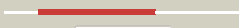


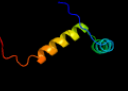



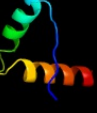

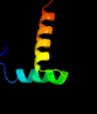
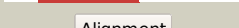

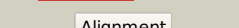

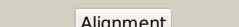

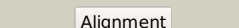

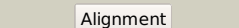


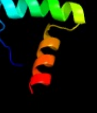











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0748 (- )_840950_841207
Date	Fri Jul 26 01:50:32 BST 2019
Unique Job ID	abe5680934c5f752

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5x3tA_</a>	 Alignment		96.5	37	<b>PDB header:</b> antitoxin/toxin <b>Chain:</b> A; <b>PDB Molecule:</b> antitoxin vapb26; <b>PDBTitle:</b> vapbc from mycobacterium tuberculosis
2	<a href="#">c2k5jB_</a>	 Alignment		95.7	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein yiif; <b>PDBTitle:</b> solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
3	<a href="#">d2bsqe1</a>	 Alignment		95.4	28	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Trafficking protein A-like
4	<a href="#">c2bj3D_</a>	 Alignment		95.3	23	<b>PDB header:</b> transcription <b>Chain:</b> D; <b>PDB Molecule:</b> nickel responsive regulator; <b>PDBTitle:</b> nikr-apo
5	<a href="#">c2h1oH_</a>	 Alignment		95.0	28	<b>PDB header:</b> gene regulation/dna complex <b>Chain:</b> H; <b>PDB Molecule:</b> trafficking protein a; <b>PDBTitle:</b> structure of fitab bound to ir36 dna fragment
6	<a href="#">c6a7vU_</a>	 Alignment		95.0	33	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> U; <b>PDB Molecule:</b> antitoxin vapb11; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
7	<a href="#">c1q5vB_</a>	 Alignment		94.8	28	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> nickel responsive regulator; <b>PDBTitle:</b> apo-nikr
8	<a href="#">d2bj7a1</a>	 Alignment		94.7	23	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
9	<a href="#">c2ca9B_</a>	 Alignment		94.2	23	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> putative nickel-responsive regulator; <b>PDBTitle:</b> apo-nikr from helicobacter pylori in closed trans-2 conformation
10	<a href="#">d2hzaa1</a>	 Alignment		92.4	28	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
11	<a href="#">d1p94a_</a>	 Alignment		92.3	19	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like

12	<a href="#">d2hzab1</a>	Alignment		91.6	28	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
13	<a href="#">c3kk4B_</a>	Alignment		89.2	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein bp1543; <b>PDBTitle:</b> uncharacterized protein bp1543 from bordetella pertussis tohama i
14	<a href="#">c6g1nB_</a>	Alignment		87.1	18	<b>PDB header:</b> antitoxin <b>Chain:</b> B; <b>PDB Molecule:</b> antitoxin hicb; <b>PDBTitle:</b> crystal structure of the burkholderia pseudomallei antitoxin hicb
15	<a href="#">c2an7A_</a>	Alignment		86.1	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> protein pard; <b>PDBTitle:</b> solution structure of the bacterial antidote pard
16	<a href="#">c4aaiB_</a>	Alignment		85.3	15	<b>PDB header:</b> viral protein <b>Chain:</b> B; <b>PDB Molecule:</b> orf e73; <b>PDBTitle:</b> thermostable protein from hyperthermophilic virus ssv-rh
17	<a href="#">c4a1qB_</a>	Alignment		85.3	15	<b>PDB header:</b> viral protein <b>Chain:</b> B; <b>PDB Molecule:</b> orf e73; <b>PDBTitle:</b> solution structure of the transcription regulator svtr from the2 shaped virus ragged hills, a hyperthermophilic3 crenarchaeal virus from yellowstone national park
18	<a href="#">c2kelB_</a>	Alignment		85.1	13	<b>PDB header:</b> transcription repressor <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein 56b; <b>PDBTitle:</b> structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1
19	<a href="#">d1mnta_</a>	Alignment		83.5	15	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
20	<a href="#">c4p7dA_</a>	Alignment		83.1	11	<b>PDB header:</b> toxin <b>Chain:</b> A; <b>PDB Molecule:</b> antitoxin hicb3; <b>PDBTitle:</b> antitoxin hicb3 crystal structure
21	<a href="#">c2k29A_</a>	Alignment	not modelled	81.1	15	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> antitoxin relb; <b>PDBTitle:</b> structure of the dbd domain of e. coli antitoxin relb
22	<a href="#">c1u9pA_</a>	Alignment	not modelled	78.3	22	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> parc; <b>PDBTitle:</b> permuted single-chain arc
23	<a href="#">c5yrzC_</a>	Alignment	not modelled	75.8	26	<b>PDB header:</b> antitoxin/hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> hicb; <b>PDBTitle:</b> toxin-antitoxin complex from streptococcus pneumoniae
24	<a href="#">c1xrxD_</a>	Alignment	not modelled	73.0	25	<b>PDB header:</b> replication inhibitor <b>Chain:</b> D; <b>PDB Molecule:</b> seqa protein; <b>PDBTitle:</b> crystal structure of a dna-binding protein
25	<a href="#">d1xrxal</a>	Alignment	not modelled	73.0	25	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> SeqA N-terminal domain-like
26	<a href="#">c6iyaD_</a>	Alignment	not modelled	70.0	20	<b>PDB header:</b> antitoxin <b>Chain:</b> D; <b>PDB Molecule:</b> transcriptional regulator copg family; <b>PDBTitle:</b> structure of the dna binding domain of antitoxin copaso
27	<a href="#">c4fxeB_</a>	Alignment	not modelled	68.6	13	<b>PDB header:</b> toxin/toxin inhibitor <b>Chain:</b> B; <b>PDB Molecule:</b> antitoxin relb; <b>PDBTitle:</b> crystal structure of the intact e. coli relbe toxin-antitoxin complex
28	<a href="#">c3goqC_</a>	Alignment	not modelled	61.1	16	<b>PDB header:</b> transcription/dna <b>Chain:</b> C; <b>PDB Molecule:</b> alginate and motility regulator z; <b>PDBTitle:</b> crystal structure of the transcription factor amrz in complex with the2 18 base pair amrz1 binding site
29	<a href="#">c3kvaD_</a>	Alignment	not modelled	59.1	26	<b>PDB header:</b> protein binding <b>Chain:</b> D; <b>PDB Molecule:</b> antitoxin protein pard-1;

29	<a href="#">c3kx6D</a>	Alignment	not modelled	59.1	20	<b>PDBTitle:</b> a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex <b>PDB header:</b> toxin/antitoxin
30	<a href="#">c3h87D</a>	Alignment	not modelled	58.3	26	<b>Chain:</b> D: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
31	<a href="#">d2cpga</a>	Alignment	not modelled	57.3	33	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
32	<a href="#">c1ea4K</a>	Alignment	not modelled	57.3	33	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> K: <b>PDB Molecule:</b> transcriptional repressor copg; <b>PDBTitle:</b> transcriptional repressor copg/22bp dsdna complex
33	<a href="#">c4hv0B</a>	Alignment	not modelled	56.0	22	<b>PDB header:</b> transcription, viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> avtr; <b>PDBTitle:</b> structure and function of avtr, a novel transcriptional regulator from2 a hyperthermophilic archaeal lipothrixvirus
34	<a href="#">c3fmtF</a>	Alignment	not modelled	48.8	19	<b>PDB header:</b> replication inhibitor/dna <b>Chain:</b> F: <b>PDB Molecule:</b> protein seqa; <b>PDBTitle:</b> crystal structure of seqa bound to dna
35	<a href="#">c6a6xC</a>	Alignment	not modelled	48.5	28	<b>PDB header:</b> toxin <b>Chain:</b> C: <b>PDB Molecule:</b> antitoxin maze7; <b>PDBTitle:</b> the crystal structure of the mtb maze-mazf-mt9 complex
36	<a href="#">c2k6IA</a>	Alignment	not modelled	47.6	24	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the solution structure of xabc0070 from xanthomonas2 axonopodis pv citri reveals this new protein is a member of3 the rhh family of transcriptional repressors
37	<a href="#">c2rbfB</a>	Alignment	not modelled	44.8	15	<b>PDB header:</b> oxidoreductase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein puta; <b>PDBTitle:</b> structure of the ribbon-helix-helix domain of escherichia coli puta2 (puta52) complexed with operator dna (o2)
38	<a href="#">c4q2uM</a>	Alignment	not modelled	33.4	10	<b>PDB header:</b> toxin/toxin repressor <b>Chain:</b> M: <b>PDB Molecule:</b> antitoxin dinj; <b>PDBTitle:</b> crystal structure of the e. coli dinj-yafq toxin-antitoxin complex
39	<a href="#">d1rkt2</a>	Alignment	not modelled	32.8	11	<b>Fold:</b> Tetracyclin repressor-like, C-terminal domain <b>Superfamily:</b> Tetracyclin repressor-like, C-terminal domain <b>Family:</b> Tetracyclin repressor-like, C-terminal domain
40	<a href="#">c5cegC</a>	Alignment	not modelled	30.9	17	<b>PDB header:</b> toxin <b>Chain:</b> C: <b>PDB Molecule:</b> addiction module antidote protein, copg/arc/metj family; <b>PDBTitle:</b> x-ray structure of toxin/anti-toxin complex from mesorhizobium2 opportunistum
41	<a href="#">c2mdvB</a>	Alignment	not modelled	27.8	31	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> designed protein; <b>PDBTitle:</b> nmr structure of beta alpha alpha 38
42	<a href="#">c6ajnF</a>	Alignment	not modelled	26.3	14	<b>PDB header:</b> toxin <b>Chain:</b> F: <b>PDB Molecule:</b> duf1778 domain-containing protein; <b>PDBTitle:</b> crystal structure of atatr bound with accoa
43	<a href="#">c4me7E</a>	Alignment	not modelled	25.9	20	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> E: <b>PDB Molecule:</b> antitoxin endoai; <b>PDBTitle:</b> crystal structure of bacillus subtilis toxin mazf in complex with2 cognate antitoxin maze
44	<a href="#">d1b28a</a>	Alignment	not modelled	25.5	24	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
45	<a href="#">c6bwqB</a>	Alignment	not modelled	24.8	20	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> pyridinium-3,5-bisthiocarboxylic acid mononucleotide nickel <b>PDBTitle:</b> larc2, the c-terminal domain of a cyclometallase involved in the2 synthesis of the npn cofactor of lactate racemase, in complex with3 mnctp
46	<a href="#">d1q9ja2</a>	Alignment	not modelled	24.2	24	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> NRPS condensation domain (amide synthase)
47	<a href="#">d1y9ba1</a>	Alignment	not modelled	21.4	17	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> VCA0319-like
48	<a href="#">d1x93a1</a>	Alignment	not modelled	21.4	22	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
49	<a href="#">c1x93B</a>	Alignment	not modelled	21.4	22	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein hp0222; <b>PDBTitle:</b> nmr structure of helicobacter pylori hp0222
50	<a href="#">c2cw1A</a>	Alignment	not modelled	18.0	18	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> sn4m; <b>PDBTitle:</b> solution structure of the de novo-designed lambda cro fold2 protein
51	<a href="#">c6gtsC</a>	Alignment	not modelled	17.5	14	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> duf1778 domain-containing protein; <b>PDBTitle:</b> structure of the atat-atar complex bound dna
52	<a href="#">d1s4ka</a>	Alignment	not modelled	16.0	30	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> YdiL-like
53	<a href="#">c2qezC</a>	Alignment	not modelled	16.0	24	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> ethanolamine ammonia-lyase heavy chain; <b>PDBTitle:</b> crystal structure of ethanolamine ammonia-lyase heavy chain2 (yp_013784.1) from listeria monocytogenes 4b f2365 at 2.15 a3 resolution
54	<a href="#">d1ox0a2</a>	Alignment	not modelled	15.9	16	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Thiolase-related

55	<a href="#">d1rfma</a>	Alignment	not modelled	13.5	17	<b>Fold:</b> L-sulfolactate dehydrogenase-like <b>Superfamily:</b> L-sulfolactate dehydrogenase-like <b>Family:</b> L-sulfolactate dehydrogenase-like
56	<a href="#">c5vgmA</a>	Alignment	not modelled	13.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> crystal structure of dihydroorotase pyrc from vibrio cholerae in2 complex with zinc at 1.95 a resolution.
57	<a href="#">c3t98A</a>	Alignment	not modelled	12.5	20	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear pore complex protein nup54; <b>PDBTitle:</b> molecular architecture of the transport channel of the nuclear pore2 complex: nup54/nup58
58	<a href="#">d2eg6a1</a>	Alignment	not modelled	12.5	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Dihydroorotase
59	<a href="#">c3t98C</a>	Alignment	not modelled	12.3	20	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> nuclear pore complex protein nup54; <b>PDBTitle:</b> molecular architecture of the transport channel of the nuclear pore2 complex: nup54/nup58
60	<a href="#">c2lxmB</a>	Alignment	not modelled	11.6	18	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> charged multivesicular body protein 5; <b>PDBTitle:</b> lip5-chmp5
61	<a href="#">d1myla</a>	Alignment	not modelled	11.5	21	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
62	<a href="#">c3c19A</a>	Alignment	not modelled	11.2	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mk0293; <b>PDBTitle:</b> crystal structure of protein mk0293 from methanopyrus kandleri av19
63	<a href="#">c6noyB</a>	Alignment	not modelled	10.9	22	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> maintenance of carboxysome positioning b protein, mcsb; <b>PDBTitle:</b> structure of cyanothecce mcdb
64	<a href="#">c3pnuA</a>	Alignment	not modelled	10.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> 2.4 angstrom crystal structure of dihydroorotase (pyrc) from2 campylobacter jejuni.
65	<a href="#">d2ve8a1</a>	Alignment	not modelled	9.5	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> FtsK C-terminal domain-like
66	<a href="#">c3kk1B</a>	Alignment	not modelled	9.1	15	<b>PDB header:</b> transferase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> reverse transcriptase p51 subunit; <b>PDBTitle:</b> hiv-1 reverse transcriptase-dna complex with nuceotide inhibitor gs-2 9148-diphosphate bound in nucleotide site
67	<a href="#">c3jzeC</a>	Alignment	not modelled	9.1	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> 1.8 angstrom resolution crystal structure of dihydroorotase (pyrc)2 from salmonella enterica subsp. enterica serovar typhimurium str. lt2
68	<a href="#">c5ovnA</a>	Alignment	not modelled	8.9	20	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> pol protein; <b>PDBTitle:</b> crystal strcure of fiv reverse transcriptase
69	<a href="#">c1oxhD</a>	Alignment	not modelled	8.7	16	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> beta ketoacyl-acyl carrier protein synthase; <b>PDBTitle:</b> the crystal structure of beta-ketoacyl-[acyl carrier protein] synthase2 ii from streptococcus pneumoniae, triclinic form
70	<a href="#">d1baza</a>	Alignment	not modelled	8.1	24	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
71	<a href="#">d2cqaa1</a>	Alignment	not modelled	8.1	19	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> TIP49 domain
72	<a href="#">c2e4jA</a>	Alignment	not modelled	8.0	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> prostaglandin-h2 d-isomerase; <b>PDBTitle:</b> solution structure of mouse lipocalin-type prostaglandin d2 synthase
73	<a href="#">c2kz3A</a>	Alignment	not modelled	7.7	24	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein rad5113; <b>PDBTitle:</b> backbone 1h, 13c, and 15n chemical shift assignments for human rad51d2 from 1 to 83
74	<a href="#">c3gvG_A</a>	Alignment	not modelled	7.5	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from mycobacterium2 tuberculosis
75	<a href="#">c1d15A</a>	Alignment	not modelled	7.3	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-l-isoaspartate o-methyltransferase; <b>PDBTitle:</b> protein-l-isoaspartate o-methyltransferase
76	<a href="#">c2mn4A</a>	Alignment	not modelled	7.3	25	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> computational designed protein based on structure template <b>PDBTitle:</b> nmr solution structure of a computational designed protein based on2 structure template 1cy5
77	<a href="#">d1myka</a>	Alignment	not modelled	6.9	22	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
78	<a href="#">c5eywB</a>	Alignment	not modelled	6.8	14	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of litopenaeus vannamei triosephosphate isomerase2 complexed with 2-phosphoglycolic acid
79	<a href="#">c5v0gE</a>	Alignment	not modelled	6.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> dihydroorotase; <b>PDBTitle:</b> crystal structure of dihydroorotase pyrc from yersinia pestis in2 complex with zinc and unknown ligand at 2.4 a resolution.
80	<a href="#">c2kebA</a>	Alignment	not modelled	6.5	7	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase subunit alpha b; <b>PDBTitle:</b> nmr solution structure of the n-terminal domain of the

						dna polymerase2 alpha p68 subunit <b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> wiskott-aldrich syndrome protein; <b>PDBTitle:</b> ternary complex of the wh2 domain of wasp with actin-dnase i
81	<a href="#">c2a3zC_</a>	Alignment	not modelled	6.4	33	
82	<a href="#">d1bdta_</a>	Alignment	not modelled	6.4	22	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
83	<a href="#">c5htA_</a>	Alignment	not modelled	6.3	23	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> msha biogenesis protein mshe; <b>PDBTitle:</b> structure of mshe with cdg
84	<a href="#">c5ibxB_</a>	Alignment	not modelled	6.1	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> 1.65 angstrom crystal structure of triosephosphate isomerase (tim)2 from streptococcus pneumoniae
85	<a href="#">c6dy3G_</a>	Alignment	not modelled	6.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> n-acylethanolamine-hydrolyzing acid amidase alpha-subunit; <b>PDBTitle:</b> caenorhabditis elegans n-acylethanolamine-hydrolyzing acid amidase2 (naaa) ortholog
86	<a href="#">c5zg5B_</a>	Alignment	not modelled	6.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase sadsubaaa mutant from2 opisthorchis viverrini
87	<a href="#">d1vrpa1</a>	Alignment	not modelled	5.8	14	<b>Fold:</b> Guanido kinase N-terminal domain <b>Superfamily:</b> Guanido kinase N-terminal domain <b>Family:</b> Guanido kinase N-terminal domain
88	<a href="#">c3m9yB_</a>	Alignment	not modelled	5.8	12	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from methicillin2 resistant staphylococcus aureus at 1.9 angstrom resolution
89	<a href="#">d1o5xa_</a>	Alignment	not modelled	5.7	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
90	<a href="#">d1g0wa1</a>	Alignment	not modelled	5.6	18	<b>Fold:</b> Guanido kinase N-terminal domain <b>Superfamily:</b> Guanido kinase N-terminal domain <b>Family:</b> Guanido kinase N-terminal domain
91	<a href="#">c4obtA_</a>	Alignment	not modelled	5.5	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase, cytosolic; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana cytosolic triose phosphate2 isomerase
92	<a href="#">d1u6ra1</a>	Alignment	not modelled	5.3	14	<b>Fold:</b> Guanido kinase N-terminal domain <b>Superfamily:</b> Guanido kinase N-terminal domain <b>Family:</b> Guanido kinase N-terminal domain
93	<a href="#">c5ounA_</a>	Alignment	not modelled	5.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ruvb-like protein 2; <b>PDBTitle:</b> nmr solution structure of the external dii domain of rvb2 from2 saccharomyces cerevisiae
94	<a href="#">d1i0ea1</a>	Alignment	not modelled	5.2	14	<b>Fold:</b> Guanido kinase N-terminal domain <b>Superfamily:</b> Guanido kinase N-terminal domain <b>Family:</b> Guanido kinase N-terminal domain
95	<a href="#">c3wrwE_</a>	Alignment	not modelled	5.1	24	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> tm-1 protein; <b>PDBTitle:</b> crystal structure of the n-terminal domain of resistance protein
96	<a href="#">d1qh4a1</a>	Alignment	not modelled	5.1	18	<b>Fold:</b> Guanido kinase N-terminal domain <b>Superfamily:</b> Guanido kinase N-terminal domain <b>Family:</b> Guanido kinase N-terminal domain