Supplementary Material

A genetically encoded photocaged N^{ϵ} -methyl-L-lysine

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Table of Contents

1.	General Experimental S2
2.	Chemical Synthesis S2
3.	DNA and Protein Sequences
4.	Construction of Plasmids
5.	Construction of the pRS1 LibraryS10
6.	Selection Procedure for Evolving Pyrrolysyl-tRNA Synthetase S11
7.	Protein Expression and Purification S11
8.	Photolysis to Form the Monomethylated Protein ······S12
9.	Protein LC-ESI-MS AnalysisS12
10.	ReferencesS13
11.	Supplementary Tables, Schemes, and Figures
12.	NMR and MS Spectra of Synthesized CompoundsS23

1. General Experimental

All reactions involving moisture sensitive reagents were conducted in ovendried glassware under an argon atmosphere. Anhydrous solvents were obtained through standard laboratory protocols. Analytical thin-layer chromatography (TLC) was preformed on Whatman SiO₂ 60 F-254 plates. Visualization was accomplished by UV irradiation at 254 nm or by staining with ninhydrin (0.3% w/v in glacial acetic acid/n-butyl alcohol 3:97). Flash column chromatography was performed with flash silica gel (particle size 32-63 μ m) from Dynamic Adsorbents Inc (Atlanta, GA).

Specific rotations of chiral compounds were obtained at the designated concentration and temperature on a Rudolph Research Analytical Autopol II polarimeter using a 0.5 dm cell. Proton and carbon NMR spectra were obtained on Varian 300 and 500 MHz NMR spectrometers. Chemical shifts are reported as δ values in parts per million (ppm) as referenced to the residual solvents: chloroform (7.27 ppm for ¹H and 77.23 ppm for ¹³C) or water (4.80 ppm for ¹H). A minimal amount of 1,4-dioxane was added as the reference standard (67.19 ppm for ¹³C) for carbon NMR spectra in deuterium oxide, and a minimal amount of sodium hydroxide pellet was added to the NMR sample to aid in the solvation of amino acids which have low solubility in deuterium oxide under neutral or acidic conditions. ¹H NMR spectra are tabulated as follows: chemical shift, multiplicity (s = singlet, bs = broad singlet, d = doublet, t = triplet, q = quartet, m = multiplet), number of protons, and coupling constant(s). Mass spectra were obtained at the Laboratory for Biological Mass Spectrometry at the Department of Chemistry, Texas A&M University.

H-Lys(Z)-OH (5) and H-Lys(Me)-OH·HCl (17) were obtained from Chem-Impex International, Inc. (Wood Dale, IL). Compound 7 was synthesized as reported.¹ All other reagents were obtained from commercial suppliers and used as received.

2. Chemical Synthesis

Compounds 6 and 8 were synthesized from 12^2 in a scalable route (Supplementary Scheme 1). For comparison, a shorter synthesis from the relatively expensive N^{ϵ} -methyl-L-lysine hydrochloride (17) following the standard protocol of

copper complexation, reaction with appropriate chloroformate, and decomplexation with 8-hydroxyquinoline³ was also developed (Supplementary Scheme 2).

OH Cl₂COCOCl, (*i*-Pr)₂NEt OCCl₃ CH₂Cl₂ NO₂ NO₂ NO_2 9 98% 10 11 (minor) NHCbz ΗŅ 1) H₂, Pd/Al₂O₂, MeOH HCHO, NaBH₄ MeOH 2) C₆H₅CHO, NaBH₄, MeOH BocHN COOCH₃ COOCH₃ BocHN 13 12 1) H₂, Pd/Al₂O₃, MeOH 2) 10 or PhCH₂OCOCl, (*i*-Pr)₂NEt, ĆH₂Cl₂ BocHN COOCH3 BocHN COOCH3 R = H, **15** NO2, **16** 14 0 1) LiOH, THF/H₂O O_2N 2) HCl, p-dioxane or H_2N COOH H_2N СООН 8 6

Supplementary Scheme 1. Longer synthesis of 6 and 8.

Supplementary Scheme 2. Shorter synthesis of 6 and 8.



2-Nitrobenzyl chloroformate (10) and 2-nitrobenzyl trichloromethyl carbonate (11). To a solution of 2-nitrobenzyl alcohol (9, 1.97 g, 12.9 mmol) in anhydrous dichloromethane (55 mL) cooled in an ice bath was added diphosgene (1.71 mL, 14.2 mmol) in dichloromethane (10 mL) dropwise over 10 min followed by diisopropylethylamine (2.25 mL, 12.9 mmol) in dichloromethane (10 mL) dropwise over 10 min. The reaction mixture was then stirred at room temperature for 2 h, and sodium hydroxide (1 N, 20 mL) was added and stirred further at room temperature for 30 min. The mixture was washed with water (30 mL), saturated sodium bicarbonate (30 mL x 2) and brine (30 mL), dried (Na₂SO₄), and flash chromatographed (EtOAc/hexanes, 1:20) to give a mixture of 10 and 11 (2.71 g, 98%) as a yellow oil. A minor fraction of impurity, presumably 11, was evident from NMR analysis but did not interfere with the next step reaction. No further purification was performed. For 10^{4} : ¹H NMR (CDCl₃, 500 MHz) δ 8.19 (d, 1 H, J = 8.0 Hz), 7.74 (t, 1 H, J = 7.8 Hz), 7.65 (d, 1 H, J = 8.0 Hz), 7.58 (t, 1 H, J = 7.8 Hz), 5.75 (s, 2 H); ¹³C NMR (CDCl₃, 125 MHz) δ 150.6, 147.7, 134.4, 129.9, 129.8, 129.2, 125.6, 69.7. For **11**: ¹H NMR $(CDCl_3, 500 \text{ MHz}) \delta 8.20 \text{ (d, 1 H, } J = 6.5 \text{ Hz}), 7.74 \text{ (t, 1 H, } J = 7.7 \text{ Hz}), 7.68 \text{ (d, 1 H, } J = 7.7 \text{ Hz}), 7.68$ J = 8.0 Hz), 7.58 (t, 1 H, J = 7.7 Hz), 5.75 (s, 2 H); ¹³C NMR (CDCl₃, 125 MHz) δ 147.3, 147.2, 134.5, 130.2, 129.8, 129.0, 108.0, 68.0,

 N^{α} -Boc- N^{ε} -benzyl-L-lysine methyl ester (13). A solution of 12 (4.20 g, 10.6 mmol) in methanol (100 mL) was hydrogenated under a H₂ balloon in the presence of palladium on alumina (10 wt.% Pd, 0.71 g, 0.67 mmol) at room temperature for 3 h, and TLC analysis showed a complete conversion. The mixture was then filtered over a pad of Celite and the solution was directly used for the next step reaction. The material should be immediately used without purification since prolonged storage at room temperature or flash chromatography would contribute to lactam formation.

To a solution of the above amine (~10.6 mmol) in methanol was added benzaldehyde (4.00 mL, 39.4 mmol), and the reaction mixture was stirred at room temperature for 30 min. The mixture was then cooled in an ice bath, and sodium borohydride (0.75 g, 19.8 mmol) was added portionwise. The mixture was then stirred at room temperature overnight, and water (10 mL) was added dropwise to quench the reaction. Most of the methanol was evaporated under a reduced pressure, and the residue was dissolved in ethyl acetate (100 mL), washed with water (30 mL), saturated sodium bicarbonate (30 mL) and brine (30 mL), dried (Na₂SO₄), and evaporated to give the crude 13 as a yellow oil, which was used in the next step reaction without further purification. A small fraction of pure 13 was obtained by flash chromatography (10% methanol with 5% triethylamine in dichloromethane) for characterization. $[\alpha]_D^{19}$ +7.4 (*c* 4.85, CH₂Cl₂); ¹H NMR (CDCl₃, 500 MHz) δ 7.35-7.30 (m, 4 H), 7.27-7.24 (m, 1 H), 5.05 (d, 1 H, J = 7.0 Hz), 4.32-4.28 (m, 1 H), 3.78 (s, 2 H), 3.74 (s, 3 H), 2.63 (t, 2 H, J = 7.0 Hz), 1.83-1.78 (m, 1 H), 1.67-1.60 (m, 1 H), 1.58-1.48 (m, 3 H), 1.44 (s, 9 H), 1.41-1.36 (m, 2 H); ¹³C NMR (CDCl₃, 125 MHz) δ 173.5, 155.5, 140.5, 128.5, 128.2, 127.0, 79.9, 54.1, 53.5, 52.3, 49.1, 32.7, 29.7, 28.4, 23.2; HRMS (ESI) calcd for $C_{19}H_{31}N_2O_4$ ([M + H]⁺) 351.2284, found 351.2282.

 N^{α} -Boc- N^{ε} -benzyl- N^{ε} -methyl-L-lysine methyl ester (14). To a solution of crude 13 (~10.6 mmol) in methanol (100 mL) in methanol was added formaldehyde (37% aqueous solution, 3.00 mL, 40.3 mmol), and the reaction mixture was stirred at room temperature for 30 min. The mixture was then cooled in an ice bath, and sodium borohydride (0.77 g, 20.4 mmol) was added portionwise. The mixture was then stirred further at room temperature for 4 h, and water (30 mL) was added dropwise to quench the reaction. Most of the methanol was evaporated under a reduced pressure, and the residue was dissolved in ethyl acetate (100 mL), washed with water (30 mL), hydrochloric acid (1 N, 30 mL), sodium hydroxide (1 N, 30 mL) and brine (30 mL), dried (Na₂SO₄), evaporated, and flash chromatographed (EtOAc/hexanes, 1:1 then 5% to 10% methanol in dichloromethane) to give 14 (3.32 g, 86% yield for three steps) as a yellow oil. $[\alpha]_D^{20}$ +7.7 (c 2.37, CH₂Cl₂); ¹H NMR (CDCl₃, 500 MHz) δ 7.33-7.29 (m, 4 H), 7.26-7.23 (m, 1 H), 5.08 (d, 1 H, J = 8.5 Hz), 4.31-4.27 (m, 1 H), 3.73 (s, 3 H), 3.46 (s, 2 H), 2.35 (t, 2 H, J = 7.2 Hz), 2.17 (s, 3 H), 1.82-1.76 (m, 1 H), 1.66-1.47 (m, 3 H), 1.44 (s, 9 H), 1.40-1.32 (m, 2 H); ¹³C NMR (CDCl₃, 125 MHz) δ 173.6, 155.6, 139.3, 129.2, 128.4, 127.1, 80.0, 62.5, 57.1, 53.6, 52.4, 42.4, 32.7, 28.5, 27.0, 23.3; HRMS (ESI) calcd for $C_{20}H_{33}N_2O_4$ ([M + H]⁺) 365.2440, found 365.2437.

N^α-Boc-*N*^ε-Cbz-*N*^ε-methyl-L-lysine methyl ester (15). A solution of 14 (2.58 g, 7.07 mmol) in methanol (50 mL) was hydrogenated under a H₂ balloon in the presence of palladium on alumina (10 wt.% Pd, 0.50 g, 0.47 mmol) at room temperature for 5 h. The mixture was then filtered over a pad of Celite and evaporated to give the crude amine (Boc-Lys(Me)-OMe) as a grey oil. A small fraction of pure amine was obtained by flash chromatography (10% methanol with 5% triethylamine in dichloromethane) for characterization. $[\alpha]_D^{19}$ +6.9 (*c* 1.90, CH₂Cl₂); ¹H NMR (CDCl₃, 500 MHz) δ 5.38 (d, 1 H, *J* = 7.0 Hz), 4.14-4.12 (m, 1 H), 3.59 (s, 3 H), 2.95 (s, 1 H), 2.46 (t, 2 H, *J* = 7.2 Hz), 2.29 (s, 3 H), 1.69-1.64 (m, 1 H), 1.55-1.48 (m, 1 H), 1.43-1.33 (m, 2 H), 1.30 (s, 9 H), 1.27-1.22 (m, 2 H); ¹³C NMR (CDCl₃, 125 MHz) δ 173.4, 155.5, 79.6, 53.3, 52.1, 51.2, 35.8, 32.2, 28.8, 28.2, 23.0; HRMS (ESI) calcd for C₁₃H₂₇N₂O₄ ([M + H]⁺) 275.1971, found 275.1968.

To a solution of the above amine (~7.07 mmol) and diisopropylethylamine (2.00 mL, 11.5 mmol) in anhydrous dichloromethane (40 mL) cooled in an ice bath was added benzyl chloroformate (95%, 1.50 mL, 10.5 mmol) dropwise over 10 min, and the mixture was stirred at room temperature for 12 h. The mixture was then diluted in ethyl acetate (100 mL), washed with sodium hydroxide (0.5 *N*, 40 mL) and brine (40 mL), dried (Na₂SO₄), evaporated, and flash chromatographed (EtOAc/hexanes, 1:3) to give **15** (2.59 g, 90% for two steps) as a colorless oil. $[\alpha]_D^{19}$ +1.2 (*c* 1.51, CH₂Cl₂); ¹H NMR analysis showed a 1.5:1 mixture of rotamers at room temperature. Major rotamer: ¹H NMR (CDCl₃, 500 MHz) δ 7.33-7.32 (m, 4 H), 7.29-7.26 (m, 1 H), 5.26 (d, 1 H, *J* = 6.0 Hz), 5.10 (s, 2 H), 4.24 (m, 1 H), 3.69 (s, 3 H), 3.32-3.19 (m, 2 H), 2.87 (s, 3 H), 1.78-1.66 (m, 2 H), 1.57-1.51 (m, 2 H), 1.41 (s, 9 H), 1.36-1.28 (m, 2 H); ¹³C NMR (CDCl₃, 125 MHz) δ 173.4, 156.5, 155.6, 137.0, 128.5, 128.0, 127.9, 79.7, 67.0, 53.4, 52.2, 48.4, 33.9, 32.0, 28.4, 26.9, 22.2; Characteristic peaks of the minor rotamer: ¹H NMR (CDCl₃, 500 MHz) δ 5.05 (d, 1 H, *J* = 6.0 Hz);

¹³C NMR (CDCl₃, 125 MHz) δ 156.3, 155.4, 79.9, 53.3, 34.6, 32.4, 27.5, 22.5; HRMS (ESI) calcd for $C_{21}H_{33}N_2O_6$ ([M + H]⁺) 409.2339, found 409.2332.



 N^{α} -Boc- N^{ε} -(2-nitrobenzyl)oxycarbonyl- N^{ε} -methyl-L-lysine methyl ester (16) and N^{α} -Boc- N^{ε} -chlorocarbonyl- N^{ε} -methyl-L-lysine methyl ester (18). Compound 14 (1.06 g, 2.91 mmol) was converted into the corresponding amine by hydrogenolysis, which was then treated with crude 10 (0.94 g, 4.38 mmol) according to the procedure for 15 to give 16 (0.91g, 69% for two steps) as a yellow oil. A small amount of 18 (yield not determined), the structure of which was assigned based on NMR and MS analysis data, was obtained as a colorless oil. Presumably Boc-Lys(Me)-OMe reacts with 11 to give 16 and generates one molecule of phosgene at the same time, which then acylates the residual Boc-Lys(Me)-OMe to afford 18.

For **16**: $[\alpha]_D^{20}$ +8.9 (*c* 1.70, CH₂Cl₂); R_f = 0.46 (EtOAc/hexanes, 1:1); ¹H NMR analysis showed a 1.1:1 mixture of rotamers at room temperature. Major rotamer: ¹H NMR (CDCl₃, 500 MHz) δ 7.96 (d, 1 H, *J* = 8.0 Hz), 7.58 (t, 1 H, *J* = 7.5 Hz), 7.50-7.47 (m, 1 H), 7.39 (t, 1 H, *J* = 8.2 Hz), 5.42 (s, 2 H), 5.21 (d, 1 H, *J* = 7.5 Hz), 4.20-4.16 (m, 1 H), 3.63 (s, 3 H), 3.21 (appar. nonet, 2 H, *J* = 7.1 Hz), 2.86 (s, 3 H), 1.74-1.44 (m, 4 H), 1.34 (s, 9 H), 1.30-1.24 (m, 2 H); ¹³C NMR (CDCl₃, 125 MHz) δ 173.2, 155.6, 155.4, 147.5, 133.6, 133.1, 128.7, 128.5, 124.8, 79.6, 63.7, 53.2, 48.5, 33.8, 31.9, 28.2, 26.7, 22.2; Characteristic peaks of the minor rotamer: ¹H NMR (CDCl₃, 500 MHz) δ 5.13 (d, 1 H, *J* = 7.5 Hz), 2.83 (s, 3 H); ¹³C NMR (CDCl₃, 125 MHz) δ 173.1, 155.5, 155.4, 147.5, 128.9, 128.5, 79.7, 52.1, 48.4, 34.6, 32.3, 27.4, 22.4; HRMS (ESI) calcd for C₂₁H₃₁N₃O₈Li ([M + Li]⁺) 460.2271, found 460.2272.

For **18**: $[\alpha]_D^{20}$ +6.6 (*c* 2.20, CH₂Cl₂); R_f = 0.61 (EtOAc/hexanes, 1:1); ¹H NMR analysis showed a 1.2:1 mixture of rotamers at room temperature. Major rotamer: ¹H NMR (CDCl₃, 500 MHz) δ 5.06 (d, 1 H, *J* = 8.0 Hz), 4.30 (m, 1 H), 4.20-3.73 (s, 3 H), 3.44 (t, 1 H, *J* = 7.5 Hz), 3.40-3.36 (m, 1 H), 3.10 (s, 3 H), 1.85-1.56 (m, 4 H), 1.43 (s, 9 H), 1.40-1.31 (m, 2 H); ¹³C NMR (CDCl₃, 125 MHz) δ 173.3, 155.5, 149.8, 80.1, 53.2, 52.8, 51.2, 38.6, 32.5, 28.5, 26.7, 22.4; Characteristic peaks of the

minor rotamer: ¹H NMR (CDCl₃, 500 MHz) δ 3.74 (s, 3 H), 3.02 (s, 3 H); ¹³C NMR (CDCl₃, 125 MHz) δ 149.3, 80.2, 52.5, 36.8, 32.7, 27.4, 22.4; HRMS (ESI) calcd for C₁₄H₂₅ClN₂O₅Na ([M + Na]⁺) 361.1320 (³⁷Cl)/359.1350 (³⁵Cl), found 361.1348/ 359.1359; calcd for C₁₄H₂₆ClN₂O₅ ([M + H]⁺) 339.1505/337.1530, found 339.1585/ 337.1557.

 N^{e} -Benzyloxycarbonyl- N^{e} -methyl-L-lysine (6). To a solution of 15 (2.59 g, 6.34 mmol) in THF (20 mL) was added lithium hydroxide solution (0.5 M, 25.0 mL, 12.5 mmol), and the mixture was stirred at room temperature for 3 h. The mixture was diluted in water (20 mL) and extracted with ether (30 mL x 2). The ether extracts were discarded, and the remaining aqueous solution was adjusted to pH 3 with hydrochloric acid (3 N), with the concomitant formation of white precipitate. The suspension was extracted with ethyl acetate (50 mL x 2), and the combined organic phases were washed once with brine (30 mL), dried (Na₂SO₄), and evaporated to give the crude carboxylic acid as a colorless oil, which was directly used without further purification.

The above crude acid (~6.34 mmol) was dissolved in 1,4-dioxane (15 mL), and hydrogen chloride in 1,4-dioxane (4.0 M, 5.0 mL, 20.0 mmol) was added. The resulting white suspension was stirred at room temperature for 12 h, evaporated, redissolved in a minimal amount of water, and loaded onto an ion-exchange column made from Dowex 50WX4-400 cation-exchange resin (~14 mL bed volume). The column was washed with excessive water (300 mL) and then eluted with pyridine (1 M, 450 mL) to give **6** (1.51 g, 81% for two steps) as a white powder. $[\alpha]_D^{20}$ +14.1 (*c* 1.07, 3 *N* HCl) (lit.⁵ $[\alpha]_D^{25}$ +14.0 (*c* 0.5, acetic acid)); ¹H NMR analysis showed a 1:1 mixture of rotamers at room temperature. Major rotamer: ¹H NMR (D₂O, 500 MHz) δ 7.46-7.42 (m, 5 H), 5.16 (s, 2 H), 3.68 (m, 1 H), 3.34 (m, 2 H), 2.90 (s, 3 H), 1.83 (m, 2 H), 1.60 (quintet, 2 H, *J* = 7.3 Hz), 1.34 (m, 2 H); ¹³C NMR (D₂O, 75 MHz) δ 184.1, 158.4, 137.1, 129.4, 129.0, 128.5, 68.0, 56.5, 49.0, 35.1, 34.8, 27.6, 22.8; Characteristic peaks of the minor rotamer: ¹H NMR (D₂O, 500 MHz, pH = 14) δ 2.95 (s, 3 H); ¹³C NMR (D₂O, 75 MHz) δ 128.2, 67.2, 49.2, 34.2, 27.3. HRMS (ESI) calcd for C₁₅H₂₃N₂O₄ ([M + H]⁺) 295.1658, found 295.1656.

N^ε-(2-Nitrobenzyl)oxycarbonyl-*N*^ε-methyl-L-lysine (8). According to the same procedure for **6**, **16** (0.914 g, 2.02 mmol) afforded **8** (0.514 g, 75% for two steps) as a pale yellow solid. $[\alpha]_D^{20}$ +14.2 (*c* 1.16, 3 *N* HCl); ¹H NMR analysis showed a 1.1:1 mixture of rotamers at room temperature. Major rotamer: ¹H NMR (D₂O, 500 MHz, pH = 14) δ 8.00 (d, 1 H, *J* = 8.0 Hz), 7.64 (t, 1 H, *J* = 7.7 Hz), 7.50 (d, 1 H, *J* = 8.5 Hz), 7.47 (t, 1 H, *J* = 8.2 Hz), 5.32 (s, 2 H), 3.95 (m, 1 H), 3.20 (m, 2 H), 2.77 (s, 3 H), 1.84 (m, 2 H), 1.49 (m, 2 H), 1.31-1.27 (m, 2 H); ¹³C NMR (D₂O, 75 MHz) δ 184.2, 158.0, 147.6, 135.1, 132.7, 129.8, 129.4, 125.7, 65.0, 56.5, 49.2, 35.1, 34.9, 27.6, 22.8; Characteristic peaks of the minor rotamer: ¹H NMR (D₂O, 500 MHz, pH = 14) δ 2.82 (s, 3 H); ¹³C NMR (D₂O, 75 MHz) δ 133.0, 129.7, 64.9, 49.3, 34.2, 27.2; HRMS (ESI) calcd for C₁₅H₂₂N₃O₆ ([M + H]⁺) 340.1509, found 340.1513.

Synthesis of 6 from the shorter pathway. To a solution of 17 (1.50 g, 7.63 mmol) in

water (30 mL) was added cupric sulfate pentahydrate (1.00 g, 4.00 mmol), followed by sodium bicarbonate (1.42 g, 16.90 mmol) in small portions to prevent excessive bubble formation. Benzyl chloroformate (2.53 g, 13.36 mmol) in dioxane (5 mL) was then added dropwise in 5 min, followed by sodium hydroxide (0.49 g, 12.25 mmol) in one portion. The reaction mixture was stirred at room temperature for 16 h, filtered, washed with water (100 mL), ethanol (50 mL) and diethyl ether (50 mL), and dried in the open air for 1 h to give the crude copper complex (2.40 g, 97%) as a blue solid.

All the above copper complex (2.40 g, ~7.40 mmol) was suspended in sodium hydroxide solution (0.2 *N*, 100 mL, 20 mmol), and a solution of 8-hydroxylquinoline (1.40 g, 9.64 mmol) in 1,4-dioxane (10 mL). The resulting green suspension was stirred at room temperature overnight and filtered. The filtrate was adjusted to pH 3 with hydrochloric acid (3 *N*) and extracted with ethyl acetate (40 mL x 2). The organic extracts were discarded, and the aqueous phase was concentrated to about 20 mL and loaded onto an ion-exchange column made from Dowex 50WX4-400 cation-exchange resin (~14 mL bed volume). The column was washed with excessive water (300 mL) and then eluted with pyridine (1 M, 450 mL) to give a yellow solid upon evaporation, which was suspended in ethanol, filtered, washed ethyl acetate dried to give **6** (1.46 g, 65% for two steps) as a white solid. $[\alpha]_D^{22}$ +15.3 (*c* 1.02, 3 *N* HCl). All other characterization data were identical to that of **6** from the longer route.

Synthesis of 8 from the shorter pathway. According to the same procedure for 6, 17 (0.50 g, 2.54 mmol) afforded 8 (0.39 g, 45% yield for two steps). The compound was identical to 8 from the longer route in all aspects.

3. DNA and Protein Sequences

3.1 DNA Sequences

Z Domain:

atgactagtgtagacaactagatcaacaaagaacaacaaaacgccttctatgagatcttacatttacctaacctgaatgagga gcagcgtgatgccttcatccaaagtttaaaagatgacccaagccaaagcgctaaccttttagcagaagctaaaaagctaaat gatgctcaggcgcctaagggatctgagctccatcaccatcaccatcactaa

GFP_{UV}:

pylT:

 $ggaaacctgatcatgtagatcgaatggact {\it cta} aatccgttcagccgggttagattcccggggtttccgcca$

Methanosarcina mazei PylRS:

accacgaagtctctcgaagcaaaatctatattgaaatggcatgcggagaccaccttgttgtaaacaactccaggagcagcaggactgcaagagcgctcaggcaccacaaatacaggaagacctgcaaacgctgcagggtttcggatgaggatctcaataagttcctcacaaaggcaaacgaagaccagacaagcgtaaaagtcaaggtcgtttctgcccctaccagaacgaaaaaggca atgccaaaatccgttgcgagagccccgaaacctcttgagaatacagaagcggcacaggctcaaccttctggatctaaatttt cacctgcgataccggtttccacccaagagtcagtttctgtcccggcatctgtttcaacatcaatatcaagcatttctacaggagttacgaagagccagactgacaggcttgaagtcctgttaaacccaaaagatgagatttccctgaattccggcaagcctttcagggagcttgagtccgaattgctctctcgcagaaaaaaaagacctgcagcagatctacgcggaagaaagggagaattatctgg ggaaactcgagcgtgaaattaccaggttctttgtggacaggggttttctggaaataaaatccccgatcctgatcctcttgagt atatcgaaaggatgggcattgataatgataccgaactttcaaaacagatcttcagggttgacaagaacttctgcctgagacccatgettgetccaaacetttacaactacetgegcaagettgacagggccetgectgatccaataaaaatttttgaaataggccca tgctacagaaaagagtccgacggcaaagaacacctcgaagagtttaccatgctgaacttctgccagatgggatcgggatgcacacgggaaaatcttgaaagcataattacggacttcctgaaccacctgggaattgatttcaagatcgtaggcgattcctgcatggtctatggggatacccttgatgtaatgcacggagacctggaactttcctctgcagtagtcggacccataccgcttgaccgggaatggggtattgataaaccctggataggggcaggtttcgggctcgaacgccttctaaaggttaaacacgactttaaaaat at caag ag ag ctg caag gt ccg ag t ctt a cta a cgg ga t t t cta cca a cctg t a a construction of the second seco

3.2 Proteins Sequences

Z Domain:

MTSVDN<mark>X</mark>INKEQQNAFYEILHLPNLNEEQRDAFIQSLKDDPSQSANLLAEAKK LNDAQAPKGSELHHHHHH

X represents a noncanonical amino acid.

GFP_{UV}:

MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKL PVPWPTLVTTFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTISFKDDGN YKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYITADKQK NGIKANFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTXSALSKDP NEKRDHMVLLEFVTAAGITHGMDELYKELHHHHHH

X represents a noncanonical amino acid.

Methanosarcina mazei PylRS:

MDKKPLNTLISATGLWMSRTGTIHKIKHHEVSRSKIYIEMACGDHLVVNNSRS SRTARALRHHKYRKTCKRCRVSDEDLNKFLTKANEDQTSVKVKVVSAPTRT KKAMPKSVARAPKPLENTEAAQAQPSGSKFSPAIPVSTQESVSVPASVSTSISSI STGATASALVKGNTNPITSMSAPVQASAPALTKSQTDRLEVLLNPKDEISLNS GKPFRELESELLSRRKKDLQQIYAEERENYLGKLEREITRFFVDRGFLEIKSPIL IPLEYIERMGIDNDTELSKQIFRVDKNFCLRPMLAPNLYNYLRKLDRALPDPIK IFEIGPCYRKESDGKEHLEEFTMLNFCQMGSGCTRENLESIITDFLNHLGIDFKI VGDSCMVYGDTLDVMHGDLELSSAVVGPIPLDREWGIDKPWIGAGFGLERL LKVKHDFKNIKRAARSESYYNGISTNL

4. Construction of plasmids

4.1 Constructions of pY+ and pY-

The plasmid pY+ was derived from the pRep plasmid by replacing the suppressor tRNA in pRep by pylT.⁶ The gene of pylT flanked by the lpp promoter at the 5' end and the *rrnC* terminator at the 3' end was amplified from pBK-AcKRS-pylT.^{7,8} The plasmid pY- was derived from the pNeg plasmid by replacing the suppressor tRNA with pylT.⁶ Similarly, the gene of pylT flanked by the lpp promoter at the 5' end and the *rrnC* terminator at the 3' end was amplified from pBK-AcKRS-pylT.^{7,8} pY+ has a tetracycline selection marker and a chloramphenicol acetyltransferase gene with an amber mutation at D112. pY- has an ampicillin selection marker and a barnase gene with two amber mutations at Q2 and D44. The barnase gene is under control of a pBad promoter.

4.2 Construction of pET-pyIT-GFP

Plasmid pET-pylT-GFP was derived from the plasmid pAcKRS-pylT-GFP1Amber in which GFP_{UV} has an amber mutation at Q204.^{7,8} The restriction enzyme *BglII* was used to cut off the ACKRS gene. The digested pAcKRS-pylT-GFP1Amber plasmid was ligated to form pET-pylT-GFP.

4.3 Construction of pET-pyIT-Z

The pET-pyIT-Z plasmid was derived from pET-pyIT-GFP. This gene was amplified from the pLeiZ plasmid.⁹ Two restriction sites, *NdeI* at the 5' end and *SacI* at the 3' end, were introduced in the PCR product which was subsequently digested and used to replace GFP_{UV} in pET-pyIT-GFP.

5. Construction of the pRS1 Library

The plasmid pBK-mmPyIRS that encodes wild-type Methanosarcina mazei PyIRS was derived from a pBK plasmid containing *p*-iodophenylalanyl-tRNA synthetase.¹⁰ The pyIRS gene is under the control of E. coli glnS promoter and terminator. It was amplified from genomic DNA of Methanosarcina mazei strain DSM 3647 (ATCC) by flanking primers, pBK-mmPylRS-NdeI-F and pBK-mmPylRS-PstI~NsiI-R. To construct the pRS1 library, NNK (N=A or C or G or T, K=G or T) mutations were introduced at six sites by overlap extension PCR.¹¹ The following pairs of primers were used to generate a PyIRS gene library with randomization at six sites: (1) pBK-(5'-gaatcccatatggataaaaaaccactaaacactctg-3') mmPylRS-NdeI-F and mmPylRS-Mutlib01-R (5'-ggccctgtcaagcttgcgmnngtagttmnnmngtttggagcaagca tggg-3'); (2) mmPylRS-Mutlib02-F (5'-cgcaagcttgacagggccctgcctgatcc-3') and mmPvlRS-Mutlib03-R (5'-gcatcccgatcccatctgmnngaamnncagcatggtaaactcttc-3'); (3) mmPyIRSand mmPyIRS-Mutlib05-R (5'-cagatgggatggatgcacacg-3') Mutlib04-F (5'ccgaaacctgcccctatmnngggtttatcaatacccca-3'); mmPyIRS-Mutlib06-F (4) (5'pBK-mmPylRS-PstI~NsiI-R ataggggcaggtttcgggctcgaacgcc-3') and (5'gtttgaaaatgcatttacaggttggtagaaatccc-3'). The gene library was digested with the restriction enzymes NdeI and NsiI, gel-purified, and ligated back into the pBK vector digested by *NdeI* and *PstI* to afford the pRS1 plasmid library. 1 µg of the ligation products were then electroporated into *E. coli* Top10 cells. Electroporated cells were recovered in SOC medium for 60 min at 37 °C, transferred into a 2 L 2YT medium with kanamycin (25 µg/mL) and were incubated at 37 °C to an OD₆₀₀ of 1.0. To calculate the library size, 1 µL of the recovered SOC culture was subjected to serial dilutions in 2YT, plated on LB agar plates with kanamycin (25 µg/mL), and grown overnight in a 37 °C incubator. Based on the colony numbers on these plates, the pRS1 library contains approximately 1.01×10^9 independent transformants. Sequencing pyIRS variants in 20 clones did not reveal any significant bias at the randomization sites.

6. Selection Procedure for Evolving Pyrrolysyl-tRNA Synthetase

The selections followed the scheme shown in **Supplementary Scheme 3**. For the positive selection, the pRS1 library was used to transform E. coli TOP10 competent cells harboring pY+ to yield a cell library greater than 1×10^9 cfu, ensuring complete coverage of the pRS1 library. Cells were plated on minimal agar plates containing 12 µg/mL tetracycline (Tet), 25 µg/mL kanamycin (Kan), 68 µg/mL chloramphenicol (Cm) and 1 mM 5. After incubation at 37 °C for 72 h, colonies on the plates were collected. Total plasmids were isolated and separated by 1% agarose gel electrophoresis. pRS1 plasmids were extracted using a gel-extraction kit (QIAGEN). The extracted pRS1 plasmids from the positive selection were used to transform E. coli TOP10 cells harboring pY- for the negative selection. After electroporation, the cells were allowed to recover for 1 h at 37 °C in SOC media before being plated on LB agar plates containing 50 µg/mL Kan, 200 µg/mL ampicillin (Amp), and 0.2% arabinose. The plates were incubated for 16 h at 37 °C. Survived cells were then pooled and the pRS1 plasmids were extracted. The selection power to exclude the mutants that also took endogenous amino acids was tested on LB agar plates containing 50 µg/mL Kan, 200 µg/mL Amp, 0.2% arabinose, and 1mM 5. The plates containing 1 mM 5 showed fewer and fewer colony numbers as the alternative selections were repeated. Five alternative selections (three positive + two negative) finally vielded many colonies. After the final third positive selection 22 single colonies were selected and the plasmids were isolated for sequencing, and another 96 single colonies were chosen to test their ability to grow on plates with 102 µg/mL Cm, 25 µg/mL Kan, 12 µg/mL Tet, and 1 mM of 5, 6, 7 or 8. An LB agar plate without any NAA was used as the control. Images of colonies growing on different plates are shown in Supplementary Fig. 7. Sequences of PyIRS variants that charge pyIT with different NAAs are presented in Supplementary Table 1.

7. Protein Expression and Purification

To express GFP_{UV} incorporated with a NAA, we cotransformed *E. Coli* BL21(DE3) cells with pBK-mKRS1 and pET-pylT-GFP. Cells were recovered in 1 mL of LB medium for 1 h at 37 °C before being plated on LB agar plate containing

Kan (25 μ g/mL) and Amp (100 μ g/mL). A single colony was then selected and grown overnight in a 10 mL culture, which was then used to inoculate 100 mL of M9 minimal media supplemented with 1% glycerol, 300 µM leucine, 2 mM MgSO₄, 0.1 mM CaCl₂, 0.2% NaCl, 25 µg/mL Kan, and 100 µg/mL Amp. Cells were grown at 37 $^{\circ}$ C in an incubator (300 r.p.m.) and protein expression was induced when the OD₆₀₀ reached 0.7 by adding both IPTG and 5 to a final concentration of 1 mM. After 6 h induction, cells were harvested, resuspended in a lysis buffer (50 mM NaH₂PO₄, 300 mM NaCl, 10 mM imidazole, pH 8.0), and sonicated. The cell lysate was clarified by centrifugation (60 min, 11,000 r.p.m., 4 °C). The supernatant was injected onto a Ni²⁺-NTA column (30 mL) equipped on a GE Healthcare ÄKTApurifier FPLC system and washed with 45 mL of lysis buffer and 45 mL of wash buffer (50 mM NaH₂PO₄, 300 mM NaCl, 40 mM imidazole, pH 8.0). Proteins were then eluted out by running an imidazole gradient from 40 mM to 250 mM in lysis buffer. Pure fractions were collected and concentrated. The buffer was later changed to 1 mM ammonium bicarbonate using an Amicon Ultra-15 Centrifugal Filter Device (Millopore, 10,000 MWCO cut). The purified proteins were analyzed by 15% SDS-PAGE. GFP_{UV} proteins incorporated with other NAAs were expressed and purified similarly except that the supplemented NAA was changed. For all NAAs, 1 mM final concentration was used.

Z domain proteins incorporated with different NAAs were expressed and purified in the same way as for GFP_{UV} proteins except that pET-pylT-Z was used to cotransform *E. coli* BL21(DE3) together with pBK-mKRS1.

8. Photolysis to Form the Monomethylated Protein

Z-7, **Z-8**, and **GFP-8** (1 mg/mL) in 1 mM ammonium bicarbonate buffer were treated with 365 nm UV light from a hand-held UV lamp for one hour.

9. Protein LC-ESI-MS Analysis

An Agilent (Santa Clara, CA) 1200 capillary HPLC system was interfaced to an API QSTAR Pulsar Hybrid QTOF mass spectrometer (Applied Biosystems/MDS Sciex, Framingham, MA) equipped with an electrospray ionization (ESI) source. Liquid chromatography (LC) separation was achieved using a Phenomenex Jupiter C4 microbore column (150×0.50 mm, 300 Å) (Torrance, CA) at a flow rate of 10 µL per min. The proteins were eluted using a gradient of (A) 0.1% formic acid versus (B) 0.1% formic acid in acetonitrile. The gradient timetable was as follows: 2% B for 5 min, 2-30% in 3 min, 30-60% in 44 min, 60-95% in 8 min, followed by holding the gradient at 95% for 5 min, for a total run time of 65 min. The MS data were acquired in positive ion mode (500-1800 Da) using spray voltage of +5000 V. BioAnalyst software (Applied Biosystems) was used for spectral deconvolution. For the GFPuv protein analysis, a mass range of m/z 500-1800 was used for deconvolution and the output range was 10000-50000 Da using a step mass of 0.1 Da and a S/N threshold of 20. For the Z-Domain protein analysis, a mass range of m/z 500-2000 was used for deconvolution and the output range was 5000-15000 Da for Z-domain-His6X using a step mass of 0.1 Da and a S/N threshold of 20.

10. References

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11. Supplementary Tables, Schemes, and Figures

Position	305	306	309	346	348	477	Remark ¹
WT	L	Y	L	N	С	W	
mKRS1 ²	L	М	А	Ν	Т	W	5, 7, 6, 8
mKRS2	L	V	А	Ν	А	W	5, 7, 6
mKRS3 ³	L	М	А	Ν	С	W	5, 7, 6, 8
mKRS4	L	А	А	Н	L	W	5, 6
mKRS5	L	М	Р	Ν	С	W	5, 6, 7, 8
mKRS6	L	М	А	Ν	S	W	5
mKRS7	L	Y	А	Ν	А	W	5
mKRS8 ⁴	L	М	Т	Ν	А	W	5
mKRS9	L	А	А	Ν	А	W	5
mKRS10	L	А	L	Ν	А	W	5, 7
mKRS11 ⁵	L	А	L	Ν	С	W	5, 7

Supplementary Table 1. Evolved PylRS variants that charge pylT with different NAAs.

¹ This column represents the NAAs that can be taken by the mutant PylRS variants. The order of compounds also indicates decreasing encoding efficiency based on the screening results.

 2 The mutant was found seven times out of 22 sequenced mutants and has an extra mutation T364K.

³ The mutant was found six times out of 22 sequenced mutants.

⁴The mutant has extra mutation P297S.

⁵ The mutant was found twice out of 22 sequenced mutants.



Supplementary Scheme 3. The selection scheme to identify PylRS variants specific for a noncanonical amino acid.



Supplementary Fig. 1. Mass determination of Protein Z-5 (A) ESI-MS spectrum of Z-5 (B) The deconvoluted ESI-MS spectrum of Z-5.



Supplementary Fig. 2. Mass determination of Protein Z-6 (A) ESI-MS spectrum of Z-6 (B) The deconvoluted ESI-MS spectrum of Z-6.



Supplementary Fig. 3. Mass determination of Protein Z-7 (A) ESI-MS spectrum of Z-7 (B) The deconvoluted ESI-MS spectrum of Z-7.



Supplementary Fig. 4. Mass determination of Protein **Z-8** (A) ESI-MS spectrum of **Z-8** (B) The deconvoluted ESI-MS spectrum of **Z-8**.



Supplementary Fig. 5. Mass determination of Protein GFP-8 (A) ESI-MS spectrum of GFP-8 (B) The deconvoluted ESI-MS spectrum of GFP-8.



Supplementary Fig. 6. Mass determination of Protein **GFP-8** after photolysis. (A) ESI-MS spectrum of **GFP-8** (B) The deconvoluted ESI-MS spectrum of **GFP-8**.



Supplementary Fig. 7. Growth of 96 single colonies from the final third positive selection of 5 on LB plates with different supplements: (A) 68 µg/mL Cm, 25 µg/mL Kan and 12 µg/mL Tet; (B) 102 µg/mL Cm, 25 µg/mL Kan and 12 µg/mL Tet; (C) 1 mM 5, 102 µg/mL Cm, 25 µg/mL Kan and 12 µg/mL Tet; (D) 1 mM 6, 102 µg/mL Cm, 25 µg/mL Kan and 12 µg/mL Tet; (E) 1 mM 7, 102 µg/mL Cm, 25 µg/mL Kan and 12 µg/mL Tet; (F) 1 mM 8, 102 µg/mL Cm, 25 µg/mL Kan and 12 µg/mL Tet. The pY+ plasmid has a GFP_{UV} gene under control of a T7 promoter. Its expression is promoted by the suppression of two amber mutations at positions 1 and 107 of a T7 RNA polymerase gene in pREP. The fluorescent intensity of the expressed full-length GFP_{UV} roughly represents the suppression efficiency at amber codons.









































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