



























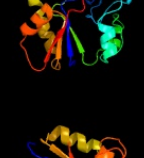
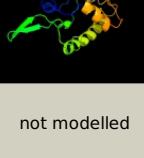


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2976c_(ung)_3332081_3332764
Date	Thu Aug 8 16:20:14 BST 2019
Unique Job ID	3f85fc2883ab64a0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2zhxG_</a>	 Alignment		100.0	100	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> G; <b>PDB Molecule:</b> uracil-dna glycosylase; <b>PDBTitle:</b> crystal structure of uracil-dna glycosylase from mycobacterium2 tuberculosis in complex with a proteinaceous inhibitor
2	<a href="#">c3zoqA_</a>	 Alignment		100.0	46	<b>PDB header:</b> hydrolase/viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> uracil-dna glycosylase; <b>PDBTitle:</b> structure of bsudg-p56 complex
3	<a href="#">c3tr7A_</a>	 Alignment		100.0	41	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> uracil-dna glycosylase; <b>PDBTitle:</b> structure of a uracil-dna glycosylase (ung) from coxiella burnetii
4	<a href="#">d1okba_</a>	 Alignment		100.0	39	<b>Fold:</b> Uracil-DNA glycosylase-like <b>Superfamily:</b> Uracil-DNA glycosylase-like <b>Family:</b> Uracil-DNA glycosylase
5	<a href="#">c3cxmA_</a>	 Alignment		100.0	40	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> uracil-dna glycosylase; <b>PDBTitle:</b> leishmania naiffi uracil-dna glycosylase in complex with 5-bromouracil
6	<a href="#">c2booA_</a>	 Alignment		100.0	46	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> uracil-dna glycosylase; <b>PDBTitle:</b> the crystal structure of uracil-dna n-glycosylase (ung) from2 deinococcus radiodurans.
7	<a href="#">d3euga_</a>	 Alignment		100.0	38	<b>Fold:</b> Uracil-DNA glycosylase-like <b>Superfamily:</b> Uracil-DNA glycosylase-like <b>Family:</b> Uracil-DNA glycosylase
8	<a href="#">d2hxma1</a>	 Alignment		100.0	39	<b>Fold:</b> Uracil-DNA glycosylase-like <b>Superfamily:</b> Uracil-DNA glycosylase-like <b>Family:</b> Uracil-DNA glycosylase
9	<a href="#">c5x55A_</a>	 Alignment		100.0	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> probable uracil-dna glycosylase; <b>PDBTitle:</b> crystal structure of mimivirus uracil-dna glycosylase
10	<a href="#">d1laue_</a>	 Alignment		100.0	36	<b>Fold:</b> Uracil-DNA glycosylase-like <b>Superfamily:</b> Uracil-DNA glycosylase-like <b>Family:</b> Uracil-DNA glycosylase
11	<a href="#">c5nn7A_</a>	 Alignment		100.0	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> uracil-dna glycosylase; <b>PDBTitle:</b> kshv uracil-dna glycosylase, apo form

12	<a href="#">d2j8xa1</a>	Alignment		100.0	36	<b>Fold:</b> Uracil-DNA glycosylase-like <b>Superfamily:</b> Uracil-DNA glycosylase-like <b>Family:</b> Uracil-DNA glycosylase
13	<a href="#">c2owrD</a>	Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> uracil-dna glycosylase; <b>PDBTitle:</b> crystal structure of vaccinia virus uracil-dna glycosylase
14	<a href="#">c5x3hA</a>	Alignment		100.0	25	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> uracil-dna glycosylase; <b>PDBTitle:</b> the y81g mutant of the ung crystal structure from nitratifactor2 salsuginis
15	<a href="#">c2rbaB</a>	Alignment		96.9	11	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> g/t mismatch-specific thymine dna glycosylase; <b>PDBTitle:</b> structure of human thymine dna glycosylase bound to abasic and 2 undamaged dna
16	<a href="#">d1muga</a>	Alignment		94.6	17	<b>Fold:</b> Uracil-DNA glycosylase-like <b>Superfamily:</b> Uracil-DNA glycosylase-like <b>Family:</b> Mug-like
17	<a href="#">d1ui0a</a>	Alignment		94.4	19	<b>Fold:</b> Uracil-DNA glycosylase-like <b>Superfamily:</b> Uracil-DNA glycosylase-like <b>Family:</b> Mug-like
18	<a href="#">c2d3yA</a>	Alignment		94.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uracil-dna glycosylase; <b>PDBTitle:</b> crystal structure of uracil-dna glycosylase from thermophilus2 hb8
19	<a href="#">c2c2pA</a>	Alignment		94.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> g/u mismatch-specific dna glycosylase; <b>PDBTitle:</b> the crystal structure of mismatch specific uracil-dna2 glycosylase (mug) from deinococcus radiodurans
20	<a href="#">d1oe4a</a>	Alignment		93.4	21	<b>Fold:</b> Uracil-DNA glycosylase-like <b>Superfamily:</b> Uracil-DNA glycosylase-like <b>Family:</b> Single-strand selective monofunctional uracil-DNA glycosylase SMUG1
21	<a href="#">c3ikbB</a>	Alignment	not modelled	93.4	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized conserved protein; <b>PDBTitle:</b> the structure of a conserved protein from streptococcus2 mutans ua159.
22	<a href="#">c5h93C</a>	Alignment	not modelled	92.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> geobacter metallireducens smug1; <b>PDBTitle:</b> crystal structure of geobacter metallireducens smug1
23	<a href="#">c4zbzA</a>	Alignment	not modelled	90.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uracil-dna glycosylase; <b>PDBTitle:</b> family 4 uracil-dna glycosylase from sulfolobus tokodaii (free form, 2 x-ray wavelength=1.5418)
24	<a href="#">d1vk2a</a>	Alignment	not modelled	88.8	20	<b>Fold:</b> Uracil-DNA glycosylase-like <b>Superfamily:</b> Uracil-DNA glycosylase-like <b>Family:</b> Mug-like
25	<a href="#">c6ajrA</a>	Alignment	not modelled	88.8	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> uracil dna glycosylase superfamily protein; <b>PDBTitle:</b> complex form of uracil dna glycosylase x and uracil
26	<a href="#">c2h2wA</a>	Alignment	not modelled	55.6	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine o-succinyltransferase; <b>PDBTitle:</b> crystal structure of homoserine o-succinyltransferase (ec 2.3.1.46)2 (homoserine o-transsuccinylase) (hts) (tm0881) from thermotoga3 maritima at 2.52 a resolution
27	<a href="#">c5grkA</a>	Alignment	not modelled	48.8	100	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> blr0248 protein; <b>PDBTitle:</b> crystal structure of uracil dna glycosylase -xanthine complex from2 bradyrhizobium diazoefficiens
28	<a href="#">c2l3fA</a>	Alignment	not modelled	45.8	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of a putative uracil dna glycosylase from2 methanosarcina acetivorans, northeast structural genomics

					consortium3 target mvr76
29	<a href="#">d2ghra1</a>	Alignment	not modelled	44.3	21 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> HTS-like
30	<a href="#">c5tbfB</a>	Alignment	not modelled	38.3	29 <b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> translation elongation factor; <b>PDBTitle:</b> crystal structure of semet derivatives of domain2 and domain 3 of rctb
31	<a href="#">c5cjjA</a>	Alignment	not modelled	36.3	20 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase; <b>PDBTitle:</b> the crystal structure of phosphoribosylglycinamide formyltransferase2 from campylobacter jejuni subsp. jejuni nctc 11168
32	<a href="#">c3av3A</a>	Alignment	not modelled	31.5	26 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase; <b>PDBTitle:</b> crystal structure of glycinamide ribonucleotide transformylase 1 from2 geobacillus kaustophilus
33	<a href="#">d1meoa</a>	Alignment	not modelled	30.8	20 <b>Fold:</b> Formyltransferase <b>Superfamily:</b> Formyltransferase <b>Family:</b> Formyltransferase
34	<a href="#">c3p9xB</a>	Alignment	not modelled	29.4	24 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase; <b>PDBTitle:</b> crystal structure of phosphoribosylglycinamide formyltransferase from2 bacillus halodurans
35	<a href="#">c2i5kB</a>	Alignment	not modelled	29.1	15 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> utp--glucose-1-phosphate uridylyltransferase; <b>PDBTitle:</b> crystal structure of ugp1p
36	<a href="#">c2ywrA</a>	Alignment	not modelled	28.3	24 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase; <b>PDBTitle:</b> crystal structure of gar transformylase from aquifex aeolicus
37	<a href="#">c2q4jB</a>	Alignment	not modelled	27.7	16 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable utp-glucose-1-phosphate uridylyltransferase 2; <b>PDBTitle:</b> ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at3g03250, a putative udp-glucose3 pyrophosphorylase
38	<a href="#">c3aufA</a>	Alignment	not modelled	27.2	31 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycinamide ribonucleotide transformylase 1; <b>PDBTitle:</b> crystal structure of glycinamide ribonucleotide transformylase 1 from2 symbiobacterium toebii
39	<a href="#">c5d88A</a>	Alignment	not modelled	26.7	18 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> predicted protease of the collagenase family; <b>PDBTitle:</b> the structure of the u32 peptidase mk0906
40	<a href="#">c3tqrA</a>	Alignment	not modelled	25.3	17 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase; <b>PDBTitle:</b> structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii
41	<a href="#">c4bmaB</a>	Alignment	not modelled	25.3	15 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-n-acetylglucosamine pyrophosphorylase; <b>PDBTitle:</b> structural of aspergillus fumigatus udp-n-acetylglucosamine2 pyrophosphorylase
42	<a href="#">d2icya2</a>	Alignment	not modelled	24.0	14 <b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> UDP-glucose pyrophosphorylase
43	<a href="#">c4s1nA</a>	Alignment	not modelled	23.7	17 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase; <b>PDBTitle:</b> the crystal structure of phosphoribosylglycinamide formyltransferase2 from streptococcus pneumoniae tigr4
44	<a href="#">c3oc9A</a>	Alignment	not modelled	23.5	10 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine pyrophosphorylase; <b>PDBTitle:</b> crystal structure of putative udp-n-acetylglucosamine2 pyrophosphorylase from entamoeba histolytica
45	<a href="#">c4zyaA</a>	Alignment	not modelled	22.6	23 <b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> asparagine--trna ligase, cytoplasmic; <b>PDBTitle:</b> the n-terminal extension domain of human asparaginyl-trna synthetase
46	<a href="#">d1r2aa</a>	Alignment	not modelled	22.0	28 <b>Fold:</b> Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit <b>Superfamily:</b> Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit <b>Family:</b> Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
47	<a href="#">d1jkxa</a>	Alignment	not modelled	21.3	23 <b>Fold:</b> Formyltransferase <b>Superfamily:</b> Formyltransferase <b>Family:</b> Formyltransferase
48	<a href="#">c2yqsA</a>	Alignment	not modelled	21.2	12 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine pyrophosphorylase; <b>PDBTitle:</b> crystal structure of uridine-diphospho-n-acetylglucosamine2 pyrophosphorylase from candida albicans, in the product-binding form
49	<a href="#">c4ds3A</a>	Alignment	not modelled	20.1	23 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase; <b>PDBTitle:</b> crystal structure of phosphoribosylglycinamide formyltransferase from2 brucella melitensis
					<b>PDB header:</b> oxidoreductase

50	<a href="#">c4d6uL</a>	Alignment	not modelled	19.5	47	<b>Chain:</b> I: <b>PDB Molecule:</b> cytochrome b-c1 complex subunit rieske, mitochondrial; <b>PDBTitle:</b> cytochrome bc1 bound to the 4(1h)-pyridone gsk932121
51	<a href="#">c5zyoD</a>	Alignment	not modelled	19.0	30	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> ribosomal rna large subunit methyltransferase h; <b>PDBTitle:</b> crystal structure of domain-swapped circular-permuted ybea (cp74) from2 escherichia coli
52	<a href="#">d2hwna1</a>	Alignment	not modelled	18.7	27	<b>Fold:</b> Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit <b>Superfamily:</b> Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit <b>Family:</b> Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
53	<a href="#">c3dcjA</a>	Alignment	not modelled	17.5	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable 5'-phosphoribosylglycinamide formyltransferase <b>PDBTitle:</b> crystal structure of glycinamide formyltransferase (purn) from2 mycobacterium tuberculosis in complex with 5-methyl-5,6,7,8-3 tetrahydrofolic acid derivative
54	<a href="#">c4xzcB</a>	Alignment	not modelled	17.4	21	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> nucleoprotein; <b>PDBTitle:</b> the crystal structure of kupe virus nucleoprotein
55	<a href="#">c5ubfB</a>	Alignment	not modelled	17.2	29	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> rctb replication initiator protein; <b>PDBTitle:</b> crystal structure of the rctb domains 2-3, rctb-155-483
56	<a href="#">c4f4mA</a>	Alignment	not modelled	17.0	45	<b>PDB header:</b> hydrolase regulator <b>Chain:</b> A: <b>PDB Molecule:</b> papain peptidoglycan amidase effector tse1; <b>PDBTitle:</b> structure of the type vi peptidoglycan amidase effector tse1 (c30a)2 from pseudomonas aeruginosa
57	<a href="#">d1maba2</a>	Alignment	not modelled	16.7	29	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase <b>Family:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase
58	<a href="#">c5jpbA</a>	Alignment	not modelled	16.6	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative polysaccharide deacetylase; <b>PDBTitle:</b> bdellovibrio bacteriovorus peptidoglycan deacetylase bd3279
59	<a href="#">d1vm8a</a>	Alignment	not modelled	16.4	12	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> UDP-glucose pyrophosphorylase
60	<a href="#">c4f0wA</a>	Alignment	not modelled	16.2	45	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of type effector tse1 c30a mutant from pseudomonas2 aeruginosa
61	<a href="#">d1jv1a</a>	Alignment	not modelled	15.6	12	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> UDP-glucose pyrophosphorylase
62	<a href="#">c1fmtA</a>	Alignment	not modelled	15.2	23	<b>PDB header:</b> formyltransferase <b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna fmet formyltransferase; <b>PDBTitle:</b> methionyl-trnafmet formyltransferase from escherichia coli
63	<a href="#">c4bwsE</a>	Alignment	not modelled	15.1	55	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> polyglutamine-binding protein 1; <b>PDBTitle:</b> crystal structure of the heterotrimer of pqbp1, u5-15kd and2 u5-52kd.
64	<a href="#">c4bwqD</a>	Alignment	not modelled	14.3	75	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> polyglutamine-binding protein 1; <b>PDBTitle:</b> crystal structure of u5-15kd in a complex with pqbp1
65	<a href="#">c4bwqH</a>	Alignment	not modelled	14.3	75	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> polyglutamine-binding protein 1; <b>PDBTitle:</b> crystal structure of u5-15kd in a complex with pqbp1
66	<a href="#">c2y8uA</a>	Alignment	not modelled	14.1	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chitin deacetylase; <b>PDBTitle:</b> a. nidulans chitin deacetylase
67	<a href="#">c4bwqB</a>	Alignment	not modelled	13.9	75	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> polyglutamine-binding protein 1; <b>PDBTitle:</b> crystal structure of u5-15kd in a complex with pqbp1
68	<a href="#">c4bwqF</a>	Alignment	not modelled	13.5	75	<b>PDB header:</b> transcription <b>Chain:</b> F: <b>PDB Molecule:</b> polyglutamine-binding protein 1; <b>PDBTitle:</b> crystal structure of u5-15kd in a complex with pqbp1
69	<a href="#">d1fmta2</a>	Alignment	not modelled	13.0	22	<b>Fold:</b> Formyltransferase <b>Superfamily:</b> Formyltransferase <b>Family:</b> Formyltransferase
70	<a href="#">d1skyb2</a>	Alignment	not modelled	12.9	25	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase <b>Family:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase
71	<a href="#">c3r0qA</a>	Alignment	not modelled	12.9	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable protein arginine n-methyltransferase 4.2; <b>PDBTitle:</b> a uniquely open conformation revealed in the crystal structure of2 arabidopsis thaliana protein arginine methyltransferase 10
72	<a href="#">d1fx0a2</a>	Alignment	not modelled	12.6	25	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase <b>Family:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase
73	<a href="#">c4zhjA</a>	Alignment	not modelled	12.6	15	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> mg-chelatase subunit chlH; <b>PDBTitle:</b> crystal structure of the catalytic subunit of magnesium chelatase

74	<a href="#">d2blna2</a>	Alignment	not modelled	12.3	17	<b>Fold:</b> Formyltransferase <b>Superfamily:</b> Formyltransferase <b>Family:</b> Formyltransferase
75	<a href="#">c4bwsB</a>	Alignment	not modelled	12.2	75	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> polyglutamine-binding protein 1; <b>PDBTitle:</b> crystal structure of the heterotrimer of pqbp1, u5-15kd and2 u5-52kd.
76	<a href="#">c1yrwA</a>	Alignment	not modelled	12.2	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein arna; <b>PDBTitle:</b> crystal structure of e.coli arna transformylase domain
77	<a href="#">c2p2qD</a>	Alignment	not modelled	12.1	16	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> ornithine carbamoyltransferase; <b>PDBTitle:</b> crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
78	<a href="#">c5vytD</a>	Alignment	not modelled	11.9	22	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> gdp-mannose 4,6-dehydratase / gdp-4-amino-4,6-dideoxy-d- <b>PDBTitle:</b> crystal structure of the wbkc n-formyltransferase (f142a variant) from2 brucella melitensis
79	<a href="#">c2q62A</a>	Alignment	not modelled	11.7	4	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> arsh; <b>PDBTitle:</b> crystal structure of arsh from sinorhizobium meliloti
80	<a href="#">c3h0dB</a>	Alignment	not modelled	11.6	13	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> ctsr; <b>PDBTitle:</b> crystal structure of ctsr in complex with a 26bp dna duplex
81	<a href="#">c5h77B</a>	Alignment	not modelled	11.5	29	<b>PDB header:</b> signaling protein, immune system <b>Chain:</b> B: <b>PDB Molecule:</b> camp-dependent protein kinase type ii-alpha regulatory <b>PDBTitle:</b> crystal structure of the pka-protein a fusion protein
82	<a href="#">d2jdia2</a>	Alignment	not modelled	11.2	29	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase <b>Family:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase
83	<a href="#">c3nrbd</a>	Alignment	not modelled	11.1	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (puru_2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
84	<a href="#">c3u3iA</a>	Alignment	not modelled	11.0	22	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleocapsid protein; <b>PDBTitle:</b> a rna binding protein from crimean-congo hemorrhagic fever virus
85	<a href="#">c3o1B</a>	Alignment	not modelled	11.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
86	<a href="#">c4rr2D</a>	Alignment	not modelled	10.4	35	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> dna primase large subunit; <b>PDBTitle:</b> crystal structure of human primase
87	<a href="#">c4zdtB</a>	Alignment	not modelled	10.1	36	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> structure-specific endonuclease subunit slx4; <b>PDBTitle:</b> crystal structure of the ring finger domain of slx1 in complex with2 the c-terminal domain of slx4
88	<a href="#">d2bw0a2</a>	Alignment	not modelled	9.9	22	<b>Fold:</b> Formyltransferase <b>Superfamily:</b> Formyltransferase <b>Family:</b> Formyltransferase
89	<a href="#">d1q3qa2</a>	Alignment	not modelled	9.6	19	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> GroEL apical domain-like <b>Family:</b> Group II chaperonin (CCT, TRIC), apical domain
90	<a href="#">c3k1yE</a>	Alignment	not modelled	9.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> x-ray structure of oxidoreductase from corynebacterium diphtheriae.2 orthorhombic crystal form, northeast structural genomics consortium3 target cdr100d
91	<a href="#">c3n0vD</a>	Alignment	not modelled	9.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
92	<a href="#">c5oeoC</a>	Alignment	not modelled	9.5	30	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> transient receptor potential cation channel subfamily v <b>PDBTitle:</b> solution structure of the complex of trpv5(655-725) with a calmodulin2 e32q/e68q double mutant
93	<a href="#">c4c9vA</a>	Alignment	not modelled	9.5	26	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> rnf43; <b>PDBTitle:</b> xenopus rnf43 ectodomain in complex with xenopus rspo2 fu1-fu2
94	<a href="#">c5zwlG</a>	Alignment	not modelled	9.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> atp synthase gamma chain; <b>PDBTitle:</b> crystal structure of the gamma - epsilon complex of photosynthetic2 cyanobacterial f1-atpase
95	<a href="#">d1tska</a>	Alignment	not modelled	9.1	39	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Scorpion toxin-like <b>Family:</b> Short-chain scorpion toxins
96	<a href="#">c3rfoA</a>	Alignment	not modelled	8.9	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna formyltransferase; <b>PDBTitle:</b> crystal structure of methionyl-trna formyltransferase from bacillus2 anthracis
97	<a href="#">c5uaiA</a>	Alignment	not modelled	8.9	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna formyltransferase; <b>PDBTitle:</b> crystal structure of methionyl-trna formyltransferase from pseudomonas2 aeruginosa
98	<a href="#">c4c84B</a>	Alignment	not modelled	8.6	25	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase znr3;

				<b>PDBTitle:</b> zebrafish znrf3 ectodomain crystal form i	
99	<a href="#">c3q0iA_</a>	Alignment	not modelled	8.6	29
				<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna formyltransferase; <b>PDBTitle:</b> methionyl-trna formyltransferase from vibrio cholerae	