Two-strain, cell-selective protein labeling in mixed bacterial cultures

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Supporting Information

	Connolly Solvent Excluded Volume (Å^3)	Connolly Molecular Area (Å^2)
Methionine	126.964	154.321
Methionine Side Chain	94.736	124.784
Propargylglycine	93.655	120.317
Propargylglycine Side Chain	58.185	87.38

Table SI 1: Dimensions of methionine and propargylglycine. Values were calculated in ChemBio3D Ultra.

	Mutations	Normalized Fluorescence with Pra
MO2b_13-2	L13P, A256G, P257T, Y260Q, H301F	100%
Clone 1	**V328M**, V389L	143%
Clone 5	S207N, Q379H, Δ548W	151%
Clone 12	**V328L**	131%
Clone 15	**T339S**, I515S	136%
Clone 16	**A331V**	163%

Table SI 2: Selection of the best performing mutants from MO9c_4 screened population compared to MO2b_13-2. KMSKS motif is located at amino acids 332-336 in *E. coli* methionyl-tRNA synthetase. Mutations in bold are located in the flexible regions adjacent to the KMSKS sequence.

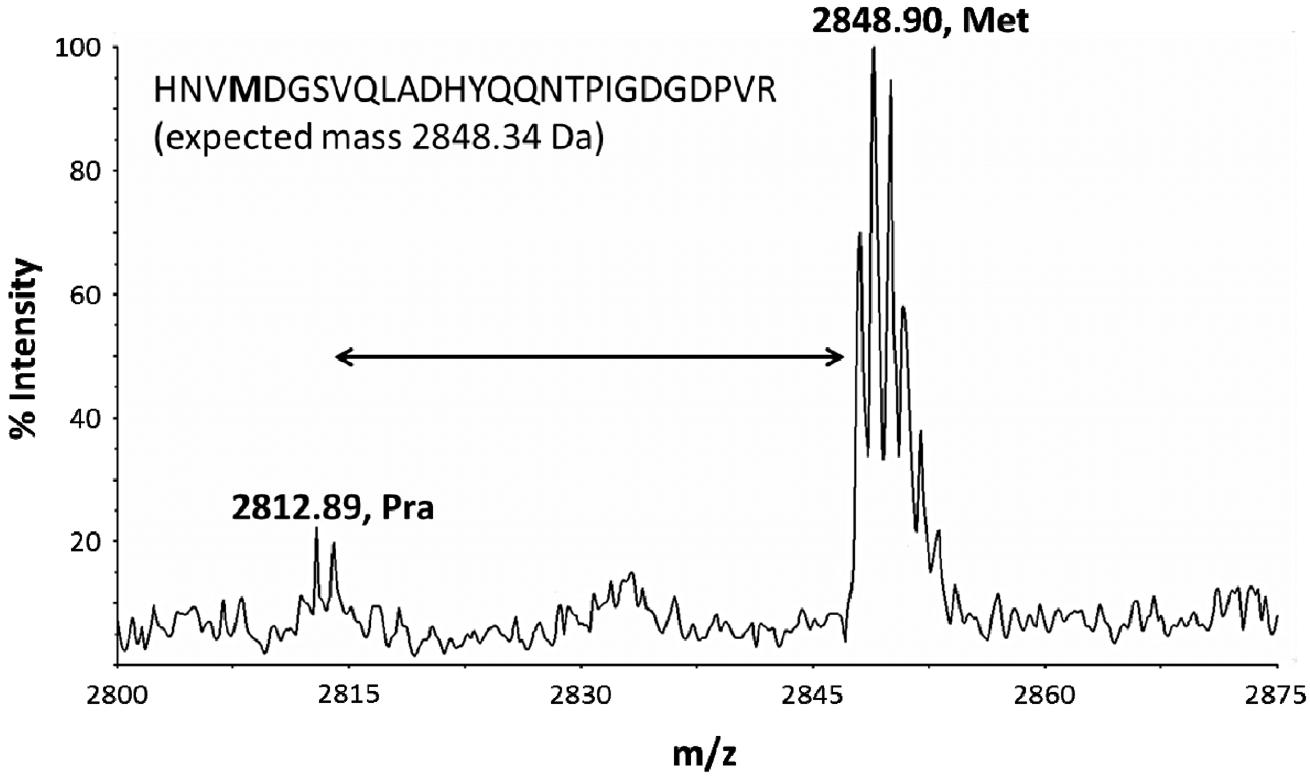

Figure SI 1: MALDI-TOF spectrum of tryptic digest of purified GFPrm_AM. His-tagged protein was expressed in a Met-auxotrophic strain of *E. coli* harboring PraRS in medium supplemented with 20 amino acids (269 µM Met) plus 4 mM Pra. Replacement of Met by Pra in the peptide HNV**M**DGSVQLADHYQQNTPIGDGDPVR results in a decrease in mass of 36 Da.