TABLE 3. *Quantities of synthetases in E. coli NC3 growing on glucose*[a]

Synthetase	Polypeptide	Holoenzyme	
	Wt fraction of total protein[b] ($\times 10^3$)	Wt fraction of total protein[c] ($\times 10^3$)	No. of molecules per genome[d]
ArgRS	0.81 ± 0.03	0.81	510
GlnRS	1.06 ± 0.02	1.06	676
GluRS	0.68 ± 0.06 (α)	1.25	539
GlyRS	1.50 ± 0.08 (β)	2.11	412
IleRS	2.29 ± 0.19	2.29	885
LeuRS	1.41 ± 0.18	1.41	597
LysRS	1.05 ± 0.05	1.05	333
PheRS	1.12 ± 0.02 (α) 1.93 ± 0.03 (β)	3.94	649
ThrRS	0.92 ± 0.14	0.92	346
ValRS	1.01 ± 0.09	1.01	425

[a] The values are for cells of *E. coli* strain NC3 growing in glucose plus MOPS minimal medium at 37°C, $k = 1.03^{-1}$.

[b] A gel was prepared from a culture grown with [^{14}C]glucose as described in Materials and Methods. Each polypeptide identified in Table 1 was cut out of the gel quantitatively and its total radioactivity was counted after oxidation to CO_2. The total radioactivity of the protein in the gel was similarly measured. These values were used to obtain an estimate of the weight fraction of the total protein which each polypeptide represented. The standard error of the mean is shown.

[c] The values for weight fraction given in column 1 for the polypeptides were corrected to include expected amounts of the other subunits of the same proteins, assuming the stoichiometry present in purified holoenzyme. In the case of PheRS, both subunits were measured, but the values for the β subunit were highly variable and therefore implied incomplete recovery. Only the values for the α chain were used to calculate the holoenzyme weight fraction.

[d] These values were obtained by multiplying the amount of protein per genome-equivalent of DNA (4×10^8 amino acid residues $\times$ 110 daltons per amino acid = 4.4×10^{10} daltons; reference 5) by the weight fraction characteristic of a particular enzyme (column 2), and then converting this value to number of molecules per genome by dividing by the holoenzyme molecular weight shown in Table 1.