TABLE 2. *Estimated specific costs of component processes of protein turnover*

Process	Metabolic cost (ATP per amino acid)[a]
Protein breakdown (to amino acids)	0·13–2
Protein synthesis (from amino acids)[b]	
Amino acid activation	2[c]
Editing for misaminoacylation of tRNAs	0–0·15
Polypeptide initiation and elongation	$2 + 1/n$[d]
Editing noncognate aminoacyl-tRNA	0–0·01
Methylation, acetylation, glycosylation, etc.	0·1[e]
Phosphorylation	0·1–0·3[e]
mRNA turnover[f]	0·16–0·36
Signal sequences	0·18–1·0
Total synthesis	4·5–5·9[g]
Total (breakdown + synthesis)	4·7–7·9

Based on Zerihun *et al.* (1998); some values are speculative.

[a] Cost is expressed as ATP cleavage to ADP and P_i.

[b] Some amino acids produced by protein breakdown are recycled (i.e. repolymerized in subsequent protein synthesis) and some are catabolized. Synthesis of amino acids to replace those catabolized increases the cost of protein turnover (not shown); according to Zerihun *et al.* (1998), resynthesizing all the amino acids would increase total protein turnover cost by more than 83 % (see also Penning de Vries, 1975*a*; de Visser *et al.*, 1992).

[c] One ATP is cleaved to AMP and PP_i per amino acid. This is equated with 2 ATP through the action of adenylate kinase (i.e. ATP + AMP→2 ADP). Note that PP_i might serve as an energy source in other maintenance processes (e.g. active transport through tonoplasts).

[d] n is number of amino acid residues in a protein.

[e] From de Visser *et al.* (1992).

[f] mRNA turnover accounts for mRNA 'lifetime', i.e. number of protein molecules polymerized before an mRNA molecule is broken down.

[g] Assumes n is large (i.e. cost of polypeptide initiation and elongation is 2 ATP/peptide).