Phyre^2

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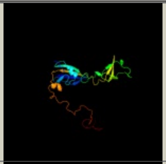
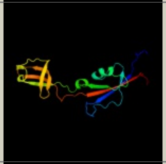
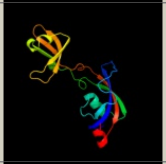
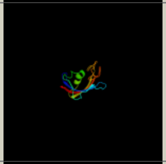
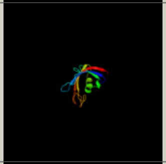
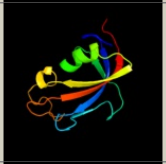
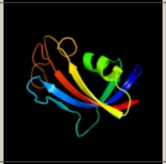
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kfwA_	Alignment		100.0	100	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase **PDBTitle:** solution structure of full-length slyd from e.coli
2	c2k8iA_	Alignment		100.0	99	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** solution structure of e.coli slyd
3	c3cgnA_	Alignment		100.0	49	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** crystal structure of thermophilic slyd
4	c2kr7A_	Alignment		100.0	32	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase slyd; **PDBTitle:** solution structure of helicobacter pylori slyd
5	c3prdA_	Alignment		100.0	25	**PDB header:**chaperone, isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase; **PDBTitle:** structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26
6	c3pr9A_	Alignment		100.0	25	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase; **PDBTitle:** structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26
7	d1ix5a_	Alignment		100.0	38	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
8	c2pbcD_	Alignment		99.7	34	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**fk506-binding protein 2; **PDBTitle:** fk506-binding protein 2
9	d1q6ha_	Alignment		99.7	26	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
10	c1q6uA_	Alignment		99.7	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase fkpa; **PDBTitle:** crystal structure of fkpa from escherichia coli
11	d1c9ha_	Alignment		99.7	24	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase

12	d1fd9a_	Alignment		99.6	24	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
13	c3jxvA_	Alignment		99.6	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**70 kda peptidyl-prolyl isomerase; **PDBTitle:** crystal structure of the 3 fkbp domains of wheat fkbp73
14	c2vcdA_	Alignment		99.6	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**outer membrane protein mip; **PDBTitle:** solution structure of the fkbp-domain of legionella2 pneumophila mip in complex with rapamycin
15	d1yata_	Alignment		99.6	25	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
16	c2lgoA_	Alignment		99.6	30	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp; **PDBTitle:** solution nmr structure of a fkbp-type peptidyl-prolyl cis-trans2 isomerase from giardia lamblia, seattle structural genomics center3 for infectious disease target gilaa.00840.a
17	d2ppna1	Alignment		99.6	25	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
18	c1rouA_	Alignment		99.6	24	**PDB header:**rotamase (isomerase) **Chain:** A: **PDB Molecule:**fkbp59-i; **PDBTitle:** structure of fkbp59-i, the n-terminal domain of a 59 kda2 fk506-binding protein, nmr, 22 structures
19	d1pbka_	Alignment		99.6	32	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
20	d1q1ca1	Alignment		99.6	24	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
21	d1r9ha_	Alignment	not modelled	99.6	24	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
22	c3o5fA_	Alignment	not modelled	99.6	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase fkbp5; **PDBTitle:** fk1 domain of fkbp51, crystal form vii
23	c2vn1A_	Alignment	not modelled	99.5	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**70 kda peptidylprolyl isomerase; **PDBTitle:** crystal structure of the fk506-binding domain of plasmodium2 falciparum fkbp35 in complex with fk506
24	c2f4eB_	Alignment	not modelled	99.5	27	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**atfkbp42; **PDBTitle:** n-terminal domain of fkbp42 from arabidopsis thaliana
25	c2jwxA_	Alignment	not modelled	99.5	26	**PDB header:**apoptosis, isomerase **Chain:** A: **PDB Molecule:**fk506-binding protein 8 variant; **PDBTitle:** solution structure of the n-terminal domain of human fkbp382 (fkbp38ntd)
26	c3o5dB_	Alignment	not modelled	99.5	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase fkbp5; **PDBTitle:** crystal structure of a fragment of fkbp51 comprising the fk1 and fk22 domains
27	c2ke0A_	Alignment	not modelled	99.5	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** solution structure of peptidyl-prolyl cis-trans isomerase from2 burkholderia pseudomallei
28	c2d9fA_	Alignment	not modelled	99.5	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fk506-binding protein 8 variant; **PDBTitle:** solution structure of ruh-047, an fkbp domain from human2 cdna

29	c1hxvA_	Alignment	not modelled	99.5	26	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**trigger factor; **PDBTitle:** ppiase domain of the mycoplasma genitalium trigger factor
30	d1hxva_	Alignment	not modelled	99.5	26	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
31	c3oe2A_	Alignment	not modelled	99.5	33	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** 1.6 a crystal structure of peptidyl-prolyl cis-trans isomerase ppiase2 from pseudomonas syringae pv. tomato str. dc3000 (pspto dc3000)
32	d1l1pa_	Alignment	not modelled	99.5	25	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
33	d1jvwa_	Alignment	not modelled	99.5	26	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
34	c1q1cA_	Alignment	not modelled	99.5	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fk506-binding protein 4; **PDBTitle:** crystal structure of n(1-260) of human fkbp52
35	d1kt0a2	Alignment	not modelled	99.5	24	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
36	d1u79a_	Alignment	not modelled	99.4	26	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
37	d1kt0a3	Alignment	not modelled	99.4	19	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
38	d1q1ca2	Alignment	not modelled	99.4	24	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
39	d1kt1a3	Alignment	not modelled	99.3	21	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
40	c1kt0A_	Alignment	not modelled	99.3	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**51 kda fk506-binding protein; **PDBTitle:** structure of the large fkbp-like protein, fkbp51, involved in steroid2 receptor complexes
41	d1w26a3	Alignment	not modelled	99.3	27	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
42	d1t11a3	Alignment	not modelled	99.3	27	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
43	c3b7xA_	Alignment	not modelled	99.2	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fk506-binding protein 6; **PDBTitle:** crystal structure of human fk506-binding protein 6
44	d1kt1a2	Alignment	not modelled	99.1	18	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
45	c2if4A_	Alignment	not modelled	99.1	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**atfkbp42; **PDBTitle:** crystal structure of a multi-domain immunophilin from2 arabidopsis thaliana
46	c1w26B_	Alignment	not modelled	99.0	27	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**trigger factor; **PDBTitle:** trigger factor in complex with the ribosome forms a2 molecular cradle for nascent proteins
47	c1qz2B_	Alignment	not modelled	99.0	28	**PDB header:**isomerase/chaperone **Chain:** B: **PDB Molecule:**fk506-binding protein 4; **PDBTitle:** crystal structure of fkbp52 c-terminal domain complex with2 the c-terminal peptide meevd of hsp90
48	c1t11A_	Alignment	not modelled	98.9	26	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**trigger factor; **PDBTitle:** trigger factor
49	c3gtyX_	Alignment	not modelled	98.5	20	**PDB header:**chaperone/ribosomal protein **Chain:** X: **PDB Molecule:**trigger factor; **PDBTitle:** promiscuous substrate recognition in folding and assembly activities2 of the trigger factor chaperone
50	c3htxA_	Alignment	not modelled	97.6	19	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**hen1; **PDBTitle:** crystal structure of small rna methyltransferase hen1
51	d1pkma1	Alignment	not modelled	86.3	16	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
52	d2g50a1	Alignment	not modelled	85.9	15	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
53	d1liua1	Alignment	not modelled	79.8	18	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
54	d1pkla1	Alignment	not modelled	79.7	15	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
55	d1e0ta1	Alignment	not modelled	73.3	25	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain

56	d1oi1a1	Alignment	not modelled	71.4	16	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
57	c2e6zA_	Alignment	not modelled	70.1	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt5; **PDBTitle:** solution structure of the second kow motif of human2 transcription elongation factor spt5
58	d1a3xa1	Alignment	not modelled	68.6	16	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
59	c1aqfB_	Alignment	not modelled	65.8	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** pyruvate kinase from rabbit muscle with mg, k, and l-2 phospholactate
60	d1oz2a1	Alignment	not modelled	65.0	18	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
61	c1t5aB_	Alignment	not modelled	64.9	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase, m2 isozyme; **PDBTitle:** human pyruvate kinase m2
62	d1oz2a3	Alignment	not modelled	63.2	22	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
63	d2etna2	Alignment	not modelled	61.9	22	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
64	d1wjqa_	Alignment	not modelled	60.1	14	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
65	d1oz2a2	Alignment	not modelled	60.0	31	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
66	d1qfha2	Alignment	not modelled	58.3	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
67	d1oi1a2	Alignment	not modelled	57.7	24	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
68	d2f23a2	Alignment	not modelled	56.2	17	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
69	c3e0vB_	Alignment	not modelled	56.2	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from leishmania mexicana in2 complex with sulphate ions
70	c3feoB_	Alignment	not modelled	54.9	18	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**mbt domain-containing protein 1; **PDBTitle:** the crystal structure of mbtd1
71	d2qn6a2	Alignment	not modelled	50.7	15	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain **Family:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
72	d1wjsa_	Alignment	not modelled	49.0	11	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
73	d1vhka1	Alignment	not modelled	48.9	19	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**YggJ N-terminal domain-like
74	d1wjra_	Alignment	not modelled	47.7	16	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
75	d1kk1a2	Alignment	not modelled	47.4	11	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain **Family:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
76	c2r58A_	Alignment	not modelled	46.4	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**polycomb protein scm; **PDBTitle:** crystal structure of the two mbt repeats from sex-comb on midleg (scm)2 in complex with di-methyl lysine
77	d1s0ua2	Alignment	not modelled	46.2	13	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain **Family:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
78	c2vytA_	Alignment	not modelled	44.9	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**sex comb on midleg-like protein 2; **PDBTitle:** the mbt repeats of human scml2 bind to peptides containing2 mono methylated lysine.
79	c3bmbB_	Alignment	not modelled	41.7	26	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**regulator of nucleoside diphosphate kinase; **PDBTitle:** crystal structure of a new rna polymerase interacting2 protein
80	d1qfha1	Alignment	not modelled	41.3	24	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
81	c3h6zA_	Alignment	not modelled	40.8	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**polycomb protein sfmbt; **PDBTitle:** crystal structure of the four mbt repeats of drosophila melanogaster2 sfmbt in complex with peptide rhr (me)k vlr
82	d1ea9c2	Alignment	not modelled	39.8	20	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain

83	d1nxza1	Alignment	not modelled	39.2	16	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**YggJ N-terminal domain-like
84	c3ceyA_	Alignment	not modelled	39.0	19	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**lethal(3)malignant brain tumor-like 2 protein; **PDBTitle:** crystal structure of l3mbtl2
85	c2etnA_	Alignment	not modelled	38.8	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**anti-cleavage anti-grea transcription factor **PDBTitle:** crystal structure of thermus aquaticus gfh1
86	c2pn0D_	Alignment	not modelled	38.4	26	**PDB header:**transcription **Chain:** D: **PDB Molecule:**prokaryotic transcription elongation factor **PDBTitle:** prokaryotic transcription elongation factor grea/greb from2 nitrosomonas europaea
87	c2ds4A_	Alignment	not modelled	38.1	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tripartite motif protein 45; **PDBTitle:** solution structure of the filamin domain from human2 tripartite motif protein 45
88	d1c8za_	Alignment	not modelled	37.4	19	**Fold:**Tubby C-terminal domain-like **Superfamily:**Tubby C-terminal domain-like **Family:**Transcriptional factor tubby, C-terminal domain
89	c1pklB_	Alignment	not modelled	36.2	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyruvate kinase); **PDBTitle:** the structure of leishmania pyruvate kinase
90	d1js8a2	Alignment	not modelled	35.9	14	**Fold:**C-terminal domain of mollusc hemocyanin **Superfamily:**C-terminal domain of mollusc hemocyanin **Family:**C-terminal domain of mollusc hemocyanin
91	c2ba0A_	Alignment	not modelled	34.7	24	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**archeal exosome rna binding protein rrp4; **PDBTitle:** archaeal exosome core
92	c3ma8A_	Alignment	not modelled	33.2	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of cgd1_2040, a pyruvate kinase from cryptosporidium2 parvum
93	c3o44G_	Alignment	not modelled	32.8	20	**PDB header:**toxin **Chain:** G: **PDB Molecule:**hemolysin; **PDBTitle:** crystal structure of the vibrio cholerae cytolysin (hlya) heptameric2 pore
94	c3besR_	Alignment	not modelled	32.3	22	**PDB header:**immune system **Chain:** R: **PDB Molecule:**interferon-gamma binding protein c4r; **PDBTitle:** structure of a poxvirus ifngbp/ifng complex
95	c2jz2A_	Alignment	not modelled	32.3	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ssl0352 protein; **PDBTitle:** solution nmr structure of ssl0352 protein from synechocystis sp. pcc2 6803. northeast structural genomics consortium target sgr42
96	d1f00i1	Alignment	not modelled	31.3	24	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments
97	c2je6I_	Alignment	not modelled	31.2	15	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**exosome complex rna-binding protein 1; **PDBTitle:** structure of a 9-subunit archaeal exosome
98	c1xezA_	Alignment	not modelled	30.6	20	**PDB header:**toxin **Chain:** A: **PDB Molecule:**hemolysin; **PDBTitle:** crystal structure of the vibrio cholerae cytolysin (hlya)2 pro-toxin with octylglucoside bound
99	c1e0tD_	Alignment	not modelled	29.8	25	**PDB header:**phosphotransferase **Chain:** D: **PDB Molecule:**pyruvate kinase; **PDBTitle:** r292d mutant of e. coli pyruvate kinase
100	c1qfhB_	Alignment	not modelled	28.8	22	**PDB header:**actin binding protein **Chain:** B: **PDB Molecule:**protein (gelation factor); **PDBTitle:** dimerization of gelation factor from dictyostelium2 discoideum: crystal structure of rod domains 5 and 6
101	c2egwB_	Alignment	not modelled	27.7	4	**PDB header:**rna methyltransferase **Chain:** B: **PDB Molecule:**upf0088 protein aq_165; **PDBTitle:** crystal structure of rrna methyltransferase with sah ligand
102	c2eqmA_	Alignment	not modelled	26.5	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 20-like 1; **PDBTitle:** solution structure of the tudor domain of phd finger2 protein 20-like 1 [homo sapiens]
103	d1fw8a_	Alignment	not modelled	26.4	33	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
104	d1gesa2	Alignment	not modelled	26.3	12	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
105	d1v10a2	Alignment	not modelled	25.5	16	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
106	c3pxpA_	Alignment	not modelled	25.0	22	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**helix-turn-helix domain protein; **PDBTitle:** crystal structure of a pas and dna binding domain containing protein2 (caur_2278) from chloroflexus aurantiacus j-10-fl at 2.30 a3 resolution
107	c3q1jA_	Alignment	not modelled	24.1	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 20; **PDBTitle:** crystal structure of tudor domain 1 of human phd finger protein 20
108	c1oz3C_	Alignment	not modelled	23.9	24	**PDB header:**transcription **Chain:** C: **PDB Molecule:**lethal(3)malignant brain tumor-like protein;

						PDBTitle: crystal structure of 3-mbt repeats of lethal (3) malignant brain tumor2 (native-i) at 1.85 angstrom
109	d3lada2	Alignment	not modelled	23.7	14	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
110	d2bi0a2	Alignment	not modelled	23.3	13	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
111	d1nz9a_	Alignment	not modelled	22.2	9	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
112	c2e28A_	Alignment	not modelled	21.8	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure analysis of pyruvate kinase from bacillus2 stearothermophilus
113	c2kvqG_	Alignment	not modelled	21.7	11	**PDB header:**transcription **Chain:** G: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of nuse:nusg-ctd complex
114	c2jvvA_	Alignment	not modelled	21.7	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of e. coli nusg carboxyterminal domain
115	c3eoeC_	Alignment	not modelled	21.5	15	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from toxoplasma gondii, 55.m00007
116	d1jnsa_	Alignment	not modelled	21.0	9	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
117	d2hi6a1	Alignment	not modelled	21.0	11	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**AF0055-like