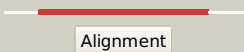

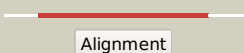

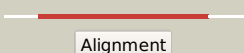

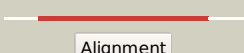





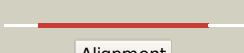

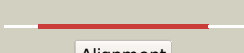













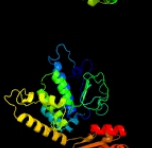

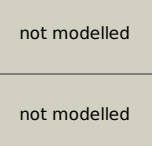


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2837c_(-)_3143645_3144655
Date	Wed Aug 7 12:50:50 BST 2019
Unique Job ID	9e931a1add8c8d9f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5o1uB_</a>	 Alignment		100.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphodiesterase; <b>PDBTitle:</b> structure of wildtype t.maritima pde (tm1595) with amp and mn2+
2	<a href="#">c3dmaA_</a>	 Alignment		100.0	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> exopolyphosphatase-related protein; <b>PDBTitle:</b> crystal structure of an exopolyphosphatase-related protein from2 bacteroides fragilis. northeast structural genomics target bfr192
3	<a href="#">c3devB_</a>	 Alignment		100.0	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> sh1221; <b>PDBTitle:</b> crystal structure of sh1221 protein from staphylococcus haemolyticus,2 northeast structural genomics consortium target shr87
4	<a href="#">c5j21C_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> bifunctional oligoribonuclease and pap phosphatase nrna; <b>PDBTitle:</b> structure of bacillus nanornase a (wt)
5	<a href="#">c5xspB_</a>	 Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphodiesterase acting on cyclic dinucleotides; <b>PDBTitle:</b> the catalytic domain of gdpp with 5'-papa
6	<a href="#">c1ir6A_</a>	 Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exonuclease recj; <b>PDBTitle:</b> crystal structure of exonuclease recj bound to manganese
7	<a href="#">d1ir6a_</a>	 Alignment		100.0	22	<b>Fold:</b> DHH phosphoesterases <b>Superfamily:</b> DHH phosphoesterases <b>Family:</b> Exonuclease RecJ
8	<a href="#">c5f56A_</a>	 Alignment		100.0	23	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> single-stranded-dna-specific exonuclease; <b>PDBTitle:</b> structure of recj complexed with dna and ssb-ct
9	<a href="#">c5ghrA_</a>	 Alignment		100.0	20	<b>PDB header:</b> dna binding protein/replication <b>Chain:</b> A: <b>PDB Molecule:</b> ssdna-specific exonuclease; <b>PDBTitle:</b> dna replication protein
10	<a href="#">d1k20a_</a>	 Alignment		100.0	16	<b>Fold:</b> DHH phosphoesterases <b>Superfamily:</b> DHH phosphoesterases <b>Family:</b> Manganese-dependent inorganic pyrophosphatase (family II)
11	<a href="#">d1i74a_</a>	 Alignment		100.0	16	<b>Fold:</b> DHH phosphoesterases <b>Superfamily:</b> DHH phosphoesterases <b>Family:</b> Manganese-dependent inorganic pyrophosphatase (family II)

12	<a href="#">d2hawa1</a>	Alignment		100.0	16	<b>Fold:</b> DHH phosphoesterases <b>Superfamily:</b> DHH phosphoesterases <b>Family:</b> Manganese-dependent inorganic pyrophosphatase (family II)
13	<a href="#">c2zxrA</a>	Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> single-stranded dna specific exonuclease recj; <b>PDBTitle:</b> crystal structure of recj in complex with mg2+ from thermus2 thermophilus hb8
14	<a href="#">c4rpaA</a>	Alignment		100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable manganese-dependent inorganic pyrophosphatase; <b>PDBTitle:</b> crystal structure of inorganic pyrophosphatase from staphylococcus2 aureus in complex with mn2+
15	<a href="#">c5yh1A</a>	Alignment		100.0	15	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> member of s1p family of ribosomal proteins; <b>PDBTitle:</b> member of s1p family of ribosomal proteins pf0399 dhh domain
16	<a href="#">d1wpna</a>	Alignment		100.0	19	<b>Fold:</b> DHH phosphoesterases <b>Superfamily:</b> DHH phosphoesterases <b>Family:</b> Manganese-dependent inorganic pyrophosphatase (family II)
17	<a href="#">c2eb0B</a>	Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> manganese-dependent inorganic pyrophosphatase; <b>PDBTitle:</b> crystal structure of methanococcus jannaschii putative family ii2 inorganic pyrophosphatase
18	<a href="#">c6mtzB</a>	Alignment		100.0	18	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hepc.19480.a.b1; <b>PDBTitle:</b> crystal structure of an uncharacterized protein from helicobacter2 pylori g27
19	<a href="#">c2qb6A</a>	Alignment		99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exopolyphosphatase; <b>PDBTitle:</b> saccharomyces cerevisiae cytosolic exopolyphosphatase, sulfate complex
20	<a href="#">c5ghrC</a>	Alignment		99.9	18	<b>PDB header:</b> dna binding protein/replication <b>Chain:</b> C: <b>PDB Molecule:</b> ssdna-specific exonuclease; <b>PDBTitle:</b> dna replication protein
21	<a href="#">c6cc2A</a>	Alignment	not modelled	97.7	14	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division control protein 45 cdc45 putative; <b>PDBTitle:</b> crystal structure of cdc45 from entamoeba histolytica
22	<a href="#">c3jc6E</a>	Alignment	not modelled	97.1	25	<b>PDB header:</b> replication <b>Chain:</b> E: <b>PDB Molecule:</b> cell division control protein 45; <b>PDBTitle:</b> structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
23	<a href="#">c5dgoA</a>	Alignment	not modelled	96.9	15	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division control protein 45 homolog; <b>PDBTitle:</b> crystal structure of cell division cycle protein 45 (cdc45)
24	<a href="#">c4fc5A</a>	Alignment	not modelled	95.2	20	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of ton_0340
25	<a href="#">c3g98B</a>	Alignment	not modelled	91.4	23	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> alanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of the c-ala domain from aquifex aeolicus2 alanyl-trna synthetase
26	<a href="#">d1ybha1</a>	Alignment	not modelled	87.7	16	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
27	<a href="#">c4ivnB</a>	Alignment	not modelled	87.0	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> the vibrio vulnificus nanr protein complexed with mannac-6p
28	<a href="#">c2zvfG</a>	Alignment	not modelled	86.4	14	<b>PDB header:</b> ligase <b>Chain:</b> G: <b>PDB Molecule:</b> alanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of archaeoglobus fulgidus alanyl-trna2 synthetase c-terminal dimerization domain <b>PDB header:</b> ligase/rna

29	<a href="#">c3wqyB_</a>	Alignment	not modelled	84.7	12	<b>Chain:</b> B: <b>PDB Molecule:</b> alanine--trna ligase; <b>PDBTitle:</b> crystal structure of archaeoglobus fulgidus alanyl-trna synthetase in2 complex with wild-type trna(ala) having g3.u70
30	<a href="#">c3shoA_</a>	Alignment	not modelled	83.6	27	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, rpir family; <b>PDBTitle:</b> crystal structure of rpir transcription factor from sphaerobacter2 thermophilus (sugar isomerase domain)
31	<a href="#">c3cf4G_</a>	Alignment	not modelled	78.4	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> acetyl-coa decarboxylase/synthase epsilon subunit; <b>PDBTitle:</b> structure of the codh component of the m. barkeri acds complex
32	<a href="#">d2ihta1</a>	Alignment	not modelled	76.0	24	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
33	<a href="#">c5uqiA_</a>	Alignment	not modelled	74.2	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphosugar isomerase; <b>PDBTitle:</b> e. coli cft073 c3406 in complex with a5p
34	<a href="#">d1m3sa_</a>	Alignment	not modelled	70.1	12	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
35	<a href="#">c3d3jA_</a>	Alignment	not modelled	69.2	17	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> enhancer of mrna-decapping protein 3; <b>PDBTitle:</b> crystal structure of human edc3p
36	<a href="#">c3trjC_</a>	Alignment	not modelled	66.8	10	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphoheptose isomerase; <b>PDBTitle:</b> structure of a phosphoheptose isomerase from francisella tularensis
37	<a href="#">d1vima_</a>	Alignment	not modelled	66.6	18	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
38	<a href="#">c2xhzC_</a>	Alignment	not modelled	66.0	14	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> arabinose 5-phosphate isomerase; <b>PDBTitle:</b> probing the active site of the sugar isomerase domain from e. coli2 arabinose-5-phosphate isomerase via x-ray crystallography
39	<a href="#">c3fxaA_</a>	Alignment	not modelled	65.1	13	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sis domain protein; <b>PDBTitle:</b> crystal structure of a putative sugar-phosphate isomerase2 (lmof2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution
40	<a href="#">d2djia1</a>	Alignment	not modelled	64.3	13	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
41	<a href="#">d1jeoa_</a>	Alignment	not modelled	60.5	12	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
42	<a href="#">d2ez9a1</a>	Alignment	not modelled	60.3	13	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
43	<a href="#">c5i01B_</a>	Alignment	not modelled	60.2	11	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoheptose isomerase; <b>PDBTitle:</b> structure of phosphoheptose isomerase gmha from neisseria gonorrhoeae
44	<a href="#">d1d7ya2</a>	Alignment	not modelled	59.5	21	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
45	<a href="#">c3cvjB_</a>	Alignment	not modelled	59.4	8	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative phosphoheptose isomerase; <b>PDBTitle:</b> crystal structure of a putative phosphoheptose isomerase (bh3325) from2 bacillus halodurans c-125 at 2.00 a resolution
46	<a href="#">d1ozha1</a>	Alignment	not modelled	59.1	15	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
47	<a href="#">c1vmeB_</a>	Alignment	not modelled	57.6	23	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> flavoprotein; <b>PDBTitle:</b> crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
48	<a href="#">d1p3da1</a>	Alignment	not modelled	55.1	13	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
49	<a href="#">c2f00A_</a>	Alignment	not modelled	54.9	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate--l-alanine ligase; <b>PDBTitle:</b> escherichia coli murc
50	<a href="#">d1j6ua1</a>	Alignment	not modelled	54.3	18	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
51	<a href="#">c5zvqA_</a>	Alignment	not modelled	54.3	23	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> recombination protein recr; <b>PDBTitle:</b> crystal structure of recombination mediator protein recr
52	<a href="#">c3pnxF_</a>	Alignment	not modelled	53.7	18	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> putative sulfurtransferase dsre; <b>PDBTitle:</b> crystal structure of a putative sulfurtransferase dsre (swol_2425)2 from syntrophomonas wolfei str. goettingen at 1.92 a resolution
53	<a href="#">c2qs7D_</a>	Alignment	not modelled	53.4	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase of the dsre/dsrf-like2 family (sso1126) from sulfobolus solfataricus p2 at 2.09 a resolution
54	<a href="#">d1iuka_</a>	Alignment	not modelled	52.9	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain

55	<a href="#">c5zbyA</a>	Alignment	not modelled	52.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase maturation protease hyci; <b>PDBTitle:</b> crystal structure of a [nife] hydrogenase maturation protease hyci2 from thermococcus kodakarensis kod1
56	<a href="#">d1q1ra2</a>	Alignment	not modelled	51.7	23	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
57	<a href="#">c2puwA</a>	Alignment	not modelled	51.7	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> isomerase domain of glutamine-fructose-6-phosphate <b>PDBTitle:</b> the crystal structure of isomerase domain of glucosamine-6-phosphate2 synthase from candida albicans
58	<a href="#">d1okga1</a>	Alignment	not modelled	50.5	17	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
59	<a href="#">d1vdda</a>	Alignment	not modelled	50.0	13	<b>Fold:</b> Recombination protein RecR <b>Superfamily:</b> Recombination protein RecR <b>Family:</b> Recombination protein RecR
60	<a href="#">d2d59a1</a>	Alignment	not modelled	49.9	12	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
61	<a href="#">c1okgA</a>	Alignment	not modelled	47.4	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> possible 3-mercaptopyruvate sulfurtransferase; <b>PDBTitle:</b> 3-mercaptopyruvate sulfurtransferase from leishmania major
62	<a href="#">c3lzcA</a>	Alignment	not modelled	41.1	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> dph2; <b>PDBTitle:</b> crystal structure of dph2 from pyrococcus horikoshii
63	<a href="#">c3fofD</a>	Alignment	not modelled	40.9	11	<b>PDB header:</b> isomerase/dna <b>Chain:</b> D: <b>PDB Molecule:</b> dna topoisomerase 4 subunit b; <b>PDBTitle:</b> structural insight into the quinolone-dna cleavage complex2 of type iia topoisomerases
64	<a href="#">d2ji7a1</a>	Alignment	not modelled	40.6	16	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
65	<a href="#">c4wb1B</a>	Alignment	not modelled	40.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cals8; <b>PDBTitle:</b> crystal structure of cals8 from micromonospora echinospora (p294s2 mutant)
66	<a href="#">c3q3vA</a>	Alignment	not modelled	40.3	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglycerate kinase; <b>PDBTitle:</b> crystal structure of phosphoglycerate kinase from campylobacter2 jejuni.
67	<a href="#">d1zpdA1</a>	Alignment	not modelled	39.0	16	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
68	<a href="#">d1gv4a2</a>	Alignment	not modelled	38.8	13	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
69	<a href="#">d1ovma1</a>	Alignment	not modelled	38.6	15	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
70	<a href="#">c1vddC</a>	Alignment	not modelled	38.3	13	<b>PDB header:</b> recombination <b>Chain:</b> C: <b>PDB Molecule:</b> recombination protein recr; <b>PDBTitle:</b> crystal structure of recombinational repair protein recr
71	<a href="#">c2zjtB</a>	Alignment	not modelled	37.7	14	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> dna gyrase subunit b; <b>PDBTitle:</b> crystal structure of dna gyrase b' domain sheds lights on the2 mechanism for t-segment navigation
72	<a href="#">d2gk3a1</a>	Alignment	not modelled	37.1	29	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> STM3548-like
73	<a href="#">c2qlcC</a>	Alignment	not modelled	36.9	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> dna repair protein radc homolog; <b>PDBTitle:</b> the crystal structure of dna repair protein radc from chlorobium2 tepidum t1s
74	<a href="#">c2k5eA</a>	Alignment	not modelled	35.9	31	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of putative uncharacterized protein2 gsu1278 from methanocaldococcus jannaschii, northeast3 structural genomics consortium (nesh) target gsr195
75	<a href="#">c3guxA</a>	Alignment	not modelled	34.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative zn-dependent exopeptidase; <b>PDBTitle:</b> crystal structure of a putative zn-dependent exopeptidase (bv1_1317)2 from bacteroides vulgatus atcc 8482 at 1.80 a resolution
76	<a href="#">c5xk2A</a>	Alignment	not modelled	34.6	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> diacylglycerol lipase; <b>PDBTitle:</b> crystal structure of mono- and diacylglycerol lipase from aspergillus2 oryzae
77	<a href="#">c3euaD</a>	Alignment	not modelled	33.7	13	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> putative fructose-aminoacid-6-phosphate deglycase; <b>PDBTitle:</b> crystal structure of a putative phosphosugar isomerase (bsu32610) from2 bacillus subtilis at 1.90 a resolution
78	<a href="#">d3pma3</a>	Alignment	not modelled	33.6	21	<b>Fold:</b> Phosphoglucomutase, first 3 domains <b>Superfamily:</b> Phosphoglucomutase, first 3 domains <b>Family:</b> Phosphoglucomutase, first 3 domains
79	<a href="#">d1q6za1</a>	Alignment	not modelled	33.3	16	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
80	<a href="#">c2i2A</a>	Alignment	not modelled	33.1	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucosamine--fructose-6-phosphate

80	<a href="#">c2z3A</a>	Alignment	not modelled	33.1	14	<b>PDBTitle:</b> isomerase domain of human glucose:fructose-6-phosphate2 amidotransferase
81	<a href="#">c3d3kD</a>	Alignment	not modelled	32.9	17	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> enhancer of mrna-decapping protein 3; <b>PDBTitle:</b> crystal structure of human edc3p
82	<a href="#">c2duwA</a>	Alignment	not modelled	32.1	17	<b>PDB header:</b> ligand binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative coa-binding protein; <b>PDBTitle:</b> solution structure of putative coa-binding protein of2 klebsiella pneumoniae
83	<a href="#">c3rhtB</a>	Alignment	not modelled	31.9	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> (gatase1)-like protein; <b>PDBTitle:</b> crystal structure of type 1 glutamine amidotransferase (gatase1)-like2 protein from planctomyces limnophilus
84	<a href="#">d1r3sa</a>	Alignment	not modelled	31.5	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> UROD/MetE-like <b>Family:</b> Uroporphyrinogen decarboxylase, UROD
85	<a href="#">c3nuhB</a>	Alignment	not modelled	31.5	11	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> dna gyrase subunit b; <b>PDBTitle:</b> a domain insertion in e. coli gyrb adopts a novel fold that plays a2 critical role in gyrase function
86	<a href="#">c1u57A</a>	Alignment	not modelled	29.6	26	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> gag polyprotein; <b>PDBTitle:</b> nmr structure of the (345-392)gag sequence from hiv-1
87	<a href="#">c4tmaH</a>	Alignment	not modelled	28.2	11	<b>PDB header:</b> isomerase/isomerase inhibitor <b>Chain:</b> H: <b>PDB Molecule:</b> dna gyrase subunit b; <b>PDBTitle:</b> crystal structure of gyrase bound to its inhibitor yacg
88	<a href="#">c4s1wA</a>	Alignment	not modelled	27.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine--fructose-6-phosphate aminotransferase <b>PDBTitle:</b> structure of a putative glutamine--fructose-6-phosphate2 aminotransferase from staphylococcus aureus subsp. aureus mu50
89	<a href="#">d1tjya</a>	Alignment	not modelled	27.6	11	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
90	<a href="#">c5t76A</a>	Alignment	not modelled	27.3	14	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> alanine--trna ligase, cytoplasmic; <b>PDBTitle:</b> a fragment of a human trna synthetase
91	<a href="#">d1vmea2</a>	Alignment	not modelled	27.3	23	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> ROO N-terminal domain-like
92	<a href="#">d1j93a</a>	Alignment	not modelled	26.6	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> UROD/MetE-like <b>Family:</b> Uroporphyrinogen decarboxylase, UROD
93	<a href="#">c1jpkA</a>	Alignment	not modelled	26.2	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> uroporphyrinogen decarboxylase; <b>PDBTitle:</b> gly156asp mutant of human urod, human uroporphyrinogen iii2 decarboxylase
94	<a href="#">c1yi1A</a>	Alignment	not modelled	26.2	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetolactate synthase; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana acetoxyacid synthase in2 complex with a sulfonylurea herbicide, tribenuron methyl
95	<a href="#">c5btaD</a>	Alignment	not modelled	26.1	14	<b>PDB header:</b> isomerase/dna <b>Chain:</b> D: <b>PDB Molecule:</b> dna gyrase subunit b; <b>PDBTitle:</b> crystal structure of a topoisomerase ii complex
96	<a href="#">c4z2cD</a>	Alignment	not modelled	24.8	11	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> dna gyrase subunit b; <b>PDBTitle:</b> quinolone(moxifloxacin)-dna cleavage complex of gyrase from s.2 pneumoniae
97	<a href="#">c3mc3A</a>	Alignment	not modelled	24.4	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> dsre/dsrf-like family protein; <b>PDBTitle:</b> crystal structure of dsre/dsrf-like family protein (np_342589.1) from2 sulfolobus solfataricus at 1.49 a resolution
98	<a href="#">c4a7pA</a>	Alignment	not modelled	24.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-glucose dehydrogenase; <b>PDBTitle:</b> se-met derivatized ugdg, udp-glucose dehydrogenase from sphingomonas2 elodea
99	<a href="#">d1xhca2</a>	Alignment	not modelled	23.4	16	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
100	<a href="#">c1zmrA</a>	Alignment	not modelled	23.1	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglycerate kinase; <b>PDBTitle:</b> crystal structure of the e. coli phosphoglycerate kinase
101	<a href="#">d1kfia3</a>	Alignment	not modelled	22.7	29	<b>Fold:</b> Phosphoglucomutase, first 3 domains <b>Superfamily:</b> Phosphoglucomutase, first 3 domains <b>Family:</b> Phosphoglucomutase, first 3 domains
102	<a href="#">d1j5xa</a>	Alignment	not modelled	22.2	12	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> double-SIS domain
103	<a href="#">d1pvda1</a>	Alignment	not modelled	21.8	12	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
104	<a href="#">c3tbfA</a>	Alignment	not modelled	21.7	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucosamine--fructose-6-phosphate aminotransferase <b>PDBTitle:</b> c-terminal domain of glucosamine-fructose-6-phosphate aminotransferase2 from francisella tularensis.
105	<a href="#">c4erhB</a>	Alignment	not modelled	21.5	7	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> outer membrane protein a; <b>PDBTitle:</b> the crystal structure of ompa domain of ompa from salmonella enterica2 subsp. enterica serovar typhimurium str. 14028s
						<b>PDB header:</b> isomerase

106	<a href="#">c3fkjA_</a>	Alignment	not modelled	21.2	11	<b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphosugar isomerases; <b>PDBTitle:</b> crystal structure of a putative phosphosugar isomerase (stm_0572) from2 salmonella typhimurium lt2 at 2.12 a resolution
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