Phyre^2

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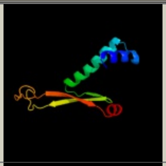
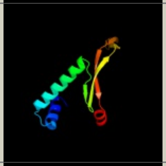
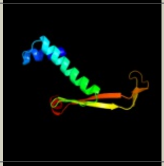
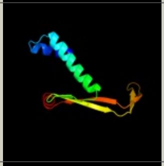
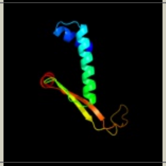
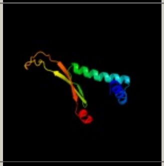
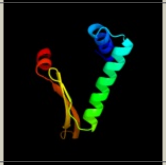
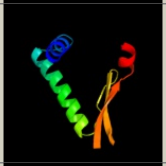
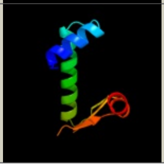
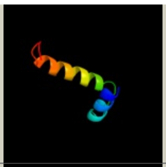
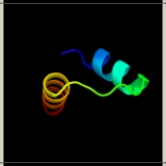
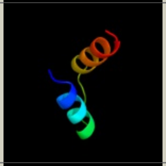
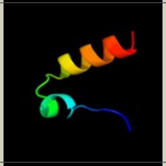
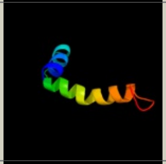
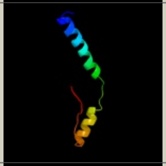
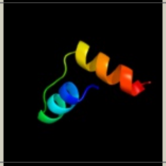
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2iifA_	Alignment		99.9	37	**PDB header:**recombination/dna **Chain:** A: **PDB Molecule:**integration host factor; **PDBTitle:** single chain integration host factor mutant protein (scihf2-2 k45ae) in complex with dna
2	d1p71a_	Alignment		99.9	47	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
3	c3c4iA_	Alignment		99.9	42	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding protein hu homolog; **PDBTitle:** crystal structure analysis of n terminal region containing the2 dimerization domain and dna binding domain of hu protein(histone like3 protein-dna binding) from mycobacterium tuberculosis [h37rv]
4	d1owfa_	Alignment		99.9	37	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
5	d1owfb_	Alignment		99.9	34	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
6	c2np2B_	Alignment		99.9	32	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**hbb; **PDBTitle:** hbb-dna complex
7	d1exea_	Alignment		99.9	39	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
8	d1huua_	Alignment		99.8	58	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
9	d1mula_	Alignment		99.8	95	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
10	d2o97b1	Alignment		99.6	70	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
11	d1b8za_	Alignment		99.6	54	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein

12	c2yskA_	Alignment		42.6	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha1432; **PDBTitle:** crystal structure of a hypothetical protein ttha1432 from thermus2 thermophilus
13	d1o17a1	Alignment		42.5	17	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
14	d1brwa1	Alignment		41.2	17	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
15	d1dula_	Alignment		41.0	10	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
16	d1z67a1	Alignment		30.8	21	**Fold:**YidB-like **Superfamily:**YidB-like **Family:**YidB-like
17	d1nria_	Alignment		29.2	16	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
18	c1nriA_	Alignment		29.2	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein hi0754; **PDBTitle:** crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
19	d1khda1	Alignment		28.9	0	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
20	d2tpta1	Alignment		28.7	10	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
21	c3mzyA_	Alignment	not modelled	26.7	14	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**rna polymerase sigma-h factor; **PDBTitle:** the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
22	c3cvjB_	Alignment	not modelled	26.6	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative phosphoheptose isomerase; **PDBTitle:** crystal structure of a putative phosphoheptose isomerase (bh3325) from2 bacillus halodurans c-125 at 2.00 a resolution
23	d1i27a_	Alignment	not modelled	25.7	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal domain of the rap74 subunit of TFIIF
24	d1z6ra1	Alignment	not modelled	25.5	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ROK associated domain
25	c1o17A_	Alignment	not modelled	24.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** anthranilate phosphoribosyl-transferase (trpd)
26	d2cp9a1	Alignment	not modelled	24.5	19	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
27	d1aipc1	Alignment	not modelled	23.8	27	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
28	c2krcA_	Alignment	not modelled	22.8	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-directed rna polymerase subunit delta; **PDBTitle:** solution structure of the n-terminal domain of bacillus2 subtilis delta subunit of rna polymerase
						Fold: Methionine synthase domain-like

29	d1uoua1	Alignment	not modelled	21.7	15	**Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
30	d2o4ta1	Alignment	not modelled	21.7	13	**Fold:**Left-handed superhelix **Superfamily:**BH3980-like **Family:**BH3980-like
31	d1nh2d1	Alignment	not modelled	21.0	21	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
32	c2v79B_	Alignment	not modelled	20.8	13	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**dna replication protein dnad; **PDBTitle:** crystal structure of the n-terminal domain of dnad from2 bacillus subtilis
33	c2vn2B_	Alignment	not modelled	20.4	17	**PDB header:**replication **Chain:** B: **PDB Molecule:**chromosome replication initiation protein; **PDBTitle:** crystal structure of the n-terminal domain of dnad protein2 from geobacillus kaustophilus hta426
34	d1xb2b1	Alignment	not modelled	19.9	21	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
35	c3tsuA_	Alignment	not modelled	18.6	37	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
36	d1hq1a_	Alignment	not modelled	18.4	12	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
37	d1ee8a1	Alignment	not modelled	17.4	14	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
38	d1tdza1	Alignment	not modelled	16.6	14	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
39	c1otpA_	Alignment	not modelled	16.5	10	**PDB header:**phosphorylase **Chain:** A: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
40	d1qzxa2	Alignment	not modelled	16.5	27	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
41	d1k82a1	Alignment	not modelled	16.0	18	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
42	d1vola2	Alignment	not modelled	15.8	17	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Transcription factor IIB (TFIIB), core domain
43	d1ussa_	Alignment	not modelled	15.5	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Linker histone H1/H5
44	d1qb2a_	Alignment	not modelled	14.9	16	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
45	c3g2bA_	Alignment	not modelled	14.8	6	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**coenzyme pqq synthesis protein d; **PDBTitle:** crystal structure of pqqd from xanthomonas campestris
46	d2ffha2	Alignment	not modelled	14.7	12	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
47	c2jqeA_	Alignment	not modelled	14.3	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** soution structure of af54 m-domain
48	c1khdD_	Alignment	not modelled	14.2	0	**PDB header:**transferase **Chain:** D: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** crystal structure analysis of the anthranilate2 phosphoribosyltransferase from erwinia carotovora at 1.93 resolution (current name, pectobacterium carotovorum)
49	d1r2za1	Alignment	not modelled	13.9	29	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
50	c1l0oC_	Alignment	not modelled	13.6	24	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**sigma factor; **PDBTitle:** crystal structure of the bacillus stearothermophilus anti-2 sigma factor spoiiab with the sporulation sigma factor3 sigmaf
51	d1l0oc_	Alignment	not modelled	13.6	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
52	d1g8ia_	Alignment	not modelled	13.6	7	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
53	d1k3xa1	Alignment	not modelled	13.4	19	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
54	c3bwgA_	Alignment	not modelled	13.2	31	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**uncharacterized hth-type transcriptional regulator yydk; **PDBTitle:** the crystal structure of possible transcriptional regulator yydk from2 bacillus subtilis subsp. subtilis str. 168

55	c1tr8A_	Alignment	not modelled	13.0	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**conserved protein (mth177); **PDBTitle:** crystal structure of archaeal nascent polypeptide-associated complex2 (aenac)
56	d1njra_	Alignment	not modelled	11.9	21	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
57	c1vquB_	Alignment	not modelled	11.4	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase 2; **PDBTitle:** crystal structure of anthranilate phosphoribosyltransferase 22 (17130499) from nostoc sp. at 1.85 a resolution
58	d1nvpd1	Alignment	not modelled	11.1	17	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
59	d1uxda_	Alignment	not modelled	11.1	35	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
60	d1smyf2	Alignment	not modelled	11.0	3	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
61	d1z05a1	Alignment	not modelled	11.0	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ROK associated domain
62	c3a4cA_	Alignment	not modelled	10.4	11	**PDB header:**cell cycle, replication **Chain:** A: **PDB Molecule:**dna replication factor cdt1; **PDBTitle:** crystal structure of cdt1 c terminal domain
63	d1efub3	Alignment	not modelled	10.2	21	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
64	d1v8ga1	Alignment	not modelled	10.2	12	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
65	c2kloA_	Alignment	not modelled	10.0	11	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dna replication factor cdt1; **PDBTitle:** structure of the cdt1 c-terminal domain
66	c1brwB_	Alignment	not modelled	10.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyrimidine nucleoside phosphorylase); **PDBTitle:** the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
67	d1mkma1	Alignment	not modelled	9.9	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator IclR, N-terminal domain
68	c2l8nA_	Alignment	not modelled	9.8	30	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional repressor cytr; **PDBTitle:** nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
69	c2dsjA_	Alignment	not modelled	9.8	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside (thymidine) phosphorylase; **PDBTitle:** crystal structure of project id tt0128 from thermus thermophilus hb8
70	d2elca1	Alignment	not modelled	9.6	12	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
71	d1uxca_	Alignment	not modelled	9.6	35	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
72	d1aisb2	Alignment	not modelled	9.6	22	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Transcription factor IIB (TFIIB), core domain
73	c1aipG_	Alignment	not modelled	9.5	27	**PDB header:**complex of two elongation factors **Chain:** G: **PDB Molecule:**elongation factor ts; **PDBTitle:** ef-tu ef-ts complex from thermus thermophilus
74	d2bjca1	Alignment	not modelled	9.4	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
75	c2v3cC_	Alignment	not modelled	9.4	19	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** crystal structure of the srp54-srp19-7s.s srp rna complex2 of m. jannaschii
76	c3edpB_	Alignment	not modelled	9.2	28	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**lin2111 protein; **PDBTitle:** the crystal structure of the protein lin2111 (functionally unknown)2 from listeria innocua clip11262
77	c2kjwA_	Alignment	not modelled	8.8	14	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s6; **PDBTitle:** solution structure and backbone dynamics of the permutant2 p54-55
78	d1qpza1	Alignment	not modelled	8.8	25	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
79	c2lcvA_	Alignment	not modelled	8.6	30	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional repressor cytr; **PDBTitle:** structure of the cytidine repressor dna-binding domain; an alternate2 calculation
						Fold: Ferredoxin-like

80	d2j5aa1	Alignment	not modelled	8.4	26	**Superfamily:**Ribosomal protein S6 **Family:**Ribosomal protein S6
81	c3thgA_	Alignment	not modelled	8.4	7	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ribulose bisphosphate carboxylase/oxygenase activase 1, **PDBTitle:** crystal structure of the creosote rubisco activase c-domain
82	c3kfoA_	Alignment	not modelled	8.3	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**nucleoporin nup133; **PDBTitle:** crystal structure of the c-terminal domain from the nuclear pore2 complex component nup133 from saccharomyces cerevisiae
83	d1x92a_	Alignment	not modelled	8.3	16	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
84	d1tk9a_	Alignment	not modelled	8.1	20	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
85	d2hsga1	Alignment	not modelled	8.0	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
86	d1lcda_	Alignment	not modelled	8.0	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
87	d1qjha_	Alignment	not modelled	7.7	14	**Fold:**Ferredoxin-like **Superfamily:**Ribosomal protein S6 **Family:**Ribosomal protein S6
88	c3r3tA_	Alignment	not modelled	7.6	15	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s6; **PDBTitle:** crystal structure of 30s ribosomal protein s from bacillus anthracis
89	d2fq4a1	Alignment	not modelled	7.3	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
90	d2i10a1	Alignment	not modelled	7.1	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
91	d1u5ta1	Alignment	not modelled	7.0	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
92	d1vr3a1	Alignment	not modelled	7.0	23	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acireductone dioxygenase
93	c1dpuA_	Alignment	not modelled	6.8	12	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**replication protein a (rpa32) c-terminal domain; **PDBTitle:** solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)
94	d1dpua_	Alignment	not modelled	6.8	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal domain of RPA32
95	c2bpqB_	Alignment	not modelled	6.8	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** anthranilate phosphoribosyltransferase (trpd) from2 mycobacterium tuberculosis (apo structure)
96	c1xb2B_	Alignment	not modelled	6.7	29	**PDB header:**translation **Chain:** B: **PDB Molecule:**elongation factor ts, mitochondrial; **PDBTitle:** crystal structure of bos taurus mitochondrial elongation2 factor tu/ts complex
97	c2kz3A_	Alignment	not modelled	6.5	26	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein rad51l3; **PDBTitle:** backbone 1h, 13c, and 15n chemical shift assignments for human rad51d2 from 1 to 83
98	d1x2na1	Alignment	not modelled	6.5	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
99	c1rp3G_	Alignment	not modelled	6.4	18	**PDB header:**transcription **Chain:** G: **PDB Molecule:**rna polymerase sigma factor sigma-28 (flia); **PDBTitle:** cocrystal structure of the flagellar sigma/anti-sigma2 complex, sigma-28/flgm