complex tae3-2 tai3 from ralstonia pickettii
50	<a href="#">c6bjuD_</a>	Alignment	not modelled	80.4	14	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> atzh; <b>PDBTitle:</b> the structure of atzh: a little known member of the atrazine breakdown2 pathway
51	<a href="#">d3cnxa1</a>	Alignment	not modelled	78.6	8	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SAV4671-like
52	<a href="#">d3e99a1</a>	Alignment	not modelled	74.3	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
53	<a href="#">c3gwrA_</a>	Alignment	not modelled	73.9	12	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> putative calcium/calmodulin-dependent protein kinase type <b>PDBTitle:</b> crystal structure of putative calcium/calmodulin-dependent protein2 kinase type ii association domain (yp_315894.1) from thiobacillus3 denitrificans atcc 25259 at 2.00 a resolution
						<b>Fold:</b> Cystatin-like

54	<a href="#">d3bb9a1</a>	Alignment	not modelled	72.7	10	<b>Superfamily:</b> NTF2-like <b>Family:</b> SO0125-like
55	<a href="#">d2owpa1</a>	Alignment	not modelled	71.8	14	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BxeB1374-like
56	<a href="#">c2rsxA</a>	Alignment	not modelled	71.3	32	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yoeb; <b>PDBTitle:</b> solution structure of isea, an inhibitor protein of dl-endopeptidases2 from bacillus subtilis
57	<a href="#">c5uwaB</a>	Alignment	not modelled	60.8	8	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable phospholipid-binding protein mlac; <b>PDBTitle:</b> structure of e. coli phospholipid binding protein mlac
58	<a href="#">c3kspA</a>	Alignment	not modelled	58.6	13	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> calcium/calmodulin-dependent kinase ii association domain; <b>PDBTitle:</b> crystal structure of a putative ca/calmodulin-dependent kinase ii2 association domain (exig_1688) from exiguobacterium sibiricum 255-153 at 2.59 a resolution
59	<a href="#">c3fsdA</a>	Alignment	not modelled	57.1	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ntf2-like protein of unknown function in nutrient uptake; <b>PDBTitle:</b> crystal structure of ntf2-like protein of unknown function in nutrient2 uptake (yp_427473.1) from rhodospirillum rubrum atcc 11170 at 1.70 a3 resolution
60	<a href="#">c3ub1C</a>	Alignment	not modelled	56.8	13	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> orf13-like protein; <b>PDBTitle:</b> ntf2 like protein involved in plasmid conjugation
61	<a href="#">c3dukD</a>	Alignment	not modelled	53.7	13	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> ntf2-like protein of unknown function; <b>PDBTitle:</b> crystal structure of a ntf2-like protein of unknown function2 (mfla_0564) from methylobacillus flagellatus kt at 2.200 a resolution
62	<a href="#">d1vqqa1</a>	Alignment	not modelled	45.7	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Penicillin binding protein 2a (PBP2A), N-terminal domain
63	<a href="#">c2qguA</a>	Alignment	not modelled	43.1	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> probable signal peptide protein; <b>PDBTitle:</b> three-dimensional structure of the phospholipid-binding protein from2 ralstonia solanacearum q8xv73_ralsq in complex with a phospholipid at3 the resolution 1.53 a. northeast structural genomics consortium4 target rsr89
64	<a href="#">c4ouqA</a>	Alignment	not modelled	42.7	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf4783 family protein (bf1468) from2 bacteroides fragilis ych46 at 1.55 a resolution
65	<a href="#">c4ce4i</a>	Alignment	not modelled	41.1	16	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> mrpI9; <b>PDBTitle:</b> 39s large subunit of the porcine mitochondrial ribosome
66	<a href="#">c4or1A</a>	Alignment	not modelled	40.8	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf4783 family protein (bacova_04304) from2 bacteroides ovatus atcc 8483 at 1.40 a resolution
67	<a href="#">c1mwuA</a>	Alignment	not modelled	37.2	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 2a; <b>PDBTitle:</b> structure of methicillin acyl-penicillin binding protein 2a from2 methicillin resistant staphylococcus aureus strain 27r at 2.60 a3 resolution.
68	<a href="#">c4fczB</a>	Alignment	not modelled	29.9	15	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> toluene-tolerance protein; <b>PDBTitle:</b> crystal structure of toluene-tolerance protein from pseudomonas putida2 (strain kt2440), northeast structural genomics consortium (nesg)3 target ppr99
69	<a href="#">c3ke7A</a>	Alignment	not modelled	27.3	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative ketosteroid isomerase; <b>PDBTitle:</b> crystal structure of putative ketosteroid isomerase (yp_001303366.1)2 from parabacteroides distasonis atcc 8503 at 1.45 a resolution
70	<a href="#">c3fkaD</a>	Alignment	not modelled	26.7	15	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized ntf-2 like protein; <b>PDBTitle:</b> crystal structure of a ntf-2 like protein of unknown function2 (spo1084) from silicibacter pomeroyi dss-3 at 1.69 a resolution
71	<a href="#">c3hzpA</a>	Alignment	not modelled	24.2	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ntf2-like protein of unknown function; <b>PDBTitle:</b> crystal structure of ntf2-like protein of unknown function mn2a_05052 from prochlorococcus marinus (yp_291699.1) from prochlorococcus sp.3 nat12a at 1.40 a resolution
72	<a href="#">c5djQ_N</a>	Alignment	not modelled	23.7	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> N: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the structure of cbb3 cytochrome oxidase.
73	<a href="#">c5djQ_P</a>	Alignment	not modelled	23.7	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> P: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the structure of cbb3 cytochrome oxidase.
74	<a href="#">c5djQ_O</a>	Alignment	not modelled	23.7	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the structure of cbb3 cytochrome oxidase.
75	<a href="#">c5djQ_Q</a>	Alignment	not modelled	23.7	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> Q: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the structure of cbb3 cytochrome oxidase.
76	<a href="#">d1ulib</a>	Alignment	not modelled	22.6	9	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Ring hydroxylating beta subunit
77	<a href="#">c5vq0C</a>	Alignment	not modelled	22.4	25	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> microtubule-actin cross-linking factor 1,

77	<a href="#">c3ve3c</a>	Alignment	not modelled	22.4	23	isoforms 1/2/3/5; <b>PDB header:</b> structure of hacf7 ef1-ef2-gar domains
78	<a href="#">c3qk9B</a>	Alignment	not modelled	20.9	10	<b>PDB header:</b> protein transport <b>Chain:</b> B; <b>PDB Molecule:</b> mitochondrial import inner membrane translocase subunit <b>PDBTitle:</b> yeast tim44 c-terminal domain complexed with cymal-3
79	<a href="#">c4r4gA</a>	Alignment	not modelled	20.5	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> putative lipoprotein ycda; <b>PDBTitle:</b> crystal structure of a putative lipoprotein (ycda) from bacillus2 subtilis subsp. subtilis str. 168 at 2.62 a resolution
80	<a href="#">c5wqhE</a>	Alignment	not modelled	19.7	14	<b>PDB header:</b> isomerase <b>Chain:</b> E; <b>PDB Molecule:</b> isomerase trt14; <b>PDBTitle:</b> structure of fungal meroterpenoid isomerase trt14 complexed with2 substrate analog and endo-terretonin d
81	<a href="#">d1v5ra1</a>	Alignment	not modelled	19.3	25	<b>Fold:</b> N domain of copper amine oxidase-like <b>Superfamily:</b> GAS2 domain-like <b>Family:</b> GAS2 domain
82	<a href="#">c2n6uA</a>	Alignment	not modelled	18.3	43	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> astexin2-dc4; <b>PDBTitle:</b> solution study of astexin2-dc4
83	<a href="#">c2pg1L</a>	Alignment	not modelled	16.4	44	<b>PDB header:</b> structural protein <b>Chain:</b> J; <b>PDB Molecule:</b> cytoplasmic dynein 1 intermediate chain 2; <b>PDBTitle:</b> structural analysis of a cytoplasmic dynein light chain-2 intermediate chain complex
84	<a href="#">c2pg1L</a>	Alignment	not modelled	16.4	44	<b>PDB header:</b> structural protein <b>Chain:</b> L; <b>PDB Molecule:</b> cytoplasmic dynein 1 intermediate chain 2; <b>PDBTitle:</b> structural analysis of a cytoplasmic dynein light chain-2 intermediate chain complex
85	<a href="#">d2cw9a1</a>	Alignment	not modelled	16.3	8	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> TIM44-like
86	<a href="#">c5up5A</a>	Alignment	not modelled	16.1	43	<b>PDB header:</b> de novo protein <b>Chain:</b> A; <b>PDB Molecule:</b> ehee_rd1_0284; <b>PDBTitle:</b> solution structure of the de novo mini protein ehee_rd1_0284
87	<a href="#">c3r2cL</a>	Alignment	not modelled	16.0	20	<b>PDB header:</b> transcription/rna <b>Chain:</b> J; <b>PDB Molecule:</b> 30s ribosomal protein s10; <b>PDBTitle:</b> crystal structure of antitermination factors nusB and nusE in complex2 with boxA rna
88	<a href="#">c3efyB</a>	Alignment	not modelled	15.0	9	<b>PDB header:</b> cell cycle <b>Chain:</b> B; <b>PDB Molecule:</b> cif (cell cycle inhibiting factor); <b>PDBTitle:</b> structure of the cyclomodulin cif from pathogenic2 escherichia coli
89	<a href="#">c6f0kA</a>	Alignment	not modelled	13.1	10	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> cytochrome c family protein; <b>PDBTitle:</b> alternative complex iii
90	<a href="#">c2z8nB</a>	Alignment	not modelled	12.7	25	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> 27.5 kda virulence protein; <b>PDBTitle:</b> structural basis for the catalytic mechanism of phosphothreonine lyase
91	<a href="#">d2rcda1</a>	Alignment	not modelled	12.1	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> BxeB1374-like
92	<a href="#">c5x9jB</a>	Alignment	not modelled	11.9	8	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> prhc; <b>PDBTitle:</b> structure of prhc from penicillium brasilianum nbrC 6234
93	<a href="#">c2ytxA</a>	Alignment	not modelled	11.0	12	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> cold shock domain-containing protein e1; <b>PDBTitle:</b> solution structure of the second cold-shock domain of the human2 kiaa0885 protein (unr protein)
94	<a href="#">c2h3oA</a>	Alignment	not modelled	10.8	40	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> merf; <b>PDBTitle:</b> structure of merf, a membrane protein with two trans-2 membrane helices
95	<a href="#">c2mewA</a>	Alignment	not modelled	10.6	15	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> 30s ribosomal protein s10; <b>PDBTitle:</b> solution structure of nuse (s10) from thermotoga maritima
96	<a href="#">c5wdaL</a>	Alignment	not modelled	10.6	9	<b>PDB header:</b> protein transport <b>Chain:</b> L; <b>PDB Molecule:</b> general secretion pathway protein g; <b>PDBTitle:</b> structure of the pulg pseudopilus
97	<a href="#">c1wazA</a>	Alignment	not modelled	10.5	38	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> merf; <b>PDBTitle:</b> nmr structure determination of the bacterial mercury transporter,2 merf, in micelles
98	<a href="#">c5ts4A</a>	Alignment	not modelled	9.9	10	<b>PDB header:</b> de novo protein <b>Chain:</b> A; <b>PDB Molecule:</b> denovo ntf2; <b>PDBTitle:</b> crystal structure of a de novo designed protein with curved beta-sheet
99	<a href="#">c2kncA</a>	Alignment	not modelled	9.5	10	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> integrin alpha-iiB; <b>PDBTitle:</b> platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex