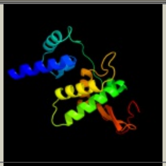
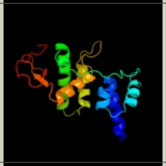
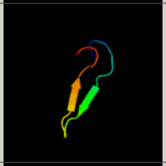
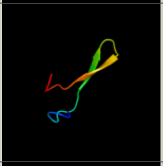
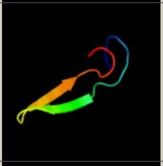
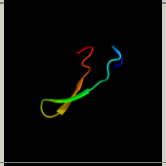
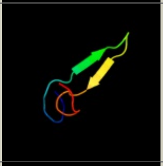
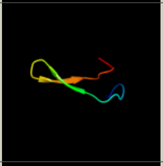
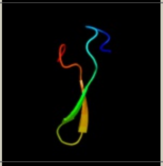
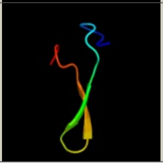
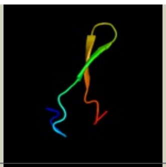
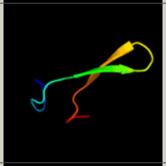
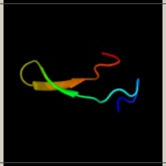
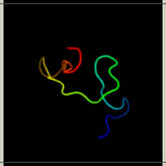
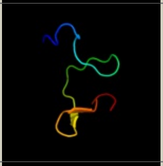
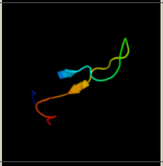
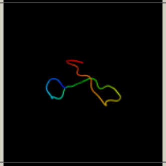
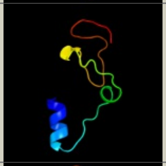
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0ABY7
Date	Thu Jan 5 11:16:42 GMT 2012
Unique Job ID	7d2e382eb99dba87

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2avue1	Alignment		100.0	100	**Fold:**FlhC-like **Superfamily:**FlhC-like **Family:**FlhC-like
2	c2avuF_	Alignment		100.0	100	**PDB header:**transcription activator **Chain:** F: **PDB Molecule:**flagellar transcriptional activator flhc; **PDBTitle:** structure of the escherichia coli flhdc complex, a2 prokaryotic heteromeric regulator of transcription
3	c1ee8A_	Alignment		88.8	26	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mutm (fpg) protein; **PDBTitle:** crystal structure of mutm (fpg) protein from thermus thermophilus hb8
4	c1k82D_	Alignment		86.8	31	**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
5	c1zgwA_	Alignment		86.3	24	**PDB header:**transcription regulator/dna **Chain:** A: **PDB Molecule:**ada polyprotein; **PDBTitle:** nmr structure of e. coli ada protein in complex with dna
6	c1nnjA_	Alignment		85.1	27	**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
7	c2opfA_	Alignment		84.7	23	**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
8	d1ee8a3	Alignment		82.0	24	**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
9	c2f5qA_	Alignment		81.4	27	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosidase; **PDBTitle:** catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
10	d1tdza3	Alignment		79.2	27	**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
11	d1r2za3	Alignment		78.7	27	**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

12	d1k82a3	Alignment		78.5	31	**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
13	d1l1ta3	Alignment		78.4	27	**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
14	d1k3xa3	Alignment		78.3	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
15	c3eg9B_	Alignment		75.3	21	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**sec24 related gene family, member d; **PDBTitle:** crystal structure of the mammalian copii-coat protein2 sec23/24 bound to the transport signal sequence of membrin
16	c3eh2B_	Alignment		72.5	24	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein transport protein sec24c; **PDBTitle:** crystal structure of the human copii-coat protein sec24c
17	c3a46B_	Alignment		72.5	7	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure of mvnei1/thf complex
18	c1pd0A_	Alignment		71.7	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**protein transport protein sec24; **PDBTitle:** crystal structure of the copii coat subunit, sec24,2 complexed with a peptide from the snare protein sed53 (yeast syntaxin-5)
19	c1m2vB_	Alignment		71.1	15	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein transport protein sec24; **PDBTitle:** crystal structure of the yeast sec23/24 heterodimer
20	c2hr5B_	Alignment		65.6	21	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**rubrerythrin; **PDBTitle:** pf1283- rubrerythrin from pyrococcus furiosus iron bound form
21	c3iz6X_	Alignment		63.4	15	**PDB header:**ribosome **Chain:** X: **PDB Molecule:**40s ribosomal protein s27 (s27e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
22	d2akla2	Alignment	not modelled	63.3	19	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**PhnA zinc-binding domain
23	c1m2oA_	Alignment	not modelled	62.9	20	**PDB header:**protein transport/signaling protein **Chain:** A: **PDB Molecule:**protein transport protein sec23; **PDBTitle:** crystal structure of the sec23-sar1 complex
24	d1qxfa_	Alignment		62.9	13	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein S27e
25	c3izbX_	Alignment	not modelled	62.2	20	**PDB header:**ribosome **Chain:** X: **PDB Molecule:**40s ribosomal protein rps27 (s27e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
26	c2aklA_	Alignment	not modelled	60.9	19	**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

27	c2x48B_	Alignment	not modelled	56.5	21	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**cag38821; **PDBTitle:** orf 55 from sulfolobus islandicus rudivirus 1
28	c1dvbA_	Alignment	not modelled	52.7	24	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubrerythrin; **PDBTitle:** rubrerythrin
29	c2kn9A_	Alignment	not modelled	51.0	17	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubredoxin; **PDBTitle:** solution structure of zinc-substituted rubredoxin b (rv3250c) from2 mycobacterium tuberculosis. seattle structural genomics center for3 infectious disease target mytud.01635.a
30	d1bl0a1	Alignment	not modelled	48.8	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
31	c3a44D_	Alignment	not modelled	46.0	15	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
32	c1yuzB_	Alignment	not modelled	45.4	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nigerythrin; **PDBTitle:** partially reduced state of nigerythrin
33	d1vdda_	Alignment	not modelled	45.2	24	**Fold:**Recombination protein RecR **Superfamily:**Recombination protein RecR **Family:**Recombination protein RecR
34	c3rfaA_	Alignment	not modelled	44.5	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribosomal rna large subunit methyltransferase n; **PDBTitle:** x-ray structure of rlmn from escherichia coli in complex with s-2 adenosylmethionine
35	d2gnra1	Alignment	not modelled	44.4	27	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**SSO2064-like
36	d2dsxa1	Alignment	not modelled	43.8	23	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
37	c3egxB_	Alignment	not modelled	43.6	26	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein transport protein sec24a; **PDBTitle:** crystal structure of the mammalian copii-coat protein2 sec23a/24a complexed with the snare protein sec22b and3 bound to the transport signal sequence of the snare protein4 bet1
38	c2kdxA_	Alignment	not modelled	43.4	14	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**hydrogenase/urease nickel incorporation protein **PDBTitle:** solution structure of hypa protein
39	c1vddC_	Alignment	not modelled	42.9	24	**PDB header:**recombination **Chain:** C: **PDB Molecule:**recombination protein recr; **PDBTitle:** crystal structure of recombinational repair protein recr
40	d1mm2a_	Alignment	not modelled	42.1	29	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**PHD domain
41	d1ywsa1	Alignment	not modelled	41.8	25	**Fold:**Rubredoxin-like **Superfamily:**CSL zinc finger **Family:**CSL zinc finger
42	c2pptA_	Alignment	not modelled	40.7	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin-2; **PDBTitle:** crystal structure of thioredoxin-2
43	d1pd0a5	Alignment	not modelled	39.7	14	**Fold:**Rubredoxin-like **Superfamily:**Zn-finger domain of Sec23/24 **Family:**Zn-finger domain of Sec23/24
44	c2xzm6_	Alignment	not modelled	38.9	10	**PDB header:**ribosome **Chain:** 6: **PDB Molecule:**rps27e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
45	d1dx8a_	Alignment	not modelled	38.6	20	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
46	d1bl0a2	Alignment	not modelled	36.7	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
47	d1d5ya1	Alignment	not modelled	36.1	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
48	d1lkoa2	Alignment	not modelled	35.8	17	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
49	c2gb5B_	Alignment	not modelled	35.0	27	**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
50	d1nnqa2	Alignment	not modelled	33.5	22	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
51	d1k78a1	Alignment	not modelled	32.6	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
52	d6rxna_	Alignment	not modelled	32.3	25	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
						Fold: Rubredoxin-like

53	d4rxna_	Alignment	not modelled	31.8	25	**Superfamily:**Rubredoxin-like **Family:**Rubredoxin
54	d1yuza2	Alignment	not modelled	31.6	29	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
55	d1u5ka2	Alignment	not modelled	31.2	16	**Fold:**ArfGap/RecO-like zinc finger **Superfamily:**ArfGap/RecO-like zinc finger **Family:**RecO C-terminal domain-like
56	d1iroa_	Alignment	not modelled	30.0	25	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
57	c2v3bB_	Alignment	not modelled	28.1	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**rubredoxin 2; **PDBTitle:** crystal structure of the electron transfer complex2 rubredoxin - rubredoxin reductase from pseudomonas3 aeruginosa.
58	d1olta_	Alignment	not modelled	28.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**Oxygen-independent coproporphyrinogen III oxidase HemN
59	d1wgea1	Alignment	not modelled	27.9	29	**Fold:**Rubredoxin-like **Superfamily:**CSL zinc finger **Family:**CSL zinc finger
60	d1s24a_	Alignment	not modelled	27.9	18	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
61	c1s24A_	Alignment	not modelled	27.9	18	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubredoxin 2; **PDBTitle:** rubredoxin domain ii from pseudomonas oleovorans
62	c1u78A_	Alignment	not modelled	27.5	12	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**transposable element tc3 transposase; **PDBTitle:** structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
63	d2gmga1	Alignment	not modelled	27.2	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PF0610-like
64	d1wfha_	Alignment	not modelled	26.5	27	**Fold:**AN1-like Zinc finger **Superfamily:**AN1-like Zinc finger **Family:**AN1-like Zinc finger
65	d1qcva_	Alignment	not modelled	25.0	13	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
66	d1dl6a_	Alignment	not modelled	24.9	17	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
67	c3mn2B_	Alignment	not modelled	24.8	21	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**probable arac family transcriptional regulator; **PDBTitle:** the crystal structure of a probable arac family transcriptional2 regulator from rhodopseudomonas palustris cga009
68	d1wfpa_	Alignment	not modelled	24.7	32	**Fold:**AN1-like Zinc finger **Superfamily:**AN1-like Zinc finger **Family:**AN1-like Zinc finger
69	d6paxa1	Alignment	not modelled	24.5	35	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
70	d2rdva_	Alignment	not modelled	23.7	28	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
71	d1wg2a_	Alignment	not modelled	23.7	32	**Fold:**AN1-like Zinc finger **Superfamily:**AN1-like Zinc finger **Family:**AN1-like Zinc finger
72	c2js4A_	Alignment	not modelled	23.3	28	**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
73	d1rb9a_	Alignment	not modelled	23.0	22	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
74	d1iu5a_	Alignment	not modelled	21.9	22	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
75	d1h7va_	Alignment	not modelled	21.9	19	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
76	d1wfla_	Alignment	not modelled	21.7	23	**Fold:**AN1-like Zinc finger **Superfamily:**AN1-like Zinc finger **Family:**AN1-like Zinc finger
77	c1x4iA_	Alignment	not modelled	21.5	17	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**inhibitor of growth protein 3; **PDBTitle:** solution structure of phd domain in inhibitor of growth2 protein 3 (ing3)
78	d1y02a2	Alignment	not modelled	21.4	33	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**FYVE, a phosphatidylinositol-3-phosphate binding domain
79	d1twfb_	Alignment	not modelled	21.2	27	**Fold:**beta and beta-prime subunits of DNA dependent RNA-polymerase **Superfamily:**beta and beta-prime subunits of DNA dependent RNA-polymerase

						Family:RNA-polymerase beta
80	c3lsgD_	Alignment	not modelled	20.9	33	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**two-component response regulator yesn; **PDBTitle:** the crystal structure of the c-terminal domain of the two-2 component response regulator yesn from fusobacterium3 nucleatum subsp. nucleatum atcc 25586
81	d1d5ya2	Alignment	not modelled	19.8	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
82	c1x4wA_	Alignment	not modelled	19.5	32	**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
83	d1z60a1	Alignment	not modelled	19.5	26	**Fold:**Cysteine-rich domain **Superfamily:**Cysteine-rich domain **Family:**TFIIH p44 subunit cysteine-rich domain
84	d1wffa_	Alignment	not modelled	19.4	32	**Fold:**AN1-like Zinc finger **Superfamily:**AN1-like Zinc finger **Family:**AN1-like Zinc finger
85	c3mv2A_	Alignment	not modelled	18.9	8	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**coatomer subunit alpha; **PDBTitle:** crystal structure of a-cop in complex with e-cop
86	c2pmzB_	Alignment	not modelled	18.8	22	**PDB header:**translation, transferase **Chain:** B: **PDB Molecule:**dna-directed rna polymerase subunit b; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
87	c2y0fD_	Alignment	not modelled	18.2	21	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; **PDBTitle:** structure of gcpe (ispg) from thermus thermophilus hb27
88	c3mkrB_	Alignment	not modelled	18.2	11	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**coatomer subunit alpha; **PDBTitle:** crystal structure of yeast alpha/epsilon-cop subcomplex of the copi2 vesicular coat
89	c3k7aM_	Alignment	not modelled	17.8	24	**PDB header:**transcription **Chain:** M: **PDB Molecule:**transcription initiation factor iib; **PDBTitle:** crystal structure of an rna polymerase ii-tfiib complex
90	d1wiia_	Alignment	not modelled	17.7	27	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Putative zinc binding domain
91	d2ayja1	Alignment	not modelled	17.7	11	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L40e
92	d1brfa_	Alignment	not modelled	17.7	28	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
93	d2eppa1	Alignment	not modelled	17.1	20	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
94	c2adrA_	Alignment	not modelled	16.9	36	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**adr1; **PDBTitle:** adr1 dna-binding domain from saccharomyces cerevisiae, nmr,2 25 structures
95	c3mklB_	Alignment	not modelled	16.6	15	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator gadx; **PDBTitle:** crystal structure of dna-binding transcriptional dual regulator from2 escherichia coli k-12
96	c2yrcA_	Alignment	not modelled	16.6	23	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**protein transport protein sec23a; **PDBTitle:** solution structure of the zf-sec23_sec24 from human sec23a
97	c3c8fA_	Alignment	not modelled	16.6	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate formate-lyase 1-activating enzyme; **PDBTitle:** 4fe-4s-pyruvate formate-lyase activating enzyme with2 partially disordered adomet
98	d1mm3a_	Alignment	not modelled	16.6	28	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**PHD domain
99	c2jr6A_	Alignment	not modelled	16.4	16	**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