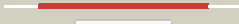



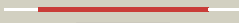












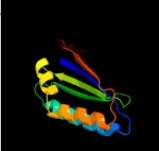






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0793 (-) _886722_887027
Date	Fri Jul 26 01:50:37 BST 2019
Unique Job ID	20a4ee1a1d1b6f52

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1y0ha_</a>	 Alignment		100.0	100	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> PA3566-like
2	<a href="#">c4zosA_</a>	 Alignment		99.9	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> protein ye0340 from yersinia enterocolitica subsp. <b>PDBTitle:</b> 2.20 angstrom resolution crystal structure of protein ye0340 of2 unidentified function from yersinia enterocolitica subsp.3 enterocolitica 8081]
3	<a href="#">c3bm7A_</a>	 Alignment		99.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> protein of unknown function with ferredoxin-like fold; <b>PDBTitle:</b> crystal structure of a putative antibiotic biosynthesis monooxygenase2 (cc_2132) from caulobacter crescentus cb15 at 1.35 a resolution
4	<a href="#">d2pd1a1</a>	 Alignment		99.9	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> PA3566-like
5	<a href="#">c2omoC_</a>	 Alignment		99.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> duf176; <b>PDBTitle:</b> putative antibiotic biosynthesis monooxygenase from nitrosomonas2 europaea
6	<a href="#">c2bbeA_</a>	 Alignment		99.9	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein so0527; <b>PDBTitle:</b> crystal structure of protein so0527 from shewanella oneidensis
7	<a href="#">d2omoa1</a>	 Alignment		99.9	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> PA3566-like
8	<a href="#">d1x7va_</a>	 Alignment		99.9	32	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> PA3566-like
9	<a href="#">c3e8oB_</a>	 Alignment		99.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein with ferredoxin-like fold; <b>PDBTitle:</b> crystal structure of a putative antibiotic biosynthesis monooxygenase2 (dr_2100) from deinococcus radiodurans at 1.40 a resolution
10	<a href="#">c3fgvB_</a>	 Alignment		99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein with ferredoxin-like fold; <b>PDBTitle:</b> crystal structure of a putative antibiotic biosynthesis monooxygenase2 (spo2313) from silicibacter pomeroyi dss-3 at 1.30 a resolution
11	<a href="#">c2gffB_</a>	 Alignment		99.9	22	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> lsrg protein; <b>PDBTitle:</b> crystal structure of yersinia pestis lsrg

12	<a href="#">c3mcsB_</a>	Alignment		99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative monooxygenase; <b>PDBTitle:</b> crystal structure of putative monooxygenase (fn1347) from2 fusobacterium nucleatum subsp. nucleatum atcc 25586 at 2.55 a3 resolution
13	<a href="#">c4dn9B_</a>	Alignment		99.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> antibiotic biosynthesis monooxygenase; <b>PDBTitle:</b> crystal structure of putative antibiotic biosynthesis monooxygenase2 from chloroflexus aurantiacus j-10-fl
14	<a href="#">c4dpoA_</a>	Alignment		99.9	22	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved protein; <b>PDBTitle:</b> crystal structure of a conserved protein mm_1583 from methanosarcina2 mazeri go1
15	<a href="#">d1tuva_</a>	Alignment		99.9	26	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> PA3566-like
16	<a href="#">c2fb0A_</a>	Alignment		99.9	18	<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 conserved protein of unknown function from2 bacteroides thetaiotaomicron vpi-5482 at 2.10 a resolution, possible3 oxidoreductase
17	<a href="#">c3gz7B_</a>	Alignment		99.9	18	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative antibiotic biosynthesis monooxygenase; <b>PDBTitle:</b> crystal structure of putative antibiotic biosynthesis monooxygenase2 (np_888398.1) from bordetella bronchiseptica at 2.15 a resolution
18	<a href="#">c4hl9B_</a>	Alignment		99.9	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> antibiotic biosynthesis monooxygenase; <b>PDBTitle:</b> crystal structure of antibiotic biosynthesis monooxygenase
19	<a href="#">c3kkfA_</a>	Alignment		99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative antibiotic biosynthesis monooxygenase; <b>PDBTitle:</b> crystal structure of putative antibiotic biosynthesis monooxygenase2 (np_810307.1) from bacteriodes thetaiotaomicron vpi-5482 at 1.30 a3 resolution
20	<a href="#">c3f44A_</a>	Alignment		99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative monooxygenase; <b>PDBTitle:</b> crystal structure of putative monooxygenase (yp_193413.1) from2 lactobacillus acidophilus ncfm at 1.55 a resolution
21	<a href="#">c3kngA_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> snoab; <b>PDBTitle:</b> crystal structure of snoab, a cofactor-independent oxygenase2 from streptomyces nogalater, determined to 1.9 resolution
22	<a href="#">c3hx9B_</a>	Alignment	not modelled	99.8	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> protein rv3592; <b>PDBTitle:</b> structure of heme-degrader, mhud (rv3592), from2 mycobacterium tuberculosis with two hemes bound in its3 active site
23	<a href="#">d1iuja_</a>	Alignment	not modelled	99.8	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> PG130-like
24	<a href="#">d1q8ba_</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Hypothetical protein YjCS
25	<a href="#">c6fxdB_</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> mupz; <b>PDBTitle:</b> crystal structure of mupz from pseudomonas fluorescens
26	<a href="#">c5f9pA_</a>	Alignment	not modelled	99.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> anthrone oxidase-like protein; <b>PDBTitle:</b> crystal structure study of anthrone oxidase-like protein
27	<a href="#">c2riIA_</a>	Alignment	not modelled	99.4	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> antibiotic biosynthesis monooxygenase; <b>PDBTitle:</b> crystal structure of a putative monooxygenase (yp_001095275.1) from2 shewanella loihica pv-4 at 1.26 a resolution
28	<a href="#">d2zdp1</a>	Alignment	not modelled	99.4	7	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> PG130-like
29	<a href="#">c3fi2A_</a>	Alignment	not modelled	99.4	11	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> monooxygenase-like protein;

29	<a href="#">c3jzA</a>	Alignment	not modelled	99.4	11	<b>PDBTitle:</b> crystal structure of a monooxygenase-like protein (lin2316) from <i>Listeria innocua</i> at 1.85 Å resolution
30	<a href="#">c3tvzA</a>	Alignment	not modelled	99.4	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein yhgC; <b>PDBTitle:</b> structure of <i>Bacillus subtilis</i> Hmob
31	<a href="#">c4ae5C</a>	Alignment	not modelled	99.3	16	<b>PDB header:</b> signaling protein <b>Chain:</b> C; <b>PDB Molecule:</b> signal transduction protein trap; <b>PDBTitle:</b> structure of a major regulator of staphylococcal pathogenesis
32	<a href="#">d1lq9a</a>	Alignment	not modelled	99.3	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Actinorhodin biosynthesis monooxygenase ActVa-Orf6
33	<a href="#">d1xbwa</a>	Alignment	not modelled	99.2	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> PG130-like
34	<a href="#">d1tz0a</a>	Alignment	not modelled	99.2	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> PG130-like
35	<a href="#">c5y02D</a>	Alignment	not modelled	97.9	9	<b>PDB header:</b> lyase <b>Chain:</b> D; <b>PDB Molecule:</b> hydroxynitrile lyase; <b>PDBTitle:</b> c-terminal peptide depleted mutant of hydroxynitrile lyase from <i>Passiflora edulis</i> (pehnl) bound with (r)-mandelonitrile
36	<a href="#">c3bn7A</a>	Alignment	not modelled	97.9	16	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> ferredoxin-like protein; <b>PDBTitle:</b> crystal structure of a dimeric ferredoxin-like protein (cc_2267) from <i>Caulobacter crescentus</i> cb15 at 1.64 Å resolution
37	<a href="#">d1q4ra</a>	Alignment	not modelled	97.9	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Plant stress-induced protein
38	<a href="#">c3bdcA</a>	Alignment	not modelled	97.9	7	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> mll5499 protein; <b>PDBTitle:</b> crystal structure of a dabb family protein with a ferredoxin-like fold2 (mll5499) from <i>Mesorhizobium loti</i> maff303099 at 1.79 Å resolution
39	<a href="#">d1tr0a</a>	Alignment	not modelled	97.8	10	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Plant stress-induced protein
40	<a href="#">c2qvcA</a>	Alignment	not modelled	97.8	16	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> ferredoxin-like protein; <b>PDBTitle:</b> crystal structure of a dimeric ferredoxin-like protein (bb1511) from <i>Bordetella bronchiseptica</i> rb50 at 1.90 Å resolution
41	<a href="#">c3bguA</a>	Alignment	not modelled	97.7	13	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> ferredoxin-like protein of unknown function; <b>PDBTitle:</b> crystal structure of a dimeric ferredoxin-like protein of unknown2 function (tfu_0763) from <i>Thermobifida fusca</i> yx at 1.50 Å resolution
42	<a href="#">d1rja</a>	Alignment	not modelled	97.5	12	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Plant stress-induced protein
43	<a href="#">c3bb5B</a>	Alignment	not modelled	97.5	11	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> stress responsive alpha-beta protein; <b>PDBTitle:</b> crystal structure of a dimeric ferredoxin-like protein of unknown2 function (jann_3925) from <i>Jannaschia</i> sp. ccs1 at 2.30 Å resolution
44	<a href="#">c3hfkB</a>	Alignment	not modelled	97.4	10	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> 4-methylmuconolactone methylisomerase; <b>PDBTitle:</b> crystal structure of 4-methylmuconolactone methylisomerase (h52a) in2 complex with 4-methylmuconolactone
45	<a href="#">c5ixuA</a>	Alignment	not modelled	97.4	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 an uncharacterized nipsnap domain protein from <i>Burkholderia xenovorans</i>
46	<a href="#">c3fmbA</a>	Alignment	not modelled	97.3	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> dimeric protein of unknown function and ferredoxin-like <b>PDBTitle:</b> crystal structure of dimeric protein of unknown function and2 ferredoxin-like fold (yp_212648.1) from <i>Bacteroides fragilis</i> nctc3 9343 at 1.85 Å resolution
47	<a href="#">d2cb2a1</a>	Alignment	not modelled	97.3	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> SOR-like
48	<a href="#">d1x8da1</a>	Alignment	not modelled	97.1	9	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Yjil-like
49	<a href="#">c2qlwA</a>	Alignment	not modelled	96.9	9	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> rhau; <b>PDBTitle:</b> crystal structure of rhamnose mutarotase rhau of <i>Rhizobium</i> 2 leguminosarum
50	<a href="#">c2qlxA</a>	Alignment	not modelled	96.9	9	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> l-rhamnose mutarotase; <b>PDBTitle:</b> crystal structure of rhamnose mutarotase rhau of <i>Rhizobium</i> 2 leguminosarum in complex with l-rhamnose
51	<a href="#">c5b0aA</a>	Alignment	not modelled	96.6	5	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> olivetolic acid cyclase; <b>PDBTitle:</b> polyketide cyclase oac from <i>Cannabis sativa</i> , h5q mutant
52	<a href="#">d1vqya1</a>	Alignment	not modelled	96.5	10	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> NIPSNAP
53	<a href="#">d2ftra1</a>	Alignment	not modelled	96.5	12	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> EthD-like
54	<a href="#">c5k9fA</a>	Alignment	not modelled	96.4	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> nipsnap domain protein; <b>PDBTitle:</b> crystal structure of a nipsnap domain protein from

						burkholderia2 xenovorans
55	<a href="#">d1vqsa_</a>	Alignment	not modelled	96.3	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> NIPSNAP
56	<a href="#">d2hiqa1</a>	Alignment	not modelled	96.1	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Hypothetical protein YdhR
57	<a href="#">c1wd6B_</a>	Alignment	not modelled	95.7	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> protein ydhr; <b>PDBTitle:</b> crystal structure of jw1657 from escherichia coli
58	<a href="#">d2go8a1</a>	Alignment	not modelled	95.7	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> PG130-like
59	<a href="#">c2djb_</a>	Alignment	not modelled	95.2	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> redy-like protein; <b>PDBTitle:</b> crystal structure of hapk from hahella chejuensis
60	<a href="#">c5kakE_</a>	Alignment	not modelled	95.1	16	<b>PDB header:</b> unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of an uncharacterized nipsnap-like domain protein2 from burkholderia xenovorans
61	<a href="#">c6hnnA_</a>	Alignment	not modelled	94.9	8	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> l-rhamnose mutarotase; <b>PDBTitle:</b> crystal structure of l-rhamnose mutarotase fa22100 from formosa2 agariphila
62	<a href="#">c3dcaC_</a>	Alignment	not modelled	94.5	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> rpa0582; <b>PDBTitle:</b> crystal structure of the rpa0582- protein of unknown2 function from rhodopseudomonas palustris- a structural3 genomics target
63	<a href="#">d2fiua1</a>	Alignment	not modelled	94.4	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Atu0297-like
64	<a href="#">c3lo3E_</a>	Alignment	not modelled	94.2	10	<b>PDB header:</b> structure genomics, unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> uncharacterized conserved protein; <b>PDBTitle:</b> the crystal structure of a conserved functionally unknown protein from2 colwellia psycherythraea 34h.
65	<a href="#">c3bf4B_</a>	Alignment	not modelled	89.4	14	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ethyl tert-butyl ether degradation ethd protein; <b>PDBTitle:</b> crystal structure of an ethd-like protein (reut_b5694) from ralstonia2 eutropha jmp134 at 2.10 a resolution
66	<a href="#">c3gn6B_</a>	Alignment	not modelled	79.2	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ct0912, orfan protein with a ferredoxin-like domain repeat; <b>PDBTitle:</b> crystal structure of ct0912, orfan protein from chlorobium tepidum2 with a ferredoxin-like domain repeat (np_661805.1) from chlorobium3 tepidum t1s at 1.80 a resolution
67	<a href="#">c3a16C_</a>	Alignment	not modelled	75.3	16	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> aldoxime dehydratase; <b>PDBTitle:</b> crystal structure of aldoxime dehydratase (oxdre) in complex2 with propionaldoxime
68	<a href="#">d2ifxa1</a>	Alignment	not modelled	66.6	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> MmlI-like
69	<a href="#">c2kl8A_</a>	Alignment	not modelled	45.6	30	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> or15; <b>PDBTitle:</b> solution nmr structure of de novo designed ferredoxin-like fold2 protein, northeast structural genomics consortium target or15
70	<a href="#">c5cw9A_</a>	Alignment	not modelled	43.5	33	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> de novo designed ferredoxin-ferredoxin domain insertion <b>PDBTitle:</b> crystal structure of de novo designed ferredoxin-ferredoxin domain2 insertion protein
71	<a href="#">d2cfxa2</a>	Alignment	not modelled	29.1	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Lrp/AsnC-like transcriptional regulator C-terminal domain
72	<a href="#">c4hhuA_</a>	Alignment	not modelled	24.2	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> or280; <b>PDBTitle:</b> crystal structure of engineered protein. northeast structural genomics2 consortium target or280.
73	<a href="#">c4ky3A_</a>	Alignment	not modelled	22.3	26	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> designed protein or327; <b>PDBTitle:</b> three-dimensional structure of the orthorhombic crystal of2 computationally designed insertion domain , northeast structural3 genomics consortium (nesg) target or327
74	<a href="#">d2cs4a1</a>	Alignment	not modelled	17.1	31	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ras-binding domain, RBD
75	<a href="#">c2e1aD_</a>	Alignment	not modelled	16.4	14	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> 75aa long hypothetical regulatory protein asnc; <b>PDBTitle:</b> crystal structure of ffrp-dm1
76	<a href="#">c1zr9A_</a>	Alignment	not modelled	11.4	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein 593; <b>PDBTitle:</b> solution structure of a human c2h2-type zinc finger protein
77	<a href="#">d1zr9a1</a>	Alignment	not modelled	11.4	15	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> HkH motif-containing C2H2 finger
78	<a href="#">c3znul_</a>	Alignment	not modelled	10.2	16	<b>PDB header:</b> lyase <b>Chain:</b> I: <b>PDB Molecule:</b> 5-chloromuconolactone dehalogenase; <b>PDBTitle:</b> crystal structure of clcf in crystal form 2
79	<a href="#">c5yh1A_</a>	Alignment	not modelled	9.3	8	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> member of s1p family of ribosomal proteins;

						<b>PDBTitle:</b> member of s1p family of ribosomal proteins pf0399 dhh domain
80	<a href="#">c4iyqB_</a>	Alignment	not modelled	9.2	15	<b>PDB header:</b> protein binding <b>Chain:</b> B; <b>PDB Molecule:</b> divalent ion tolerance protein cuta1; <b>PDBTitle:</b> crystal structure of divalent ion tolerance protein cuta1 from2 ehrlichia chaffeensis
81	<a href="#">d1wi0a_</a>	Alignment	not modelled	7.9	17	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> CAD & PB1 domains <b>Family:</b> PB1 domain
82	<a href="#">d2atza1</a>	Alignment	not modelled	7.7	18	<b>Fold:</b> Prim-pol domain <b>Superfamily:</b> Prim-pol domain <b>Family:</b> HP0184-like
83	<a href="#">d2pc6a1</a>	Alignment	not modelled	7.3	4	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> IlvH-like
84	<a href="#">c4lqbA_</a>	Alignment	not modelled	7.2	7	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein kfla3161
85	<a href="#">c2djwF_</a>	Alignment	not modelled	6.9	19	<b>PDB header:</b> unknown function <b>Chain:</b> F; <b>PDB Molecule:</b> probable transcriptional regulator, asnc family; <b>PDBTitle:</b> crystal structure of ttha0845 from thermus thermophilus hb8
86	<a href="#">c4ic7B_</a>	Alignment	not modelled	6.8	17	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> dual specificity mitogen-activated protein kinase kinase 5; <b>PDBTitle:</b> crystal structure of the erk5 kinase domain in complex with an mkk52 binding fragment
87	<a href="#">d2cyya2</a>	Alignment	not modelled	6.7	12	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Lrp/AsnC-like transcriptional regulator C-terminal domain
88	<a href="#">d2f1fa2</a>	Alignment	not modelled	6.5	9	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> IlvH-like
89	<a href="#">d2r85a2</a>	Alignment	not modelled	6.4	16	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> PurP ATP-binding domain-like
90	<a href="#">d2fgca1</a>	Alignment	not modelled	5.5	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> IlvH-like
91	<a href="#">c3bpjD_</a>	Alignment	not modelled	5.5	8	<b>PDB header:</b> translation <b>Chain:</b> D; <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 subunit j; <b>PDBTitle:</b> crystal structure of human translation initiation factor 3, subunit 12 alpha
92	<a href="#">d2npta1</a>	Alignment	not modelled	5.3	20	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> CAD & PB1 domains <b>Family:</b> PB1 domain