



HAL
open science

Traceless Staudinger Ligation to Access Stable Aminoacyl- or Peptidyl-Dinucleotide

Camélia Kitoun, Saidbakhrom Saidjalolov, Delphine Bouquet, Fabiola Djago,
Quentin Blancart Remaury, Bruno Sargueil, Pauline Poinot, Mélanie
Etheve-Quelquejeu, Laura Iannazzo

► **To cite this version:**

Camélia Kitoun, Saidbakhrom Saidjalolov, Delphine Bouquet, Fabiola Djago, Quentin Blancart Remaury, et al.. Traceless Staudinger Ligation to Access Stable Aminoacyl- or Peptidyl-Dinucleotide. ACS Omega, 2023, 8 (4), pp.3850-3860. 10.1021/acsomega.2c06135 . hal-04294940

HAL Id: hal-04294940

<https://hal.science/hal-04294940v1>

Submitted on 20 Nov 2023

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Traceless Staudinger Ligation to Access Stable Aminoacyl- or Peptidyl-Dinucleotide

Camélia Kitoun, Saidbakhrom Saidjalolov, Delphine Bouquet, Fabiola Djago, Quentin Blancart Remaury, Bruno Sargueil, Pauline Pointot, Mélanie Etheve-Quellejeu,* and Laura Iannazzo*



Cite This: <https://doi.org/10.1021/acsomega.2c06135>



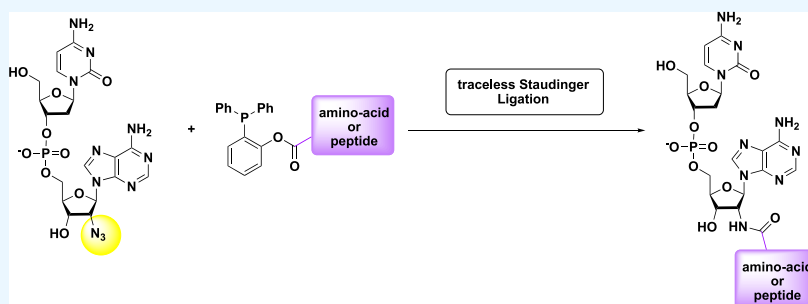
Read Online

ACCESS |

Metrics & More

Article Recommendations

Supporting Information



ABSTRACT: Aminoacyl- and peptidyl-tRNA are specific biomolecules involved in many biological processes, from ribosomal protein synthesis to the synthesis of peptidoglycan precursors. Here, we report a post-synthetic approach based on traceless Staudinger ligation for the synthesis of a stable amide bond to access aminoacyl- or peptidyl-di-nucleotide. A series of amino-acid and peptide ester phenyl phosphines were synthesized, and their reactivity was studied on a 2'-N₃ di-nucleotide. The corresponding 2'-amide di-nucleotides were obtained and characterized by LC-HRMS, and mechanistic interpretations of the influence of the amino acid phenyl ester phosphine were proposed. We also demonstrated that enzymatic 5'-OH phosphorylation is compatible with the acylated di-nucleotide, allowing the possibility to access stable aminoacylated-tRNA.

INTRODUCTION

Amino acyl- and peptidyl-tRNAs are natural or synthetic¹ biomolecules composed of an RNA part covalently linked to an amino acid or a peptide. The most well-known natural RNAs containing an amino acid residue are the aminoacyl-tRNAs (aa-tRNA), in which the amino acid is connected at a 3'- or 2'-position of the terminal ribose by an ester link (Figure 1). Aa-tRNAs are used in ribosomal protein synthesis but also in non-ribosomal peptide synthesis (NRPS). This NRPS includes the synthesis of peptidoglycan precursors² or tetrapyrrole,³ modification of bacterial membrane lipids,⁴ and N-terminal labeling of proteins targeted for proteolysis.⁵ Aminoacyl-tRNAs also participate in secondary metabolism,⁶ including the synthesis of cyclic dipeptides⁷ and natural antibiotics.⁸

The exploration of the role of aminoacyl-tRNA in biological processes requires stable molecules. Stable aa-tRNA analogues have been first designed by replacing the terminal ribose by a deoxy-ribose to avoid the isomerization of the amino acid moiety between the 2'- and 3'-hydroxyl of the ribose. The replacement of the ester bond by a stable function such as a triazole ring,⁹ an oxadiazole,¹⁰ or an amide bond¹¹ could also be used to stabilize the link between the amino acid and the RNA (Figure 1). These stable analogues have been efficiently used to obtain crystallographic structures of complexes between aa-tRNA analogues and the enzyme¹² or to decipher

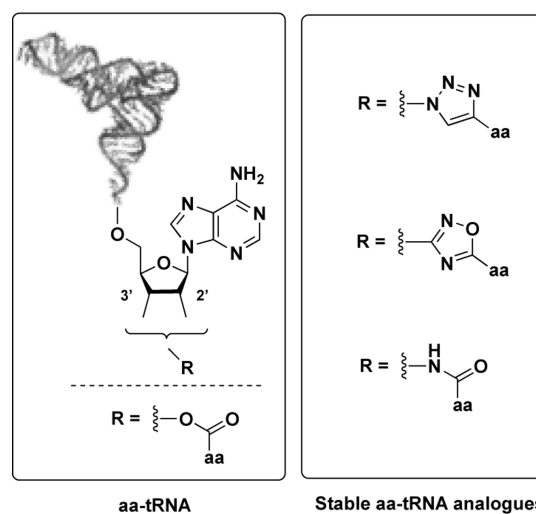
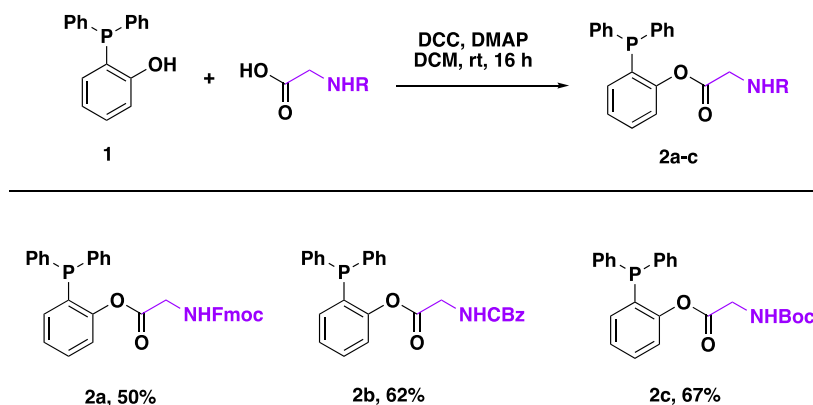


Figure 1. Structure of aa-tRNA and stable analogues.

Received: September 22, 2022

Accepted: October 26, 2022

Scheme 1. Synthesis of *N*-Protected Glycine Phosphines

the specificity or regioselectivity of the transfer of the amino acid.¹³

For the synthesis of aminoacyl-RNA analogues containing an amide bond, two approaches have been used: (i) the pre-synthetic approach, which involves the formation of the amide bond on the nucleoside and then its incorporation into the RNA by solid phase synthesis or enzymatic ligation, or (ii) the post-synthetic approach, which involves the post-functionalization of an amino-RNA. The first approach was performed using standard peptide coupling^{11,14} or Staudinger–Vilarrasa reaction¹⁵ to link activated amino acids to amino- or azido-deoxyadenosine, respectively. This method requires relatively large amounts of modified nucleotide monomers obtained by multi-step syntheses. The second approach has been described in a single report, in which the direct coupling of an activated amino acid to an 18 nt 3'-amino-RNA has been efficiently used only for formyl-methionine.^{11b} The challenge in the post-synthetic strategy is to find a chemoselective reaction, allowing site-specific acylation starting from a non-protected RNA, which contains several other nucleophilic groups. Here we propose to use the chemoselective traceless Staudinger ligation¹⁶ in the presence of amino acids or peptide phosphines for the post-functionalization of an azido-di-nucleotide, which is a known precursor for the synthesis of aa-tRNA.^{10,17}

The use of amino acids in the traceless variant of the Staudinger ligation has been first introduced for the synthesis of peptides in the presence of phosphinothiol by the work of Raines.¹⁸ Thanks to this Staudinger peptide ligation (SPL) approach, two peptides have been efficiently ligated from glycine-azido derivatives.¹⁹ The ligation with non-glycinic amino-acid turns out to be more complex since an aza-Wittig by-product could be observed. To overcome this issue, an effort has been made to design a novel phosphinothiol in which the phenyl groups have been substituted by an *O*-methoxy group at the *para* position.²⁰ Long²¹ and cyclic²² peptides were also synthesized by classical traceless Staudinger ligation using phosphino-ester or, more recently, with 2-(diphenylphosphanyl)phenyl)methane.²³ The group of Bernardi²⁴ applied such a methodology for the synthesis of amide-substituted glycosyl derivatives, while Guo and co-workers described the preparation of glycan-peptide conjugates.²⁵ Interestingly, all these examples mainly report the use of phosphines substituted with protected amino acids or peptides, and no study has ever depicted the reactivity of ester phenyl phosphine carrying unprotected amino acids for traceless Staudinger ligation, which could be useful in a post-synthetic strategy.

RESULTS AND DISCUSSION

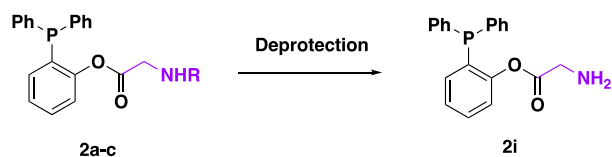
To explore the traceless Staudinger ligation to access aminoacyl- or peptidyl-RNA analogues, the dCpA-2'-N₃ dinucleotide **4** containing an azido group at the 2' position of the terminal adenosine was used. This dinucleotide has already been used in many studies to mimic the terminal CA motif present in all tRNAs, and the 2'-deoxy-cytidine does not impair the functionality of aa-tRNA.¹⁰ The development of post-functionalization reaction conditions went through the preparation of phosphines substituted with an amino acid or a peptide as a second partner for the ligation step. The reactivity of phosphines was investigated, and a mechanistic interpretation was proposed to rationalize the experimental results.

We first started our investigation with the synthesis of NH₂-protected amino acid phenyl ester phosphines with different protecting groups. For this purpose, the commercially available 2-hydroxyphenyl diphenylphosphine **1** was esterified in the presence of protected glycine, DCC, and DMAP in DCM at room temperature for 16 h. Glycine was selected as the model amino acid for our study. This reaction allowed the formation of three glycine phenyl ester phosphines **2a-c** containing a variety of protecting groups including Fmoc, benzyloxycarbonyl (CBz), and Boc in 50, 62, and 67% yields, respectively (Scheme 1).

The phosphines **2a-c** were then submitted to classical deprotection conditions. Under basic conditions (Scheme 2, entry 1), the degradation of the reaction mixture was observed, which led to the oxidation of phosphine and the cleavage of the ester linkage. Compound **2b** was treated with a catalytic amount of Pd/C under hydrogen pressure, and degradation of only the starting material was observed (Scheme 2, entry 2). The synthesis of the NH₂-free glycine phenyl ester phosphine was finally obtained starting from compound **2c** treated with a 15% solution of TFA in DCM at room temperature for 2 h. Compound **2i** was then obtained in 86% yield as a trifluoroacetate salt (Scheme 2, entry 3). This study shows that the best option to protect the amine to synthesize amino acid-phosphine phenol ester is the *tert*-butoxycarbonyl (Boc).

To expand the scope of NH₂-unprotected amino-acid phosphine, a range of five amino-acids and peptides were selected. *N*-Boc-protected phosphines were obtained by coupling an alanine, a valine, and a phenylalanine in the presence of compound **1** using DCC and DMAP according to the route previously described for the synthesis of glycine phenyl ester phosphine (Scheme 1). The desired amino-acid phosphine esters **2d**, **2e**, and **2f** were isolated in 85, 96, and

Scheme 2. Optimization of Deprotection Conditions



Entry	Phosphine	Conditions	2i
1	2a	Piperidine 20% DMF, 16h, rt	Degradation
2	2b	H_2 , Pd/C THF, 16 h, rt	Degradation
3	2c	TFA 15% DCM, 2 h, rt	86% ^a

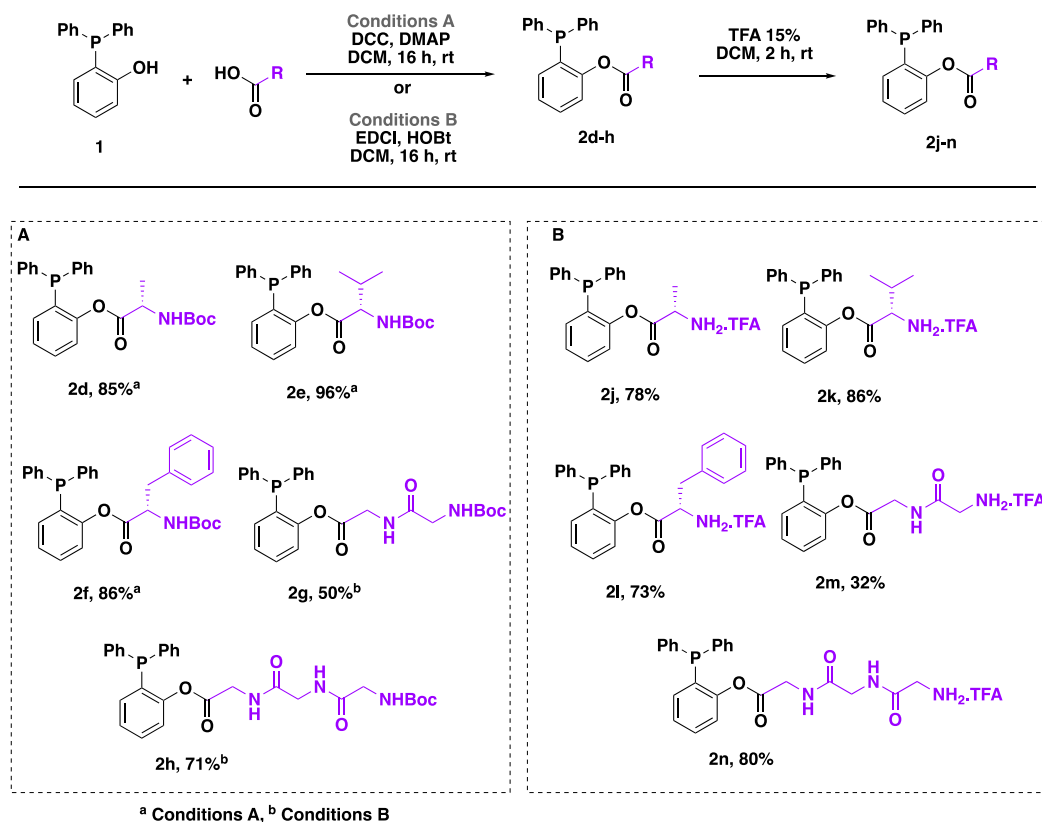
^a compound **2i** isolated in a trifluoroacetate salt.

86% yields, respectively (Scheme 3A). Di- and tri-peptides were also engaged in a coupling reaction in the presence of the phenol phosphine **1**, with EDCI and HOBt as coupling reagents (Conditions B, Scheme 3). The corresponding phosphines **2g** and **2h** with a di-glycine and tri-glycine peptide were obtained in 50 and 71% yields, respectively (Scheme 3A). The deprotection conditions using a solution of 15% TFA in DCM were then applied, and five unprotected amino-acid or peptide phenyl ester phosphines **2j-n** were isolated in 32 to 80% yields (Scheme 3B).

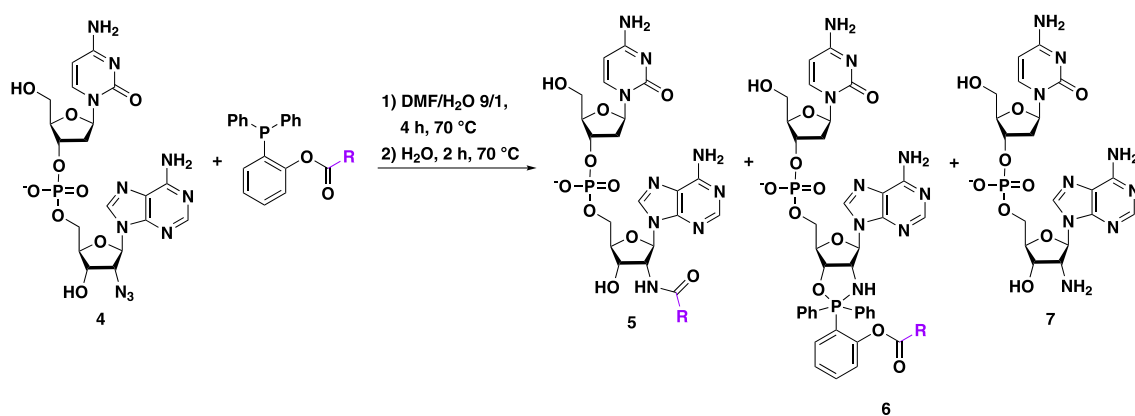
Among the series of previously synthesized phosphines, we next focused our attention on the reactivity of amino acid and peptide phosphines **2i**, **2j**, **2m**, and **2n** substituted with Gly and Ala groups. The reactions were carried out on 0.83 μmol of dinucleotide **4** and analyzed by LC-HRMS.

The dinucleotide substrate **4** was first treated in the presence of 10 equivalents of phosphine **2i** and heated for 4 h at 70 °C, followed by the addition of water and 2 h of stirring at 70 °C to get a full conversion. Under these conditions, the formation of the ligated compound **5i** was observed in 12% yield in competition with the reduced derivative **7** (Scheme 4, entry 1). Phosphine **2j** and **2k** lead to the same ratio in favor of the reduced dinucleotide **7** (Scheme 4, entries 2 and 3). When dipeptide **2m** is used, no compound from the traceless Staudinger ligation was detected by LC-HRMS, and the reduction of dinucleotide **4** afforded compound **7**. In addition, a cyclic oxazaphospholane derivative,²⁶ **6m**, was obtained in 28% yield (Scheme 4, entry 4). The formation of such a cyclic derivative could be explained by the 1,2-*cis* position²⁷ of the 2'-N₃ function and the 3'-OH hydroxyl of the ribose. In the presence of phosphine **2n** substituted with a glycine tripeptide, di-nucleotide **4** was converted into the expected ligated compound **2n** in 10% yield (Scheme 4, entry 5). The access to the amide function was in competition with the formation of the oxazaphospholane derivative **6n** observed in 47% yield and the reduction of the azide (compound **7**) observed in 37% yield.

Based on the modest yield of traceless Staudinger ligation obtained with unprotected amino acid or peptide phosphines, we next examined the reactivity of *N*-Boc-protected phosphine derivatives. Traceless Staudinger ligation was then applied to di-nucleotide **4** in the presence of protected phosphines **2c**, **2d**,

Scheme 3. Synthesis of Phosphine Phenol Esters Containing (A) *N*-Boc-Protected Amine and (B) Unprotected Amine

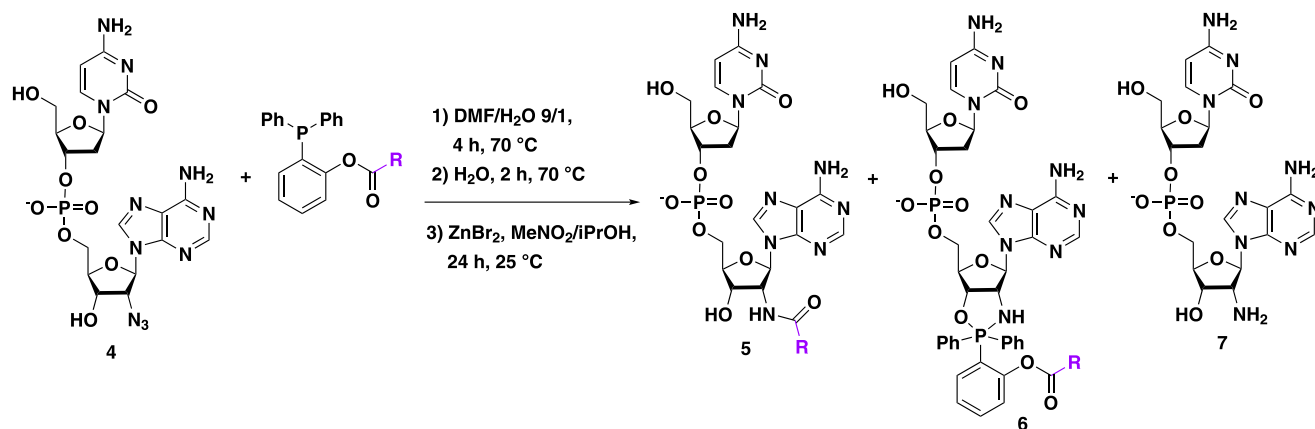
Scheme 4. Substrate Scope



Entry	Phosphine	5 ^a	6 ^a	7 ^a
1		5i: 12%	6i: -	88%
2		5j: 18%	6j: -	82%
3		5k: 4%	6k: 8%	88%
4		5m: -	6m: 28%	72%
5		5n: 10%	6n: 47%	37%
6		5c: 29%	6c: 63%	6%
7		5d: 35%	6d: 46%	19%
8		5g: 13%	6g: 83%	4%
9		5h: 21%	6h: 48%	31%

^a Product yield based on LC-HRMS data by relative quantification of dinucleotides.

Scheme 5. One-Pot Procedure



Entry	Phosphine	5 ^a	6 ^a	7 ^a
1		5i: 13%	6i: 4%	83%
2		5j: 30%	6j: -	70%

^a Product yield based on LC-HRMS data by relative quantification of dinucleotides.

2g, and **2h**. By contrast, the protection of the amino group allowed an increase in the yield of the formation of the amide bond up to 35% for compound **2d**. Although the reduced dinucleotide **7** was observed in the reaction mixture, the yield drastically decreased with protected phosphines (4 to 31% vs 37 to 88%). The formation of the oxazaphospholane derivatives was also detected with different yields (between 46 and 83% yields), depending on the phosphine.

These experimental results indicate that the use of *N*-Boc-protected phenyl ester phosphines impacts the yield of the reaction in favor of the amide derivative. We then reinvestigated our strategy and developed a three-step procedure to ligate a protected amino acid or peptide-phosphine by traceless Staudinger ligation (Scheme 5). After the ligation step of dCpA-2'-N₃ di-nucleotide **4** in the presence of phosphines **2c** and **2d** at 70 °C for 4 h, followed by an additional 2 h of stirring at 70 °C in water, the crude mixture was treated with ZnBr₂ salts²⁸ for 24 h in a mixture of isopropanol and nitromethane. These conditions enabled the formation of the amide derivatives **5i** and **5j** in 13 and 30% yields, starting with phosphine **2c** and **2d**. This three-step procedure allows higher ligation yields than the use of unprotected amino acid or peptide phosphines.

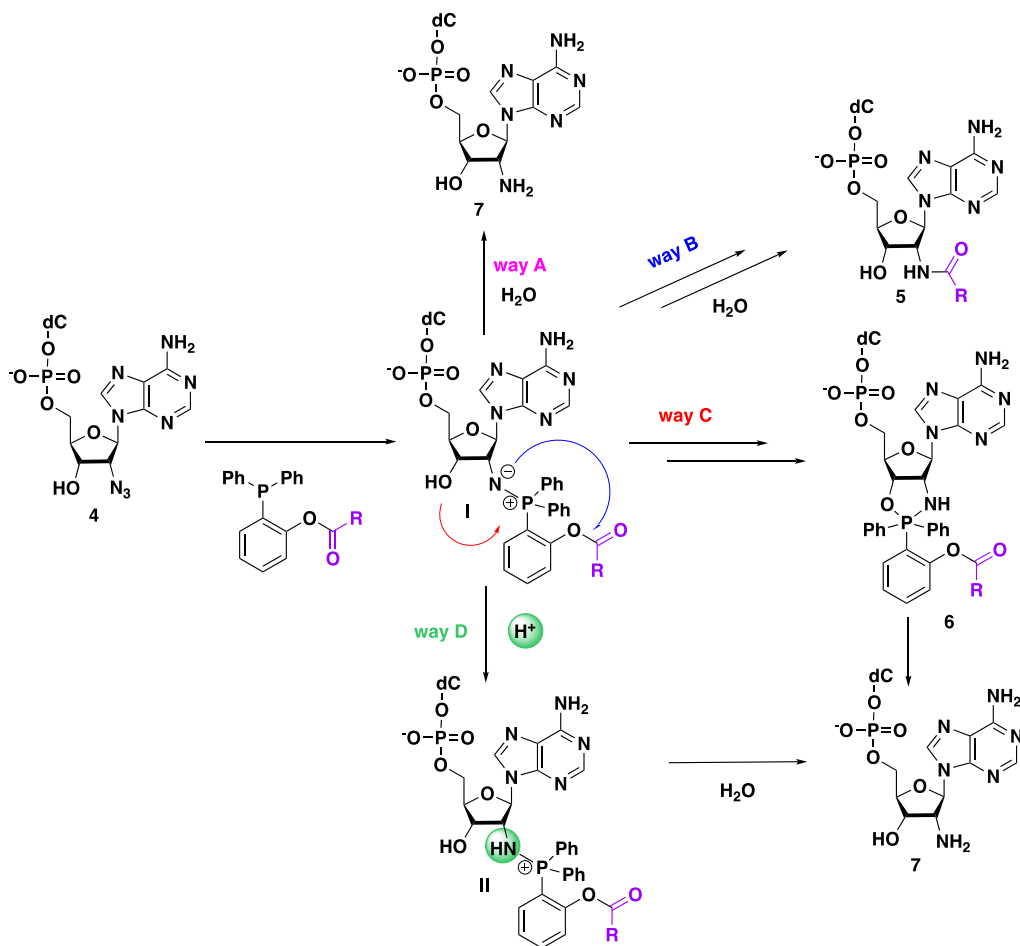
The results observed in this study show that the substituent on the amino group of the amino-acid or peptide linked to the ester phenyl phosphine has a strong impact on the ligation through a traceless Staudinger pathway. When the amino-acid is deprotected, the reduction of azide **4** is favored. In contrast, the yield increased in favor of the desired ligated derivative with *N*-Boc-protected phosphines, but an important amount of

cyclic oxazaphospholane could be observed. To rationalize these results, a putative mechanism is proposed in Scheme 6.

After the formation of the iminophosphorane intermediate **I**, Staudinger reduction could lead directly to the formation of the reduced di-nucleotide **7** (way A). In a previous study,²⁶ we have demonstrated that the reaction occurred in competition with the acyl transfer from the phosphine to the nitrogen on the iminophosphorane through a six-membered ring formed during the transition state (way B) and the formation of the cyclic oxazaphospholane derivative promoted by the vicinal *cis* configuration of the nitrogen of the iminophosphorane and the hydroxyl at the 3' position (way C). In the presence of *N*-Boc-protected phosphine, the nucleophilic attack of nitrogen on electrophilic carbonyl could be disadvantageous due to the steric hindrance of the Boc group and lead to the formation of compound **6**. With NH₂-free amino acid or peptide phenyl ester phosphines, it offers an additional source of proton (coming from the TFA salt) that could easily protonate the nitrogen at the 3'-position, reported as a strong base,²⁹ affording intermediate **II**. Then, the hydrolysis with water could provide reduced compound **7**.

The crude mixture obtained after traceless Staudinger ligation with phosphine **2j** was then submitted to enzymatic 5'-phosphorylation using bacteriophage T4 polynucleotide kinase to yield dinucleotide **8** in 24% yield (Scheme 7). This was confirmed by LC-HRMS analyses (see Supporting Information S37-38). An additional enzymatic ligation step, starting from **8**, could provide a series of stable aa-tRNAs since T4 RNA ligase is known to efficiently catalyze the ligation of the 3'-OH terminus of an RNA with a 5'-phosphorylated dinucleotide.^{11a}

Scheme 6. Proposed Mechanism



CONCLUSIONS

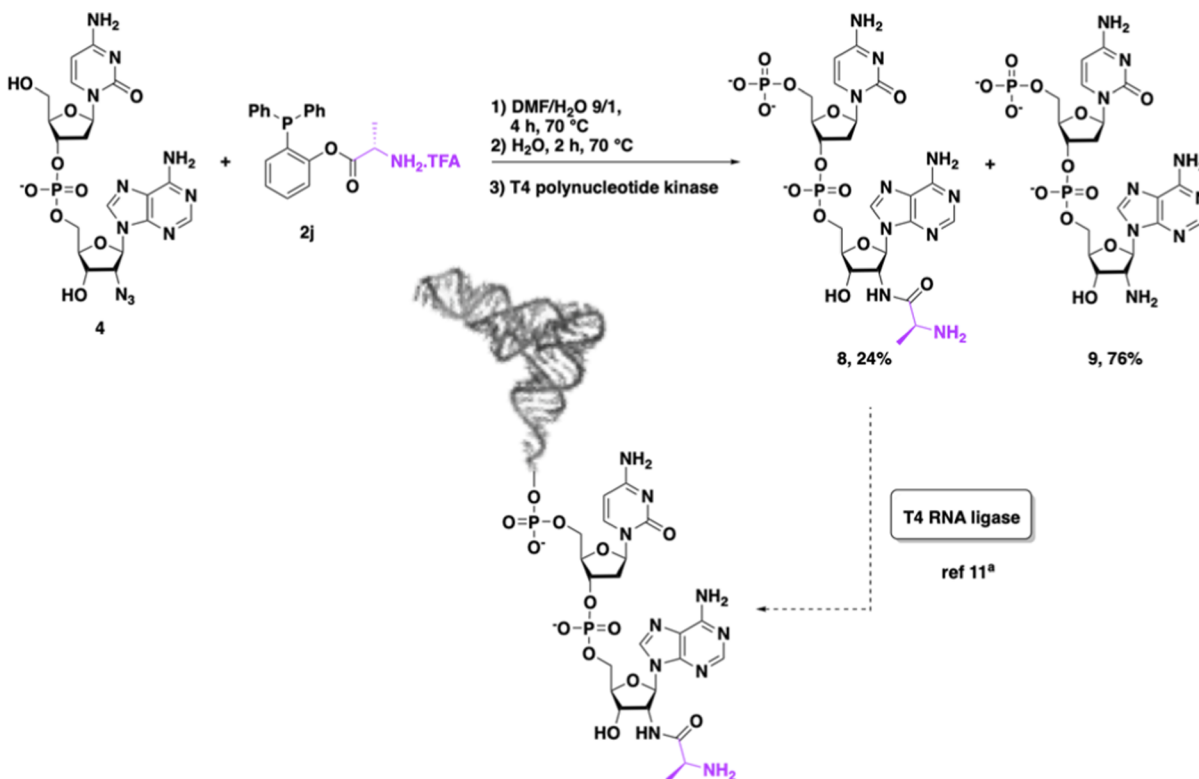
In conclusion, we have reported the first application of traceless Staudinger ligation to functionalize, in a post-synthetic approach, di-nucleotides with amino-acid or peptide phosphines. We synthesized a series of ester phosphines containing various amino acids or peptides. Boc was used as the protecting group for the amine since the deprotection step to remove other groups led to the degradation of the phosphine ester. Traceless Staudinger ligation was performed on a 2'-azido di-nucleotide in the presence of the protected and unprotected Gly and Ala phosphines. The use of unprotected phosphine ester provided the direct formation of the amino acid dinucleotide, although with moderate yields (12 and 18% yield). Inversely, the use of the protected amino phosphine ester allows us to obtain a better yield in favor of the amino acid dinucleotide (29 and 35%). We then perform a one-pot three-step procedure in the presence of *N*-BocAla and NBocGly phosphines to form two desired amino acylated dinucleotides in 13 and 30% yields.

The post-synthetic traceless Staudinger ligation reported here is a versatile method allowing us to obtain a variety of stable amino acyl-tRNAs from a single acylated di-nucleotide. Of note, our synthetic route could also be of interest for studying RNAs containing non-canonical bases modified with amino acids.³⁰ Indeed, it has recently been suggested that such modifications of RNA could be living molecular fossils, and the group of T. Carell synthesized amino-acyl RNAs to support the idea of a molecular RNA-peptide world.³¹

EXPERIMENTAL SECTION

General Information. Reactions were carried out under an argon atmosphere and performed using freshly distilled solvents. THF was dried over sodium/benzophenone; DCM, DMF, and MeOH were dried over calcium hydride. Di-nucleotide 4 was synthesized according to the procedure previously reported by our group.²⁶ (2-Hydroxyphenyl) diphenylphosphine was purchased from Merck. The progress of the reactions was monitored by thin layer chromatography (TLC). TLC: precoated silica gel thin layer sheets 60 F₂₅₄(Merck) and detection by charring with 10% H₂SO₄ in ethanol or phosphomolybdic acid in ethanol, followed by heating. Flash chromatography was carried out over silica gel (60 Å, 180–240 mesh) from Merck. Preparative HPLC was performed using a HPLC system with a reverse phase C-18 NUCLEOSIL column (250 mm × 21.2 mm, 5 μm) using a solvent system consisting of A: 50 mM aqueous NH₄OAc pH 4.5 and B: MeCN (linear gradient from 0% B to 63% B in 30 min) at a flow rate of 15 mL/min and UV detection at 254 nm. NMR spectra were recorded on Bruker spectrometers (Avance II 500 and Avance III HD 4000). Chemical shifts (δ) are reported in parts per million (ppm) and referenced to the residual proton or carbon resonance of the solvents: CDCl₃ (δ 7.26), D₂O (δ 4.79), DMSO (δ 2.50), CD₃OD (δ 3.31) or D₂O (δ 4.79) for ¹H and CDCl₃ (δ 77.16) or (CD₃)₂SO (δ 39.52), or CD₃OD (δ 49.00) for ¹³C. Signals were assigned using 1D (¹H and ¹³C) and 2D (HSQC, COSY, and HMBC) experiments. NMR coupling constants (*J*) are reported in

Scheme 7. Access to Stable Aa-tRNA by Enzymatic Phosphorylation and Ligation



Hertz (Hz), and splitting patterns are indicated as follows: s (singlet), bs (broad singlet), d (doublet), t (triplet), q (quartet), dd (doublet of doublet), and m (multiplet).

LC/HRMS Conditions: Conditions A. HPLC analysis was performed on a Hypersil GOLD aQ (ThermoFisher Scientific) column (100 mm × 2.1 mm, 1.9 μm) using a solvent system consisting of A: H₂O with 0.02% AcOH and B: MeCN with 0.02% AcOH (linear gradient from 0 to 100% B in 30 min) at a flow rate of 0.2 mL/min at 30 °C and UV detection at 254 nm. Fractions detected using low-resolution mass spectra (HRMS) were obtained on a LC QTOF mass spectrometer.

Conditions B: LC-HRMS analyses were performed on a Q Exactive mass spectrometer (Thermo Fisher Scientific), equipped with an electrospray ionization source (H-ESI II probe) coupled with an Accela 1250 Pump (Thermo Fisher Scientific). Samples were injected onto a Thermo Fisher Hypersil GOLD aQ chromatography column (100 mm × 2.1 mm, 1.9 μm particle size). The flow rate was set at 0.3 mL/min, and the mobile phase consisted of water containing 0.02% acetic acid (solvent A) and acetonitrile containing 0.02% acetic acid (solvent B). The gradient program was as follows: 0 to 5 min, 2% B; 5 to 20 min, up to 70% B; 20 to 30 min, came back to 98% B and 2 min of equilibration. The column temperature was maintained at 30 °C, and the temperature of the autosampler was set at 4 °C. MS analyses were performed in a full scan negative ion mode with a scan range from 200 to 1500 *m/z*.

General Procedure 1 for the Preparation of Phosphine 2a-f: Conditions A. To a solution of (2-hydroxyphenyl)diphenylphosphine (1 equiv) in DCM were successively added DCC (3 equiv), DMAP (4 equiv), and a *N*-protected amino acid (3 equiv). The mixture was stirred overnight at room temperature, then filtered through a pad of Celite, and concentrated under reduced pressure. The crude

product was purified by flash chromatography using cyclohexane/EtOAc as an eluent to afford the desired phosphine.

General Procedure 2 for the Preparation of Phosphine 2g-h: Conditions B. To a solution of *N*-Boc di- or tri-peptide (1 equiv) in DCM were successively added EDCI (2 equiv) and HOBT (2 equiv). The mixture was stirred for 30 min at room temperature, and (2-hydroxyphenyl) diphenylphosphine (2 equiv) was added at 0 °C. The reaction mixture was then stirred at room temperature for 16 h. DCM and brine were added, and the organic phase was washed three times with brine. The organic layer was dried over MgSO₄, filtered, and concentrated. The residue was purified by silica gel chromatography using cyclohexane/EtOAc as the eluent to afford the desired phosphine.

Compound (2a). Following general procedure 1 for the preparation of amino acid-phosphine, compound 2a was obtained (150 mg, 50%) as a white foam after purification by flash chromatography using cyclohexane/EtOAc (7/3) as the eluent, starting from (2-hydroxyphenyl) diphenylphosphine (150 mg, 0.54 mmol) and *N*-Fmoc-Gly (480 mg, 1.62 mmol) in DCM (5 mL). ¹H NMR (500 MHz, CDCl₃): δ = 7.70 (d, *J* = 7.5 Hz, 2 H, H^{Ar}), 7.53 (d, *J* = 7.3 Hz, 2 H, H^{Ar}), 7.34 (d, *J* = 7.3 Hz, 2 H, H^{Ar}), 7.28–7.24 (m, 13 H, H^{Ar}), 7.11–7.08 (m, 2 H, H^{Ar}), 6.83–6.80 (m, 1 H, H_{Ar}), 4.99 (br s, 1 H, NH), 4.34 (d, *J* = 7.0 Hz, 2 H, CH₂^{Fmoc}), 4.18–4.15 (m, 1 H, CH^{Fmoc}), 3.85–3.84 (m, 2 H, CH₂^{Gly}). ¹³C NMR (126 MHz, CDCl₃): δ = 168.1 (C=O), 156.1 (C=O), 152.4, 143.9, 141.4, 135.4, 134.2, 134.0, 130.4, 130.2, 129.3, 128.8, 127.8, 127.2, 126.7, 125.2, 122.5, 120.1, 67.3 (CH₂^{Fmoc}), 47.3 (CH^{Fmoc}), 42.8 (CH₂^{Gly}). ³¹P NMR (202 MHz, CDCl₃): δ = -15.7. HRMS (ESI) *m/z*: [M + H]⁺ calcd for C₃₅H₂₉NO₄P 558.18342; found, 558.18175.

Compound (2b). Following general procedure 1 for the preparation of amino acid-phosphine, compound 2b was

obtained (157 mg, 62%) as a white foam, after purification by flash chromatography using cyclohexane/EtOAc (8/2) as the eluent, starting from (2-hydroxyphenyl) diphenylphosphine (150 mg, 0.54 mmol) and *N*-Cbz-Gly (338 mg, 1.62 mmol) in DCM (10 mL). ^1H NMR (500 MHz, CDCl_3): δ = 7.28–7.23 (m, 16 H, 5 H^{ArCbz} , 12 H H^{ArPhos}), 7.08–7.05 (m, 2 H, H^{ArPhos}), 6.78–6.76 (m, 1 H, H^{ArPhos}), 5.02 (s, 2 H, CH_2^{Cbz}), 3.80–3.79 (m, 2 H, CH_2^{Gly}). ^{13}C NMR (126 MHz, CDCl_3): δ = 168.1 (C=O), 156.2 (C=O), 152.3, 136.3, 135.4, 135.3, 134.1 (2C), 133.9 (2C), 130.5, 130.3, 130.2, 129.3 (2C), 128.8 (2C), 128.7 (2C), 128.6 (2C), 128.5, 128.3, 128.2, 126.7, 122.5, 67.21 (CH_2^{Cbz}), 42.71 (CH_2^{Gly}). ^{31}P NMR (202 MHz, CDCl_3): δ = –15.8. HRMS (ESI) m/z : $[\text{M} + \text{H}]^+$ calcd for $\text{C}_{28}\text{H}_{25}\text{NO}_4\text{P}$ 470.15212; found, 470.15210.

Compound (2c). Following general procedure 1 for the preparation of amino acid-phosphine, compound **2c** was obtained (262 mg, 67%) as a white foam, after purification by flash chromatography using cyclohexane/EtOAc (8/2) as the eluent, starting from (2-hydroxyphenyl) diphenylphosphine (250 mg, 0.89 mmol) and *N*-Boc-Gly (472 mg, 2.67 mmol) in DCM (10 mL). ^1H NMR (500 MHz, CDCl_3): δ = 7.40–7.33 (m, 11 H, H^{Ar}), 7.20–7.16 (m, 2 H, H^{Ar}), 6.90–6.88 (m, 1 H, H^{Ar}), 4.70 (br s, 1 H, NH), 3.84 (d, J = 5.0 Hz, 2 H, CH_2^{Gly}), 1.49 (s, 9 H, $t\text{Bu}^{\text{Boc}}$). ^{13}C NMR (126 MHz, CDCl_3): δ = 168.5, 155.6, 152.3, 135.5, 134.1, 134.0, 133.7, 133.5, 130.5, 130.4, 130.2, 129.3, 129.2, 128.8, 128.7, 126.6, 122.6, 80.1 (Cq^{Boc}), 42.4 (CH_2^{Gly}), 28.4 ($t\text{Bu}^{\text{Boc}}$). ^{31}P NMR (202 MHz, CDCl_3): δ = –15.7. HRMS (ESI) m/z : $[\text{M} + \text{H}]^+$ calcd for $\text{C}_{25}\text{H}_{27}\text{NO}_4\text{P}$ 436.16777; found, 436.16634.

Compound (2d). Following general procedure 1 for the preparation of amino acid-phosphine, compound **2d** was obtained (276 mg, 85%) as a white foam, after purification by flash chromatography using cyclohexane/EtOAc (8/2) as the eluent, starting from (2-hydroxyphenyl) diphenylphosphine (200 mg, 0.7 mmol) and *N*-Boc-Ala (407 mg, 2.1 mmol) in DCM (10 mL). ^1H NMR (500 MHz, CDCl_3): δ = 7.28–7.17 (m, 11 H, H^{Ar}), 7.09–7.06 (m, 1 H, H^{Ar}), 7.02 (t, J = 7.5 Hz, 1 H, H^{Ar}), 6.71–6.69 (m, 1 H, H^{Ar}), 4.82 (br s, 1 H, NH), 4.26 (br s, 1 H, $\text{H}\alpha$), 1.35 (s, 9 H, $t\text{Bu}^{\text{Boc}}$), 1.16 (d, J = 5 Hz, 3 H, CH_3^{Ala}). ^{13}C NMR (126 MHz, CDCl_3): δ = 171.2, 152.6, 135.4, 134.0, 133.8, 133.5, 133.3, 131.9, 132.5, 130.0, 129.9, 129.1, 128.9, 128.6, 126.4, 122.2, 121.0, 116.1, 79.8 (Cq^{Boc}), 49.5 ($\text{CH}\alpha$), 28.3 ($t\text{Bu}^{\text{Boc}}$), 18.1 (CH_3^{Ala}). ^{31}P NMR (202 MHz, CDCl_3): δ = –16.8. HRMS (ESI) m/z : $[\text{M}]^+$ calcd for $\text{C}_{26}\text{H}_{28}\text{NO}_4\text{P}$ 449.1555; found, 449.1744.

Compound (2e). Following general procedure 1 for the preparation of amino acid-phosphine, compound **2e** was obtained (329 mg, 96%) as a white foam, after purification by flash chromatography using cyclohexane/EtOAc (9/1) as the eluent, starting from (2-hydroxyphenyl) diphenylphosphine (200 mg, 0.7 mmol) and *N*-Boc-Val (390 mg, 2.1 mmol) in DCM (10 mL). ^1H NMR (500 MHz, CDCl_3): δ = 7.39–7.32 (m, 7 H, H^{Ar}), 7.31–7.37 (m, 4 H, H^{Ar}), 7.19–7.17 (m, 1 H, H^{Ar}), 7.14 (t, J = 10 Hz, 1 H, H^{Ar}), 6.83–6.81 (m, 1 H, H^{Ar}), 4.88 (d, J = 10 Hz, 1 H, NH), 4.29–4.27 (m, 1 H, $\text{H}\alpha$), 4.18–4.16 (m, 1 H, $\text{H}\beta$), 1.46 (s, 9 H, $t\text{Bu}^{\text{Boc}}$), 0.94 (d, J = 5 Hz, 3 H, CH_3^{Val}), 0.82 (d, J = 5 Hz, 3 H, CH_3^{Val}). ^{13}C NMR (126 MHz, CDCl_3): δ = 170.4, 155.8, 153.1, 152.9, 135.9, 135.8, 135.7, 134.2, 134.1, 134.0, 130.3, 130.2, 129.3, 129.2, 128.9, 128.8, 126.5, 122.3, 79.8 (Cq^{Boc}), 58.8 ($\text{C}\alpha$), 31.1 ($\text{C}\beta$), 28.5 ($t\text{Bu}^{\text{Boc}}$), 19.4 (CH_3^{Val}), 17.3 (CH_3^{Val}). ^{31}P NMR (202 MHz, CDCl_3): δ = –17.2. HRMS (ESI) m/z : $[\text{M}]^+$ calcd for $\text{C}_{28}\text{H}_{32}\text{NO}_4\text{P}$ 477.2069; found, 477.2057.

Compound (2f). Following general procedure 1 for the preparation of amino acid-phosphine, compound **2f** was obtained (324 mg, 86%) as a white foam, after purification by flash chromatography using cyclohexane/EtOAc (9/1) as the eluent, starting from (2-hydroxyphenyl) diphenylphosphine (200 mg, 0.7 mmol) and *N*-Boc-Phe (551 mg, 2.1 mmol) in DCM (10 mL). ^1H NMR (500 MHz, CDCl_3): δ = 7.41–7.31 (m, 11 H, H^{Ar}), 7.30–7.26 (m, 2 H, H^{Ar}), 7.24–7.20 (m, 1 H, H^{Ar}), 7.15–7.12 (m, 4 H, H^{Ar}), 6.84–6.81 (m, 1 H, H^{Ar}), 4.78 (br s, 1 H, NH), 4.52 (br s, 1 H, $\text{H}\alpha$), 3.14–3.10 (m, 1 H, $\text{CH}_2\beta$), 2.80–2.76 (m, 1 H, $\text{CH}_2\beta$), 1.39 (s, 9 H, $t\text{Bu}^{\text{Boc}}$). ^{13}C NMR (126 MHz, CDCl_3): δ = 169.8, 155.1, 152.7, 136.6, 135.5, 134.2, 134.0, 133.9, 133.6, 133.4, 130.1, 129.6, 129.2, 129.1, 128.8, 128.6, 127.0, 126.5, 122.2, 121.7, 116.2, 80.0 (Cq^{Boc}), 54.7 ($\text{CH}\alpha$), 31.9 (CH_2^{Phe}), 28.4 ($t\text{Bu}^{\text{Boc}}$). ^{31}P NMR (202 MHz, CDCl_3): δ = –16.6. HRMS (ESI) m/z : $[\text{M}]^+$ calcd for $\text{C}_{32}\text{H}_{32}\text{NO}_4\text{P}$ 525.2069; found, 525.2051.

Compound (2g). Following general procedure 2 for the preparation of amino acid-phosphine, compound **2g** was obtained (260 mg, 50%) as a white foam, after purification by flash chromatography using cyclohexane/EtOAc (6/4) as the eluent, starting from (2-hydroxyphenyl) diphenylphosphine (300 mg, 1.0 mmol), EDCI (412 mg, 2.0 mmol), HOBT (290 mg, 2.0 mmol), and *N*-Boc-GlyGly (505 mg, 2.0 mmol) in DCM (10 mL). ^1H NMR (500 MHz, CDCl_3): δ = 7.36–7.11 (m, 13 H, H^{Ar}), 6.80–6.74 (m, 1 H, H^{Ar}), 3.91–3.87 (m, 2 H, CH_2), 3.71–3.67 (m, 2 H, CH_2), 1.40 (s, 9 H, $t\text{Bu}^{\text{Boc}}$). ^{13}C NMR (126 MHz, CDCl_3): δ = 171.5 (C=O), 1697.9 (C=O), 159.2, 156.9 (C=O), 152.8, 136.7, 135.5, 134.4, 133.6, 133.5, 133.4, 133.3, 129.9, 129.8, 128.8, 128.3, 128.2, 127.9, 126.1, 122.2, 119.4, 114.2, 79.3 (Cq^{Boc}), 40.4 (CH_2), 40.3 (CH_2), 27.2 (2 $t\text{Bu}^{\text{Boc}}$), 24.6 ($t\text{Bu}^{\text{Boc}}$). ^{31}P NMR (202 MHz, CDCl_3): δ = –19.4. HRMS (ESI) m/z : $[\text{M} + \text{H}]^+$ calcd for $\text{C}_{27}\text{H}_{30}\text{N}_2\text{O}_5\text{P}$ 493.18923; found, 493.18743.

Compound (2h). Following general procedure 2 for the preparation of amino acid-phosphine, compound **2h** was obtained (140 mg, 71%) as a white foam, after purification by flash chromatography using cyclohexane/EtOAc (3/7) as the eluent, starting from (2-hydroxyphenyl) diphenylphosphine (100 mg, 0.36 mmol), EDCI (138 mg, 0.72 mmol), HOBT (97 mg, 0.72 mmol), and *N*-Boc-GlyGlyGly (208 mg, 0.72 mmol) in DCM (10 mL). ^1H NMR (500 MHz, MeOD): δ = 7.36–7.27 (m, 7 H, H^{Ar}), 7.24–7.21 (m, 4 H, H^{Ar}), 7.14–7.11 (m, 2 H, H^{Ar}), 6.81–6.79 (m, 1 H, H^{Ar}), 3.89 (s, 2 H, CH_2^{Gly}), 3.86 (s, 2 H, CH_2^{Gly}), 3.71 (s, 2 H, CH_2^{Gly}), 1.41 (s, 9 H, $t\text{Bu}^{\text{Boc}}$). ^{13}C NMR (126 MHz, MeOD): δ = 173.0, 122.0, 169.3, 158.3, 155.6, 138.2, 136.9, 136.8, 134.9, 134.7, 134.5, 131.7, 131.6, 131.4, 131.1, 130.2, 129.8, 129.7, 129.6, 129.4, 129.3, 127.5, 123.6, 120.8, 115.9, 80.9 (Cq^{Boc}), 43.1 (CH_2^{Gly}), 41.8 (CH_2^{Gly}), 41.7 (CH_2^{Gly}), 28.7 ($t\text{Bu}^{\text{Boc}}$). ^{31}P NMR (202 MHz, MeOD): δ = –17.2. HRMS (ESI) m/z : $[\text{M} + \text{H}]^+$ calcd for $\text{C}_{29}\text{H}_{33}\text{N}_3\text{O}_6\text{P}$ 550.21070; found, 550.20908.

General Procedure 3 for the Deprotection of the Boc-Protecting Group. *N*-Boc amino acid/peptide-phosphine (1 equiv) was suspended in a 2 M TFA solution (11 equiv) in DCM, and the reaction was stirred for 2 h at room temperature. The reaction mixture was concentrated under reduced pressure, and the residue was purified by flash chromatography (DCM/MeOH 9/1) to yield the corresponding TFA salt.

Compound (2i). Following general procedure 3 for the deprotection of *N*-Boc amino acid-phosphine, compound **2i** was obtained (49 mg, 86%) as a white foam, after the removal

of TFA by co-evaporation (3 × toluene, 3 × DCM), starting from compound **2c** (55 mg, 0.12 mmol) and TFA (0.69 mL, 1.38 mmol). ¹H NMR (500 MHz, MeOD): δ = 7.49–7.46 (m, 1 H, H^{Ar}), 7.39–7.38 (m, 6 H, H^{Ar}), 7.30–7.24 (m, 6 H, H^{Ar}), 6.91–6.89 (m, 1 H, H^{Ar}), 3.82 (s, 2 H, CH₂^{Gly}). ¹³C NMR (126 MHz, MeOD): δ = 167.2, 153.7, 136.7, 135.3, 134.9, 134.7, 132.8, 131.6, 130.4, 130.1, 129.8, 129.6, 128.2, 123.3, 40.9 (CH₂^{Gly}). ³¹P NMR (202 MHz, MeOD): δ = –17.6. ¹⁹F NMR (471 MHz, MeOD): δ = –76.9. HRMS (ESI) *m/z*: [M + H]⁺ calcd for C₂₀H₁₉NO₂P 336.11479; found, 336.11480.

Compound (2j). Following general procedure 3 for the deprotection of *N*-Boc amino acid-phosphine, compound **2j** was obtained (212 mg, 78%) as a white foam, after purification by flash chromatography using DCM/MeOH (9/1) as the eluent, starting from compound **2d** (262 mg, 0.58 mmol) and TFA (3.2 mL, 6.38 mmol). ¹H NMR (500 MHz, CDCl₃): δ = 7.27–7.20 (m, 7 H, H^{Ar}), 7.18–7.14 (m, 4 H, H^{Ar}), 7.06–7.01 (m, 2 H, H^{Ar}), 6.71–6.69 (m, 1 H, H^{Ar}), 3.89–3.82 (m, 1 H, H_α), 1.26 (d, *J* = 5 Hz, 3 H, CH₃^{Ala}). ¹³C NMR (126 MHz, CDCl₃): δ = 168.5, 152.1, 152.0, 135.1, 135.0, 134.9, 134.0, 133.9, 130.4, 130.0, 129.9, 129.4, 128.9, 128.8, 122.1, 49.3 (C_α), 15.3 (CH₃^{Ala}). ³¹P NMR (202 MHz, CDCl₃): δ = –17.1. ¹⁹F NMR (471 MHz, CDCl₃): δ = –75.8. HRMS (ESI) *m/z*: [M]⁺ calcd for C₂₁H₂₀NO₂P 349.1231; found 349.1230.

Compound (2k). Following general procedure 3 for the deprotection of *N*-Boc amino acid-phosphine, compound **2k** was obtained (239 mg, 86%) as a white foam, after purification by flash chromatography using DCM/MeOH (96/4) as the eluent, starting from compound **2e** (271 mg, 0.56 mmol) and TFA (3.1 mL, 6.16 mmol). ¹H NMR (500 MHz, CDCl₃): δ = 7.39–7.32 (m, 7 H, H^{Ar}), 7.29–7.22 (m, 5 H, H^{Ar}), 6.84–6.82 (m, 1 H, H^{Ar}), 3.86 (br s, 1 H, H_α), 2.30–2.27 (m, 1 H, H_β), 1.00 (d, *J* = 5 Hz, 3 H, CH₃^{Val}), 0.92 (d, *J* = 5 Hz, 3 H, CH₃^{Val}). ¹³C NMR (126 MHz, CDCl₃): δ = 167.8, 152.5, 152.4, 135.4, 135.3, 134.2, 134.1, 134.0, 133.9, 133.8, 130.4, 129.7, 129.3, 128.9, 127.0, 122.1, 58.7 (C_α), 29.4 (C_β), 16.9 (CH₃^{Val}). ³¹P NMR (202 MHz, CDCl₃): δ = –17.6. ¹⁹F NMR (471 MHz, CDCl₃): δ = –75.6. HRMS (ESI) *m/z*: [M]⁺ calcd for C₂₃H₂₄NO₂P 377.1545; found, 377.1544.

Compound (2l). Following general procedure 3 for the deprotection of *N*-Boc amino acid-phosphine, compound **2l** was obtained (170 mg, 73%) as a white foam, after purification by flash chromatography using DCM/MeOH (96/4) as the eluent, starting from compound **2f** (227 mg, 0.43 mmol) and TFA (2.37 mL, 4.73 mmol). ¹H NMR (500 MHz, CDCl₃): δ = 7.41–7.32 (m, 11 H, H^{Ar}), 7.31–7.24 (m, 3 H, H^{Ar}), 7.20–7.13 (m, 4 H, H^{Ar}), 6.85–6.83 (m, 1 H, H^{Ar}), 3.73–3.71 (m, 1 H, H_α), 3.11 (dd, *J* = 5, 10 Hz, 1 H, H_β), 2.83–2.78 (m, 1 H, H_β). ¹³C NMR (126 MHz, CDCl₃): δ = 171.0, 159.2, 152.4, 136.0, 135.3, 134.6, 134.4, 134.0, 133.9, 133.6, 133.5, 131.5, 130.2, 129.6, 129.3, 129.0, 128.9, 128.8, 128.7, 127.3, 126.6, 122.2, 121.3, 121.0, 115.6, 55.4 (C_α), 38.6 (C_β). ³¹P NMR (202 MHz, CDCl₃): δ = –17.1. ¹⁹F NMR (471 MHz, CDCl₃): δ = –75.5. HRMS (ESI) *m/z*: [M]⁺ calcd for C₂₇H₂₄NO₂P 425.1544; found, 425.1551.

Compound (2m). Following general procedure 3 for the deprotection of *N*-Boc peptide-phosphine, compound **2m** was obtained (20 mg, 32%) as a white foam, after purification by HPLC starting from compound **2g** (60 mg, 0.12 mmol) and TFA (0.7 mL, 1.32 mmol). ¹H NMR (500 MHz, CDCl₃): δ = 7.27–7.15 (m, 11 H, H^{Ar}), 7.01–6.96 (m, 2 H, H^{Ar}), 6.74–6.71 (m, 1 H, H^{Ar}), 3.74 (m, 2 H, CH₂), 3.6 (s, 2 H, CH₂). ¹³C NMR (126 MHz, CDCl₃): δ = 168.2 (C=O), 167.0 (C=O),

152.4, 135.4, 135.3, 134.1, 133.9, 132.2, 132.1, 130.3, 130.4, 129.3 (2C), 128.9 (2C), 128.8 (2C), 126.7, 122.6, 41.2 (CH₂^{Gly}), 41.6 (CH₂^{Gly}). ³¹P NMR (202 MHz, CDCl₃): δ = –16.2. HRMS (ESI) *m/z*: [M + H]⁺ calcd for C₂₂H₂₂N₂O₃P 393.13626; found, 393.13669.

Compound (2n). Following general procedure 3 for the deprotection of *N*-Boc peptide-phosphine, compound **2n** was obtained (45 mg, 80%) as a white foam, after purification by HPLC, starting from compound **2h** (60 mg, 0.1 mmol) and TFA (0.55 mL, 1.1 mmol). ¹H NMR (500 MHz, MeOD): δ = 7.44–7.16 (m, 13 H, H^{Ar}), 6.89–6.84 (m, 1 H, H^{Ar}), 3.96 (d, *J* = 5.25, 2 H; CH₂), 3.74 (s, 2 H, CH₂), 3.26 (s, 2H, CH₂). ¹³C NMR (126 MHz, MeOD): δ = 171.6 (C=O), 169.4 (C=O), 168 (C=O), 154, 136.9, 136.8, 135.0 (2C), 134.8 (2C), 131.8, 131.7, 131.3, 130.3 (2C), 129.8 (2C), 129.7 (2C), 127.6, 129.6, 42.9 (CH₂^{Gly}), 41.9 (CH₂^{Gly}), 41.5 (CH₂^{Gly}). ³¹P NMR (202 MHz, MeOD): δ = –17.1. HRMS (ESI) *m/z*: [M + H]⁺ calcd for C₂₄H₂₅N₃O₄P 450.15772; found, 450.15811.

General Procedure 4 for Traceless Staudinger Ligation with Di-nucleotide 4. To a solution of di-nucleotide **4** (0.83 μmol, 1 equiv) in an Eppendorf tube in DMF/H₂O (9/1, 1 mL) was added phosphine (10 equiv), and the mixture was stirred for 4 h at 70 °C in a thermo-shaker plate. Then, an excess of water (3 mL) was added, and the mixture was stirred for 2 h at 70 °C. After lyophilization, the residue was analyzed by LC/HRMS.

General Procedure 5 for Traceless Staudinger Ligation with Di-nucleotide 4 with *N*-Boc-Protected Amino Acid Phosphine. To a solution of di-nucleotide **4** (0.5 mg, 0.83 μmol) in an Eppendorf tube in DMF/H₂O (9/1, 1 mL) was added phosphine **2c** (3.7 mg, 8.3 μmol) or **2d** (3.8 mg, 8.3 μmol), and the mixture was stirred for 4 h at 70 °C in a thermo-shaker plate. Then, an excess of water (3 mL) was added, and the mixture was stirred for 2 h at 70 °C. After lyophilization, the residue was dissolved in a 5 M solution of ZnBr₂ in a 1/1 (v/v) mixture of iPrOH/MeNO₂ (69 μL, 344 μmol), and the reaction mixture was stirred at room temperature for 24 h. Water was added, and the mixture was lyophilized and analyzed by UPLC-HRMS.

General Procedure 6 for Traceless Staudinger Ligation and Enzymatic Phosphorylation. To a solution of dinucleotide **4** (1 mg, 1.67 μmol) in DMF/H₂O (9/1, 1 mL) in an Eppendorf tube was added phosphine (7 mg, 16.7 μmol), and the mixture was stirred for 4 h at 70 °C in a thermo-shaker plate (Grant Bio). Then, an excess of water (3 mL) was added, and the mixture was stirred for 2 h at 70 °C. After lyophilization, the residue was resuspended in 770 μL of water. The phosphorylation reaction was then carried out in a 1 mL reaction containing 70 mM Tris–HCl pH7.6, 10 mM MgCl₂, 5 mM DTT, 5 mM ATP, and 200 μL of T4 polynucleotide kinase (New England Biolabs ref #M0201L) for 3 h at 37 °C. T4 PNK was then inactivated for 20 min at 65 °C. The crude mixture was then analyzed by LC-HRMS.

■ ASSOCIATED CONTENT

Supporting Information

The Supporting Information is available free of charge at <https://pubs.acs.org/doi/10.1021/acsomega.2c06135>.

LC/HRMS analysis for compound **5c–d**, **5g–k**, **5m–n**, **6c–d**, **6g–h**, **6m–n**, **7**, **8**, and ⁹NMR spectra for compounds **2a–n** FAIR data, including the primary NMR FID files (PDF)

AUTHOR INFORMATION

Corresponding Authors

Mélanie Etheve-Quelquejeu – Université Paris Cité, CNRS, Laboratoire de Chimie et Biochimie Pharmacologiques et Toxicologiques, Paris F-75006, France; orcid.org/0000-0002-4105-3243; Phone: (33) 1 76 53 42 50; Email: laura.iannazzo@u-paris.fr

Laura Iannazzo – Université Paris Cité, CNRS, Laboratoire de Chimie et Biochimie Pharmacologiques et Toxicologiques, Paris F-75006, France; orcid.org/0000-0002-2181-4885; Phone: (33) 1 76 53 42 22; Email: melanie.etheve-quelquejeu@u-paris.fr

Authors

Camélia Kitoun – Université Paris Cité, CNRS, Laboratoire de Chimie et Biochimie Pharmacologiques et Toxicologiques, Paris F-75006, France

Saidbakhrom Saidjalolov – Université Paris Cité, CNRS, Laboratoire de Chimie et Biochimie Pharmacologiques et Toxicologiques, Paris F-75006, France

Delphine Bouquet – Université Paris Cité, CNRS, Laboratoire de Chimie et Biochimie Pharmacologiques et Toxicologiques, Paris F-75006, France

Fabiola Djago – Institut de Chimie des Milieux et Matériaux de Poitiers IC2MP, Université de Poitiers, UMR 7285, Poitiers 86073, France

Quentin Blancart Remaury – Institut de Chimie des Milieux et Matériaux de Poitiers IC2MP, Université de Poitiers, UMR 7285, Poitiers 86073, France

Bruno Sargueil – Université Paris Cité, CNRS, UMR 8038/CiTCOM, Paris F-75006, France

Pauline Poinot – Institut de Chimie des Milieux et Matériaux de Poitiers IC2MP, Université de Poitiers, UMR 7285, Poitiers 86073, France; orcid.org/0000-0002-7927-1887

Complete contact information is available at:

<https://pubs.acs.org/10.1021/acsomega.2c06135>

Notes

The authors declare no competing financial interest.

ACKNOWLEDGMENTS

This research was funded by grants from the Agence National de la Recherche (ANR), Project SyntRNA [ANR-17-CE07-0041-02], Project Volatolomix [ANR-21-CE18-0009], and La Ligue contre le cancer.

REFERENCES

- (1) Klabenkova, K.; Fokina, A.; Stetsenko, D. Chemistry of peptide-oligonucleotide conjugates: a review. *Molecules* **2021**, *26*, 5420.
- (2) (a) Shepherd, J.; Ibba, M. Direction of aminoacylated transfer RNAs into antibiotic synthesis and peptidoglycan-mediated antibiotic resistance. *FEBS Lett.* **2013**, *587*, 2895–2904. (b) Fonvielle, M.; Chemama, M.; Villet, R.; Lecerf, M.; Bouhss, A.; Valéry, J. M.; Etheve-Quelquejeu, M.; Arthur, M. Aminoacyl-tRNA recognition by the FemX_{Wv} transferase for bacterial cell wall synthesis. *Nucleic Acids Res.* **2009**, *37*, 1589–1601.
- (3) Jahn, D.; Verkamp, E.; Söll, D. Glutamyl-transfer RNA: a precursor of heme and chlorophyll biosynthesis. *Trends Biochem. Sci.* **1992**, *17*, 215–218.
- (4) Roy, H.; Ibba, M. Broad range amino acid specificity of RNA-dependent lipid remodeling by multiple peptide resistance factors. *J. Biol. Chem.* **2009**, *284*, 29677–29683.

(5) Mogk, A.; Schmidt, R.; Bukau, B. The N-end rule pathway for regulated proteolysis: prokaryotic and eukaryotic strategies. *Trends Cell Biol.* **2007**, *17*, 165–172.

(6) (a) Katz, A.; Elgamal, S.; Rajkovic, A.; Ibba, M. Non-canonical roles of tRNAs and tRNA mimics in bacterial cell biology. *Mol. Microbiol.* **2016**, *101*, 545–558. (b) Moutiez, M.; Belin, P.; Gondry, M. Aminoacyl-tRNA-Utilizing Enzymes in Natural Product Biosynthesis. *Chem. Rev.* **2017**, *117*, 5578–5618.

(7) Gondry, M.; Sauguet, L.; Belin, P.; Thai, R.; Amouroux, R.; Teller, C.; Tuphile, K.; Jacquet, M.; Braud, S.; Courçon, M.; Masson, C.; Dubois, S.; Lautru, S.; Lecoq, A.; Hashimoto, S.-i.; Genet, R.; Pernodet, J.-L. Cyclodipeptide synthases are a family of tRNA-dependent peptide bond-forming enzymes. *Nat. Chem. Biol.* **2009**, *5*, 414–420.

(8) (a) Garg, R. P.; Qian, X. L.; Alemany, L. B.; Moran, S.; Parry, R. J. Investigation of valanimycin biosynthesis: elucidation of the role of seryl-tRNA. *Proc. Natl. Acad. Sci. U.S.A.* **2008**, *105*, 6543–6547.

(b) Zhang, W.; Ntai, I.; Kelleher, N. L.; Walsh, C. T. tRNA-dependent peptide bond formation by the transferase PacB in biosynthesis of the pacidamycin group of pentapeptidyl nucleoside antibiotics. *Proc. Natl. Acad. Sci. U.S.A.* **2011**, *108*, 12249–12253.

(c) Bougioukou, D. J.; Mukherjee, S.; van der Donk, W. A. Revisiting the biosynthesis of dehydrophos reveals a tRNA-dependent pathway. *Proc. Natl. Acad. Sci. U.S.A.* **2013**, *110*, 10952–10957. (d) Ortega, M. A.; Hao, Y.; Zhang, Q.; Walker, M. C.; van der Donk, W. A.; Nair, S. K. Structure and mechanism of the tRNA-dependent lantibiotic dehydratase NisB. *Nature* **2015**, *517*, 506–512.

(9) Chemama, M.; Fonvielle, M.; Arthur, M.; Valéry, J. M.; Etheve-Quelquejeu, M. Synthesis of stable aminoacyl-tRNA analogues containing triazole as a bioisoster of esters. *Chem. Eur. J.* **2009**, *15*, 1929–1938.

(10) Chemama, M.; Fonvielle, M.; Villet, R.; Arthur, M.; Valéry, J. M.; Etheve-Quelquejeu, M. Stable analogues of aminoacyl-tRNA for inhibition of an essential step of bacterial cell-wall synthesis. *J. Am. Chem. Soc.* **2007**, *129*, 12642–12643.

(11) (a) Mellal, D.; Fonvielle, M.; Santarem, M.; Chemama, M.; Schneider, Y.; Iannazzo, L.; Braud, E.; Arthur, M.; Etheve-Quelquejeu, M. Synthesis and biological evaluation of non-isomerizable analogues of Ala-tRNA^{Ala}. *Org. Biomol. Chem.* **2013**, *11*, 6161–6169. (b) Steger, J.; Graber, D.; Moroder, H.; Geiermann, A. S.; Aigner, M.; Micura, R. Efficient access to nonhydrolyzable initiator tRNA based on the synthesis of 3'-azido-3'-deoxyadenosine RNA. *Angew. Chem., Int. Ed.* **2010**, *49*, 7470–7472.

(12) Fonvielle, M.; Li de La Sierra-Gallay, I.; El-Sagheer, A.; Lecerf, M.; Patin, D.; Mellal, D.; Mayer, C.; Blanot, D.; Gale, N.; Brown, T.; van Tilbeurgh, H.; Etheve-Quelquejeu, M.; Arthur, M. The structure of FemX_{Wv} in complex with a peptidyl-RNA conjugate: mechanism of aminoacyl transfer from Ala-tRNA^{Ala} to peptidoglycan precursors. *Angew. Chem., Int. Ed.* **2013**, *52*, 7278–7281.

(13) Fonvielle, M.; Chemama, M.; Lecerf, M.; Villet, R.; Busca, P.; Bouhss, A.; Etheve-Quelquejeu, M.; Arthur, M. Decoding the logic of the tRNA regiospecificity of nonribosomal FemX_{Wv} aminoacyl transferase. *Angew. Chem., Int. Ed.* **2010**, *49*, 5115–5119.

(14) Terenzi, S.; Biala, E.; Nguyen-Trung, N. Q.; Strazewski, P. Amphiphilic 3'-peptidyl-RNA conjugates. *Angew. Chem. Int. Ed.* **2003**, *42*, 2909–2912.

(15) Moroder, H.; Steger, J.; Graber, D.; Fauster, K.; Trapp, K.; Trapp, V.; Marquez, N.; Polacek, D. N.; Wilson, R.; Micura, R. Non-hydrolyzable RNA-peptide conjugates: a powerful advance in the synthesis of mimics for 3'-peptidyl tRNA termini. *Angew. Chem., Int. Ed.* **2009**, *48*, 4056–4060.

(16) Saxon, E.; Armstrong, J. I.; Bertozzi, C. R. A "tracless" Stauffer ligation for the chemoselective synthesis of amide bonds. *Org. Lett.* **2000**, *2*, 2141–2143.

(17) (a) Robertson, S. A.; Noren, C. J.; Anthony-Cahill, S. J.; Griffith, M. C.; Schultz, P. G. The use of 5'-phospho-2-deoxyribocytidylriboadenosine as a facile route to chemical aminoacylation of tRNA. *Nucleic Acids Res.* **1989**, *17*, 9649–9660. (b) Fahmi, N. E.; Dedkova, L.; Wang, B.; Golovine, S.; Hecht, S.

M. Site-specific incorporation of glycosylated serine and tyrosine derivatives into proteins. *J. Am. Chem. Soc.* **2007**, *129*, 3586–3597.

(18) Nilsson, B. L.; Kiessling, L.; Raines, R. T. Staudinger ligation: a peptide from a thioester and azide. *Org. Lett.* **2000**, *2*, 1939–1941.

(19) Nilsson, B. L.; Kiessling, L.; Raines, R. T. High-yielding Staudinger ligation of a phosphinothioester and azide to form a peptide. *Org. Lett.* **2001**, *3*, 9–12.

(20) Tam, A.; Soellner, M. B.; Raines, R. T. Electronic and steric effects on the rate of the traceless Staudinger ligation. *Org. Biomol. Chem.* **2008**, *6*, 1173–1175.

(21) Nilsson, B. L.; Hondal, J. R.; Soellner, M. B.; Raines, R. T. Protein assembly by orthogonal chemical ligation methods. *J. Am. Chem. Soc.* **2003**, *125*, 5268–5269.

(22) David, O.; Meester, W. J. N.; Bieräugel, H.; Schoemaker, H. E.; Hiemstra, H.; van Maarseveen, J. H. Intramolecular Staudinger ligation: a powerful ring-closure method to form medium-sized lactams. *Angew. Chem., Int. Ed.* **2003**, *42*, 4373–4375.

(23) Bajaj, K.; Pillai, G. G.; Sakhuja, R.; Kumar, D. Expansion of phosphane treasure box for Staudinger peptide ligation. *J. Org. Chem.* **2020**, *85*, 12147–12159.

(24) (a) Bianchi, A.; Bernardi, A. Traceless Staudinger ligation of glycosyl azides with triaryl phosphines: stereoselective synthesis of glycosyl amides. *J. Org. Chem.* **2006**, *71*, 4565–4577. (b) Nisic, F.; Andreini, M.; Bernardi, A. Stereoselective synthesis of N-glycosyl amino acids by traceless Staudinger ligation of unprotected glycosyl azides. *Eur. J. Org. Chem.* **2009**, *2009*, 5744–5751.

(25) Zhu, S.; Guo, Z. Chemical synthesis of GPI glycan-peptide conjugates by traceless Staudinger ligation. *Org. Lett.* **2017**, *19*, 3063–3066.

(26) (a) Kitoun, C.; Fonvielle, M.; Sakkas, F.; Lefresne, N.; Djago, M.; Blancart Remaury, Q.; Poinot, P.; Arthur, M.; Etheve-Quelquejeu, M.; Iannazzo, L. Phosphine-mediated bioconjugation of the 3'-end of RNA. *Org. Lett.* **2020**, *22*, 8034–8038. (b) Kitoun, C.; Fonvielle, M.; Arthur, M.; Etheve-Quelquejeu, M.; Iannazzo, L. Traceless Staudinger ligation for bioconjugation of RNA. *Current Protocols in Nucleic Acid Chemistry* **2021**, *1*, No. e42.

(27) Nisic, F.; Speciale, G.; Bernardi, A. Stereoselective synthesis of α - and β -glycofuranosyl amides by traceless ligation of glycofuranosyl azides. *Chem. Eur. J.* **2012**, *18*, 6895–6906.

(28) (a) Kaul, K.; Brouillette, Y.; Sajjadi, Z.; Hansford, K. A.; Lubell, W. D. Selective *tert*-butyl ester deprotection in the presence of acid labile protecting groups with use of $ZnBr_2$. *J. Org. Chem.* **2004**, *69*, 6131–6133. (b) Ferreira, F.; Morvan, F. Silyl protecting groups for oligonucleotide synthesis removed by a $ZnBr_2$ treatment. *Nucleoside Nucleotides and Nucleic Acids* **2005**, *24*, 1009–1013.

(29) Núñez, M. G.; Farley, A. J.; Dixon, D. J. Bifunctional iminophosphorane organocatalysts for enantioselective synthesis: application to the ketimine nitro-Mannich reaction. *J. Am. Chem. Soc.* **2013**, *135*, 16348–16351.

(30) Nainytė, M.; Müller, F.; Ganazzoli, G.; Chan, C. Y.; Crisp, A.; Globisch, D.; Carell, T. Amino acid modified RNA bases as building blocks of an early earth RNA-peptide world. *Chem. Eur. J.* **2020**, *26*, 14856–14860.

(31) Müller, F.; Escobar, L.; Xu, F.; Węgrzyn, A.; Nainytė, M.; Amatov, T.; Chan, C. Y.; Pichler, A.; Carell, T. A prebiotically plausible scenario of an RNA-peptide world. *Nature* **2022**, *605*, 279–284.