Phyre2

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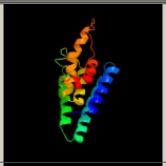
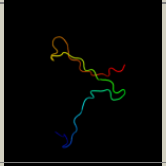
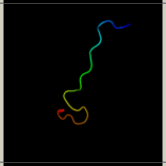
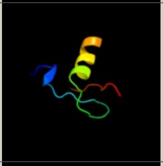
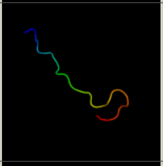
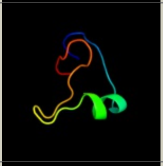
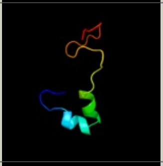
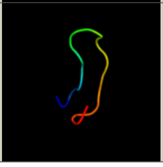
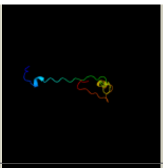
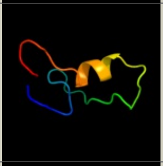
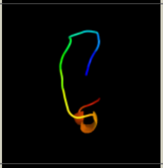
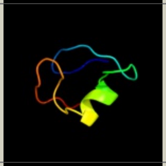
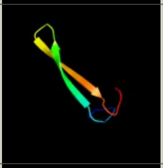
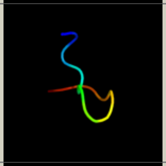
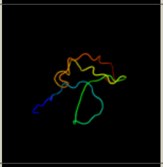
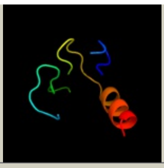
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3s0xB_	Alignment		98.7	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidase a24b, flak domain protein; **PDBTitle:** the crystal structure of gxgd membrane protease flak
2	c2owoA_	Alignment		86.6	16	**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
3	c1v9pB_	Alignment		81.9	12	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase
4	c2k5cA_	Alignment		81.7	25	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein pf0385; **PDBTitle:** nmr structure for pf0385
5	c3py7A_	Alignment		78.6	21	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein,paxillin ld1,protein e6 **PDBTitle:** crystal structure of full-length bovine papillomavirus oncoprotein e62 in complex with ld1 motif of paxillin at 2.3a resolution
6	c1dgsB_	Alignment		76.6	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase from t.2 filiformis
7	d1dgsa1	Alignment		74.9	27	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**NAD+-dependent DNA ligase, domain 3
8	d2fk4a1	Alignment		69.5	19	**Fold:**E6 C-terminal domain-like **Superfamily:**E6 C-terminal domain-like **Family:**E6 C-terminal domain-like
9	d1vd4a_	Alignment		69.2	27	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
10	d2fiya1	Alignment		66.5	22	**Fold:**FdhE-like **Superfamily:**FdhE-like **Family:**FdhE-like
11	c2qgpA_	Alignment		66.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hnh endonuclease; **PDBTitle:** x-ray structure of the nhn endonuclease from geobacter2 metallireducens. northeast structural genomics consortium3 target gmr87.

12	c3zyqA_	Alignment		64.9	18	**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
13	d1vfya_	Alignment		63.6	29	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**FYVE, a phosphatidylinositol-3-phosphate binding domain
14	d1pfva3	Alignment		63.0	27	**Fold:**Rubredoxin-like **Superfamily:**Methionyl-tRNA synthetase (MetRS), Zn-domain **Family:**Methionyl-tRNA synthetase (MetRS), Zn-domain
15	c2ea6A_	Alignment		62.8	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ring finger protein 4; **PDBTitle:** solution structure of the ring domain of the human ring2 finger protein 4
16	d2jnea1	Alignment		62.1	43	**Fold:**Rubredoxin-like **Superfamily:**YfgJ-like **Family:**YfgJ-like
17	c2jneA_	Alignment		62.1	43	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hypothetical protein yfgj; **PDBTitle:** nmr structure of e.coli yfgj modelled with two zn+2 bound.2 northeast structural genomics consortium target er317.
18	c2lcqA_	Alignment		62.0	31	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative toxin vapc6; **PDBTitle:** solution structure of the endonuclease nob1 from p.horikoshii
19	d1wfpa_	Alignment		61.6	18	**Fold:**AN1-like Zinc finger **Superfamily:**AN1-like Zinc finger **Family:**AN1-like Zinc finger
20	d1dvpa2	Alignment		59.7	19	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**FYVE, a phosphatidylinositol-3-phosphate binding domain
21	c3nw0A_	Alignment	not modelled	59.4	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**non-structural maintenance of chromosomes element 1 **PDBTitle:** crystal structure of mageg1 and nse1 complex
22	c3llkA_	Alignment	not modelled	58.7	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfhydryl oxidase 1; **PDBTitle:** sulfhydryl oxidase fragment of human qsox1
23	d1wg2a_	Alignment	not modelled	58.6	18	**Fold:**AN1-like Zinc finger **Superfamily:**AN1-like Zinc finger **Family:**AN1-like Zinc finger
24	c1dvpA_	Alignment	not modelled	58.5	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine **PDBTitle:** crystal structure of the vhs and fyve tandem domains of hrs,2 a protein involved in membrane trafficking and signal3 transduction
25	d1wfka_	Alignment	not modelled	57.6	36	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**FYVE, a phosphatidylinositol-3-phosphate binding domain
26	c2kr6A_	Alignment	not modelled	57.4	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**presenilin-1; **PDBTitle:** solution structure of presenilin-1 ctf subunit

27	c3floD_	Alignment		55.8	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna polymerase alpha catalytic subunit a; **PDBTitle:** crystal structure of the carboxyl-terminal domain of yeast2 dna polymerase alpha in complex with its b subunit
28	c3pfqA_	Alignment	not modelled	55.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein kinase c beta type; **PDBTitle:** crystal structure and allosteric activation of protein kinase c beta2 ii
29	c2ecmA_	Alignment	not modelled	55.1	26	**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
30	c3odeA_	Alignment	not modelled	54.3	33	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 1; **PDBTitle:** human parp-1 zinc finger 2 (zn2) bound to dna
31	c3k1lA_	Alignment	not modelled	54.3	43	**PDB header:**ligase **Chain:** A: **PDB Molecule:**fancl; **PDBTitle:** crystal structure of fancl
32	c2dmjA_	Alignment	not modelled	54.2	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly (adp-ribose) polymerase family, member 1; **PDBTitle:** solution structure of the first zf-parp domain of human2 poly(adp-ribose)polymerase-1
33	c2hr5B_	Alignment	not modelled	53.6	17	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**rubrerythrin; **PDBTitle:** pf1283- rubrerythrin from pyrococcus furiosus iron bound form
34	c2ep4A_	Alignment	not modelled	53.6	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ring finger protein 24; **PDBTitle:** solution structure of ring finger from human ring finger2 protein 24
35	d1wfha_	Alignment	not modelled	53.5	26	**Fold:**AN1-like Zinc finger **Superfamily:**AN1-like Zinc finger **Family:**AN1-like Zinc finger
36	c2kizA_	Alignment	not modelled	52.8	26	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase arkadia; **PDBTitle:** solution structure of arkadia ring-h2 finger domain
37	c2jrpA_	Alignment	not modelled	52.6	22	**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
38	d2baya1	Alignment	not modelled	50.4	11	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
39	d2gmga1	Alignment	not modelled	50.3	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PF0610-like
40	c1x4wA_	Alignment	not modelled	50.2	35	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hypothetical protein flj13222; **PDBTitle:** solution structure of the zf-an1 domain from human2 hypothetical protein flj13222
41	c1z2qA_	Alignment	not modelled	49.8	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**lm5-1; **PDBTitle:** high-resolution solution structure of the lm5-1 fyve domain2 from leishmania major
42	c2l0bA_	Alignment	not modelled	49.6	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase praja-1; **PDBTitle:** solution nmr structure of zinc finger domain of e3 ubiquitin-protein2 ligase praja-1 from homo sapiens, northeast structural genomics3 consortium (nesg) target hr4710b
43	c2ja6L_	Alignment	not modelled	49.4	28	**PDB header:**transferase **Chain:** L: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii 7.7 **PDBTitle:** cpd lesion containing rna polymerase ii elongation complex2 b
44	c2k9hA_	Alignment	not modelled	48.4	17	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**glycoprotein; **PDBTitle:** the hantavirus glycoprotein g1 tail contains a dual cchc-2 type classical zinc fingers
45	c2d8tA_	Alignment	not modelled	47.4	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
46	d1iyma_	Alignment	not modelled	46.9	20	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
47	c2ct0A_	Alignment	not modelled	46.6	20	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**non-smc element 1 homolog; **PDBTitle:** solution structure of the ring domain of the non-smc2 element 1 protein
48	c2kdxA_	Alignment	not modelled	46.5	25	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**hydrogenase/urease nickel incorporation protein **PDBTitle:** solution structure of hypa protein
49	c2vjfB_	Alignment	not modelled	46.4	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**mdm4 protein; **PDBTitle:** crystal structure of the mdm2-mdmx ring domain heterodimer
50	c1dvbA_	Alignment	not modelled	46.0	17	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubrerythrin; **PDBTitle:** rubrerythrin
						PDB header:transferase

51	c3axtA_	Alignment	not modelled	45.4	30	**Chain:** A: **PDB Molecule:**probable n(2),n(2)-dimethylguanosine trna methyltransferase **PDBTitle:** complex structure of trna methyltransferase trm1 from aquifex aeolicus2 with s-adenosyl-l-methionine
52	c2cs2A_	Alignment	not modelled	45.2	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase-1; **PDBTitle:** solution structure of the second zn-finger domain of2 poly(adp-ribose) polymerase-1
53	c3a44D_	Alignment	not modelled	44.6	14	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
54	c3h0gL_	Alignment	not modelled	44.4	28	**PDB header:**transcription **Chain:** L: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
55	c3bjiA_	Alignment	not modelled	44.0	31	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**proto-oncogene vav; **PDBTitle:** structural basis of promiscuous guanine nucleotide exchange2 by the t-cell essential vav1
56	c3ky9B_	Alignment	not modelled	43.9	29	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**proto-oncogene vav; **PDBTitle:** autoinhibited vav1
57	d2ctda2	Alignment	not modelled	43.9	44	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
58	d2gnra1	Alignment	not modelled	43.8	29	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**SSO2064-like
59	c2xeuA_	Alignment	not modelled	43.7	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ring finger protein 4; **PDBTitle:** ring domain
60	d1rmda2	Alignment	not modelled	43.7	35	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
61	d2ayja1	Alignment	not modelled	43.6	17	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L40e
62	c1v9xA_	Alignment	not modelled	42.7	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly (adp-ribose) polymerase; **PDBTitle:** solution structure of the first zn-finger domain of2 poly(adp-ribose) polymerase-1
63	c2djbA_	Alignment	not modelled	42.5	16	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**polycomb group ring finger protein 6; **PDBTitle:** solution structure of the ring domain of the human polycomb2 group ring finger protein 6
64	c1x4jA_	Alignment	not modelled	42.0	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ring finger protein 38; **PDBTitle:** solution structure of ring finger in ring finger protein 38
65	c2qkdA_	Alignment	not modelled	41.9	24	**PDB header:**signaling protein, cell cycle **Chain:** A: **PDB Molecule:**zinc finger protein zpr1; **PDBTitle:** crystal structure of tandem zpr1 domains
66	c2f9iD_	Alignment	not modelled	41.9	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl **PDBTitle:** crystal structure of the carboxyltransferase subunit of acc2 from staphylococcus aureus
67	d1faqa_	Alignment	not modelled	41.4	37	**Fold:**Cysteine-rich domain **Superfamily:**Cysteine-rich domain **Family:**Protein kinase cysteine-rich domain (cys2, phorbol-binding domain)
68	c2ectA_	Alignment	not modelled	41.4	19	**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
69	c2i5oA_	Alignment	not modelled	41.2	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase eta; **PDBTitle:** solution structure of the ubiquitin-binding zinc finger2 (ubz) domain of the human dna y-polymerase eta
70	c3cngC_	Alignment	not modelled	41.0	20	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea
71	c2f42A_	Alignment	not modelled	40.8	17	**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
72	c3lrqB_	Alignment	not modelled	40.7	32	**PDB header:**ligase **Chain:** B: **PDB Molecule:**e3 ubiquitin-protein ligase trim37; **PDBTitle:** crystal structure of the u-box domain of human ubiquitin-2 protein ligase (e3), northeast structural genomics3 consortium target hr4604d.
73	d1uw0a_	Alignment	not modelled	40.6	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**PARP-type zinc finger
74	c2zkr2_	Alignment	not modelled	40.4	23	**PDB header:**ribosomal protein/rna **Chain:** 2: **PDB Molecule:**60s ribosomal protein l37e; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
75	d1vqo11	Alignment	not modelled	39.5	30	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37e
76	d1wjva1	Alignment	not modelled	39.2	26	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**C2HC finger

77	c2rowA_	Alignment	not modelled	39.1	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rho-associated protein kinase 2; **PDBTitle:** the c1 domain of rock ii
78	c3tsuA_	Alignment	not modelled	38.8	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
79	d1wffa_	Alignment	not modelled	38.5	28	**Fold:**AN1-like Zinc finger **Superfamily:**AN1-like Zinc finger **Family:**AN1-like Zinc finger
80	c3t7lA_	Alignment	not modelled	38.5	22	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**zinc finger fyve domain-containing protein 16; **PDBTitle:** crystal structure of the fyve domain of endofin (zfyve16) at 1.1a2 resolution
81	d2cu8a1	Alignment	not modelled	38.4	36	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
82	d2ct1a1	Alignment	not modelled	38.1	60	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
83	c2jr6A_	Alignment	not modelled	37.7	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
84	c2pmzB_	Alignment	not modelled	37.6	19	**PDB header:**translation, transferase **Chain:** B: **PDB Molecule:**dna-directed rna polymerase subunit b; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
85	c2jmdA_	Alignment	not modelled	37.4	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tnf receptor-associated factor 6; **PDBTitle:** solution structure of the ring domain of human traf6
86	c3jywY_	Alignment	not modelled	35.8	36	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**60s ribosomal protein l37(a); **PDBTitle:** structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
87	d1tjla2	Alignment	not modelled	35.7	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Prokaryotic DksA/TraR C4-type zinc finger
88	d1q1aa_	Alignment	not modelled	35.5	17	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
89	d1xa6a3	Alignment	not modelled	35.4	35	**Fold:**Cysteine-rich domain **Superfamily:**Cysteine-rich domain **Family:**Protein kinase cysteine-rich domain (cys2, phorbol-binding domain)
90	c1jocA_	Alignment	not modelled	35.3	28	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**early endosomal autoantigen 1; **PDBTitle:** eea1 homodimer of c-terminal fyve domain bound to inositol2 1,3-diphosphate
91	c2y43B_	Alignment	not modelled	35.0	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**e3 ubiquitin-protein ligase rad18; **PDBTitle:** rad18 ubiquitin ligase ring domain structure
92	c1hk8A_	Alignment	not modelled	33.7	27	**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
93	d1hk8a_	Alignment	not modelled	33.7	27	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**Class III anaerobic ribonucleotide reductase NRDD subunit
94	c3t6pA_	Alignment	not modelled	33.7	40	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**baculoviral iap repeat-containing protein 2; **PDBTitle:** iap antagonist-induced conformational change in ciap1 promotes e32 ligase activation via dimerization
95	c1s1iY_	Alignment	not modelled	33.6	36	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**60s ribosomal protein l37-a; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
96	c2db6A_	Alignment	not modelled	33.5	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sh3 and cysteine rich domain 3; **PDBTitle:** solution structure of rsgi ruh-051, a c1 domain of stac32 from human cdna
97	d1s5pa_	Alignment	not modelled	32.9	8	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
98	c2csyA_	Alignment	not modelled	32.8	16	**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
99	d2cona1	Alignment	not modelled	32.7	36	**Fold:**Rubredoxin-like **Superfamily:**NOB1 zinc finger-like **Family:**NOB1 zinc finger-like
100	d1chca_	Alignment	not modelled	32.3	16	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
101	c2eluA_	Alignment	not modelled	32.0	50	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 406; **PDBTitle:** solution structure of the 5th c2h2 zinc finger of human2 zinc finger protein 406

102	c2ecvA_	Alignment	not modelled	31.5	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tripartite motif-containing protein 5; **PDBTitle:** solution structure of the zinc finger, c3hc4 type (ring2 finger) domain of tripartite motif-containing protein 5
103	d1zbdb_	Alignment	not modelled	31.4	18	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**FYVE, a phosphatidylinositol-3-phosphate binding domain
104	c2eciA_	Alignment	not modelled	31.4	16	**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
105	c1u5kA_	Alignment	not modelled	31.0	18	**PDB header:**recombination,replication **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** recombinational repair protein reco
106	c2kgoA_	Alignment	not modelled	30.9	36	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ybii; **PDBTitle:** solution nmr structure of zn finger protein ybil from escherichia2 coli. nesg target et107, ocsp target ec0402
107	c1z6uA_	Alignment	not modelled	30.8	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**np95-like ring finger protein isoform b; **PDBTitle:** np95-like ring finger protein isoform b [homo sapiens]
108	d1jm7a_	Alignment	not modelled	30.8	32	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
109	d2c2la2	Alignment	not modelled	30.7	17	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
110	c1tjlD_	Alignment	not modelled	30.7	33	**PDB header:**transcription **Chain:** D: **PDB Molecule:**dnak suppressor protein; **PDBTitle:** crystal structure of transcription factor dksa from e. coli
111	d1wfla_	Alignment	not modelled	29.9	19	**Fold:**AN1-like Zinc finger **Superfamily:**AN1-like Zinc finger **Family:**AN1-like Zinc finger
112	c3u50C_	Alignment	not modelled	29.9	19	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**telomerase-associated protein 82; **PDBTitle:** crystal structure of the tetrahymena telomerase processivity factor2 teb1 ob-c
113	d1x3ha1	Alignment	not modelled	29.7	23	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
114	c2hcnA_	Alignment	not modelled	29.5	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rna-directed rna polymerase (ns5); **PDBTitle:** crystal structure of rna dependent rna polymerase domain from west2 nile virus
115	d1iyca_	Alignment	not modelled	29.4	35	**Fold:**Invertebrate chitin-binding proteins **Superfamily:**Invertebrate chitin-binding proteins **Family:**Antifungal peptide scarabaecin
116	c2cszA_	Alignment	not modelled	29.0	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**synaptotagmin-like protein 4; **PDBTitle:** solution structure of the ring domain of the synaptotagmin-2 like protein 4
117	d1kbea_	Alignment	not modelled	28.9	33	**Fold:**Cysteine-rich domain **Superfamily:**Cysteine-rich domain **Family:**Protein kinase cysteine-rich domain (cys2, phorbol-binding domain)
118	d1yc5a1	Alignment	not modelled	28.7	23	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
119	c2klxA_	Alignment	not modelled	28.5	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** solution structure of glutaredoxin from bartonella henselae str.2 houston
120	d1dsva_	Alignment	not modelled	28.4	29	**Fold:**Retrovirus zinc finger-like domains **Superfamily:**Retrovirus zinc finger-like domains **Family:**Retrovirus zinc finger-like domains