Phyre^2

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Description	RVBD3597c_(lsr2)_4041160_4041498
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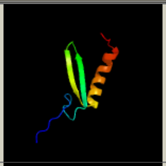
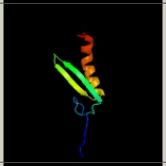
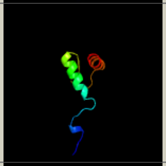
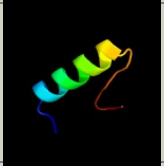
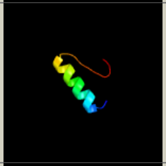
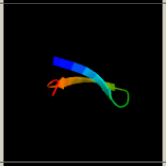
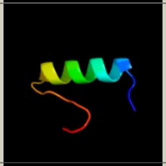
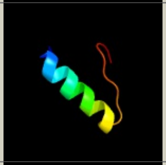
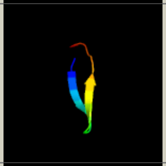
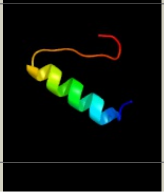
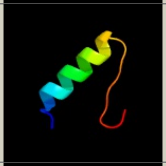
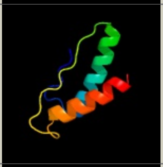
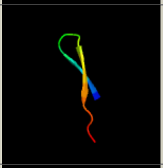
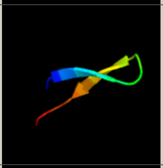
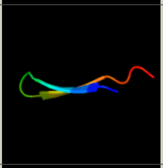
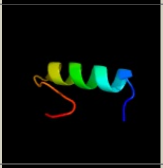
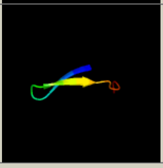
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4e1rA_	Alignment		99.9	100	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein lsr2; **PDBTitle:** crystal structure of the dimerization domain of lsr2 from2 mycobacterium tuberculosis in the p 31 2 1 space group
2	c4e1pA_	Alignment		99.9	100	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein lsr2; **PDBTitle:** crystal structure of the dimerization domain of lsr2 from2 mycobacterium tuberculosis in the p 1 21 1 space group
3	c2kngA_	Alignment		99.6	100	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein lsr2; **PDBTitle:** solution structure of c-domain of lsr2
4	d2bcqa3	Alignment		61.4	16	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like
5	c2bcuA_	Alignment		55.1	16	**PDB header:**transferase, lyase/dna **Chain:** A: **PDB Molecule:**dna polymerase lambda; **PDBTitle:** dna polymerase lambda in complex with a dna duplex2 containing an unpaired damp and a t:t mismatch
6	d1boba_	Alignment		54.2	15	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
7	d1dgja2	Alignment		53.4	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
8	d2fmpa3	Alignment		50.8	12	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like
9	c8iczA_	Alignment		46.2	12	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**protein (dna polymerase beta (e.c.2.7.7.7)); **PDBTitle:** dna polymerase beta (pol b) (e.c.2.7.7.7) complexed with2 seven base pairs of dna; soaked in the presence of of datp3 (1 millimolar), mncl2 (5 millimolar), and lithium sulfate4 (75 millimolar)
10	d1t3qa2	Alignment		45.3	6	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
11	c1nomA_	Alignment		44.9	12	**PDB header:**nucleotidyltransferase **Chain:** A: **PDB Molecule:**dna polymerase beta; **PDBTitle:** dna polymerase beta (pol b) (e.c.2.7.7.7), 31-kd domain; soaked in the2 presence of mncl2 (5 millimolar)

12	c2eq9C_	Alignment		44.0	34	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdb
13	d2vana2	Alignment		42.9	12	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like
14	c3qd7X_	Alignment		41.9	14	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**uncharacterized protein ydal; **PDBTitle:** crystal structure of ydal, a stand-alone small muts-related protein2 from escherichia coli
15	c6miwA_	Alignment		41.6	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase huwe1; **PDBTitle:** wwe domain of human huwe1
16	d1jqra_	Alignment		40.9	31	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like
17	c1x4rA_	Alignment		40.6	19	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**parp14 protein; **PDBTitle:** solution structure of wwe domain in parp14 protein
18	c2dk6A_	Alignment		40.2	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**parp11 protein; **PDBTitle:** solution structure of wwe domain in poly (adp-ribose)2 polymerase family, member 11 (parp 11)
19	d1jmsa4	Alignment		39.0	12	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like
20	d1n62a2	Alignment		38.5	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
21	c4xlgB_	Alignment	not modelled	36.5	42	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**structure-specific endonuclease subunit slx4; **PDBTitle:** c. glabrata slx1 in complex with slx4ccd.
22	c3auoB_	Alignment	not modelled	36.5	24	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna polymerase beta family (x family); **PDBTitle:** dna polymerase x from thermus thermophilus hb8 ternary complex with 1-2 nt gapped dna and ddgtp
23	c4p4oA_	Alignment	not modelled	35.7	16	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase beta; **PDBTitle:** crystal structure of leishmania infantum polymerase beta: ternary gap2 complex
24	d1rm6c2	Alignment	not modelled	35.6	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
25	d1ffva2	Alignment	not modelled	35.3	11	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
26	d1vlba2	Alignment	not modelled	35.3	6	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
27	c1t1eA_	Alignment	not modelled	34.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**kumamolisin; **PDBTitle:** high resolution crystal structure of the intact pro-2 kumamolisin, a sedolisin type proteinase (previously3 called kumamolysin or kscp)
28	d1ujra_	Alignment	not modelled	34.2	31	**Fold:**WWE domain **Superfamily:**WWE domain **Family:**WWE domain
29	c2zqeA	Alignment	not modelled	33.9	24	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**muts2 protein;

29	c2zqeA_	Alignment	not modelled	33.9	24	**PDBTitle:** crystal structure of the smr domain of thermus thermophilus muts2
30	d1au7a2	Alignment	not modelled	33.6	41	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**POU-specific domain
31	d1e3oc2	Alignment	not modelled	32.9	36	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**POU-specific domain
32	c6iwyA_	Alignment	not modelled	32.0	11	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**flagellar hook-associated protein 2; **PDBTitle:** crystal structure of the flagellar cap protein flid from helicobacter2 pylori
33	c2eq8C_	Alignment	not modelled	31.6	30	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
34	c2w9mB_	Alignment	not modelled	30.6	12	**PDB header:**dna replication **Chain:** B: **PDB Molecule:**polymerase x; **PDBTitle:** structure of family x dna polymerase from deinococcus2 radiodurans
35	c5g5gA_	Alignment	not modelled	29.9	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative xanthine dehydrogenase yagt iron-sulfur-binding **PDBTitle:** escherichia coli periplasmic aldehyde oxidase
36	c2m0kB_	Alignment	not modelled	29.7	63	**PDB header:**metal binding protein/metal transport **Chain:** B: **PDB Molecule:**peptide from cyclic nucleotide-gated olfactory channel; **PDBTitle:** 3d structure of calmodulin and calmodulin binding domain of rat2 olfactory cyclic nucleotide-gated ion channel
37	c5u4uA_	Alignment	not modelled	29.2	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mgc81300 protein; **PDBTitle:** pseudogtpase domain (pg1) of p190rhogap-a
38	c2m0jB_	Alignment	not modelled	28.5	63	**PDB header:**metal binding protein/metal transport **Chain:** B: **PDB Molecule:**peptide from cyclic nucleotide-gated olfactory channel; **PDBTitle:** 3d structure of calmodulin and calmodulin binding domain of olfactory2 cyclic nucleotide-gated ion channel complex
39	c1y56A_	Alignment	not modelled	27.5	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein ph1363; **PDBTitle:** crystal structure of l-proline dehydrogenase from p.horikoshii
40	c1rm6F_	Alignment	not modelled	27.3	19	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**4-hydroxybenzoyl-coa reductase gamma subunit; **PDBTitle:** structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
41	c5y6qA_	Alignment	not modelled	26.7	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde oxidase small subunit; **PDBTitle:** crystal structure of an aldehyde oxidase from methylobacillus sp.2 ky4400
42	d2d9ia1	Alignment	not modelled	26.0	13	**Fold:**IF3-like **Superfamily:**SMR domain-like **Family:**Smr domain
43	c4w9uD_	Alignment	not modelled	25.7	11	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**acyl-coa dehydrogenase; **PDBTitle:** crystal structure of an acyl-coa dehydrogenase from brucella2 melitensis
44	c2ihmA_	Alignment	not modelled	25.3	16	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase mu; **PDBTitle:** polymerase mu in ternary complex with gapped 11mer dna duplex and2 bound incoming nucleotide
45	c3utkA_	Alignment	not modelled	24.5	17	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**lipoprotein outs; **PDBTitle:** structure of the pilotin of the type ii secretion system
46	d2cyua1	Alignment	not modelled	24.5	19	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
47	c1w3dA_	Alignment	not modelled	23.9	37	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase component of **PDBTitle:** nmr structure of the peripheral-subunit binding domain of bacillus2 stearothermophilus e2p
48	c6gwjB_	Alignment	not modelled	23.3	9	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**ekc/keops complex subunit lage3; **PDBTitle:** protein complex
49	c4a56A_	Alignment	not modelled	22.8	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**pullulanase secretion protein puls; **PDBTitle:** crystal structure of the type 2 secretion system pilotin2 from klebsiella oxytoca
50	c1kdhA_	Alignment	not modelled	22.8	12	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**terminal deoxynucleotidyltransferase short **PDBTitle:** binary complex of murine terminal deoxynucleotidyl2 transferase with a primer single stranded dna
51	c4qoyE_	Alignment	not modelled	22.0	44	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**pyruvate dehydrogenase (dihydrolipoyltransacetylase **PDBTitle:** novel binding motif and new flexibility revealed by structural2 analysis of a pyruvate dehydrogenase-dihydrolipoyl acetyltransferase3 sub-complex from the escherichia coli pyruvate dehydrogenase multi-4 enzyme complex
52	d1w85i_	Alignment	not modelled	21.7	38	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex

						Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
53	c3hrdH_	Alignment	not modelled	21.6	25	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**nicotinate dehydrogenase small fes subunit; **PDBTitle:** crystal structure of nicotinate dehydrogenase
54	d1r7ma2	Alignment	not modelled	21.6	8	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Group I mobile intron endonuclease
55	c1t3qD_	Alignment	not modelled	21.2	6	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**quinoline 2-oxidoreductase small subunit; **PDBTitle:** crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
56	d1t1ea2	Alignment	not modelled	20.2	24	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Subtilase propeptides/inhibitors
57	c2jvfA_	Alignment	not modelled	19.9	29	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo protein m7; **PDBTitle:** solution structure of m7, a computationally-designed2 artificial protein
58	d1dcja_	Alignment	not modelled	19.3	16	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
59	d1v97a2	Alignment	not modelled	19.3	11	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
60	c1n60D_	Alignment	not modelled	19.1	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**carbon monoxide dehydrogenase small chain; **PDBTitle:** crystal structure of the cu,mo-co dehydrogenase (codh); cyanide-2 inactivated form
61	c3v3lA_	Alignment	not modelled	19.0	31	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase rnf146; **PDBTitle:** crystal structure of human rnf146 wwe domain in complex with iso-2 adpribose
62	c4wx8A_	Alignment	not modelled	18.7	9	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**ekc/keops complex subunit pcc1; **PDBTitle:** crystal structure of binary complex gon7-pcc1
63	c1au7B_	Alignment	not modelled	18.5	42	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**protein pit-1; **PDBTitle:** pit-1 mutant/dna complex
64	c1zwvA_	Alignment	not modelled	18.4	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoamide acyltransferase component of branched- **PDBTitle:** solution structure of the subunit binding domain (hbsbd) of2 the human mitochondrial branched-chain alpha-ketoacid3 dehydrogenase
65	c6dgbA_	Alignment	not modelled	18.3	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**is607 family transposase is1535; **PDBTitle:** crystal structure of the c-terminal catalytic domain of is1535 tnpa,2 an is607-like serine recombinase
66	d1je3a_	Alignment	not modelled	18.1	26	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
67	c4ochA_	Alignment	not modelled	17.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endonuclease muts2; **PDBTitle:** apo structure of smr domain of muts2 from deinococcus radiodurans
68	c1stzB_	Alignment	not modelled	17.7	21	**PDB header:**transcription **Chain:** B: **PDB Molecule:**heat-inducible transcription repressor hrca homolog; **PDBTitle:** crystal structure of a hypothetical protein at 2.2 a resolution
69	d1pava_	Alignment	not modelled	17.3	14	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
70	c1ffuA_	Alignment	not modelled	16.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cuts, iron-sulfur protein of carbon monoxide **PDBTitle:** carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor
71	d1w4ha1	Alignment	not modelled	16.4	24	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
72	c1r7mA_	Alignment	not modelled	15.9	8	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**intron-encoded endonuclease i-scei; **PDBTitle:** the homing endonuclease i-scei bound to its dna recognition2 region
73	c2gzqA_	Alignment	not modelled	15.8	8	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**phosphatidylethanolamine-binding protein; **PDBTitle:** phosphatidylethanolamine-binding protein from plasmodium vivax
74	c6hlwB_	Alignment	not modelled	15.6	21	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**genome polyprotein; **PDBTitle:** crystal structure of human acbd3 gold domain in complex with 3a2 protein of enterovirus-a71 (fusion protein)
75	c4zohC_	Alignment	not modelled	15.5	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative oxidoreductase iron-sulfur subunit; **PDBTitle:** crystal structure of glyceraldehyde oxidoreductase
76	d1jroa2	Alignment	not modelled	15.5	29	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins

77	c2cooA_	Alignment	not modelled	15.5	34	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoamide acyltransferase component of branched- **PDBTitle:** solution structure of the e3_binding domain of2 dihydrolipoamide branched chaintransacylase
78	c4je5C_	Alignment	not modelled	15.4	15	**PDB header:**transferase **Chain:** C: **PDB Molecule:**aromatic/aminoadipate aminotransferase 1; **PDBTitle:** crystal structure of the aromatic aminotransferase aro8, a putative2 alpha-aminoadipate aminotransferase in saccharomyces cerevisiae
79	d2ezha_	Alignment	not modelled	15.4	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
80	c3dv0I_	Alignment	not modelled	15.3	38	**PDB header:**oxidoreductase/transferase **Chain:** I: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase **PDBTitle:** snapshots of catalysis in the e1 subunit of the pyruvate2 dehydrogenase multi-enzyme complex
81	d1vl2a1	Alignment	not modelled	14.6	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
82	c4es2A_	Alignment	not modelled	14.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**bh0342 protein; **PDBTitle:** double-stranded endonuclease activity in b. halodurans clustered2 regularly interspaced short palindromic repeats (crispr)-associated3 cas2 protein
83	d1m0da_	Alignment	not modelled	13.7	30	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Endonuclease I (Holliday junction resolvase)
84	c4g29A_	Alignment	not modelled	13.5	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**secreted effector protein ssei; **PDBTitle:** structure of the catalytic domain of the salmonella virulence factor2 ssei
85	c3edyA_	Alignment	not modelled	13.5	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tripeptidyl-peptidase 1; **PDBTitle:** crystal structure of the precursor form of human tripeptidyl-peptidase2 1
86	d1zpwx1	Alignment	not modelled	13.3	14	**Fold:**Ferredoxin-like **Superfamily:**TTP0101/SSO1404-like **Family:**TTP0101/SSO1404-like
87	d1bala_	Alignment	not modelled	13.1	20	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
88	c3lhkA_	Alignment	not modelled	13.0	31	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna binding protein mj0014; **PDBTitle:** crystal structure of putative dna binding protein from2 methanocaldococcus jannaschii.
89	c2hlsB_	Alignment	not modelled	12.9	39	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**protein disulfide oxidoreductase; **PDBTitle:** the crystal structure of a protein disulfide oxidoreductase from2 aeropyrum pernix k1
90	d1jdqa_	Alignment	not modelled	12.9	26	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
91	c2fuvB_	Alignment	not modelled	12.9	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phosphoglucomutase; **PDBTitle:** phosphoglucomutase from salmonella typhimurium.
92	c6iw6A_	Alignment	not modelled	12.8	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**terminal uridylyltransferase 4,terminal uridylyltransferase **PDBTitle:** crystal structure of the lin28-interacting module of human tut4
93	c2p0wB_	Alignment	not modelled	12.5	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**histone acetyltransferase type b catalytic subunit; **PDBTitle:** human histone acetyltransferase 1 (hat1)
94	d2ezia_	Alignment	not modelled	12.3	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
95	d1bf4a_	Alignment	not modelled	12.3	44	**Fold:**SH3-like barrel **Superfamily:**Chromo domain-like **Family:**"Histone-like" proteins from archaea
96	c2eq7C_	Alignment	not modelled	12.0	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**2-oxoglutarate dehydrogenase e2 component; **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
97	c1w4kA_	Alignment	not modelled	12.0	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate dehydrogenase e2; **PDBTitle:** peripheral-subunit binding domains from mesophilic,2 thermophilic, and hyperthermophilic bacteria fold by3 ultrafast, apparently two-state transitions
98	c5h1pB_	Alignment	not modelled	11.9	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**crispr-associated endoribonuclease cas2; **PDBTitle:** crispr-associated protein
99	c6hltD_	Alignment	not modelled	11.9	19	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**genome polyprotein; **PDBTitle:** crystal structure of human acbd3 gold domain in complex with 3a2 protein of rhinovirus-14 (hrv14)