

TABLE 2
Properties of the most important nucleoid proteins in *E. coli*

Protein	Structure ^a	Preferred DNA target ^b	Binding site size (bp) ^c	Exponential phase		Stationary phase		PDB I.D. # ^{rmf} and reference
				Copies/cell ^d	% of chromosomal DNA bound ^e	Copies/cell ^d	% of chromosomal DNA bound ^e	
HU	Heterodimer	Kinked, gapped, 3- or 4-way junctions	36	30,000	8	10,000	6	1MUL (Ramstein <i>et al.</i> , 2003)
IHF	Heterodimer	WATCAANNNTTTR	36	12,000	4	20,000	11	Iihf (Rice <i>et al.</i> , 1996)
H-NS	Homodimer/ oligomer	Curved DNA	10	10,000	1	6,000	1	2jr1 (Rimsky, 2004; Rosselli, K. <i>et al.</i> unpublished)
StpA	Homodimer/ oligomer	Curved DNA	10	12,000	1	5,000	<1	N.A.; homologous to H-NS
Fis	Homodimer	GNTYAAWWWTTRANC	21–27	30,000	6	<1,000	<1	1ety (Cheng <i>et al.</i> , 2000)
Dps	Dodecamer	None	90?	500	<1	20,000	11	1dps (Grant <i>et al.</i> , 1998)

Protein	Growth Phenotype
HU	<i>hupA</i> or <i>hupB</i> : +; <i>hupA/hupB</i> : ±; Mutants form filaments and anucleate cells
IHF	Required for growth on several carbon sources
H-NS	Poor growth; - at 20° C
STpA	Non-essential
Fis	Non-essential
Dps	Required for survival in stationary phase and under stress conditions

^aQuaternary structure, usually determined from the atomic (X-ray) structure of the protein or using biochemical procedures.

^bEach of the proteins binds DNA nonspecifically with physiologically significant affinities. A preferred binding sequence or DNA structure is noted when known. Y = C or T, R = G or A, W = A or T, and N = any base.

^cBinding site size is estimated from atomic structures of the DNA complex (HU and IHF), footprinting data (H-NS, StpA, and Fis), or modeling based on the atomic structures of the unbound protein (Fis and Dps). For HU, 14 to 19 bp are actually contacted in the crystal structures, but contacts covering up to 46 bp are supported by the structures. The size and stoichiometry of the Dps-DNA complex is speculative (11).

^dFis, HU, and IHF are expressed in dimers per cell, and Dps is expressed in dodecamers per cell. H-NS and StpA are expressed as dimers per cell, but the functional binding form may be a tetramer or higher order complexes. Data were collated from individual studies and Talukder *et al.* (318) from *E. coli* cells cultured in rich media. All values represent approximations as different research groups have reported different values.

^ePercentage of chromosomal DNA potentially bound by each protein. Calculations are based on three and one chromosome equivalents per cell in exponential and stationary phases, respectively, where the *E. coli* chromosome is 4.6 Mbp. These values are approximate because of the assumptions used in the calculations.

^fProtein DataBase (PDB (<http://pdb.org>)) identification number (I.D. #) with reference. Many structures or partial structures of these proteins have been reported. The I.D. # of a representative full length structure is presented. These proteins are from individual studies of *E. coli* cells when available. N.A. = not available.