



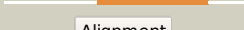

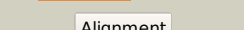

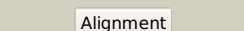






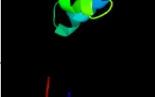
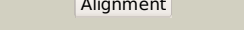

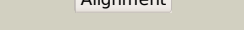

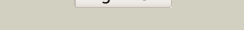

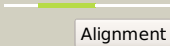

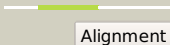
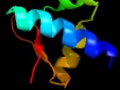
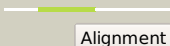





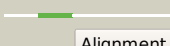

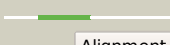

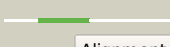



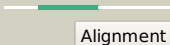
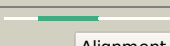
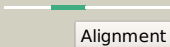
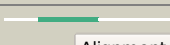


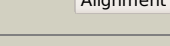
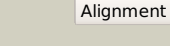



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1044 (- )_1167057_1167680
Date	Wed Jul 31 22:05:11 BST 2019
Unique Job ID	72e2ee7b4c30589b

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1zela_</a>	 Alignment		98.1	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein rv2827c; <b>PDBTitle:</b> crystal structure of rv2827c protein from mycobacterium tuberculosis
2	<a href="#">c3b73A_</a>	 Alignment		93.7	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> phiH1 repressor-like protein; <b>PDBTitle:</b> crystal structure of the phiH1 repressor-like protein from haloarcula2 marismortui
3	<a href="#">d1zela2</a>	 Alignment		88.3	17	<b>Fold:</b> Rv2827c C-terminal domain-like <b>Superfamily:</b> Rv2827c C-terminal domain-like <b>Family:</b> Rv2827c C-terminal domain-like
4	<a href="#">c2pjpA_</a>	 Alignment		83.1	13	<b>PDB header:</b> translation/rna <b>Chain:</b> A: <b>PDB Molecule:</b> selenocysteine-specific elongation factor; <b>PDBTitle:</b> structure of the mrna-binding domain of elongation factor2 selb from e.coli in complex with secis rna
5	<a href="#">c3lmmB_</a>	 Alignment		79.3	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the dip2311 protein from corynebacterium2 diphtheriae, northeast structural genomics consortium target cdr35
6	<a href="#">d1mkma1</a>	 Alignment		78.7	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Transcriptional regulator IclR, N-terminal domain
7	<a href="#">c4j2nA_</a>	 Alignment		74.4	25	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> gp37; <b>PDBTitle:</b> crystal structure of mycobacteriophage pukovnik xis
8	<a href="#">c4o6jA_</a>	 Alignment		72.4	16	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> iron-dependent transcription repressor related protein; <b>PDBTitle:</b> crystal structure of t. acidophilum ider
9	<a href="#">c2kfsA_</a>	 Alignment		72.3	18	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical regulatory protein; <b>PDBTitle:</b> nmr structure of rv2175c
10	<a href="#">d1j5ya1</a>	 Alignment		71.1	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
11	<a href="#">c4j2nB_</a>	 Alignment		70.8	25	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> gp37; <b>PDBTitle:</b> crystal structure of mycobacteriophage pukovnik xis

12	<a href="#">c2o0yB_</a>	 Alignment		66.5	15	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator rha1_ro069532 (iclr-family) from rhodococcus sp.
13	<a href="#">c2x4hA_</a>	 Alignment		66.2	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein sso2273; <b>PDBTitle:</b> crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
14	<a href="#">c2h09A_</a>	 Alignment		65.8	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator mntr; <b>PDBTitle:</b> crystal structure of diphtheria toxin repressor like protein2 from e. coli
15	<a href="#">c3i09B_</a>	 Alignment		64.9	27	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator2 (jann_22dec04_contig27_revised_gene3569) from jannaschia sp. ccs1 at3 2.81 a resolution
16	<a href="#">c2g7uB_</a>	 Alignment		58.4	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> 2.3 a structure of putative catechol degradative operon regulator from2 rhodococcus sp. rha1
17	<a href="#">c6amaO_</a>	 Alignment		56.9	27	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> O: <b>PDB Molecule:</b> putative dna-binding protein; <b>PDBTitle:</b> structure of s. coelicolor/s. venezuelae bldc-smea-ssfa complex to2 3.09 angstrom
18	<a href="#">c5whmB_</a>	 Alignment		55.7	12	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> iclr family transcriptional regulator; <b>PDBTitle:</b> crystal structure of iclr family transcriptional regulator from2 brucella abortus
19	<a href="#">c5h1aC_</a>	 Alignment		51.8	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> iclr transcription factor homolog; <b>PDBTitle:</b> crystal structure of an iclr homolog from microbacterium sp. strain2 hm58-2
20	<a href="#">c2it0A_</a>	 Alignment		50.6	13	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> iron-dependent repressor ider; <b>PDBTitle:</b> crystal structure of a two-domain ider-dna complex crystal2 form ii
21	<a href="#">c1fx7C_</a>	 Alignment	not modelled	46.5	12	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> iron-dependent repressor ider; <b>PDBTitle:</b> crystal structure of the iron-dependent regulator (ider) from2 mycobacterium tuberculosis
22	<a href="#">c1mkmA_</a>	 Alignment	not modelled	45.9	9	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> iclr transcriptional regulator; <b>PDBTitle:</b> crystal structure of the thermotoga maritima iclr
23	<a href="#">c3kfwX_</a>	 Alignment	not modelled	44.4	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> X: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> uncharacterized protein rv0674 from mycobacterium tuberculosis
24	<a href="#">c4ew6A_</a>	 Alignment	not modelled	40.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-galactose-1-dehydrogenase protein; <b>PDBTitle:</b> crystal structure of d-galactose-1-dehydrogenase protein from2 rhizobium etli
25	<a href="#">d2jn6a1</a>	 Alignment	not modelled	40.5	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Cgl2762-like
26	<a href="#">c2xroE_</a>	 Alignment	not modelled	40.5	11	<b>PDB header:</b> dna-binding protein/dna <b>Chain:</b> E: <b>PDB Molecule:</b> hth-type transcriptional regulator ttgv; <b>PDBTitle:</b> crystal structure of ttgv in complex with its dna operator
27	<a href="#">c2ia2D_</a>	 Alignment	not modelled	37.4	9	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a putative transcriptional regulator rha061952 from rhodococcus sp. rha1
28	<a href="#">d1stza1</a>	 Alignment	not modelled	37.4	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Heat-inducible transcription repressor HrcA, N-terminal domain
		 Alignment				<b>PDB header:</b> oxidoreductase

29	<a href="#">c6jnkA_</a>	Alignment	not modelled	36.5	15	<b>Chain:</b> A: <b>PDB Molecule:</b> l-arabinose 1-dehydrogenase (nad(p)(+)); <b>PDBTitle:</b> crystal structure of azospirillum brasilense l-arabinose 1-2 dehydrogenase (nadp-bound form)
30	<a href="#">d1ntca_</a>	Alignment	not modelled	35.9	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
31	<a href="#">c1g3wA_</a>	Alignment	not modelled	35.7	11	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> diphtheria toxin repressor; <b>PDBTitle:</b> cd-cys102ser dtxr
32	<a href="#">c1wsuA_</a>	Alignment	not modelled	35.7	14	<b>PDB header:</b> translation/rna <b>Chain:</b> A: <b>PDB Molecule:</b> selenocysteine-specific elongation factor; <b>PDBTitle:</b> c-terminal domain of elongation factor selb complexed with2 secis rna
33	<a href="#">c3r4kD_</a>	Alignment	not modelled	34.5	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, iclr family; <b>PDBTitle:</b> crystal structure of a putative iclr transcriptional regulator2 (tm1040_3717) from silicibacter sp. tm1040 at 2.46 a resolution
34	<a href="#">d2htja1</a>	Alignment	not modelled	32.6	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> FaeA-like
35	<a href="#">c2ev5B_</a>	Alignment	not modelled	32.2	13	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator mntr; <b>PDBTitle:</b> bacillus subtilis manganese transport regulator (mntr)2 bound to calcium
36	<a href="#">d2ev0a1</a>	Alignment	not modelled	31.6	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
37	<a href="#">c3oa0B_</a>	Alignment	not modelled	30.3	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> lipopolysaccharide biosynthesis protein wbbp; <b>PDBTitle:</b> crystal structure of the wlba (wbbp) dehydrogenase from thermus2 thermophilus in complex with nad and udp-glcna
38	<a href="#">c1z4hA_</a>	Alignment	not modelled	30.0	13	<b>PDB header:</b> protein binding, dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> stor inhibition protein; <b>PDBTitle:</b> the response regulator tori belongs to a new family of2 atypical excisionase
39	<a href="#">c1lc3A_</a>	Alignment	not modelled	29.4	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> biliverdin reductase a; <b>PDBTitle:</b> crystal structure of a biliverdin reductase enzyme-cofactor2 complex
40	<a href="#">c5y6iB_</a>	Alignment	not modelled	29.2	13	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator kdgr; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa hmgr
41	<a href="#">c3t76A_</a>	Alignment	not modelled	28.8	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator vanug; <b>PDBTitle:</b> crystal structure of transcriptional regulator vanug, form ii
42	<a href="#">c5c8eC_</a>	Alignment	not modelled	28.2	21	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> C: <b>PDB Molecule:</b> light-dependent transcriptional regulator carh; <b>PDBTitle:</b> crystal structure of thermus thermophilus carh bound to2 adenosylcobalamin and a 26-bp dna segment
43	<a href="#">c3oqbF_</a>	Alignment	not modelled	27.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of putative oxidoreductase from bradyrhizobium2 japonicum usda 110
44	<a href="#">c4ytkA_</a>	Alignment	not modelled	27.1	36	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation factor spt5; <b>PDBTitle:</b> structure of the kow1-linker1 domain of transcription elongation2 factor spt5
45	<a href="#">d1k78a1</a>	Alignment	not modelled	26.9	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
46	<a href="#">d1lc0a1</a>	Alignment	not modelled	25.5	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
47	<a href="#">d1umqa_</a>	Alignment	not modelled	25.0	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
48	<a href="#">c1umqA_</a>	Alignment	not modelled	25.0	14	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> photosynthetic apparatus regulatory protein; <b>PDBTitle:</b> solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
49	<a href="#">d2g7ga1</a>	Alignment	not modelled	24.7	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
50	<a href="#">c5w1eA_</a>	Alignment	not modelled	24.3	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> pobr in complex with phb
51	<a href="#">c5af3A_</a>	Alignment	not modelled	24.2	15	<b>PDB header:</b> dna binding <b>Chain:</b> A: <b>PDB Molecule:</b> vapbc49; <b>PDBTitle:</b> x-ray crystal structure of rv2018 from mycobacterium tuberculosis
52	<a href="#">c3e82A_</a>	Alignment	not modelled	24.1	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase from2 klebsiella pneumoniae
53	<a href="#">c5exvD_</a>	Alignment	not modelled	24.1	9	<b>PDB header:</b> heme-binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> hemin-degrading hems.chux domain protein; <b>PDBTitle:</b> crystal structure of heme binding protein hutx from vibrio cholerae
						<b>PDB header:</b> oxidoreductase

54	<a href="#">c3gfgB_</a>	Alignment	not modelled	24.1	22	<b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized oxidoreductase yvaa; <b>PDBTitle:</b> structure of putative oxidoreductase yvaa from bacillus subtilis in2 triclinic form
55	<a href="#">c3rbvA_</a>	Alignment	not modelled	24.0	22	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar 3-ketoreductase; <b>PDBTitle:</b> crystal structure of kjid10, a 3-ketoreductase from actinomadura2 kijaniata incomplex with nadp
56	<a href="#">d1tw3a1</a>	Alignment	not modelled	24.0	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Plant O-methyltransferase, N-terminal domain
57	<a href="#">d6paxa1</a>	Alignment	not modelled	22.8	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
58	<a href="#">d2fcla1</a>	Alignment	not modelled	22.7	19	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> TM1012-like
59	<a href="#">c4fb5A_</a>	Alignment	not modelled	21.2	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable oxidoreductase protein; <b>PDBTitle:</b> crystal structure of a probable oxidoreductase protein
60	<a href="#">c5tjA_</a>	Alignment	not modelled	20.8	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, iclr family; <b>PDBTitle:</b> crystal structure of icir transcriptional regulator from2 alicyclobacillus acidocaldarius
61	<a href="#">c5cviB_</a>	Alignment	not modelled	20.1	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> slor; <b>PDBTitle:</b> structure of the manganese regulator slor
62	<a href="#">c3m2tA_</a>	Alignment	not modelled	19.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable dehydrogenase; <b>PDBTitle:</b> the crystal structure of dehydrogenase from chromobacterium2 violaceum
63	<a href="#">c3btuD_</a>	Alignment	not modelled	19.8	10	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> galactose/lactose metabolism regulatory protein <b>PDBTitle:</b> crystal structure of the super-repressor mutant of gal80p2 from saccharomyces cerevisiae; gal80(s2) [e351k]
64	<a href="#">c3dtyA_</a>	Alignment	not modelled	19.1	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family; <b>PDBTitle:</b> crystal structure of an oxidoreductase from pseudomonas2 syringae
65	<a href="#">c2wgbB_</a>	Alignment	not modelled	18.9	23	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> tetr family transcriptional repressor lfrr; <b>PDBTitle:</b> crystal structure of the tetr-like transcriptional2 regulator lfrr from mycobacterium smegmatis
66	<a href="#">c3lvtA_</a>	Alignment	not modelled	18.3	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyl hydrolase, family 38; <b>PDBTitle:</b> the crystal structure of a protein in the glycosyl hydrolase family 382 from enterococcus faecalis to 2.55a
67	<a href="#">c2g7gA_</a>	Alignment	not modelled	18.2	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rha04620, putative transcriptional regulator; <b>PDBTitle:</b> the crystal structure of the putative transcriptional regulator2 rha04620 from rhodococcus sp. rha1
68	<a href="#">c3zplE_</a>	Alignment	not modelled	18.1	13	<b>PDB header:</b> transcription/dna <b>Chain:</b> E: <b>PDB Molecule:</b> putative marr-family transcriptional repressor; <b>PDBTitle:</b> crystal structure of sco3205, a marr family transcriptional regulator2 from streptomyces coelicolor, in complex with dna
69	<a href="#">c1f5tA_</a>	Alignment	not modelled	17.9	11	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> diphtheria toxin repressor; <b>PDBTitle:</b> diphtheria tox repressor (c102d mutant) complexed with2 nickel and dtxr consensus binding sequence
70	<a href="#">c1j5yA_</a>	Alignment	not modelled	17.3	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, biotin repressor family; <b>PDBTitle:</b> crystal structure of transcriptional regulator (tm1602) from2 thermotoga maritima at 2.3 a resolution
71	<a href="#">d2hq2a1</a>	Alignment	not modelled	16.8	16	<b>Fold:</b> Heme iron utilization protein-like <b>Superfamily:</b> Heme iron utilization protein-like <b>Family:</b> HemS/ChuS-like
72	<a href="#">c3f4fF_</a>	Alignment	not modelled	16.5	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> putative oxidoreductase yhhx; <b>PDBTitle:</b> crystal structure of a probable oxidoreductase yhhx in2 triclinic form. northeast structural genomics target er647
73	<a href="#">c5a06E_</a>	Alignment	not modelled	16.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> aldose-aldose oxidoreductase; <b>PDBTitle:</b> crystal structure of aldose-aldose oxidoreductase from2 caulobacter crescentus complexed with sorbitol
74	<a href="#">d1kx5b_</a>	Alignment	not modelled	16.4	33	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
75	<a href="#">c3mq0A_</a>	Alignment	not modelled	16.1	17	<b>PDB header:</b> transcription repressor <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional repressor of the blcabc operon; <b>PDBTitle:</b> crystal structure of agobacterium tumefaciens repressor blcr
76	<a href="#">c2plyB_</a>	Alignment	not modelled	16.0	15	<b>PDB header:</b> translation/rna <b>Chain:</b> B: <b>PDB Molecule:</b> selenocysteine-specific elongation factor; <b>PDBTitle:</b> structure of the mrna binding fragment of elongation factor2 selb in complex with secis rna.
77	<a href="#">c6a3fB_</a>	Alignment	not modelled	16.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative dehydrogenase; <b>PDBTitle:</b> levoglucosan dehydrogenase, apo form
78	<a href="#">c1zh8B_</a>	Alignment	not modelled	15.7	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
						<b>PDB header:</b> transcription

79	<a href="#">c2vz4A_</a>	Alignment	not modelled	15.6	19	<b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional activator tipa; <b>PDBTitle:</b> the n-terminal domain of merr-like protein tipal bound to promoter dna
80	<a href="#">c5ydcA_</a>	Alignment	not modelled	15.5	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator rv1828; <b>PDBTitle:</b> crystal structure of mercury soaked c-terminal domain of rv1828 from <i>Mycobacterium tuberculosis</i>
81	<a href="#">c3v5nA_</a>	Alignment	not modelled	15.4	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> the crystal structure of oxidoreductase from <i>Sinorhizobium meliloti</i>
82	<a href="#">c3kuxA_</a>	Alignment	not modelled	15.1	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> structure of the ypo2259 putative oxidoreductase from <i>Yersinia pestis</i>
83	<a href="#">c3bd1B_</a>	Alignment	not modelled	14.9	22	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> cro protein; <b>PDBTitle:</b> structure of the cro protein from putative prophage element xfaso 1 in <i>Xylella fastidiosa</i> strain ann-1
84	<a href="#">c3u3xj_</a>	Alignment	not modelled	14.8	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> J: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase from <i>Sinorhizobium meliloti</i> 1021
85	<a href="#">c2wyhA_</a>	Alignment	not modelled	14.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-mannosidase; <b>PDBTitle:</b> structure of the streptococcus pyogenes family gh38 alpha-2 mannosidase
86	<a href="#">c1ofgF_</a>	Alignment	not modelled	14.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> glucose-fructose oxidoreductase; <b>PDBTitle:</b> glucose-fructose oxidoreductase
87	<a href="#">c3oa2B_</a>	Alignment	not modelled	14.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> wbbp; <b>PDBTitle:</b> crystal structure of the wlba (wbbp) dehydrogenase from <i>Pseudomonas aeruginosa</i> in complex with nad at 1.5 angstrom resolution
88	<a href="#">c2ixaA_</a>	Alignment	not modelled	13.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-n-acetylgalactosaminidase; <b>PDBTitle:</b> a-zyme, n-acetylgalactosaminidase
89	<a href="#">c4hamA_</a>	Alignment	not modelled	13.8	25	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> lmo2241 protein; <b>PDBTitle:</b> crystal structure of transcriptional antiterminator from <i>Listeria monocytogenes</i> egd-e
90	<a href="#">c3e18A_</a>	Alignment	not modelled	13.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of nad-binding protein from <i>Listeria innocua</i>
91	<a href="#">c5b7jA_</a>	Alignment	not modelled	13.6	30	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> switch-activating protein 1; <b>PDBTitle:</b> structure model of sap1-dna complex
92	<a href="#">c3evnA_</a>	Alignment	not modelled	13.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family; <b>PDBTitle:</b> crystal structure of putative oxidoreductase from <i>Streptococcus agalactiae</i> 2603v/r
93	<a href="#">c3fd8A_</a>	Alignment	not modelled	13.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family; <b>PDBTitle:</b> crystal structure of an oxidoreductase from <i>Enterococcus faecalis</i>
94	<a href="#">c4hadD_</a>	Alignment	not modelled	13.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> probable oxidoreductase protein; <b>PDBTitle:</b> crystal structure of probable oxidoreductase protein from <i>Rhizobium etli</i> cfn 42
95	<a href="#">d2jxca1</a>	Alignment	not modelled	13.4	11	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Eps15 homology domain (EH domain)
96	<a href="#">c5uibA_</a>	Alignment	not modelled	13.3	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase protein; <b>PDBTitle:</b> crystal structure of an oxidoreductase from <i>Agrobacterium radiobacter</i> 2 in complex with nad <sup>+</sup> , l-tartaric acid and magnesium
97	<a href="#">d1g3wa1</a>	Alignment	not modelled	13.3	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
98	<a href="#">c2ph0A_</a>	Alignment	not modelled	13.3	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the q6d2t7_erwct protein from <i>Erwinia carotovora</i> .2 nesg target ewr41.
99	<a href="#">d1biaa1</a>	Alignment	not modelled	13.2	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like