

Supporting Information

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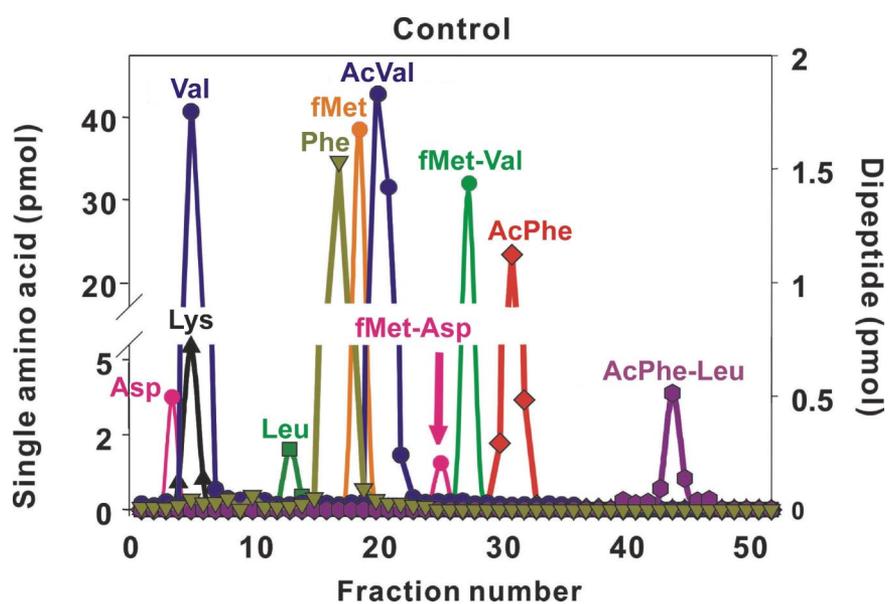


Fig. S1. HPLC pattern of superimposed control runs by using selected amino acids and the dipeptides fMet-Asp, fMet-Val, and AcPhe-Leu.

Table S1. Cognate and noncognate dipeptide formation in the absence (Pi state) and presence of an E-tRNA (POST state)

Complex			Dipeptides, pmol		Error, %
tRNA selection at the A-site	mRNA	State (E-site)	AcPhe-Lys, cognate	AcPhe-Leu, non-cognate	
Cognate versus noncognate	MFK	Pi(free)	18.8 ± 1.9	0.74 ± 0.06	3.8 ± 0.2
		POST (occupied)	12.3 ± 1.0	<0.03	0

The percent error is the ratio (incorrect dipeptides)/(correct + incorrect dipeptides) × 100.