Phyre^2

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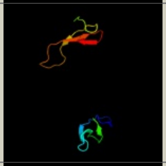
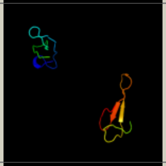
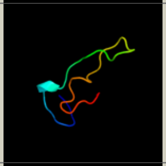
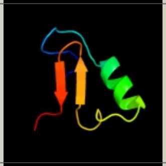
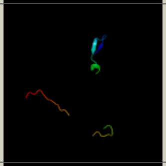
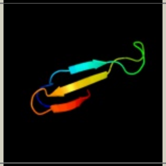
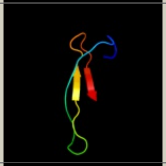
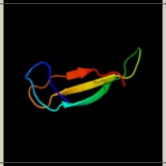
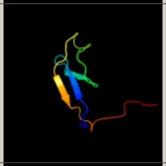
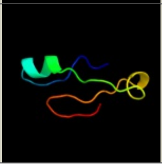
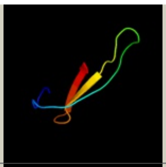
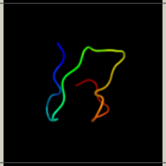
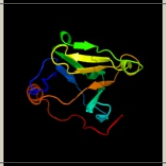
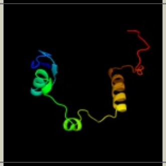
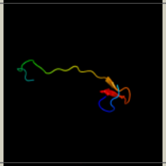
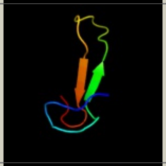
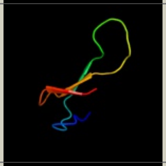
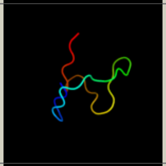
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2fiya1	Alignment		100.0	40	**Fold:**FdhE-like **Superfamily:**FdhE-like **Family:**FdhE-like
2	c1i3ql_	Alignment		96.9	15	**PDB header:**transcription **Chain:** I: **PDB Molecule:**dna-directed rna polymerase ii 14.2kd **PDBTitle:** rna polymerase ii crystal form i at 3.1 a resolution
3	c3h0gI_	Alignment		96.6	20	**PDB header:**transcription **Chain:** I: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb9; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
4	c3cngC_	Alignment		92.4	26	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea
5	c2gb5B_	Alignment		92.4	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nadh pyrophosphatase; **PDBTitle:** crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
6	c3a44D_	Alignment		91.7	27	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
7	d1tfia_	Alignment		91.2	17	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
8	c1y1yS_	Alignment		90.2	20	**PDB header:**transferase/transcription/dna-rna hybrid **Chain:** S: **PDB Molecule:**transcription elongation factor s-ii; **PDBTitle:** rna polymerase ii-tfiis-dna/rna complex
9	d1qypa_	Alignment		89.6	10	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
10	d2gnra1	Alignment		89.0	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**SSO2064-like
11	d1dl6a_	Alignment		88.9	23	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain

12	c1pqvS_	Alignment		88.7	20	**PDB header:**transferase/transcription **Chain:** S: **PDB Molecule:**transcription elongation factor s-ii; **PDBTitle:** rna polymerase ii-tfiis complex
13	c2kdxA_	Alignment		88.2	20	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**hydrogenase/urease nickel incorporation protein **PDBTitle:** solution structure of hypa protein
14	d1x6ma_	Alignment		87.8	21	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**Glutathione-dependent formaldehyde-activating enzyme, Gfa
15	c2ztgA_	Alignment		87.5	28	**PDB header:**ligase **Chain:** A: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** crystal structure of archaeoglobus fulgidus alanyl-trna2 synthetase lacking the c-terminal dimerization domain in3 complex with ala-sa
16	c3ndjA_	Alignment		86.8	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** x-ray structure of a c-3'-methyltransferase in complex with s-2 adenosyl-l-homocysteine and sugar product
17	c1nuiA_	Alignment		86.7	32	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna primase/helicase; **PDBTitle:** crystal structure of the primase fragment of bacteriophage t7 primase-2 helicase protein
18	d1twfi2	Alignment		84.9	14	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
19	d1hk8a_	Alignment		84.5	16	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**Class III anaerobic ribonucleotide reductase NRDD subunit
20	c1hk8A_	Alignment		84.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**anaerobic ribonucleotide-triphosphate reductase; **PDBTitle:** structural basis for allosteric substrate specificity2 regulation in class iii ribonucleotide reductases:3 nrdd in complex with dgtp
21	c3k7aM_	Alignment	not modelled	83.9	13	**PDB header:**transcription **Chain:** M: **PDB Molecule:**transcription initiation factor iib; **PDBTitle:** crystal structure of an rna polymerase ii-tfiib complex
22	c2opfA_	Alignment	not modelled	83.6	20	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**endonuclease viii; **PDBTitle:** crystal structure of the dna repair enzyme endonuclease-viii (nei)2 from e. coli (r252a) in complex with ap-site containing dna substrate
23	c3gn5B_	Alignment	not modelled	81.8	25	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator mqsa (ygit/b3021); **PDBTitle:** structure of the e. coli protein mqsa (ygit/b3021)
24	c2aklA_	Alignment	not modelled	80.8	38	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phna-like protein pa0128; **PDBTitle:** solution structure for phn-a like protein pa0128 from2 pseudomonas aeruginosa
25	c2lcqA_	Alignment	not modelled	80.6	17	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative toxin vapc6; **PDBTitle:** solution structure of the endonuclease nob1 from p.horikoshii
26	c2odxA_	Alignment	not modelled	80.4	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c oxidase polypeptide iv; **PDBTitle:** solution structure of zn(ii)cox4
27	d1wfka_	Alignment	not modelled	80.2	22	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**FYVE, a phosphatidylinositol-3-phosphate binding domain
28	c3eswA_	Alignment	not modelled	80.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide-n(4)-(n-acetyl-beta-glucosaminyl)asparagine **PDBTitle:** complex of yeast pngase with glcnac2-iac.

29	d1wiia_	Alignment	not modelled	79.7	17	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Putative zinc binding domain
30	d2akla2	Alignment	not modelled	79.6	35	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**PhnA zinc-binding domain
31	d1x3za1	Alignment	not modelled	79.2	15	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
32	c2y69S_	Alignment	not modelled	78.7	20	**PDB header:**electron transport **Chain:** S: **PDB Molecule:**cytochrome c oxidase subunit 5b; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
33	c2js4A_	Alignment	not modelled	78.0	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0434 protein bb2007; **PDBTitle:** solution nmr structure of bordetella bronchiseptica protein2 bb2007. northeast structural genomics consortium target3 bor54
34	d2f9yb1	Alignment	not modelled	76.2	26	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
35	c2f9yB_	Alignment	not modelled	76.2	26	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl transferase subunit **PDBTitle:** the crystal structure of the carboxyltransferase subunit of acc from2 escherichia coli
36	c2jr6A_	Alignment	not modelled	75.9	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0434 protein nma0874; **PDBTitle:** solution structure of upf0434 protein nma0874. northeast structural2 genomics target mr32
37	c2zzfA_	Alignment	not modelled	75.6	27	**PDB header:**ligase **Chain:** A: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** crystal structure of alanyl-trna synthetase without2 oligomerization domain
38	d1v54f_	Alignment	not modelled	75.4	20	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Cytochrome c oxidase Subunit F
39	c1neeA_	Alignment	not modelled	75.3	21	**PDB header:**translation **Chain:** A: **PDB Molecule:**probable translation initiation factor 2 beta **PDBTitle:** structure of archaeal translation factor aif2beta from2 methanobacterium thermoautrophicum
40	d1k81a_	Alignment	not modelled	75.2	20	**Fold:**Zinc-binding domain of translation initiation factor 2 beta **Superfamily:**Zinc-binding domain of translation initiation factor 2 beta **Family:**Zinc-binding domain of translation initiation factor 2 beta
41	c2vjfB_	Alignment	not modelled	74.9	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**mdm4 protein; **PDBTitle:** crystal structure of the mdm2-mdmx ring domain heterodimer
42	c2kyuA_	Alignment	not modelled	74.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase mll; **PDBTitle:** the solution structure of the phd3 finger of mll
43	c2f9iD_	Alignment	not modelled	74.5	23	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl **PDBTitle:** crystal structure of the carboxyltransferase subunit of acc2 from staphylococcus aureus
44	d1pfta_	Alignment	not modelled	74.3	31	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
45	c3fl2A_	Alignment	not modelled	73.1	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase uhrf1; **PDBTitle:** crystal structure of the ring domain of the e3 ubiquitin-2 protein ligase uhrf1
46	d1ywsa1	Alignment	not modelled	73.0	15	**Fold:**Rubredoxin-like **Superfamily:**CSL zinc finger **Family:**CSL zinc finger
47	c2dcuB_	Alignment	not modelled	72.7	33	**PDB header:**translation **Chain:** B: **PDB Molecule:**translation initiation factor 2 beta subunit; **PDBTitle:** crystal structure of translation initiation factor aif2betagamma2 heterodimer with gdp
48	c3pihA_	Alignment	not modelled	72.3	16	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** t. maritima uvra in complex with fluorescein-modified dna
49	d1nuia2	Alignment	not modelled	71.5	38	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**DNA primase zinc finger
50	c1z6uA_	Alignment	not modelled	71.2	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**np95-like ring finger protein isoform b; **PDBTitle:** np95-like ring finger protein isoform b [homo sapiens]
51	c3eb6A_	Alignment	not modelled	70.7	26	**PDB header:**apoptosis, ligase **Chain:** A: **PDB Molecule:**baculoviral iap repeat-containing protein 3; **PDBTitle:** structure of the ciap2 ring domain bound to ubch5b
52	c3nw0A_	Alignment	not modelled	70.3	15	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**non-structural maintenance of chromosomes element 1 **PDBTitle:** crystal structure of mageg1 and nse1 complex
53	d1chca_	Alignment	not modelled	70.3	18	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
54	c2y43B_	Alignment	not modelled	70.2	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**e3 ubiquitin-protein ligase rad18;

						PDBTitle: rad18 ubiquitin ligase ring domain structure
55	d1yuja_	Alignment	not modelled	70.2	38	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
56	c2cklA_	Alignment	not modelled	70.1	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**polycomb group ring finger protein 4; **PDBTitle:** ring1b-bmi1 e3 catalytic domain structure
57	c2e9hA_	Alignment	not modelled	69.9	16	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 5; **PDBTitle:** solution structure of the eif-5_eif-2b domain from human2 eukaryotic translation initiation factor 5
58	c1nnjA_	Alignment	not modelled	69.7	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure complex between the lactococcus lactis fpg and an2 abasic site containing dna
59	d1wgea1	Alignment	not modelled	68.7	24	**Fold:**Rubredoxin-like **Superfamily:**CSL zinc finger **Family:**CSL zinc finger
60	c2x5cB_	Alignment	not modelled	68.7	38	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**hypothetical protein orf131; **PDBTitle:** crystal structure of hypothetical protein orf131 from2 pyrobaculum spherical virus
61	c2d8tA_	Alignment	not modelled	68.4	22	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ring finger protein 146; **PDBTitle:** solution structure of the ring domain of the human ring2 finger protein 146
62	c1ee8A_	Alignment	not modelled	67.9	33	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mutm (fpg) protein; **PDBTitle:** crystal structure of mutm (fpg) protein from thermus thermophilus hb8
63	c3k35D_	Alignment	not modelled	67.5	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** crystal structure of human sirt6
64	d1pfva3	Alignment	not modelled	67.1	20	**Fold:**Rubredoxin-like **Superfamily:**Methionyl-tRNA synthetase (MetRS), Zn-domain **Family:**Methionyl-tRNA synthetase (MetRS), Zn-domain
65	d2cona1	Alignment	not modelled	67.1	17	**Fold:**Rubredoxin-like **Superfamily:**NOB1 zinc finger-like **Family:**NOB1 zinc finger-like
66	c3zyqA_	Alignment	not modelled	66.8	16	**PDB header:**signaling **Chain:** A: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine kinase **PDBTitle:** crystal structure of the tandem vhs and fyve domains of hepatocyte2 growth factor-regulated tyrosine kinase substrate (hgs-hrs) at 1.483 a resolution
67	c2csyA_	Alignment	not modelled	66.6	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**zinc finger protein 183-like 1; **PDBTitle:** solution structure of the ring domain of the zinc finger2 protein 183-like 1
68	d1p91a_	Alignment	not modelled	66.2	23	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA methyltransferase RlmA
69	d2pk7a1	Alignment	not modelled	66.2	17	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
70	c2qkdA_	Alignment	not modelled	65.9	18	**PDB header:**signaling protein, cell cycle **Chain:** A: **PDB Molecule:**zinc finger protein zpr1; **PDBTitle:** crystal structure of tandem zpr1 domains
71	c2owoA_	Alignment	not modelled	65.5	38	**PDB header:**ligase/dna **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** last stop on the road to repair: structure of e.coli dna ligase bound2 to nicked dna-adenylate
72	c1yuzB_	Alignment	not modelled	65.5	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nigerythrin; **PDBTitle:** partially reduced state of nigerythrin
73	c2jrpA_	Alignment	not modelled	64.5	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative cytoplasmic protein; **PDBTitle:** solution nmr structure of yfgj from salmonella typhimurium2 modeled with two zn+2 bound, northeast structural genomics3 consortium target str86
74	d2ct7a1	Alignment	not modelled	64.4	15	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**IBR domain
75	d2dkta1	Alignment	not modelled	64.3	21	**Fold:**CHY zinc finger-like **Superfamily:**CHY zinc finger-like **Family:**CHY zinc finger
76	d1dgsa1	Alignment	not modelled	64.1	50	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**NAD+-dependent DNA ligase, domain 3
77	c2f5qA_	Alignment	not modelled	63.8	31	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosidase; **PDBTitle:** catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
78	c2yhoE_	Alignment	not modelled	63.7	23	**PDB header:**ligase **Chain:** E: **PDB Molecule:**e3 ubiquitin-protein ligase mylip; **PDBTitle:** the idol-ube2d complex mediates sterol-dependent degradation of the2 ldl receptor
79	d1e7la2	Alignment	not modelled	63.6	29	**Fold:**His-Me finger endonucleases **Superfamily:**His-Me finger endonucleases **Family:**Recombination endonuclease VII, N-terminal domain
80	c2hjhB_	Alignment	not modelled	63.3	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nad-dependent histone deacetylase sir2;

						PDBTitle: crystal structure of the sir2 deacetylase
81	d1q1aa_	Alignment	not modelled	62.6	26	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
82	d1k3xa3	Alignment	not modelled	62.2	23	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
83	d2baya1	Alignment	not modelled	62.2	9	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
84	c1z2qA_	Alignment	not modelled	61.9	24	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**lm5-1; **PDBTitle:** high-resolution solution structure of the lm5-1 fyve domain2 from leishmania major
85	c3hi2C_	Alignment	not modelled	61.5	30	**PDB header:**dna binding protein/toxin **Chain:** C: **PDB Molecule:**hth-type transcriptional regulator mqsa(ygit); **PDBTitle:** structure of the n-terminal domain of the e. coli antitoxin mqsa2 (ygit/b3021) in complex with the e. coli toxin mqsr (ygiu/b3022)
86	c1fbvA_	Alignment	not modelled	61.4	28	**PDB header:**ligase **Chain:** A: **PDB Molecule:**signal transduction protein cbl; **PDBTitle:** structure of a cbl-ubch7 complex: ring domain function in2 ubiquitin-protein ligases
87	d1bora_	Alignment	not modelled	61.3	20	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
88	c2cttA_	Alignment	not modelled	61.1	25	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily a member 3; **PDBTitle:** solution structure of zinc finger domain from human dnaj2 subfamily a menber 3
89	c2gajA_	Alignment	not modelled	60.9	38	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna topoisomerase i; **PDBTitle:** structure of full length topoisomerase i from thermotoga maritima in2 monoclinic crystal form
90	c2jmdA_	Alignment	not modelled	60.7	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tnf receptor-associated factor 6; **PDBTitle:** solution structure of the ring domain of human traf6
91	c2kpiA_	Alignment	not modelled	60.5	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein sco3027; **PDBTitle:** solution nmr structure of streptomyces coelicolor sco30272 modeled with zn+2 bound, northeast structural genomics3 consortium target rr58
92	c1k82D_	Alignment	not modelled	60.2	28	**PDB header:**hydrolase/dna **Chain:** D: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure of e.coli formamidopyrimidine-dna2 glycosylase (fpg) covalently trapped with dna
93	d1ee8a3	Alignment	not modelled	60.1	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
94	c2qnfB_	Alignment	not modelled	60.1	26	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**recombination endonuclease vii; **PDBTitle:** crystal structure of t4 endonuclease vii h43n mutant in2 complex with heteroduplex dna containing base mismatches
95	c1nltA_	Alignment	not modelled	60.0	21	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**mitochondrial protein import protein mas5; **PDBTitle:** the crystal structure of hsp40 ydj1
96	d2ds5a1	Alignment	not modelled	59.2	25	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**ClpX chaperone zinc binding domain
97	c3glsC_	Alignment	not modelled	58.6	24	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nad-dependent deacetylase sirtuin-3, **PDBTitle:** crystal structure of human sirt3
98	c2eciA_	Alignment	not modelled	58.5	19	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**tnf receptor-associated factor 6; **PDBTitle:** solution structure of the ring domain of the human tnf2 receptor-associated factor 6 protein
99	c3pkiF_	Alignment	not modelled	58.4	15	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** human sirt6 crystal structure in complex with adp ribose
100	d1yc5a1	Alignment	not modelled	58.4	29	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
101	c2ectA_	Alignment	not modelled	58.2	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ring finger protein 126; **PDBTitle:** solution structure of the zinc finger, c3hc4 type (ring2 finger) domain of ring finger protein 126
102	d1jm7a_	Alignment	not modelled	58.2	18	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
103	d1l1ta3	Alignment	not modelled	58.1	29	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
104	c1ovxB_	Alignment	not modelled	57.9	25	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**atp-dependent clp protease atp-binding subunit clpx; **PDBTitle:** nmr structure of the e. coli clpx chaperone zinc binding domain dimer
105	c3cw2M_	Alignment	not modelled	57.6	21	**PDB header:**translation **Chain:** M: **PDB Molecule:**translation initiation factor 2 subunit beta; **PDBTitle:** crystal structure of the intact archaeal translation2

						initiation factor 2 from sulfolobus solfataricus .
106	d1yuza2	Alignment	not modelled	56.6	14	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
107	d1exka_	Alignment	not modelled	56.4	23	**Fold:**DnaJ/Hsp40 cysteine-rich domain **Superfamily:**DnaJ/Hsp40 cysteine-rich domain **Family:**DnaJ/Hsp40 cysteine-rich domain
108	d1wgma_	Alignment	not modelled	56.4	7	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
109	d1m2ka_	Alignment	not modelled	56.2	30	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
110	c2f42A_	Alignment	not modelled	56.2	7	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**stip1 homology and u-box containing protein 1; **PDBTitle:** dimerization and u-box domains of zebrafish c-terminal of hsp702 interacting protein
111	c2ea5A_	Alignment	not modelled	56.1	23	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell growth regulator with ring finger domain **PDBTitle:** solution structure of the ring domain of the human cell2 growth regulator with ring finger domain 1 protein
112	c2kwqA_	Alignment	not modelled	55.9	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein mcm10 homolog; **PDBTitle:** mcm10 c-terminal dna binding domain
113	c2cklB_	Alignment	not modelled	55.7	26	**PDB header:**transcription **Chain:** B: **PDB Molecule:**ubiquitin ligase protein ring2; **PDBTitle:** ring1b-bmi1 e3 catalytic domain structure
114	c3htkC_	Alignment	not modelled	55.7	8	**PDB header:**recombination/replication/ligase **Chain:** C: **PDB Molecule:**e3 sumo-protein ligase mms21; **PDBTitle:** crystal structure of mms21 and smc5 complex
115	d1tdza3	Alignment	not modelled	55.4	26	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
116	d1r2za3	Alignment	not modelled	55.0	29	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
117	d1vd4a_	Alignment	not modelled	54.9	35	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
118	d1vs6z1	Alignment	not modelled	54.7	11	**Fold:**L28p-like **Superfamily:**L28p-like **Family:**Ribosomal protein L31p
119	c1q14A_	Alignment	not modelled	54.3	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hst2 protein; **PDBTitle:** structure and autoregulation of the yeast hst2 homolog of sir2
120	c2ecmA_	Alignment	not modelled	54.1	24	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ring finger and chy zinc finger domain- **PDBTitle:** solution structure of the ring domain of the ring finger2 and chy zinc finger domain-containing protein 1 from mus3 musculus