Phyre2

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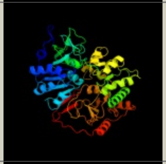
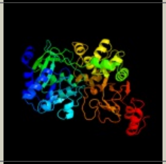
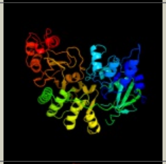
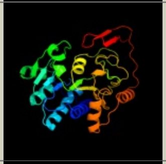
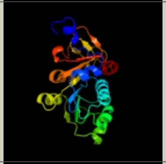
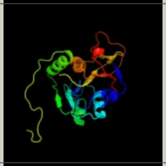
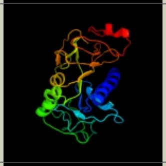
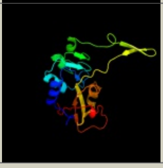
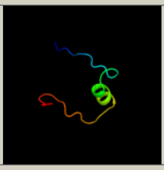
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1xr4B_	Alignment		100.0	72	**PDB header:**hydrolase/transferase **Chain:** B: **PDB Molecule:**putative citrate lyase alpha chain/citrate-acp transferase; **PDBTitle:** x-ray crystal structure of putative citrate lyase alpha chain/citrate-2 acp transferase [salmonella typhimurium]
2	c2hj0A_	Alignment		100.0	55	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative citrate lyase, alfa subunit; **PDBTitle:** crystal structure of the putative alfa subunit of citrate lyase in2 complex with citrate from streptococcus mutans, northeast structural3 genomics target smr12 (casp target).
3	c3gk7A_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coa-transferase; **PDBTitle:** crystal structure of 4-hydroxybutyrate coa-transferase from2 clostridium aminobutyricum
4	c2oasA_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coenzyme a transferase; **PDBTitle:** crystal structure of 4-hydroxybutyrate coenzyme a transferase (atoa)2 in complex with coa from shewanella oneidensis, northeast structural3 genomics target sor119.
5	c2g39A_	Alignment		100.0	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**acetyl-coa hydrolase; **PDBTitle:** crystal structure of coenzyme a transferase from pseudomonas2 aeruginosa
6	c2nvvF_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**acetyl-coa hydrolase/transferase family protein; **PDBTitle:** crystal structure of the putative acetyl-coa hydrolase/transferase2 pg1013 from porphyromonas gingivalis, northeast structural genomics3 target pgr16.
7	c3eh7A_	Alignment		100.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coa-transferase; **PDBTitle:** the structure of a putative 4-hydroxybutyrate coa-transferase from2 porphyromonas gingivalis w83
8	d1xr4a2	Alignment		100.0	72	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
9	c3d3uA_	Alignment		100.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coa-transferase; **PDBTitle:** crystal structure of 4-hydroxybutyrate coa-transferase (abft-2) from2 porphyromonas gingivalis. northeast structural genomics consortium3 target pgr26
10	d1xr4a1	Alignment		100.0	70	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
11	c2ahvC_	Alignment		100.0	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**putative enzyme ydif; **PDBTitle:** crystal structure of acyl-coa transferase from e. coli o157:h7 (ydif)-2 thioester complex with coa- 1

12	c1ooyA_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**succinyl-coa:3-ketoacid-coenzyme a transferase, **PDBTitle:** succinyl-coa:3-ketoacid coa transferase from pig heart
13	d2g39a2	Alignment		100.0	19	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
14	c3rrlC_	Alignment		100.0	24	**PDB header:**transferase **Chain:** C: **PDB Molecule:**succinyl-coa:3-ketoacid-coenzyme a transferase subunit a; **PDBTitle:** complex structure of 3-oxoadipate coa-transferase subunit a and b from2 helicobacter pylori 26695
15	c3cdkA_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**succinyl-coa:3-ketoacid-coenzyme a transferase **PDBTitle:** crystal structure of the co-expressed succinyl-coa2 transferase a and b complex from bacillus subtilis
16	d1ooya1	Alignment		100.0	15	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase beta subunit-like
17	d1ooya2	Alignment		100.0	27	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
18	d2ahua2	Alignment		100.0	17	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
19	c3cdkD_	Alignment		100.0	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**succinyl-coa:3-ketoacid-coenzyme a transferase **PDBTitle:** crystal structure of the co-expressed succinyl-coa2 transferase a and b complex from bacillus subtilis
20	d1k6da_	Alignment		100.0	23	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
21	d1poia_	Alignment	not modelled	100.0	20	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
22	d2g39a1	Alignment	not modelled	99.9	20	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
23	d2ahua1	Alignment	not modelled	99.9	20	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase beta subunit-like
24	d1poib_	Alignment	not modelled	99.9	24	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase beta subunit-like
25	c1m0sA_	Alignment	not modelled	97.7	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** northeast structural genomics consortium (nesg id ir21)
26	c1lk5C_	Alignment	not modelled	97.6	21	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**d-ribose-5-phosphate isomerase; **PDBTitle:** structure of the d-ribose-5-phosphate isomerase from2 pyrococcus horikoshii
27	c3kwmC_	Alignment	not modelled	97.5	23	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-isomerase a
28	c2f8mB_	Alignment	not modelled	97.5	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** ribose 5-phosphate isomerase from plasmodium falciparum
29	d1m0sa1	Alignment	not modelled	97.5	15	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like

						Family:D-ribose-5-phosphate isomerase (RpiA), catalytic domain
30	c1lkzB_	Alignment	not modelled	97.4	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose 5-phosphate isomerase a; **PDBTitle:** crystal structure of d-ribose-5-phosphate isomerase (rpia)2 from escherichia coli.
31	c3l7oB_	Alignment	not modelled	97.3	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from streptococcus2 mutans ua159
32	c1uj6A_	Alignment	not modelled	97.0	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** crystal structure of thermus thermophilus ribose-5-phosphate isomerase2 complexed with arabinose-5-phosphate
33	c3hheA_	Alignment	not modelled	97.0	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from bartonella2 henselae
34	d1uj4a1	Alignment	not modelled	96.7	21	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
35	d1lk5a1	Alignment	not modelled	96.2	22	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
36	c3u7jA_	Alignment	not modelled	95.6	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
37	c2pjmA_	Alignment	not modelled	95.3	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii
38	c3ecsD_	Alignment	not modelled	88.9	17	**PDB header:**translation **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b subunit **PDBTitle:** crystal structure of human eif2b alpha
39	d1vb5a_	Alignment	not modelled	86.3	18	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
40	c3a11D_	Alignment	not modelled	83.3	15	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b, delta **PDBTitle:** crystal structure of ribose-1,5-bisphosphate isomerase from2 thermococcus kodakaraensis kod1
41	c1xtzA_	Alignment	not modelled	80.2	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase; **PDBTitle:** crystal structure of the s. cerevisiae d-ribose-5-phosphate isomerase:2 comparison with the archeal and bacterial enzymes
42	c2yvkA_	Alignment	not modelled	78.5	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**methylthioribose-1-phosphate isomerase; **PDBTitle:** crystal structure of 5-methylthioribose 1-phosphate2 isomerase product complex from bacillus subtilis
43	d1t9ka_	Alignment	not modelled	77.5	15	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
44	c3e4fB_	Alignment	not modelled	75.2	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminoglycoside n3-acetyltransferase; **PDBTitle:** crystal structure of ba2930- a putative aminoglycoside n3-2 acetyltransferase from bacillus anthracis
45	d2nyga1	Alignment	not modelled	69.9	33	**Fold:**TTHA0583/YokD-like **Superfamily:**TTHA0583/YokD-like **Family:**Aminoglycoside 3-N-acetyltransferase-like
46	c3smaD_	Alignment	not modelled	66.8	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**frbf; **PDBTitle:** a new n-acetyltransferase fold in the structure and mechanism of the2 phosphonate biosynthetic enzyme frbf
47	d1o8bb1	Alignment	not modelled	64.4	13	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
48	c2ipxA_	Alignment		56.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rrna 2'-o-methyltransferase fibrillarin; **PDBTitle:** human fibrillarin
49	d1t5oa_	Alignment	not modelled	50.7	16	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
50	c1w2wJ_	Alignment	not modelled	36.8	23	**PDB header:**isomerase **Chain:** J: **PDB Molecule:**5-methylthioribose-1-phosphate isomerase; **PDBTitle:** crystal structure of yeast ypr118w, a methylthioribose-1-2 phosphate isomerase related to regulatory eif2b subunits
51	d1udxa3	Alignment	not modelled	33.1	35	**Fold:**Obg GTP-binding protein C-terminal domain **Superfamily:**Obg GTP-binding protein C-terminal domain **Family:**Obg GTP-binding protein C-terminal domain
52	d1g8sa_	Alignment	not modelled	29.2	12	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
53	d1g8aa_	Alignment	not modelled	28.3	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
54	c3myrE	Alignment	not modelled	28.0	7	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**hydrogenase (nife) small subunit hyda;

54		Alignment	not modelled			**PDBTitle:** crystal structure of [nife] hydrogenase from allochromatium vinosum in2 its ni-a state
55	d2a0ua1	Alignment	not modelled	26.1	13	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
56	d1vmha_	Alignment	not modelled	25.6	36	**Fold:**YjbQ-like **Superfamily:**YjbQ-like **Family:**YjbQ-like
57	c2q24A_	Alignment	not modelled	24.8	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative tetr family transcriptional regulator; **PDBTitle:** crystal structure of tetr transcriptional regulator sco0520 from2 streptomyces coelicolor
58	c3id5F_	Alignment	not modelled	24.6	18	**PDB header:**transferase/ribosomal protein/rna **Chain:** F: **PDB Molecule:**fibrillarin-like rrna/trna 2'-o-methyltransferase; **PDBTitle:** crystal structure of sulfolobus solfataricus c/d rnp assembled with2 nop5, fibrillarin, l7ae and a split half c/d rna
59	c3rgwS_	Alignment	not modelled	24.3	9	**PDB header:**oxidoreductase/oxidoreductase **Chain:** S: **PDB Molecule:**membrane-bound hydrogenase (nife) small subunit hoxk; **PDBTitle:** crystal structure at 1.5 a resolution of an h2-reduced, o2-tolerant2 hydrogenase from ralstonia eutropha unmasks a novel iron-sulfur3 cluster
60	d1x87a_	Alignment	not modelled	23.4	21	**Fold:**Urocanase **Superfamily:**Urocanase **Family:**Urocanase
61	d1e8oa_	Alignment	not modelled	23.2	13	**Fold:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Superfamily:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Family:**Signal recognition particle alu RNA binding heterodimer, SRP9/14
62	c2wpnA_	Alignment	not modelled	21.9	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**periplasmic [nifese] hydrogenase, small subunit; **PDBTitle:** structure of the oxidised, as-isolated nifese hydrogenase2 from d. vulgaris hildenborough
63	d1vmfa_	Alignment	not modelled	21.7	20	**Fold:**YjbQ-like **Superfamily:**YjbQ-like **Family:**YjbQ-like
64	c2qqdG_	Alignment	not modelled	20.8	20	**PDB header:**lyase **Chain:** G: **PDB Molecule:**pyruvoyl-dependent arginine decarboxylase (ec **PDBTitle:** n47a mutant of pyruvoyl-dependent arginine decarboxylase2 from methanococcus jannashii
65	c2p6hB_	Alignment	not modelled	20.0	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of hypothetical protein ape1520 from aeropyrum2 pernix k1
66	d1nt2a_	Alignment	not modelled	19.8	24	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
67	d1prya_	Alignment	not modelled	19.7	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
68	d1v7ba1	Alignment	not modelled	17.5	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
69	c2fknC_	Alignment	not modelled	17.3	21	**PDB header:**lyase **Chain:** C: **PDB Molecule:**urocanate hydratase; **PDBTitle:** crystal structure of urocanase from bacillus subtilis
70	d2gena1	Alignment	not modelled	15.7	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
71	c3qbzA_	Alignment	not modelled	15.5	20	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**ddk kinase regulatory subunit dbf4; **PDBTitle:** crystal structure of the rad53-recognition domain of saccharomyces2 cerevisiae dbf4
72	d3c07a1	Alignment	not modelled	15.5	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
73	d1ni9a_	Alignment	not modelled	15.4	13	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**GlpX-like bacterial fructose-1,6-bisphosphatase
74	d1t33a1	Alignment	not modelled	15.3	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
75	c3bnvD_	Alignment	not modelled	14.3	12	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**cj0977; **PDBTitle:** crystal structure of cj0977, a sigma28-regulated virulence protein2 from campylobacter jejuni.
76	d2o7ta1	Alignment	not modelled	14.2	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
77	d1vi0a1	Alignment	not modelled	13.4	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
78	d2vkea1	Alignment	not modelled	13.1	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
						Fold: YjbQ-like

79	d1vpha_	Alignment	not modelled	13.0	18	**Superfamily:**YjbQ-like **Family:**YjbQ-like
80	c3jsjC_	Alignment	not modelled	12.9	20	**PDB header:**transcription **Chain:** C: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** crystal structure of a putative tetr-transcriptional regulator2 (sav143) from streptomyces avermitilis ma-4680 at 2.10 a resolution
81	c2p6cB_	Alignment	not modelled	12.9	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**aq_2013 protein; **PDBTitle:** crystal structure of hypothetical protein aq_2013 from aquifex2 aeolicus vf5.
82	c1h2aS_	Alignment	not modelled	12.3	13	**PDB header:**oxidoreductase **Chain:** S: **PDB Molecule:**hydrogenase; **PDBTitle:** single crystals of hydrogenase from desulfovibrio vulgaris
83	d1wuis1	Alignment	not modelled	12.3	13	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
84	c1k5hB_	Alignment	not modelled	12.2	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**1-deoxy-d-xylulose-5-phosphate reductoisomerase; **PDBTitle:** 1-deoxy-d-xylulose-5-phosphate reductoisomerase
85	d1duvg2	Alignment	not modelled	12.1	24	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
86	d1i8fa_	Alignment	not modelled	12.0	21	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
87	d1914a1	Alignment	not modelled	12.0	13	**Fold:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Superfamily:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Family:**Signal recognition particle alu RNA binding heterodimer, SRP9/14
88	c2d6yA_	Alignment	not modelled	11.7	11	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**putative tetr family regulatory protein; **PDBTitle:** crystal structure of transcriptional factor sco4008 from streptomyces2 coelicolor a3(2)
89	c2w48D_	Alignment	not modelled	11.6	14	**PDB header:**transcription **Chain:** D: **PDB Molecule:**sorbitol operon regulator; **PDBTitle:** crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
90	c1vi0B_	Alignment	not modelled	11.5	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator
91	d2atca2	Alignment	not modelled	11.2	12	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
92	d3efba1	Alignment	not modelled	11.0	15	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
93	d1vmja_	Alignment	not modelled	10.8	32	**Fold:**YjbQ-like **Superfamily:**YjbQ-like **Family:**YjbQ-like
94	c2jvfA_	Alignment	not modelled	10.7	16	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo protein m7; **PDBTitle:** solution structure of m7, a computationally-designed2 artificial protein
95	d2nvma1	Alignment	not modelled	10.5	37	**Fold:**XisI-like **Superfamily:**XisI-like **Family:**XisI-like
96	d2nlva1	Alignment	not modelled	10.5	47	**Fold:**XisI-like **Superfamily:**XisI-like **Family:**XisI-like
97	d1dxha2	Alignment	not modelled	10.4	16	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
98	c3e0vB_	Alignment	not modelled	10.3	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from leishmania mexicana in2 complex with sulphate ions
99	d1uwka_	Alignment	not modelled	10.2	19	**Fold:**Urocanase **Superfamily:**Urocanase **Family:**Urocanase