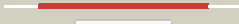



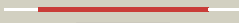






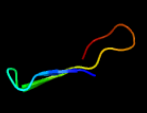



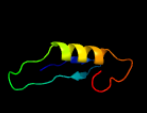

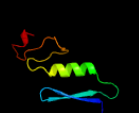

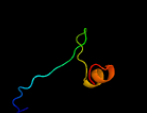

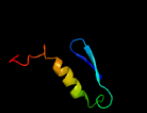


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2314c (- )_2585927_2587300
Date	Mon Aug 5 13:25:46 BST 2019
Unique Job ID	f8417e72c944c30c

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1vpba_</a>	 Alignment		100.0	15	<b>Fold:</b> Putative modulator of DNA gyrase, PmbA/TldD <b>Superfamily:</b> Putative modulator of DNA gyrase, PmbA/TldD <b>Family:</b> Putative modulator of DNA gyrase, PmbA/TldD
2	<a href="#">c5njaC_</a>	 Alignment		100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> metalloprotease tldd; <b>PDBTitle:</b> e. coli microcin-processing metalloprotease tldd/e with angiotensin2 analogue bound
3	<a href="#">d1vl4a_</a>	 Alignment		100.0	15	<b>Fold:</b> Putative modulator of DNA gyrase, PmbA/TldD <b>Superfamily:</b> Putative modulator of DNA gyrase, PmbA/TldD <b>Family:</b> Putative modulator of DNA gyrase, PmbA/TldD
4	<a href="#">c3qtdC_</a>	 Alignment		100.0	16	<b>PDB header:</b> gene regulation <b>Chain:</b> C: <b>PDB Molecule:</b> pmba protein; <b>PDBTitle:</b> crystal structure of putative modulator of gyrase (pmba) from2 pseudomonas aeruginosa pao1
5	<a href="#">d1o12a1</a>	 Alignment		49.5	38	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> N-acetylglucosamine-6-phosphate deacetylase, NagA
6	<a href="#">d1mlha1</a>	 Alignment		35.7	37	<b>Fold:</b> N-utilization substance G protein NusG, insert domain <b>Superfamily:</b> N-utilization substance G protein NusG, insert domain <b>Family:</b> N-utilization substance G protein NusG, insert domain
7	<a href="#">d1xcca_</a>	 Alignment		32.1	14	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
8	<a href="#">c2i81B_</a>	 Alignment		30.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-cys peroxiredoxin; <b>PDBTitle:</b> crystal structure of plasmodium vivax 2-cys peroxiredoxin,2 reduced
9	<a href="#">c3tkpB_</a>	 Alignment		29.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> peroxiredoxin-4; <b>PDBTitle:</b> crystal structure of full-length human peroxiredoxin 4 in the reduced2 form
10	<a href="#">c4qlpB_</a>	 Alignment		27.4	16	<b>PDB header:</b> hydrolase/protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> alanine and proline rich protein, tuberculosis necrotizing <b>PDBTitle:</b> atomic structure of tuberculosis necrotizing toxin (tnt) complexed2 with its immunity factor ift
11	<a href="#">d2h01a1</a>	 Alignment		23.4	26	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like

12	<a href="#">c2v2gC_</a>	Alignment		22.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> peroxiredoxin 6; <b>PDBTitle:</b> crystal structure of the c45s mutant of the peroxiredoxin 62 of arenicola marina. monoclinic form
13	<a href="#">c5ykjA_</a>	Alignment		21.1	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> peroxiredoxin prx1, mitochondrial; <b>PDBTitle:</b> structural basis of the thiol resolving mechanism in yeast2 mitochondrial 1-cys peroxiredoxin via glutathione/thioredoxin systems
14	<a href="#">c2vjwA_</a>	Alignment		20.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gaf family protein; <b>PDBTitle:</b> crystal structure of the second gaf domain of devs from2 mycobacterium smegmatis
15	<a href="#">c5ineA_</a>	Alignment		19.9	28	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> pre-glycoprotein polyprotein gp complex; <b>PDBTitle:</b> crystal structure of the prefusion glycoprotein of lcmv
16	<a href="#">c6feuj_</a>	Alignment		19.1	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> J: <b>PDB Molecule:</b> peroxiredoxin; <b>PDBTitle:</b> prxq2, a 1-cys peroxiredoxin of the thermo-acidophilic archaeon2 sulfobolus islandicus
17	<a href="#">c3gzkA_</a>	Alignment		18.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulase; <b>PDBTitle:</b> structure of a. acidocaldarius cellulase ccla
18	<a href="#">d1pd0a4</a>	Alignment		15.9	38	<b>Fold:</b> Gelsolin-like <b>Superfamily:</b> C-terminal, gelsolin-like domain of Sec23/24 <b>Family:</b> C-terminal, gelsolin-like domain of Sec23/24
19	<a href="#">c5vk2a_</a>	Alignment		15.2	32	<b>PDB header:</b> viral protein/immune system <b>Chain:</b> A: <b>PDB Molecule:</b> pre-glycoprotein polyprotein gp complex; <b>PDBTitle:</b> structural basis for antibody-mediated neutralization of lassa virus
20	<a href="#">c4nk8A_</a>	Alignment		14.9	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> poly(beta-d-mannuronate) c5 epimerase; <b>PDBTitle:</b> crystal structure of the periplasmic alginate epimerase algg d317a2 mutant
21	<a href="#">d1uula_</a>	Alignment	not modelled	14.1	13	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
22	<a href="#">d1n8ja_</a>	Alignment	not modelled	13.9	25	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
23	<a href="#">c5jcgC_</a>	Alignment	not modelled	13.6	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> thioredoxin-dependent peroxide reductase, mitochondrial; <b>PDBTitle:</b> structure of human peroxiredoxin 3 as three stacked rings
24	<a href="#">c2oodA_</a>	Alignment	not modelled	12.3	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> blr3880 protein; <b>PDBTitle:</b> crystal structure of guanine deaminase from bradyrhizobium japonicum
25	<a href="#">c5enuB_</a>	Alignment	not modelled	12.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alkyl hydroperoxide reductase/ thiol specific antioxidant/ <b>PDBTitle:</b> crystal structure of an alkyl hydroperoxide reductase from burkholderia2 ambifaria
26	<a href="#">c3ixrA_</a>	Alignment	not modelled	11.6	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> bacterioferritin comigratory protein; <b>PDBTitle:</b> crystal structure of xylella fastidiosa prxq c47s mutant
27	<a href="#">c4b1vM_</a>	Alignment	not modelled	10.4	29	<b>PDB header:</b> structural protein <b>Chain:</b> M: <b>PDB Molecule:</b> phosphatase and actin regulator 1; <b>PDBTitle:</b> structure of the phactr1 rpel-n domain bound to g-actin
28	<a href="#">c4b1vN_</a>	Alignment	not modelled	10.4	29	<b>PDB header:</b> structural protein <b>Chain:</b> N: <b>PDB Molecule:</b> phosphatase and actin regulator 1; <b>PDBTitle:</b> structure of the phactr1 rpel-n domain bound to g-actin

29	<a href="#">c2ov2O_</a>	Alignment	not modelled	10.3	29	<b>PDB header:</b> protein binding/transferase <b>Chain:</b> O: <b>PDB Molecule:</b> serine/threonine-protein kinase pak 4; <b>PDBTitle:</b> the crystal structure of the human rac3 in complex with the crib2 domain of human p21-activated kinase 4 (pak4)
30	<a href="#">c1bknA_</a>	Alignment	not modelled	10.2	16	<b>PDB header:</b> dna repair <b>Chain:</b> A: <b>PDB Molecule:</b> mutl; <b>PDBTitle:</b> crystal structure of an n-terminal 40kd fragment of e. coli2 dna mismatch repair protein mutl
31	<a href="#">d3dm8a1</a>	Alignment	not modelled	10.1	4	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Rpa4348-like
32	<a href="#">c4b1uM_</a>	Alignment	not modelled	10.0	29	<b>PDB header:</b> structural protein <b>Chain:</b> M: <b>PDB Molecule:</b> phosphatase and actin regulator 1; <b>PDBTitle:</b> structure of the phactr1 rpe1 domain and rpe1 motif directed2 assemblies with g-actin reveal the molecular basis for actin binding3 cooperativity.
33	<a href="#">c5d5oE_</a>	Alignment	not modelled	9.9	23	<b>PDB header:</b> unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> uncharacterized protein mj0489; <b>PDBTitle:</b> hcgc from methanocaldococcus jannaschii
34	<a href="#">d2fy6a1</a>	Alignment	not modelled	9.6	26	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
35	<a href="#">c3w6gP_</a>	Alignment	not modelled	9.3	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> P: <b>PDB Molecule:</b> probable peroxiredoxin; <b>PDBTitle:</b> structure of peroxiredoxin from anaerobic hyperthermophilic archaeon2 pyrococcus horikoshii
36	<a href="#">d1tbxa_</a>	Alignment	not modelled	9.2	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> F93-like
37	<a href="#">d1prxa_</a>	Alignment	not modelled	8.8	14	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
38	<a href="#">c3gknA_</a>	Alignment	not modelled	8.6	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> bacterioferritin comigratory protein; <b>PDBTitle:</b> insights into the alkyl peroxide reduction activity of xanthomonas2 campestris bacterioferritin comigratory protein from the trapped3 intermediate/ligand complex structures
39	<a href="#">d1pb1a_</a>	Alignment	not modelled	8.5	15	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases
40	<a href="#">c2iv0A_</a>	Alignment	not modelled	8.3	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> isocitrate dehydrogenase; <b>PDBTitle:</b> thermal stability of isocitrate dehydrogenase from2 archaeoglobus fulgidus studied by crystal structure3 analysis and engineering of chimers
41	<a href="#">d1t3ba1</a>	Alignment	not modelled	8.1	16	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbC/DsbG C-terminal domain-like
42	<a href="#">c4kb3B_</a>	Alignment	not modelled	8.1	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> peroxidoxin; <b>PDBTitle:</b> crystal structure of the mitochondrial peroxiredoxin from leishmania2 braziliensis in the decameric form
43	<a href="#">c2odbB_</a>	Alignment	not modelled	7.9	27	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase pak 6; <b>PDBTitle:</b> the crystal structure of human cdc42 in complex with the crib domain2 of human p21-activated kinase 6 (pak6)
44	<a href="#">c5zteA_</a>	Alignment	not modelled	7.7	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-cys peroxiredoxin bas1, chloroplastic; <b>PDBTitle:</b> crystal structure of prxa c119s mutant from arabidopsis thaliana
45	<a href="#">c3blxM_</a>	Alignment	not modelled	7.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> M: <b>PDB Molecule:</b> isocitrate dehydrogenase [nad] subunit 1; <b>PDBTitle:</b> yeast isocitrate dehydrogenase (apo form)
46	<a href="#">c5jheA_</a>	Alignment	not modelled	7.5	27	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> peptidyl-prolyl cis-trans isomerase cyp7; <b>PDBTitle:</b> the crystal structure of the saccharomyces cerevisiae co-chaperone2 cpr7
47	<a href="#">d1w0da_</a>	Alignment	not modelled	7.5	23	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases
48	<a href="#">d1hqsa_</a>	Alignment	not modelled	7.4	8	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases
49	<a href="#">d1bkna2</a>	Alignment	not modelled	7.4	16	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> DNA gyrase/MutL, N-terminal domain
50	<a href="#">c2w0cL_</a>	Alignment	not modelled	7.2	11	<b>PDB header:</b> virus <b>Chain:</b> L: <b>PDB Molecule:</b> protein 2; <b>PDBTitle:</b> x-ray structure of the entire lipid-containing bacteriophage pm2
51	<a href="#">c1x0lB_</a>	Alignment	not modelled	7.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> homoisocitrate dehydrogenase; <b>PDBTitle:</b> crystal structure of tetrameric homoisocitrate dehydrogenase from an2 extreme thermophile, thermus thermophilus
52	<a href="#">c1tyoA_</a>	Alignment	not modelled	6.9	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> isocitrate dehydrogenase; <b>PDBTitle:</b> isocitrate dehydrogenase from the hyperthermophile aeropyrum pernix in2 complex with etheno-nadp
53	<a href="#">d1a05a_</a>	Alignment	not modelled	6.8	8	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases
						<b>PDB header:</b> oxidoreductase

54	<a href="#">c3vj3A_</a>	Alignment	not modelled	6.4	8	<b>Chain:</b> A: <b>PDB Molecule:</b> 3-isopropylmalate dehydrogenase; <b>PDBTitle:</b> 3-isopropylmalate dehydrogenase from shewanella oneidensis mr-1 at 3402 mpa
55	<a href="#">c1htrP_</a>	Alignment	not modelled	6.4	7	<b>PDB header:</b> aspartyl protease <b>Chain:</b> P: <b>PDB Molecule:</b> progastricsin (pro segment); <b>PDBTitle:</b> crystal and molecular structures of human progastricsin at 1.622 angstroms resolution
56	<a href="#">c3r8wC_</a>	Alignment	not modelled	6.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-isopropylmalate dehydrogenase 2, chloroplastic; <b>PDBTitle:</b> structure of 3-isopropylmalate dehydrogenase isoform 2 from2 arabidopsis thaliana at 2.2 angstrom resolution
57	<a href="#">c2kiA_</a>	Alignment	not modelled	6.2	8	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> nmr structure of the h103g mutant so2144 h-nox domain from2 shewanella oneidensis in the fe(ii)co ligation state
58	<a href="#">d1xcra1</a>	Alignment	not modelled	6.1	20	<b>Fold:</b> AF0104/ALDC/Ptd012-like <b>Superfamily:</b> AF0104/ALDC/Ptd012-like <b>Family:</b> PTD012-like
59	<a href="#">d1vp7b_</a>	Alignment	not modelled	6.1	21	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> XseB-like <b>Family:</b> XseB-like
60	<a href="#">d1vp7a_</a>	Alignment	not modelled	6.1	21	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> XseB-like <b>Family:</b> XseB-like
61	<a href="#">c3upsA_</a>	Alignment	not modelled	6.1	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> iojap-like protein; <b>PDBTitle:</b> crystal structure of iojap-like protein from zymomonas mobilis
62	<a href="#">c3sbcG_</a>	Alignment	not modelled	6.1	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> peroxiredoxin tsa1; <b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae tsa1c47s mutant protein
63	<a href="#">c2qygC_</a>	Alignment	not modelled	6.0	20	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> ribulose biphosphate carboxylase-like protein 2; <b>PDBTitle:</b> crystal structure of a rubisco-like protein rlp2 from rhodospseudomonas2 palustris
64	<a href="#">c1o12B_</a>	Alignment	not modelled	5.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> n-acetylglucosamine-6-phosphate deacetylase; <b>PDBTitle:</b> crystal structure of n-acetylglucosamine-6-phosphate deacetylase2 (tm0814) from thermotoga maritima at 2.5 a resolution
65	<a href="#">d1cm7a_</a>	Alignment	not modelled	5.8	7	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases
66	<a href="#">d1wpwa_</a>	Alignment	not modelled	5.6	15	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases
67	<a href="#">c1e0aB_</a>	Alignment	not modelled	5.6	33	<b>PDB header:</b> signalling protein/kinase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase pak-alpha; <b>PDBTitle:</b> cdc42 complexed with the gtpase binding domain of p212 activated kinase
68	<a href="#">d1g2ua_</a>	Alignment	not modelled	5.5	15	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases
69	<a href="#">c5ovqL_</a>	Alignment	not modelled	5.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> L: <b>PDB Molecule:</b> peroxiredoxin; <b>PDBTitle:</b> crystal structure of the peroxiredoxin (ahpc2) from the2 hyperthermophilic bacteria aquifex aeolicus vf
70	<a href="#">c2rjzA_</a>	Alignment	not modelled	5.5	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> pilo protein; <b>PDBTitle:</b> crystal structure of the type 4 fimbrial biogenesis protein pilo from2 pseudomonas aeruginosa
71	<a href="#">c3ztlB_</a>	Alignment	not modelled	5.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin peroxidase; <b>PDBTitle:</b> crystal structure of decameric form of peroxiredoxin i from2 schistosoma mansoni
72	<a href="#">c2bmxB_</a>	Alignment	not modelled	5.5	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alkyl hydroperoxidase c; <b>PDBTitle:</b> mycobacterium tuberculosis ahpc
73	<a href="#">d1xaca_</a>	Alignment	not modelled	5.4	15	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases
74	<a href="#">d1vr4a1</a>	Alignment	not modelled	5.4	20	<b>Fold:</b> Dodecin subunit-like <b>Superfamily:</b> YbjQ-like <b>Family:</b> YbjQ-like
75	<a href="#">c5mnwA_</a>	Alignment	not modelled	5.3	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> guanylate cyclase soluble subunit beta-1; <b>PDBTitle:</b> solution structure of the cinaciguat bound human beta1 h-nox.
76	<a href="#">c1y2iC_</a>	Alignment	not modelled	5.3	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical protein s0862; <b>PDBTitle:</b> crystal structure of mcsg target apc27401 from shigella flexneri
77	<a href="#">d1y2ia_</a>	Alignment	not modelled	5.3	26	<b>Fold:</b> Dodecin subunit-like <b>Superfamily:</b> YbjQ-like <b>Family:</b> YbjQ-like
78	<a href="#">c2hqhB_</a>	Alignment	not modelled	5.3	9	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein mg376 homolog; <b>PDBTitle:</b> crystal structure of a small single-stranded dna binding2 protein from mycoplasma pneumoniae
79	<a href="#">d1qmva_</a>	Alignment	not modelled	5.2	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like

80	<a href="#">d1m7ja1</a>	Alignment	not modelled	5.2	17	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> D-aminoacylase
81	<a href="#">c4k59A</a>	Alignment	not modelled	5.2	23	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna binding protein rsmf; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa rsmf
82	<a href="#">d2j85a1</a>	Alignment	not modelled	5.2	9	<b>Fold:</b> STIV B116-like <b>Superfamily:</b> STIV B116-like <b>Family:</b> STIV B116-like
83	<a href="#">d1eeja1</a>	Alignment	not modelled	5.1	14	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbC/DsbG C-terminal domain-like
84	<a href="#">d2zccta1</a>	Alignment	not modelled	5.1	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like