Phyre2

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Description	P76575
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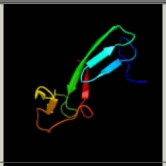
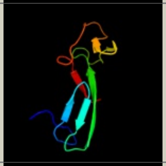
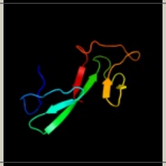
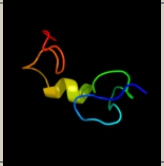
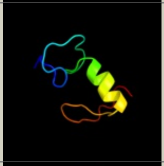
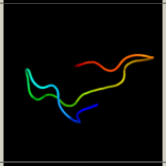
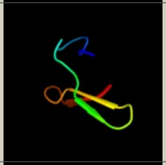
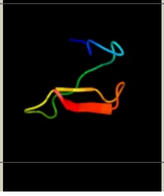
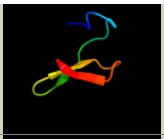
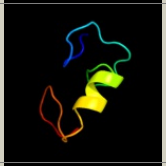
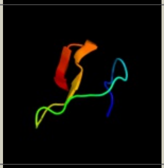
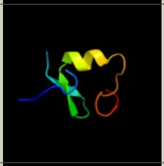
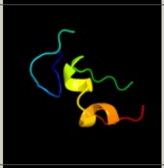
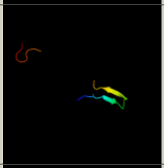
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2jnea1	Alignment		100.0	100	**Fold:**Rubredoxin-like **Superfamily:**YfgJ-like **Family:**YfgJ-like
2	c2jneA_	Alignment		100.0	100	**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.
3	c2jrpA_	Alignment		100.0	63	**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
4	c2eciA_	Alignment		73.7	33	**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
5	c2djbA_	Alignment		72.6	23	**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
6	c2ecwA_	Alignment		71.4	35	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**tripartite motif-containing protein 30; **PDBTitle:** solution structure of the zinc finger, c3hc4 type (ring2 finger) domain tripartite motif protein 30
7	d1dgsa1	Alignment		70.4	32	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**NAD+-dependent DNA ligase, domain 3
8	c2f42A_	Alignment		69.6	18	**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
9	d2jnya1	Alignment		69.6	15	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
10	c2jr6A_	Alignment		69.0	19	**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
11	d2pk7a1	Alignment		67.4	23	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like

12	c2js4A_	Alignment		66.1	23	**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
13	d1rmda2	Alignment		64.4	33	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
14	d1t1ha_	Alignment		62.7	20	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
15	d2hf1a1	Alignment		61.3	27	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
16	c2xeuA_	Alignment		60.6	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ring finger protein 4; **PDBTitle:** ring domain
17	c2ecvA_	Alignment		58.2	38	**PDB header:**ligase **Chain:** D: **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
18	c3a44D_	Alignment		57.0	31	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
19	d2baya1	Alignment		56.2	15	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
20	d1p91a_	Alignment		55.6	23	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA methyltransferase RlmA
21	c3fl2A_	Alignment	not modelled	55.2	24	**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
22	c2y43B_	Alignment	not modelled	54.8	28	**PDB header:**ligase **Chain:** B: **PDB Molecule:**e3 ubiquitin-protein ligase rad18; **PDBTitle:** rad18 ubiquitin ligase ring domain structure
23	d2dkta1	Alignment	not modelled	54.8	27	**Fold:**CHY zinc finger-like **Superfamily:**CHY zinc finger-like **Family:**CHY zinc finger
24	c2cklA_	Alignment	not modelled	54.6	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**polycomb group ring finger protein 4; **PDBTitle:** ring1b-bmi1 e3 catalytic domain structure
25	c3ztgA_	Alignment	not modelled	52.5	30	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase rbbp6; **PDBTitle:** solution structure of the ring finger-like domain of2 retinoblastoma binding protein-6 (rbbp6)
26	c2kreA_	Alignment	not modelled	52.4	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ubiquitin conjugation factor e4 b; **PDBTitle:** solution structure of e4b/ufd2a u-box domain
27	c2h0dB_	Alignment	not modelled	52.3	33	**PDB header:**metal binding protein/ligase **Chain:** B: **PDB Molecule:**ubiquitin ligase protein ring2; **PDBTitle:** structure of a bmi-1-ring1b polycomb group ubiquitin ligase complex
28	c3lrqB_	Alignment	not modelled	52.0	31	**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.
						Fold:RING/U-box

29	d1jm7a_	Alignment	not modelled	51.0	25	**Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
30	c2ecyA_	Alignment	not modelled	50.6	28	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**tnf receptor-associated factor 3; **PDBTitle:** solution structure of the zinc finger, c3hc4 type (ring2 finger)" domain of tnf receptor-associated factor 3
31	c2kpiA_	Alignment	not modelled	50.6	27	**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
32	d2c2la2	Alignment	not modelled	50.2	18	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
33	c1z6uA_	Alignment	not modelled	46.8	28	**PDB header:**ligase **Chain:** A: **PDB Molecule:**np95-like ring finger protein isoform b; **PDBTitle:** np95-like ring finger protein isoform b [homo sapiens]
34	d1g25a_	Alignment	not modelled	46.4	33	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
35	c2yurA_	Alignment	not modelled	45.3	30	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**retinoblastoma-binding protein 6; **PDBTitle:** solution structure of the ring finger of human2 retinoblastoma-binding protein 6
36	c2csyA_	Alignment	not modelled	44.9	27	**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
37	d2ct7a1	Alignment	not modelled	44.5	24	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**IBR domain
38	d1jm7b_	Alignment	not modelled	43.4	28	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
39	d2c2vv1	Alignment	not modelled	43.1	18	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
40	c3htkC_	Alignment	not modelled	42.7	27	**PDB header:**recombination/replication/ligase **Chain:** C: **PDB Molecule:**e3 sumo-protein ligase mms21; **PDBTitle:** crystal structure of mms21 and smc5 complex
41	c2owoA_	Alignment	not modelled	42.3	34	**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
42	c2lcqA_	Alignment	not modelled	40.7	30	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative toxin vapc6; **PDBTitle:** solution structure of the endonuclease nob1 from p.horikoshii
43	d1bora_	Alignment	not modelled	40.3	34	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
44	d1l1ta3	Alignment	not modelled	39.6	21	**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
45	c3tsuA_	Alignment	not modelled	39.0	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
46	d1tdza3	Alignment	not modelled	38.7	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
47	d1r2za3	Alignment	not modelled	38.7	21	**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
48	d1lv3a_	Alignment	not modelled	38.4	15	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Hypothetical zinc finger protein YacG
49	d1ee8a3	Alignment	not modelled	38.3	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
50	c2ct2A_	Alignment	not modelled	37.7	36	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tripartite motif protein 32; **PDBTitle:** solution structure of the ring domain of the tripartite2 motif protein 32
51	c3l11A_	Alignment	not modelled	37.7	33	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase rnf168; **PDBTitle:** crystal structure of the ring domain of rnf168
52	c1v9pB_	Alignment	not modelled	37.7	33	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase
53	c2ep4A_	Alignment	not modelled	37.4	30	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ring finger protein 24; **PDBTitle:** solution structure of ring finger from human ring finger2 protein 24
54	d1k82a3	Alignment	not modelled	37.3	21	**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
55	c2z2sD_	Alignment	not modelled	36.4	30	**PDB header:**transcription **Chain:** D: **PDB Molecule:**anti-sigma factor chrr, transcriptional activator chrr;

						PDBTitle: crystal structure of rhodobacter sphaeroides sige in complex with the2 anti-sigma chrr
56	d1e4ua_	Alignment	not modelled	36.0	40	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
57	d1wd2a_	Alignment	not modelled	35.8	32	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
58	c1dgsB_	Alignment	not modelled	35.5	32	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase from t.2 filiformis
59	c2egpA_	Alignment	not modelled	34.8	38	**PDB header:**antiviral protein **Chain:** A: **PDB Molecule:**tripartite motif-containing protein 34; **PDBTitle:** solution structure of the ring-finger domain from human2 tripartite motif protein 34
60	c3pihA_	Alignment	not modelled	34.5	46	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** t. maritima uvra in complex with fluorescein-modified dna
61	d1wfka_	Alignment	not modelled	34.2	25	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**FYVE, a phosphatidylinositol-3-phosphate binding domain
62	c3kp9A_	Alignment	not modelled	33.8	26	**PDB header:**blood coagulation,oxidoreductase **Chain:** A: **PDB Molecule:**vkorc1/thioredoxin domain protein; **PDBTitle:** structure of a bacterial homolog of vitamin k epoxide reductase
63	d1dl6a_	Alignment	not modelled	33.5	30	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
64	c2cklB_	Alignment	not modelled	32.7	33	**PDB header:**transcription **Chain:** B: **PDB Molecule:**ubiquitin ligase protein ring2; **PDBTitle:** ring1b-bmi1 e3 catalytic domain structure
65	c2xb1A_	Alignment	not modelled	32.7	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**pygopus homolog 2, b-cell cll/lymphoma 9-like protein; **PDBTitle:** crystal structure of the human pygo2 phd finger in complex with the2 b9l hd1 domain
66	c3hugJ_	Alignment	not modelled	31.9	32	**PDB header:**transcription/membrane protein **Chain:** J: **PDB Molecule:**probable conserved membrane protein; **PDBTitle:** crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl
67	c2kdxA_	Alignment	not modelled	31.3	17	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**hydrogenase/urease nickel incorporation protein **PDBTitle:** solution structure of hypa protein
68	c2opfA_	Alignment	not modelled	31.2	21	**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
69	c1zr9A_	Alignment	not modelled	30.7	30	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 593; **PDBTitle:** solution structure of a human c2h2-type zinc finger protein
70	d1zr9a1	Alignment	not modelled	30.7	30	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**HkH motif-containing C2H2 finger
71	c2jmdA_	Alignment	not modelled	30.3	33	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tnf receptor-associated factor 6; **PDBTitle:** solution structure of the ring domain of human traf6
72	d1k3xa3	Alignment	not modelled	30.1	17	**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
73	c3k7aM_	Alignment	not modelled	29.8	32	**PDB header:**transcription **Chain:** M: **PDB Molecule:**transcription initiation factor iib; **PDBTitle:** crystal structure of an rna polymerase ii-tfiib complex
74	c2f5qA_	Alignment	not modelled	29.7	26	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosidase; **PDBTitle:** catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
75	d1wgma_	Alignment	not modelled	29.3	18	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
76	c2riqA_	Alignment	not modelled	28.7	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 1; **PDBTitle:** crystal structure of the third zinc-binding domain of human parp-1
77	c1rmdA_	Alignment	not modelled	27.8	30	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**rag1; **PDBTitle:** rag1 dimerization domain
78	c3bvoA_	Alignment	not modelled	27.0	12	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**co-chaperone protein hscb, mitochondrial precursor; **PDBTitle:** crystal structure of human co-chaperone protein hscb
79	c2jvnA_	Alignment	not modelled	26.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 1; **PDBTitle:** domain c of human parp-1
80	c2gb5B_	Alignment	not modelled	26.3	23	**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
						PDB header:hydrolase

81	c3cngC_	Alignment	not modelled	25.2	23	**Chain:** C: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea
82	c2ectA_	Alignment	not modelled	24.8	25	**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
83	c2ecmA_	Alignment	not modelled	24.5	28	**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
84	c1loiA_	Alignment	not modelled	23.6	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cyclic 3',5'-amp specific phosphodiesterase rd1; **PDBTitle:** n-terminal splice region of rat c-amp phosphodiesterase,2 nmr, 7 structures
85	d1x4ka1	Alignment	not modelled	23.5	25	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
86	c2vpdA_	Alignment	not modelled	23.3	17	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**pygopus homolog 1; **PDBTitle:** decoding of methylated histone h3 tail by the pygo-bcl9 wnt2 signaling complex
87	c2k5rA_	Alignment	not modelled	22.6	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein xf2673; **PDBTitle:** solution nmr structure of xf2673 from xylella fastidiosa.2 northeast structural genomics consortium target xfr39
88	c1k82D_	Alignment	not modelled	21.5	21	**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
89	c3knvA_	Alignment	not modelled	21.0	30	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**tnf receptor-associated factor 2; **PDBTitle:** crystal structure of the ring and first zinc finger domains2 of traf2
90	c2l0bA_	Alignment	not modelled	20.8	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
91	d2cu8a1	Alignment	not modelled	20.4	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
92	c2d8tA_	Alignment	not modelled	20.3	20	**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
93	d1jnia_	Alignment	not modelled	20.0	57	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
94	c1jniA_	Alignment	not modelled	20.0	57	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**diheme cytochrome c napb; **PDBTitle:** structure of the napb subunit of the periplasmic nitrate2 reductase from haemophilus influenzae.
95	d3d85d1	Alignment	not modelled	18.5	24	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
96	d1pfta_	Alignment	not modelled	18.5	30	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
97	c1ee8A_	Alignment	not modelled	18.5	27	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mutm (fpg) protein; **PDBTitle:** crystal structure of mutm (fpg) protein from thermus thermophilus hb8
98	c2yslA_	Alignment	not modelled	17.8	35	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tripartite motif-containing protein 31; **PDBTitle:** solution structure of the ring domain (1-66) from2 tripartite motif-containing protein 31
99	c1nnjA_	Alignment	not modelled	17.4	29	**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