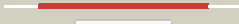
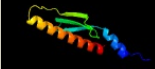


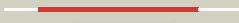
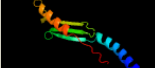



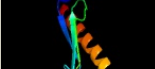


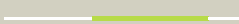


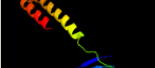










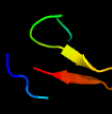
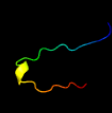
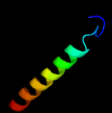




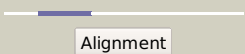
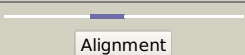
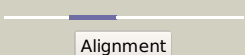


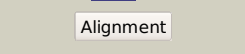

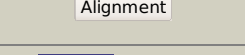
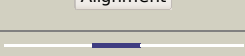

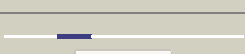

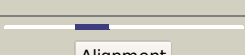
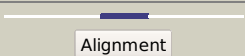
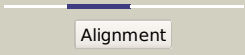
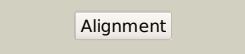
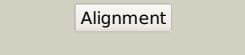
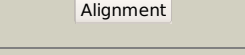





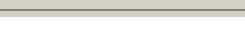

# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3880c_(-)_4360377_4360724
Date	Sat Aug 10 22:05:06 BST 2019
Unique Job ID	31a4c7e577a78216

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1j8ba_</a>	 Alignment		98.7	17	<b>Fold:</b> YbaB-like <b>Superfamily:</b> YbaB-like <b>Family:</b> YbaB-like
2	<a href="#">d1puga_</a>	 Alignment		98.6	20	<b>Fold:</b> YbaB-like <b>Superfamily:</b> YbaB-like <b>Family:</b> YbaB-like
3	<a href="#">c1ybxA_</a>	 Alignment		98.1	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> conserved hypothetical protein cth-383 from clostridium thermocellum
4	<a href="#">c3f42A_</a>	 Alignment		97.5	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein hp0035; <b>PDBTitle:</b> crystal structure of uncharacterized protein hp0035 from helicobacter2 pylori
5	<a href="#">d1pugb_</a>	 Alignment		96.6	22	<b>Fold:</b> YbaB-like <b>Superfamily:</b> YbaB-like <b>Family:</b> YbaB-like
6	<a href="#">c5yrxA_</a>	 Alignment		96.1	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoid-associated protein rv3716c; <b>PDBTitle:</b> crystal structure of a hypothetical protein rv3716c from mycobacterium2 tuberculosis
7	<a href="#">c3hnbW_</a>	 Alignment		60.4	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a basic coiled-coil protein of unknown function2 from eubacterium eligens atcc 27750
8	<a href="#">d1a87a_</a>	 Alignment		49.4	20	<b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> Colicin <b>Family:</b> Colicin
9	<a href="#">c1a87A_</a>	 Alignment		49.4	20	<b>PDB header:</b> bacteriocin <b>Chain:</b> A: <b>PDB Molecule:</b> colicin n; <b>PDBTitle:</b> colicin n
10	<a href="#">d1t3ua_</a>	 Alignment		33.0	19	<b>Fold:</b> Cell division protein ZapA-like <b>Superfamily:</b> Cell division protein ZapA-like <b>Family:</b> Cell division protein ZapA-like
11	<a href="#">d2o6pa1</a>	 Alignment		30.0	33	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> NEAT domain-like <b>Family:</b> NEAT domain

12	<a href="#">c2o6pA</a>	Alignment		29.4	33	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> iron-regulated surface determinant protein c; <b>PDBTitle:</b> crystal structure of the heme-isdc complex
13	<a href="#">d2d9ra1</a>	Alignment		25.4	21	<b>Fold:</b> Double-split beta-barrel <b>Superfamily:</b> AF2212/PG0164-like <b>Family:</b> PG0164-like
14	<a href="#">c4akrC</a>	Alignment		23.5	29	<b>PDB header:</b> actin-binding protein <b>Chain:</b> C; <b>PDB Molecule:</b> if-actin-capping protein subunit alpha; <b>PDBTitle:</b> crystal structure of the cytoplasmic actin capping protein2 cap32_34 from dictyostelium discoideum
15	<a href="#">c2k78A</a>	Alignment		20.5	36	<b>PDB header:</b> heme-binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> iron-regulated surface determinant protein c; <b>PDBTitle:</b> solution structure of the isdc neat domain bound to zinc2 protoporphyrin
16	<a href="#">c5w6pB</a>	Alignment		17.9	55	<b>PDB header:</b> viral protein, hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> tailspike protein 2; <b>PDBTitle:</b> crystal structure of bacteriophage cba120 tailspike protein 22 enzymatically active domain (tsp2dn, orf211)
17	<a href="#">d2itea1</a>	Alignment		17.8	4	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> NEAT domain-like <b>Family:</b> NEAT domain
18	<a href="#">c3teqB</a>	Alignment		17.2	24	<b>PDB header:</b> signaling protein <b>Chain:</b> B; <b>PDB Molecule:</b> stromal interaction molecule 1; <b>PDBTitle:</b> crystal structure of soar domain
19	<a href="#">d1izna</a>	Alignment		16.4	17	<b>Fold:</b> Subunits of heterodimeric actin filament capping protein Capz <b>Superfamily:</b> Subunits of heterodimeric actin filament capping protein Capz <b>Family:</b> Capz alpha-1 subunit
20	<a href="#">c2mmvA</a>	Alignment		15.7	21	<b>PDB header:</b> cell cycle <b>Chain:</b> A; <b>PDB Molecule:</b> cell division protein zapa; <b>PDBTitle:</b> zapa mutant dimer from geobacillus stearotherophilus
21	<a href="#">c4mypA</a>	Alignment	not modelled	15.3	23	<b>PDB header:</b> heme-binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> iron-regulated surface determinant protein a; <b>PDBTitle:</b> structure of the central neat domain, n2, of the listerial hbp22 protein complexed with heme
22	<a href="#">c2e7dA</a>	Alignment	not modelled	15.1	14	<b>PDB header:</b> metal binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein isdh; <b>PDBTitle:</b> crystal structure of a neat domain from staphylococcus aureus
23	<a href="#">c3sz6B</a>	Alignment	not modelled	14.2	9	<b>PDB header:</b> heme-binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> conserved domain protein; <b>PDBTitle:</b> isdx1, an anthrax hemophore
24	<a href="#">d2j9ua1</a>	Alignment	not modelled	13.7	30	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> VPS28 C-terminal domain-like <b>Family:</b> VPS28 C-terminal domain-like
25	<a href="#">d1hn0a3</a>	Alignment	not modelled	13.2	70	<b>Fold:</b> Hyaluronate lyase-like, C-terminal domain <b>Superfamily:</b> Hyaluronate lyase-like, C-terminal domain <b>Family:</b> Hyaluronate lyase-like, C-terminal domain
26	<a href="#">c5wvmA</a>	Alignment	not modelled	13.1	32	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> maltose-binding periplasmic protein,two-component system <b>PDBTitle:</b> crystal structure of baes cocrystallized with 2 mm indole
27	<a href="#">d1eh9a2</a>	Alignment	not modelled	12.2	50	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
28	<a href="#">d2co3a1</a>	Alignment	not modelled	11.5	29	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Bacterial adhesins <b>Family:</b> Pilus subunits

29	<a href="#">c3terA</a>	 Alignment	not modelled	11.5	10	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> mammalian stromal interaction molecule-1; <b>PDBTitle:</b> crystal structure of soar domain with inhibition helix from c. elegans
30	<a href="#">d2cnza1</a>	 Alignment	not modelled	11.4	29	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Bacterial adhesins <b>Family:</b> Pilus subunits
31	<a href="#">c2kq1A</a>	 Alignment	not modelled	10.8	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> bh0266 protein; <b>PDBTitle:</b> solution structure of protein bh0266 from bacillus2 halodurans. northeast structural genomics consortium target3 bhr97a
32	<a href="#">c3m86B</a>	 Alignment	not modelled	10.7	25	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> amoebiasin-2; <b>PDBTitle:</b> crystal structure of the cysteine protease inhibitor, ehicp2, from2 entamoeba histolytica
33	<a href="#">c5o6vF</a>	 Alignment	not modelled	10.2	38	<b>PDB header:</b> virus <b>Chain:</b> F: <b>PDB Molecule:</b> small envelope protein m; <b>PDBTitle:</b> the cryo-em structure of tick-borne encephalitis virus complexed with2 fab fragment of neutralizing antibody 19/1786
34	<a href="#">d3cdda2</a>	 Alignment	not modelled	9.8	22	<b>Fold:</b> Phage tail proteins <b>Superfamily:</b> Phage tail proteins <b>Family:</b> Baseplate protein-like
35	<a href="#">c4hcgA</a>	 Alignment	not modelled	9.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cupredoxin 1; <b>PDBTitle:</b> uncharacterized cupredoxin-like domain protein cupredoxin_1 with zinc2 bound from bacillus anthracis
36	<a href="#">c6f3tK</a>	 Alignment	not modelled	9.7	26	<b>PDB header:</b> transcription <b>Chain:</b> K: <b>PDB Molecule:</b> transcription initiation factor tfiid subunit 6; <b>PDBTitle:</b> crystal structure of the human taf5-taf6-taf9 complex
37	<a href="#">c2npbA</a>	 Alignment	not modelled	9.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> selenoprotein w; <b>PDBTitle:</b> nmr solution structure of mouse selw
38	<a href="#">c4b28A</a>	 Alignment	not modelled	9.5	24	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> metallopeptidase, family m24, putative; <b>PDBTitle:</b> crystal structure of dm5p lyase rddddp from roseobacter denitrificans
39	<a href="#">c2j9wB</a>	 Alignment	not modelled	9.4	25	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> vps28-prov protein; <b>PDBTitle:</b> structural insight into the escrt-ii link and its role in mvb2 trafficking
40	<a href="#">c6n1fD</a>	 Alignment	not modelled	9.3	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> oxidoreductase, 2og-fe(ii) oxygenase family; <b>PDBTitle:</b> crystal structure of oxidoreductase, 2og-fe(ii) oxygenase family, from2 burkholderia pseudomallei
41	<a href="#">c5o6vD</a>	 Alignment	not modelled	9.2	38	<b>PDB header:</b> virus <b>Chain:</b> D: <b>PDB Molecule:</b> small envelope protein m; <b>PDBTitle:</b> the cryo-em structure of tick-borne encephalitis virus complexed with2 fab fragment of neutralizing antibody 19/1786
42	<a href="#">d1sr3a</a>	 Alignment	not modelled	9.0	29	<b>Fold:</b> OB-fold <b>Superfamily:</b> Heme chaperone CcmE <b>Family:</b> Heme chaperone CcmE
43	<a href="#">c5o6vE</a>	 Alignment	not modelled	8.8	38	<b>PDB header:</b> virus <b>Chain:</b> E: <b>PDB Molecule:</b> small envelope protein m; <b>PDBTitle:</b> the cryo-em structure of tick-borne encephalitis virus complexed with2 fab fragment of neutralizing antibody 19/1786
44	<a href="#">c4ympC</a>	 Alignment	not modelled	8.6	6	<b>PDB header:</b> heme-binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> internalin; <b>PDBTitle:</b> crystal structure of the bacillus anthracis hal neat domain in complex2 with heme
45	<a href="#">c4yo3G</a>	 Alignment	not modelled	8.5	25	<b>PDB header:</b> transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> tssa; <b>PDBTitle:</b> enteroaggregative escherichia coli tssa n-terminal fragment
46	<a href="#">c3ge2A</a>	 Alignment	not modelled	8.5	16	<b>PDB header:</b> lipoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> lipoprotein, putative; <b>PDBTitle:</b> crystal structure of putative lipoprotein sp_0198 from streptococcus2 pneumoniae
47	<a href="#">c5o6aF</a>	 Alignment	not modelled	8.3	38	<b>PDB header:</b> virus <b>Chain:</b> F: <b>PDB Molecule:</b> small envelope protein m; <b>PDBTitle:</b> the cryo-em structure of tick-borne encephalitis virus mature particle
48	<a href="#">c5o6aE</a>	 Alignment	not modelled	8.3	38	<b>PDB header:</b> virus <b>Chain:</b> E: <b>PDB Molecule:</b> small envelope protein m; <b>PDBTitle:</b> the cryo-em structure of tick-borne encephalitis virus mature particle
49	<a href="#">c5o6aD</a>	 Alignment	not modelled	8.3	38	<b>PDB header:</b> virus <b>Chain:</b> D: <b>PDB Molecule:</b> small envelope protein m; <b>PDBTitle:</b> the cryo-em structure of tick-borne encephalitis virus mature particle
50	<a href="#">c3cddD</a>	 Alignment	not modelled	8.1	22	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> prophage muso2, 43 kda tail protein; <b>PDBTitle:</b> crystal structure of prophage muso2, 43 kda tail protein from2 shewanella oneidensis
51	<a href="#">c3rurB</a>	 Alignment	not modelled	7.8	4	<b>PDB header:</b> metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> iron-regulated surface determinant protein b; <b>PDBTitle:</b> staphylococcus aureus heme-bound selenomethionine-labeled isdb-n2
52	<a href="#">d1iq8a4</a>	 Alignment	not modelled	7.6	45	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Pre-PUA domain <b>Family:</b> Archaeosine tRNA-guanine transglycosylase, C2 domain
53	<a href="#">c3m6cA</a>	 Alignment	not modelled	7.6	26	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> 60 kda chaperonin 1; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis groel1 apical domain

54	<a href="#">d2oq0a1</a>	Alignment	not modelled	7.6	23	<b>Fold:</b> OB-fold <b>Superfamily:</b> HIN-2000 domain-like <b>Family:</b> HIN-200/IF120x domain
55	<a href="#">c4b6ad</a>	Alignment	not modelled	7.5	38	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> 60s ribosomal protein l5; <b>PDBTitle:</b> cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
56	<a href="#">c5vmme</a>	Alignment	not modelled	7.4	4	<b>PDB header:</b> transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> iron-regulated cell wall-anchored protein; <b>PDBTitle:</b> staphylococcus aureus isdb bound to human hemoglobin
57	<a href="#">d2a29a1</a>	Alignment	not modelled	7.1	12	<b>Fold:</b> Metal cation-transporting ATPase, ATP-binding domain N <b>Superfamily:</b> Metal cation-transporting ATPase, ATP-binding domain N <b>Family:</b> Metal cation-transporting ATPase, ATP-binding domain N
58	<a href="#">d3b5ha2</a>	Alignment	not modelled	7.0	50	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> I set domains
59	<a href="#">c3lyhB</a>	Alignment	not modelled	6.9	25	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> cobalamin (vitamin b12) biosynthesis cbix protein; <b>PDBTitle:</b> crystal structure of putative cobalamin (vitamin b12) biosynthesis2 cbix protein (yp_958415.1) from marinobacter aquaeolei vt8 at 1.60 a3 resolution
60	<a href="#">c2vzaD</a>	Alignment	not modelled	6.7	26	<b>PDB header:</b> cell adhesion <b>Chain:</b> D: <b>PDB Molecule:</b> cell filamentation protein; <b>PDBTitle:</b> type iv secretion system effector protein bepa
61	<a href="#">c4e1rA</a>	Alignment	not modelled	6.7	29	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein lsr2; <b>PDBTitle:</b> crystal structure of the dimerization domain of lsr2 from2 mycobacterium tuberculosis in the p 31 2 1 space group
62	<a href="#">c4e1pA</a>	Alignment	not modelled	6.7	29	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein lsr2; <b>PDBTitle:</b> crystal structure of the dimerization domain of lsr2 from2 mycobacterium tuberculosis in the p 1 21 1 space group
63	<a href="#">c2qjIA</a>	Alignment	not modelled	6.5	32	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-related modifier 1; <b>PDBTitle:</b> crystal structure of urm1
64	<a href="#">c3e0eA</a>	Alignment	not modelled	6.3	15	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> replication protein a; <b>PDBTitle:</b> crystal structure of a domain of replication protein a from2 methanococcus maripaludis. northeast structural genomics3 large mrr110b
65	<a href="#">c4fxtB</a>	Alignment	not modelled	6.3	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf3823 family protein (bacova_02663) from2 bacteroides ovatus atcc 8483 at 2.77 a resolution
66	<a href="#">d1qxya</a>	Alignment	not modelled	6.3	35	<b>Fold:</b> Creatinase/aminopeptidase <b>Superfamily:</b> Creatinase/aminopeptidase <b>Family:</b> Creatinase/aminopeptidase
67	<a href="#">c4qdyA</a>	Alignment	not modelled	6.1	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> crystal structure of a ybbr-like protein (sp_1560) from streptococcus2 pneumoniae tigr4 at 2.74 a resolution
68	<a href="#">c2zbtB</a>	Alignment	not modelled	6.1	27	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxal biosynthesis lyase pdxs; <b>PDBTitle:</b> crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8
69	<a href="#">c3ig4E</a>	Alignment	not modelled	6.1	30	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> xaa-pro aminopeptidase; <b>PDBTitle:</b> structure of a putative aminopeptidase p from bacillus anthracis
70	<a href="#">c4fo7B</a>	Alignment	not modelled	6.1	47	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> methionine aminopeptidase; <b>PDBTitle:</b> pseudomonas aeruginosa metap, in mn form
71	<a href="#">c6g7cF</a>	Alignment	not modelled	6.0	43	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> impa-related domain protein; <b>PDBTitle:</b> nt2-ctd domains of the tssa component from the type vi secretion2 system of aeromonas hydrophila.
72	<a href="#">c4txvB</a>	Alignment	not modelled	5.9	21	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c oxidase subunit 2; <b>PDBTitle:</b> crystal structure of the mixed disulfide intermediate between2 thioredoxin-like tlpas(c110s) and subunit ii of cytochrome c oxidase3 cox3 (c233s)
73	<a href="#">c6mzml</a>	Alignment	not modelled	5.9	25	<b>PDB header:</b> transcription/dna <b>Chain:</b> I: <b>PDB Molecule:</b> transcription initiation factor tfiid subunit 6; <b>PDBTitle:</b> human tfiid bound to promoter dna and tfiia
74	<a href="#">c4qslC</a>	Alignment	not modelled	5.7	35	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of listeria monocytogenes pyruvate carboxylase
75	<a href="#">c3lnbA</a>	Alignment	not modelled	5.7	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetyltransferase family protein; <b>PDBTitle:</b> crystal structure analysis of arylamine n-acetyltransferase c from2 bacillus anthracis
76	<a href="#">d1tafb</a>	Alignment	not modelled	5.6	26	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> TBP-associated factors, TAFs
77	<a href="#">d1wrua2</a>	Alignment	not modelled	5.6	18	<b>Fold:</b> Phage tail proteins <b>Superfamily:</b> Phage tail proteins <b>Family:</b> Baseplate protein-like
78	<a href="#">c4qr8B</a>	Alignment	not modelled	5.5	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> xaa-pro dipeptidase; <b>PDBTitle:</b> crystal structure of e coli pepq
						<b>PDB header:</b> heme-binding protein

79	<a href="#">c4h8pA_</a>	Alignment	not modelled	5.3	23	<b>Chain:</b> A; <b>PDB Molecule:</b> iron transport-associated domain protein; <b>PDBTitle:</b> neat5 domain of isdx2, a b. anthracis hemophore in complex with heme
80	<a href="#">d1o0xa_</a>	Alignment	not modelled	5.3	40	<b>Fold:</b> Creatinase/aminopeptidase <b>Superfamily:</b> Creatinase/aminopeptidase <b>Family:</b> Creatinase/aminopeptidase
81	<a href="#">d2gg2a1</a>	Alignment	not modelled	5.3	33	<b>Fold:</b> Creatinase/aminopeptidase <b>Superfamily:</b> Creatinase/aminopeptidase <b>Family:</b> Creatinase/aminopeptidase