



The First Nucleic Acid Strands May Have Grown on Peptides via Primeval Reverse Translation

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Abstract

The central dogma of molecular biology dictates that, with only a few exceptions, information proceeds from DNA to protein through an RNA intermediate. Examining the enigmatic steps from prebiotic to biological chemistry, we take another road suggesting that primordial peptides acted as template for the self-assembly of the first nucleic acids polymers. Arguing in favour of a sort of archaic “reverse translation” from proteins to RNA, our basic premise is a Hadean Earth where key biomolecules such as amino acids, polypeptides, purines, pyrimidines, nucleosides and nucleotides were available under different prebiotically plausible conditions, including meteorites delivery, shallow ponds and hydrothermal vents scenarios. Supporting a protein-first scenario alternative to the RNA world hypothesis, we propose the primeval occurrence of short two-dimensional peptides termed “selective amino acid- and nucleotide-matching oligopeptides” (henceforward SANMAOs) that non-covalently bind at the same time the polymerized amino acids and the single nucleotides dispersed in the prebiotic milieu. In this theoretical paper, we describe the chemical features of this hypothetical oligopeptide, its biological plausibility and its virtues from an evolutionary perspective. We provide a theoretical example of SANMAO’s selective pairing between amino acids and nucleosides, simulating a poly-Glycine peptide that acts as a template to build a purinic chain corresponding to the glycine’s extant triplet codon GGG. Further, we discuss how SANMAO might have endorsed the formation of low-fidelity RNA’s polymerized strains, well before the appearance of the accurate genetic material’s transmission ensured by the current translation apparatus.

Keywords Nucleoside triphosphates · Prebiotic chemistry · RNA world · Origin of life · Polypeptide

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1 Introduction

In a stable and unrestricted milieu, the minimum genetic requirement for a vital cell capable of autonomous growth counts no less than 300 genes to ensure at least cytosolic metabolism and genomic expression and preservation (Hutchison III et al. 2016; Thornburg et al. 2022). The huge structural and functional demands of extant living cells are difficult to reconcile with the enigmatic steps from inorganic to biological chemistry. In particular, the origin of the translation system is a chicken-and-egg conundrum: which came first, genes or proteins? (Wolf and Koonin 2007). An influential hypothesis put forward by Gilbert (1986) suggests that RNA was the first macromolecule in the prebiotic world, long before functional proteins and hence DNA (Kirschning 2021). The RNA-world hypothesis assumes that life on Earth started with self-recognizing and self-replicating RNA molecules, supposedly RNA ribozymes or prototypical ribonucleotide reductases (Fusz et al. 2005; Lundin et al. 2015; Schneider et al. 2018; Becker et al. 2019). Only later proteins became the catalysts of life, contributing to the genetic take-over of DNA as the information-storage molecule (Müller et al. 2022). Variant theories suggest the occurrence of pristine pre-RNA systems such as, e.g., a heterogeneous chimeric nucleic acid structure where purine deoxyribonucleosides, pyrimidine ribonucleosides and non-canonical bases may have coexisted in the same geochemical scenario (Schneider et al. 2018; Bhowmik and Krishnamurthy 2019; Xu et al. 2020). However, objections have been raised to the RNA world hypothesis, being RNA polymers' catalytic repertoire too small, chemically too homogeneous and constrained by low yield/slow turnover (Kirschning 2021).

Otherwise, the extant cooperation among peptides, small molecules, coenzymes and metal-based cofactors points towards primeval coevolution of different proto-metabolic biomolecules at a system level (Kroiss et al. 2019; Kirschning 2021). Also, it has been suggested a primordial peptide synthesis without ribosomes, evoking a primeval RNA-peptide world. Alternatively, there existed a stage prior to the RNA world termed the “polypeptide” or the “protein world” (Milner-White and James 2019), in which amino acids pairing was mandatory to allow peptide-to-peptide information transfer and ensuing synthesis of one protein sequence from another (Root-Bernstein 1982). The hypothesis is attractive, since amino acids and even peptides are easier to chemically synthesize from simple chemicals than nucleotides (Milner-White and James 2019). Further, as we will see in the sequel, simple amino acidic polymers display better binding and catalytic properties compared with RNA chains (Milner-White and James 2019).

Here we will tackle the chicken–egg problem regarding the duality between nucleic acids and proteins from a new peptidic perspective. Given the almost infinite possibilities of combinations among amino acids and nucleic acids in long timescales, it is likely that complex molecules equipped with biological activity spontaneously arose in ancient abiotic environments (Kitadai and Maruyama 2018). The real problem is not so much the spontaneous formation of complex biomolecules, but their preservation through duplication mechanisms and subsequent transmission to the next generation. The central dogma of molecular

biology states that information is transferred from DNA to protein through an RNA intermediate, apart from a few reverse transcriptases (Wolf and Koonin 2007; Chandramouly et al. 2021). Going against this dogma, we will describe the possibility that the first peptides were “retro-translated” to nucleic acid polymers. We will suggest the primeval occurrence of a short, amino acidic polymer termed “selective amino acid- and nucleotide-matching oligopeptide” (henceforward SANMAO). SANMAO was able to non-covalently bind the amino acids endowed in a peptidic chain and to selectively pair them with the single nucleosides scattered in the abiotic medium. We will describe the chemical features of this hypothetical oligopeptide, its biological plausibility and evolutionary virtues.

2 From Amino Acids to Nucleotides

The RNA world hypothesis suggests that the peptidic synthesis under prebiotic conditions was initiated by RNA molecules (Wolf and Koonin 2007). It has been proposed that non-canonical RNA bases established a rudimental and inaccurate peptide synthesis directly on RNA (Bhowmik and Krishnamurthy 2019), starting from covalently connected chimeric molecules made of peptide and RNA (Müller et al. 2022). Since the formation of peptide bonds via direct binding of amino acids to RNA templates (Yarus 1998) is stereochemically implausible, it is more likely that the primeval RNA acted as a template to synthesize aminoacylating ribozymes (Wochner et al. 2011; Torres de Farias and José 2020; Müller et al. 2022). Initially, RNA must have gained the ability to catalyze the synthesis of just small peptides (Müller et al. 2022). Translation might have started with ribozyme-catalyzed reactions involving abiogenic amino acids, followed by aspecific, non-templated synthesis of increasingly versatile peptides (Wolf and Koonin 2007). The specific amino acids recognition by proto-tRNAs might have depended just on the physical affinity between amino acids and their cognate codons/anticodons (Wolf and Koonin 2007). In the sequel, we will suggest another theory for the onset of peptide translation.

2.1 A Scenario for the Evolution of Translation: Towards a Proteic Beginning

We propose a peptide-first model in which oligopeptides capable of molecular recognition spontaneously appeared. Terminologically, we will consider oligopeptides as chains of aminoacids ≤ 20 residues, while polypeptides > 20 (Apostolopoulos et al. 2021). Here follows a list of the virtues of a peptide-first model:

1. Peptides' and proteins' polymers are easier to abiotically synthesize than nucleic acids' (Fusz et al. 2005).
2. Peptide bonds are more chemically stable than RNA bonds, the latter being more prone to hydrolysis (Schiller 2016).
3. The extant peptides and proteins have a wider breadth of chemical moieties for molecular recognition, displaying strong affinities for various types of small molecules.

4. Peptides and proteins have a much broader repertoire and efficiency as catalysts than RNAs and ribozymes. For example, the Ser-His and Gly-Gly oligopeptide can catalyze peptide bond formation (Schiller 2016), while the Pro-Pro dipeptide and the Pro-x-x-Phe tetrapeptide (x = any amino acid) display aldol condensation activity, i.e., the most significant carbon–carbon bond-forming reaction (Schiller 2016).
5. Proteins have a greater potential for the evolution of a variety of binding and catalytic capacities than RNA (Wolf and Koonin 2007).
6. Action of peptides as templates has been already demonstrated for self-replicating α -helix peptides (Schiller 2016).
7. It has been suggested that amino acids and peptides drove the evolution of translation through the intermediate stage of peptidic proto-ligases forming covalent bonds (Frenkel-Pinter et al. 2019).
8. Cationic side chains incorporated into proto-peptides possibly interacted with negatively charged RNA, catalyzing RNA oligomerization (Frenkel-Pinter et al. 2019).

In sum, several reasons plead for a versatile polypeptide world at the very origin of life. We will see in the sequel that the main problem is to understand how primeval peptides were able to produce their own copies. We suggest that, in a proteic world at the dawn of life, the issue of information transmission could be tackled through the production of nucleic acids' polymers from spontaneously generated peptidic templates. We require a sort of “reverse translation”, a primitive “protein-dependent RNA polymerase” which might provide some kind of chemical correspondence between amino acids and their extant cognate triplets (Wolf and Koonin 2007; Biro 2007).

2.2 Information Transmission from Amino Acids to Nucleotides?

We explore the possibility that some peptides were “retro-translated” into nucleic acid polymers by an oligopeptide, namely SANMAO, able to selectively pair the polymeric amino acids and the single nucleotides scattered in the abiotic medium. Once a specific series of nucleotides was brought near, covalent links were established, speeding up non-stochastic formation of biologically relevant RNA chains.

Our aim is to look for the likely chemical and biological attributes of SANMAO. It has been suggested that the first peptides were short, glycine-rich peptidic chains supplied with randomly alternating L/D racemic amino acids. Since short polypeptides flicker between structureless conformations rather than staying fixed in one, enantiomeric ring/chain structures devoid of tertiary structure were favored at the expense of helical conformations (Milner-White and Russell 2008). Like a few extant peptides that are metamorphic, i.e., quickly switch between different folds with different functions (Lella and Mahalakshmi 2017; Dishman et al. 2021), it is feasible that the early oligopeptides explored many different conformations and moved so quickly between different states that no fixed conformation was detectable (Milner-White and James 2019). The commonest primeval polypeptide conformation might

have been the nest, i.e., a biologically active 3–6 residue peptide (Milner-White and Russell 2008). For example, the synthetic hexapeptide Ser–Gly–Ala–Gly–Lys–Thr has been shown to bind phosphate, while other nests can either bind iron–sulfur centers for electrons storage/transfer, or form polymeric channels characterized by potassium-driven transmembrane potentials (Milner-White and James 2019).

SANMAO must be formed by the amino acids available on the Hadean Earth. If we hypothesize that the primordial soup might have contained ~10 natural amino acids and peptides <5 amino acids each, the possible SANMAO's sequence combinations amount to ~110,000 (Schiller 2016). To bring this number down, it should be noted that not all the possible amino acid pairs are available for bonding and higher affinities generate more persisting biomolecules (Root-Bernstein 1982; Biro 2007; Lella and Mahalakshmi 2017; Frenkel-Pinter et al. 2020). The most abundant amino acids are (and possibly were) the structurally versatile Gly and Ala (Trifonov 2004).

Peptide flexibility is guaranteed by the small, rotating Gly, rigidity is guaranteed by Ala, Tyr, Trp, Phe and conformation changes are guaranteed by His. The hydro-sulphuric bonds of Cys and Met confer resistance to denaturation, while Pro causes α - and β -chains disruption. The outer peptidic surfaces are rich of negative-charged Lys, Arg, His, while the inner surfaces are rich of hydrophobic amino acids. Occasionally, peptidic chains may exert opposite biological effects. To make an example, cationic poly(Leu-Lys) peptides favor mononucleotide diphosphates' oligomerization and increase the abundance of long RNA oligomers (Frenkel-Pinter et al. 2020), while (Leu-Lys) $_n$ or (Leu-Lys-Lys-Leu) $_n$ peptides exhibit RNA hydrolysis activities (Frenkel-Pinter et al. 2020).

Amino acids with complex side chains such as the aromatic and the cationic ones are thought to be late recruitments to the genetic code (Wolf and Koonin 2007). Despite long-range electrostatics generated by cationic amino acids (i.e., Arg, His, and Lys) plays at present a more dominant role than peptide conformation (Frenkel-Pinter et al. 2019), it must be stressed that the cationic amino acids were not abundant on the prebiotic Earth (Frenkel-Pinter et al. 2020). When coping with the primordial mediums, it must be also kept into account that different environments display different temperatures, pH and redox gradients (Holm et al. 2006; Baaske et al. 2007; Russell et al. 0; Fryer 2012; Postec et al. 2015; Lamadrid et al. 2017; Preiner et al. 2018; Cartwright and Russell 2019; Boyd et al. 2020; Russell and Ponce 2020). These variations deeply influence peptides formation, kinetics, folding and biological activity.

Our SANMAO's scenario requires a mechanism for the elongation of the nucleosides' growing chain similar to the extant mechanism for biological nucleic acids synthesis, where the 3' end of the incoming nucleotide forms a covalent phosphodiester with the 5' end of the previous nucleotide. In touch with our requirement, a plausible mechanism of ribose 3' OH orientation has been suggested which favors the formation of 5'–3', rather than the more probable 5'–2' linkage (Carter Jr and Kraut 1973).

The prebiotic peptide catalysis of phosphodiester, an issue that seems vital for the SANMAO hypothesis and may represent a link between prebiotic chemistry and the RNA world, has been investigated by Wieczorek et al. (2013). The authors used

the catalytic L-dipeptides Ser-His and Ala-His to achieve condensation of activated RNA monomers into short RNA chains, proceeding through an intermediate reaction in which dipeptides covalently bind to nucleotide monophosphates.

It is worth mentioning that SANMAO does not require polymerase, hydrolase and ligase activity. Indeed, nucleotides' polymers can spontaneously self-assemble even in abiotic environments, where the energy to form the phosphodiester bonds between the sugar base of one nucleotide and the phosphate group of the adjacent nucleotide is easily available. The biological task of SANMAO is not to create phosphodiester bonds, but rather to guarantee and expedite the possibility that two given nucleotides get closer to each other, increasing the chances of their spontaneous polymerization.

Now, we are finally ready, in the next section of the Results, to build a SANMAO and describe its interactions.

3 Results

Here we provide a simulation of an hypothetical oligopeptide supplied with the SANMAOs' required biochemical features. SANMAO must display two active zones: the first active zone selectively links a specific amino acid located in a template polypeptide, while the second active zone selectively links isolated purines or pyrimidines.

To give a proof-of-concept example, we substantiate the chemical steps from Gly to its extant corresponding codon, i.e., the triplet codon GGG. Our scenario meets specific requirements:

1. We need a peptide acting as a template for the synthesis of nucleic acids chains. For sake of simplicity, we will use a gly-gly dipeptide, the simplest to generate in every plausible primeval scenario.
2. Also, we need the spontaneous occurrence of a pool of different nucleotides dispersed in the primordial milieu, including at least a few guanosine monofosphate molecules.
3. Then, we need an oligopeptide (namely, SANMAO) able to link selectively via non-covalent interactions both the Gly and the Guanosyn monofosphate.

Among the countless feasible SANMAO conformations, we suggest a six-amino acids long oligopeptide capable of binding both Gly and Guanosyn monofosphate. Starting from the N-terminus, our SANMAO displays the following PQQQPG sequence:

Pro1-Gln2-Gly3-Gln4-Pro5-Gly6.

The hydrophilic Glu2/Gln4 and the hydrophobic Gly3/Gln6 are small, devoid of steric hindrance and provide SANMAO's conformation flexibility. Our SANMAO allows the following non-covalent interactions (Fig. 1):

- a. The acidic Glu2 and Glu4 bind the two carbonyl groups of the gly-gly dipeptide.

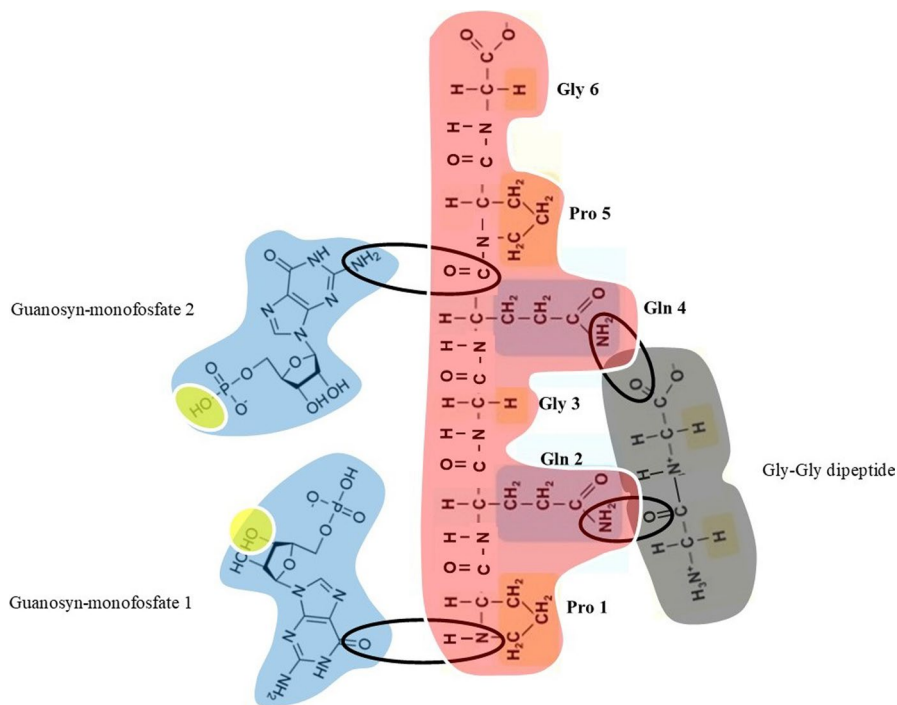


Fig. 1 Theoretical steps leading to the formation of Guanosyn polymers starting from a Gly-Gly dipeptide and an oligomer with PQQPG sequence. The Gly-Gly dipeptide (right) acts as a template for the polymerization of the purine corresponding to Gly, i.e., the guanosyn-monofosphate (left). The hollow circles depict the molecular surfaces linked by non-covalent bonds. The yellow circles depict the molecular surfaces where the covalent phosphodiester bonds will take place. For the sake of simplicity, the figure illustrates the formation of just two of the three guanosyns forming the triplet codon GGG. (Color figure online)

- b. The hydrophobic Pro1 and Gln2 bind the first molecule of guanosine monofosphate.
- c. The hydrophobic Pro5 and Gly6 bind the second molecule of guanosine monofosphate.

SANMAO attains proximity between the two molecules of guanosine monofosphate, thus expediting the formation of a covalent phosphodiester bond between the 5' end of the first guanosine monofosphate and the 3' end of the second guanosine monofosphate.

Checking for the biological plausibility of the PQQPG sequence, we ran UniProtKB for peptide search. The PQQPG sequence can be found in bacteria, fungi and eukaryotes such as *Acinetobacter baumannii* 99,063, *Streptomyces* sp. PRh5, *Oceanicoccus sagamiensis*, the fungal plant pathogen *Colletotrichum fioriniae* PJ7, the roundworm *Ancylostoma ceylanicum*, the African malaria mosquito *Anopheles gambiae*, the common eastern firefly *Photinus pyralis*, the Atlantic salmon *Salmo salar*, the European red deer *Cervus elaphus hippelaphus* and also Homo sapiens. In

humans and other mammals, the PQQQPG sequence can be detected in various collagen proteins. Also, the RCSB Protein Data Bank observed the PQQQPG sequence in the *Pseudomonas aeruginosa*'s minor pseudopilin XcpW, a type II secretion machinery carrying virulence factors into the extracellular space (Franz et al. 2011). The PQQQPG sequence, which deletion does not impair protein function, is located in a pseudolipin's unstructured proteic extremity that is relatively hydrophobic and intrinsically disordered.

Therefore, our theoretical SANMAO sequence is not just biologically plausible, but can also be currently found in different taxonomical domains and kingdoms.

Thanks to SANMAO, the extremities of the two nucleotides can be arranged in close proximity, thus facilitating spontaneous covalent bond formation. The transient interactions provided by SANMAO allow peptidic chains to act as templates to build increasingly longer chains of nucleic acids that roughly correspond to the amino acids of the template polypeptide. At this stage, it does not matter whether the nucleic acids chains are made either of RNA, DNA, uncanonical nucleosides or unconventional mixtures.

When nucleic acids are achieved from a prototype peptidic template, SANMAO allows the reverse operation too. The novel nucleic acid polymer may serve as template for building a copy of the prototype polypeptide. Figure 2 summarizes the complete theoretical sequence. In the primordial milieu containing biomolecules and polymers (Fig. 2A), different SANMAOs link specific amino acids placed inside a template peptide (Fig. 2B). Then, every SANMAO links the corresponding nucleotidic triplet, giving rise to a progressively longer nucleic acid polymer (Fig. 2C). Next, the nucleic acid polymer (Fig. 2D), through the same SANMAOs (Fig. 2E), uses the scattered amino acids available in the primordial milieu to produce a copy of the template peptide (Fig. 2F). Note that every SANMAO (say SANMAO 1) may also act as template peptide for another SANMAO (say SANMAO 2), the whole procedure leading to the duplication of the same SANMAO 1.

4 Conclusions

This paper provides a theoretical attempt to elucidate the primeval transmission of symbolic information between proteins and nucleic acids, outlining a theoretical model of "reverse translation" from short peptides to nucleic acid oligomers at the origin of life. For one polymer to faithfully transmit symbolic information to another polymer, even one built from the same composite parts, there has to be some kind of integral stoichiometric relationship between their strands. The Watson–Crick double helix solves this problem in a unique way, because the backbone structures of RNA and DNA have largely overlapping stable helix parameters. This problem has been quantitatively discussed by Carter Jr and Kraut (1973), who showed that extended polypeptide strands curve in such a way that their stable conformations include helix parameters matching those of double-stranded RNA if and only if the number of amino acids is exactly twice the number of nucleotide bases in the RNA. Such stoichiometric equivalence appears to be essential for the reproducible templating of one polymer by another. These data are in touch with our account. It might be

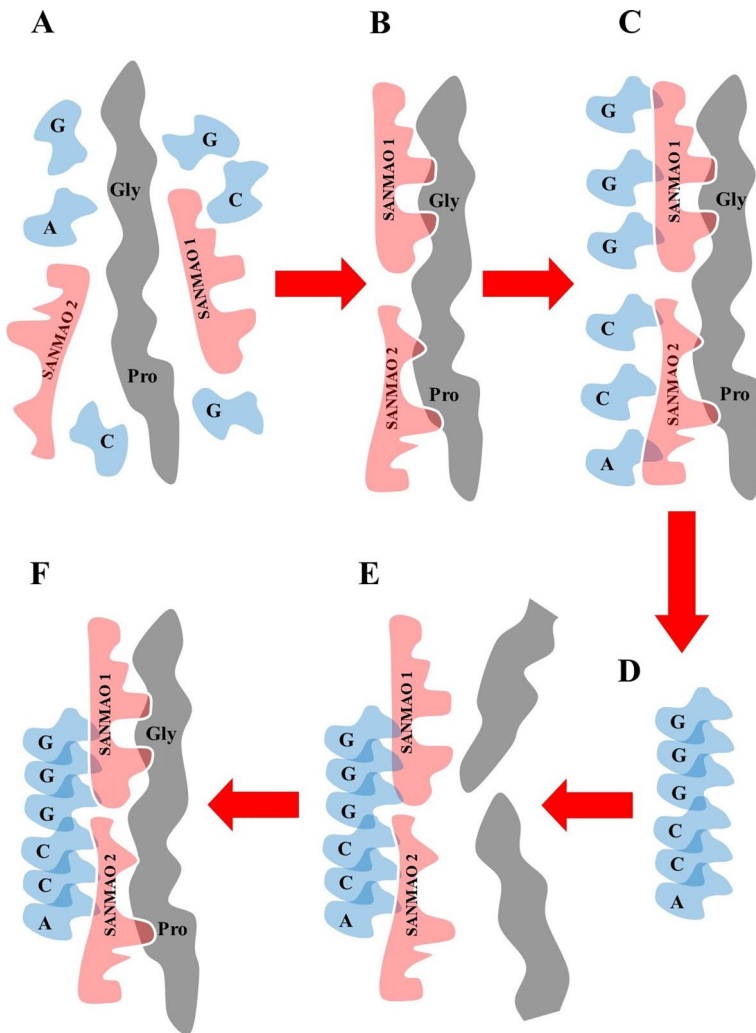


Fig. 2 Theoretical switching from template peptides to nucleic acid polymers and vice versa. The blue shapes stand for single nucleosides where *A* adenine, *C* cytosine and *G* guanine. A template polymer is depicted in grey and two of its amino acids (Gly and Pro) are highlighted. Two structurally different SANMAO molecules (red shapes) correlate distinct amino acids with specific nucleosides. For more details, see the main text. (Color figure online)

objected that the model presented in Figs. 1 and 2 is fanciful in two dimensions and that the authors would have to construct the corresponding models carefully in three dimensions in order to convey even a modicum of reality. However, the available data concerning the primeval medium point towards peptides lacking a three-dimensional structure (Milner-White and James 2019).

We suggest the random appearance on the Hadean Earth (about 4 billion years ago) of oligopeptides (SANMAOs) able to link both the amino acids and the

purines/pyrimidines scattered in the primeval abiotic medium. SANMAOs acted as a buffer between amino acids and nucleic acids, promoting a sort of “reverse translation” from peptidic templates to nucleotidic polymers.

Three fundamental premises underlie our scientific effort to address the issue of the first cellular replication and to tackle the proteins/nucleic acids’ chicken–egg problem via the SANMAO hypothesis:

1. The occurrence of a primeval environment with a continuous source of freely available energy is required for the spontaneous synthesis of biomolecules’ polymers. Many energetically plausible paths from inorganic settings to the first living cells have been outlined (Sousa et al. 2013). For example, the energetic sources for early organic synthesis and systems reactions could have been derived from the proton gradients at the hydrothermal vents-ocean alkaline interface (Sousa et al. 2013; Damer and Deamer 2020). The nanopores formed by the Fe-rich saponite sheets might have acted as confined microenvironments capable of preserving biopolymers precursors from the detrimental effects of the aqueous medium (Ménez et al. 2018). Then, manifold isolated chemical compartments generated mingled agglomerates able to last for long until the SANMAO’s replication processes began.
2. Physical constraints must be kept into account. Physical rules allow biomolecular mixtures, in particular peptides, to self-assemble and cooperate, generating self-organizing hierarchies of polymeric materials (Jacobs 2021; Trivedi et al. 2022; McMullen et al. 2022).
3. The previous prebiotic formation of complex biomolecules is mandatory. The availability of amino acids, polypeptides, proteins, purines, pyrimidines, nucleosides and nucleotides is required under prebiotically plausible conditions on the Hadean Earth. The challenge is to trace plausible physical–chemical processes that permit biomolecules’ abiotic formation and self-regenerating catalytic cycles from a handful of simple compounds such as cyanide, water ammonia, and so on (Becker et al. 2019; Wołos et al. 2020).

Hence, the availability of the amino acids and peptides in prebiotic settings must be investigated. Primordial amino acids and Gly-Gly and cyclo(Gly-Gly) oligopeptides were exogenously delivered to the Hadean Earth (and possibly to the Noachian Mars) by comets and asteroids through hypervelocity impact shocks (Shimoyama and Ogasawara 2002; Holm et al. 2015; Ménez et al. 2018; Eigenbrode et al. 2018). In the interstellar medium, carbon atoms’ condensation on the surface of cold cosmic dust leads to the spontaneous formation of isomeric polyglycine peptides (Krasnokutski et al. 2022; Broadley et al. 2022). Simulations of impacts of Fe-bearing meteorites/asteroids on CO₂- and N₂-rich oceans suggest that glycine and alanine can be spontaneously synthesized from mixtures of Fe, Ni, Mg₂SiO₄, H₂O, CO₂ and N₂ (Takeuchi 2020). Also, amino acids and peptides may have appeared on the Hadean earth under different geochemical scenario, including Fischer–Tropsch-type synthesis (Russell et al. 2010; Roumégon and Cannat 2014), Miller and Urey’s spark discharge, Sutherland’s cyanosulfidic

protometabolism (Holm et al. 2015; Takeuchi 2020; Kirschning 2021), Strecker synthesis (Ménez et al. 2018), alkylation of indole with pyruvate followed by amination under hydrothermal conditions (Ménez et al. 2018), etc. The starting blocks for building amino acids are usually pyruvate, carbohydrate-containing molecules, carboxylic acids, ammonium, glutamate, glutamine, aspartate, H_2S and thiosulfate (Kirschning 2021). Complex amino acid such as tryptophan can be abiotically formed beneath the Atlantis Massif during a serpentinites' late alteration stage, via Friedel–Crafts reactions catalyzed by iron-rich saponite clays (Ménez et al. 2018). It is noteworthy that amino acids synthesis may occur under various conditions of water supply, pH and temperature, leading, e.g., to the production of phenols that are a moiety of tyrosine (Russell et al. 2010), of phenylalanyl-phenylalanine and tyrosyl-tyrosine oligomers (Milner-White and Russell 2008), of high yields of alanine, glutamate, phenylalanine and tyrosine (Milner-White and Russell 2008). Polypeptides can be produced abiotically also in extreme conditions. For example, dry glycine polymers are formed at pressures up to ~ 250 atm during thermal cycling between 0 and 250°C (Milner-White and Russell 2008). Further, possible amino acids ancestors like depsipeptides produce polypeptides during dry-down cycles under mild conditions (Frenkel-Pinter et al. 2019).

In a SANMAO scenario, the first peptides, utilizing the nucleotides spontaneously generated in the primeval medium, acted as a template for nucleic acid polymerization. Therefore, the next step is to investigate the availability of nucleic acids in prebiotic settings.

The building blocks of RNA and DNA, i.e., the purine/pyrimidine nucleobases and their structural isomers, have been detected in carbonaceous meteorites, possibly generated by photochemical reactions in the interstellar medium and subsequently incorporated into asteroids (Oba et al. 2022). When incubated with impact and volcanic rock glasses at room temperature, ribonucleoside triphosphates are converted to a steady polyribonucleic acid of 90–150 nucleotides in length (Jerome et al. 2022). Still, purines and pyrimidines, in particular adenine, may be abiotically formed both in seafloor hydrothermal environments and shallow ponds. Purines synthesis is feasible along a pathway based on the reaction of formamidopyrimidine precursors with ribose, whereas pyrimidines require a further step involving aminooxazoles (Becker et al. 2019). Fischer–Tropsch type reactions on carbonaceous chondrites in the presence of NH_3 and short heating up to 600°C generate the familiar nucleobases, although at very low conversions (Preiner et al. 2018). An abiotic one-pot scenario has been suggested to generate purines, pyrimidines and also 5'-mono- and diphosphates in the same environment, driven solely by wet–dry cycles occurring at low temperatures in a few separated shallow ponds (Becker et al. 2019). Wet–dry cycles allow mononucleotide mixtures' polymerization up to > 100 nucleotides in length (Kirschning 2021). While isocyanates in combination with sodium nitrite generate methylated nucleosides (Schneider et al. 2018), the uranosyl-selective prebiotic synthesis of purine deoxyribonucleosides uses intermediates from the prebiotic synthesis of pyrimidines, leading to a mixture of deoxyadenosine, deoxyinosine, cytidine and uridine (Xu et al. 2020). Dry heating combinations of glycine, alanine, valine, lysine, asparagine and glutamine produce pterin riboside at

160–200 °C for 4–6 h (Preiner et al. 2018). When ultramafic rocks are exposed to fluids, the alkalinity may promote abiotic formation of pentoses, particularly ribose (Holm et al. 2006). Also, water-soluble polyphosphates like cyclotriphosphate can be generated in the vicinity of volcanoes (Kirschning 2021).

In sum, experimental and theoretical approaches suggest that key biomolecules such as amino acids, polypeptides, purines, pyrimidines, nucleotides and nucleotides were available under various prebiotically plausible conditions, including meteorites delivery, shallow ponds and hydrothermal vents scenarios. Nevertheless, biomolecules' prebiotic formation is not an easy process, being bonds formation kinetically frustrated by high energy barriers (Frenkel-Pinter et al. 2019). This would mean that spontaneously generated biomolecular polymers of reasonable length were present on the Hadean Earth, but not abundant (Preiner et al. 2018; Takeuchi 2020).

Another problem is the scarce fidelity of the first SANMAO mechanism of protein translation. Indeed, structural organization and cell order distribution of granular systems (Wanjura et al. 2019) suggest that every hierarchical level adds complexity during assembly at the expense of increases in random errors (Michel and Yunker 2019). This would mean that the first efforts to transmit the genetic material to the offspring, i.e., the first random couplings between amino acids and nucleosides, were unavoidably prone to errors. Being the primeval translational mechanisms not as accurate and efficient as the modern triplet-based version (Wolf and Koonin 2007; Schiller 2016), the ancient peptides gave rise to polymerized strains of low-fidelity RNA. Nevertheless, the many mistakes of the primeval “reverse-translational” mechanism were possibly effective to enlarge the number of codon combinations. Then, the natural selection of strong affinity intermolecular interactions and the decreased entropy of the best couplings led to increased stabilization over long timescales (Schiller 2016). Due to decoding systems' evolutionary pressures (Ottén et al. 2020; Torres de Farias and José 2020), the subsequent emergence and selection of RNA drove the separation of catalytic and genetic functions (Schiller 2016). Then, repetition and duplication of simple peptidic and nucleic acids polymers took progressively place (Milner-White and James 2019). Synergy and co-evolution among diverse classes of molecules including polyesters and depsipeptides contributed to attenuate hydrolysis rates, promote folding/solubility and accelerate ligand binding/catalysis (Frenkel-Pinter et al. 2020). Actually, cationic proto-peptides significantly increase the thermal stability of folded RNA structures, while RNA increases by > 30-fold the depsipeptides' lifetime (Frenkel-Pinter et al. 2020).

Our model holds true even in the case in which the stereochemical hypothesis of the origin of the genetic code was false. Indeed, SANMAO does not necessarily require stereochemical relationships between amino acids and codons and/or anticodons. Further, covalent interactions between the peptide moiety and the nascent nucleic acid should also be taken into account (Müller et al. 2022). The SANMAO model hypothesizes that non-covalent interactions such as hydrogen bonds allow information flow from the template peptide to the nucleic acids. Yet, the model can be reasonably modified assuming the presence of covalent bonds between the SANMAO oligopeptide and the growing nucleic acid fragments. Each template amino acid (such as, e.g., Gly) could match a single SANMAO oligopeptide covalently linked with a nucleotide fragment that corresponds to the

amino acid codon (such as, e.g., GGG in the case of Gly), leading to the formation of covalent phosphodiester bonds and nucleoside fragments. To support this claim, it has been hypothesized that a natural tendency to interactions between pre-mRNA molecules and peptidated-RNAs sustained the catalytic role in the phase that triggered the genetic code origin (Di Giulio 2015). Di Giulio's model suggests that the pairing between peptidated-RNAs and pre-mRNAs involving a base number greater than three would represent the first form of the genetic code, followed by a natural evolutionistic tendency towards the more efficient triplet conformation. Therefore, the origin of enzymatic catalysis could be traced to the early relationship between nucleotides and amino acid components, via an intermediate formed by tRNA-like molecules covalently linked to polypeptides (Di Giulio 1997). The genetic code would result from a very long era of interactions among peptidated-RNAs, the extant tmRNAs representing the molecular fossils of the evolutionary stages that led to the appearance of the first mRNAs.

Catalytic and reproducing systems prone to Darwinian selection eventually developed, generating versatile and resilient metabolic “hypercycles” that circumvented the potential “error catastrophe” due to the formation of long strings of random sequences (Mossela and Steel 2005). Further, thousands of metabolic innovations on earlier phylogenetic branches were facilitated by horizontal gene transfers, breeding stepwise adaptation to successive environments and ensuing regulatory adaptations (Pang and Lercher 2018).

It has been argued that life emerged many times via multiple different historical pathways (Kempes and Krakauer 2021). If life spontaneously arose on the Hadean Earth from rather trivial non-organic assemblies, why it has not been produced *de novo* after the appearance of the last universal common ancestor (LUCA)? We suggest a straightforward answer: any viable effort after LUCA to produce unprecedented life was doomed to fail because of natural selection. After LUCA, the likely newcomers generated from organic precursors of low complexity would have been too fragile to compete with well-adapted LUCA's heirs equipped with consolidated selective advantage and plastic immune memory (Ferro et al. 2019; Bernheim et al. 2021; Wein and Sorek 2022).

Our work has a limitation, i.e., the molecules presented here have not been synthesized and no molecular modelling has been performed. Our fully theoretical model would require experimental support, by achieving the proposed hexapeptide commercially from a custom peptide-synthesis company to investigate the proposed interactions, possibly using a technique such as surface plasma resonance. In addition to testing for the existence of interactions, there would also be the need to test for their specificity and catalytic properties, as our model would appear to require that different peptide sequences form interactions with different amino acids.

In sum, in touch with the literature, we assume that life is a spontaneous process consisting of self-assembly of complex molecules. Focusing on the crucial step of protein translation, we propose, this time against the literature and the central dogma of molecular biology, an unusual but plausible scenario in which peptides lead to nucleic acid polymers.

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Declarations

Conflict of interest The authors do not have any known or potential conflict of interest including any financial, personal or other relationships with other people or organizations within three years of beginning the submitted work that could inappropriately influence, or be perceived to influence, their work.

Ethical Approval This research does not contain any studies with human participants or animals performed by the authors.

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References

- Apostolopoulos V, Bojarska J, Chai T-T, Elnagdy S, Kaczmarek K et al (2021) A global review on short peptides: frontiers and perspectives. *Molecules* 26(2):430. <https://doi.org/10.3390/molecules26020430>
- Baaske P, Weinert F, Duhr S, Lemke K, Russell MJ, Braun D (2007) Extreme accumulation of nucleotides in simulated hydrothermal pore systems. *Proc Natl Acad Sci USA* 104:9346–9351
- Becker S, Feldmann J, Wiedemann S, Okamura H, Schneider C et al (2019) Unified prebiotically plausible synthesis of pyrimidine and purine RNA ribonucleotides. *Science* 366(6461):76–82. <https://doi.org/10.1126/science.aax2747>
- Bernheim A, Millman A, Ofir G et al (2021) Prokaryotic viperins produce diverse antiviral molecules. *Nature* 589:120–124. <https://doi.org/10.1038/s41586-020-2762-2>
- Bhowmik S, Krishnamurthy R (2019) The role of sugar-backbone heterogeneity and chimeras in the simultaneous emergence of RNA and DNA. *Nat Chem* 11:1009–1018
- Biro JC (2007) The Proteomic Code: a molecular recognition code for proteins. *Theor Biol Med Model* 4:45. <https://doi.org/10.1186/1742-4682-4-45>
- Boyd ES, Amenabar MJ, Poudel S, Templeton AS (2020) Bioenergetic constraints on the origin of autotrophic metabolism. *Philos Trans A* 378(2165):20190151. <https://doi.org/10.1098/rsta.2019.0151>. (published online 6 Jan 2020)
- Broadley MW, Bekaert DV, Piani L et al (2022) Origin of life-forming volatile elements in the inner Solar System. *Nature* 611:245–255. <https://doi.org/10.1038/s41586-022-05276-x>
- Carter CW Jr, Kraut J (1973) A proposed model for interaction of polypeptides with RNA. *Proc Natl Acad Sci USA* 71(2):283–287. <https://doi.org/10.1073/pnas.71.2.283>
- Cartwright JH, Russell MJ (2019) The origin of life: the submarine alkaline vent theory at 30. *Interface Focus*. <https://doi.org/10.1098/rsfs.2019.0104>
- Chandramouly G, Zhao J, McDevitt S, Rusanov T, Hoang T et al (2021) Polθ reverse transcribes RNA and promotes RNA-templated DNA repair. *Sci Adv* 7(24):eabf1771. <https://doi.org/10.1126/sciadv.abf1771>. (published online 11 June 2021)

- Damer B, Deamer D (2020) The hot spring hypothesis for an origin of life. *Astrobiology*. <https://doi.org/10.1089/ast.2019.2045>
- Di Giulio M (1997) On the RNA world: evidence in favor of an early ribonucleopeptide world. *J Mol Evol* 45:571–578
- Di Giulio M (2015) A model for the origin of the first mRNAs. *J Mol Evol* 81:10–17
- Dishman AF, Tyler RC, Fox JC, Kleist AB, Prehoda KE et al (2021) Evolution of fold switching in a metamorphic protein. *Science* 371(6524):86–90. <https://doi.org/10.1126/science.abd8700>
- Eigenbrode JL, Summons RE, Steele A, Freissinet C, Millan M et al (2018) Organic matter preserved in 3-billion-year-old mudstones at Gale crater, Mars. *Science* 360(6393):1096–1101. <https://doi.org/10.1126/science.aas9185>
- Ferro K, Peuß R, Yang W, Rosenstiel P, Schulenburg H, Kurtz J (2019) Experimental evolution of immunological specificity. *Proc Natl Acad Sci USA* 116(41):20598–20604. <https://doi.org/10.1073/pnas.1904828116>
- Franz LP, Douzi B, Durand E, Dyer DH, Voulhoux R, Forest KT (2011) Structure of the minor pseudopilin XcpW from the *Pseudomonas aeruginosa* type II secretion system. *Acta Crystallogr D* 67:124–130
- Frenkel-Pinter M, Haynes JW, Martin C, Petrov AS, Burcar BT et al (2019) Selective incorporation of proteinaceous over nonproteinaceous cationic amino acids in model prebiotic oligomerization reactions. *Proc Natl Acad Sci USA* 116(33):16338–16346. <https://doi.org/10.1073/pnas.1904849116>
- Frenkel-Pinter M, Haynes JW, Mohyeldin AM et al (2020) Mutually stabilizing interactions between proto-peptides and RNA. *Nat Commun* 11:3137
- Fryer P (2012) Serpentinite mud volcanism: observations, processes, and implications. *Annu Rev Mar Sci* 4:345–373. <https://doi.org/10.1146/annurev-marine-120710-100922>
- Fusz S, Eisenführ A, Srivatsan SG, Heckel A, Famulok M (2005) A ribozyme for the aldol reaction. *Chem Biol* 12(8):941–950. <https://doi.org/10.1016/j.chembiol.2005.06.008>
- Gilbert W (1986) Origin of life: the RNA world. *Nature* 319:618. <https://doi.org/10.1038/319618a0>
- Holm NG, Dumont M, Ivarsson M, Konn C (2006) Alkaline fluid circulation in ultramafic rocks and formation of nucleotide constituents: a hypothesis. *Geochem Trans* 7:7
- Holm NG, Oze C, Mousis O, Waite JH, Guilbert-Lepoutre A (2015) Serpentinization and the formation of H₂ and CH₄ on celestial bodies (planets, moons, comets). *Astrobiology* 15(7):587–600. <https://doi.org/10.1089/ast.2014.1188>
- Hutchison CA III, Chuang R-Y, Noskov VN, Assad-Garcia N, Deerinc TJ et al (2016) Design and synthesis of a minimal bacterial genome. *Science*. <https://doi.org/10.1126/science.aad6253>
- Jacobs WM (2021) Self-assembly of biomolecular condensates with shared components. *Phys Rev Lett* 126:258101 (**Published 24 June 2021**)
- Jerome CA, Kim H-J, Mojzsis SJ, Benner SA, Biondi E (2022) Catalytic synthesis of polyribonucleic acid on prebiotic rock glasses. *Astrobiology* 22(6):629–636. <https://doi.org/10.1089/ast.2022.0027>
- Kempes CP, Krakauer DC (2021) The multiple paths to multiple life. *J Mol Evol* 89:415–426
- Kirschning A (2021) The coenzyme/protein pair and the molecular evolution of life. *Nat Prod Rep* 38(5):993–1010. <https://doi.org/10.1039/d0np00037j>
- Kitadai N, Maruyama S (2018) Origins of building blocks of life: a review. *Geosci Front* 9(4):1117–1153
- Krasnokutski SA, Chuang K-J, Jäger C, Ueberschaar N, Henning TH (2022) A pathway to peptides in space through the condensation of atomic carbon. *Nat Astron* 6:381–386
- Kroiss D, Ashkenasy G, Braunschweig AB, Tuttle T, Ulijn RV (2019) Catalyst: can systems chemistry unravel the mysteries of the chemical origins of life? *Chem* 5:1917–1920
- Lamadrid HM, Donald Rimstidt J, Schwarzenbach EM, Klein F, Ulrich S et al (2017) Effect of water activity on rates of serpentinization of olivine. *Nat Commun* 8:16107
- Lella M, Mahalakshmi R (2017) Metamorphic proteins: emergence of dual protein folds from one primary sequence. *Biochemistry* 56(24):2971–2984. <https://doi.org/10.1021/acs.biochem.7b00375>. (**Publication Date 1 June 2017**)
- Lundin D, Berggren G, Logan DT, Sjöberg B-M (2015) The origin and evolution of ribonucleotide reduction. *Life* 5(1):604–636. <https://doi.org/10.3390/life5010604>
- McMullen A, Muñoz Basagoiti M, Zeravcic Z et al (2022) Self-assembly of emulsion droplets through programmable folding. *Nature* 610:502–506
- Ménez B, Pisapia C, Andreani M, Jamme F, Vanbellingen QP et al (2018) Abiotic synthesis of amino acids in the recesses of the oceanic lithosphere. *Nature* 564(7734):59–63. <https://doi.org/10.1038/s41586-018-0684-z>. (**Epub 7 Nov 2018**)

- Michel JA, Yunker PJ (2019) Structural hierarchy confers error tolerance in biological materials. *Proc Natl Acad Sci USA* 116(8):2875–2880. <https://doi.org/10.1073/pnas.1813801116>
- Milner-White EJ (2019) Protein three-dimensional structures at the origin of life. *Interface Focus* 9(6):20190057. <https://doi.org/10.1098/rsfs.2019.0057> (Published online 18 Oct 2019)
- Milner-White EJ, Russell MJ (2008) Predicting the conformations of peptides and proteins in early evolution. *Biol Direct* 3:3. <https://doi.org/10.1186/1745-6150-3-3>
- Mossela E, Steel M (2005) Random biochemical networks: the probability of self-sustaining autocatalysis. *J Theor Biol* 233(3):327–336. <https://doi.org/10.1016/j.jtbi.2004.10.011>
- Müller F, Escobar L, Xu F, Węgrzyn E, Nainytė M et al (2022) A prebiotically plausible scenario of an RNA–peptide world. *Nature* 605:279–284
- Oba Y, Takano Y, Furukawa Y, Koga T, Glavin DP et al (2022) Identifying the wide diversity of extraterrestrial purine and pyrimidine nucleobases in carbonaceous meteorites. *Nat Commun* 13:2008
- Otten R, Pádua RAP, Adrian Bunzel H, Nguyen V, Pitsawong W et al (2020) How directed evolution reshapes the energy landscape in an enzyme to boost catalysis. *Science* 370(6523):1442–1446. <https://doi.org/10.1126/science.abd3623>
- Pang TY, Lercher MJ (2018) Each of 3,323 metabolic innovations in the evolution of *E. coli* arose through the horizontal transfer of a single DNA segment. *Proc Natl Acad Sci USA* 116(1):187–192. <https://doi.org/10.1073/pnas.1718997115>
- Postec A, Quéméneur M, Bes M, Mei N, Benaïssa F et al (2015) Microbial diversity in a submarine carbonate edifice from the serpentinizing hydrothermal system of the Prony Bay (New Caledonia) over a 6-year period. *Front Microbiol*. <https://doi.org/10.3389/fmicb.2015.00857>
- Preiner M, Xavier JC, Sousa FL, Zimorski V, Neubeck A et al (2018) Serpentinization: connecting geochemistry, ancient metabolism and industrial hydrogenation. *Life* 8(4):41. <https://doi.org/10.3390/life8040041>
- Root-Bernstein RS (1982) Amino acid pairing. *J Theor Biol* 94(4):885–894. [https://doi.org/10.1016/0022-5193\(82\)90083-2](https://doi.org/10.1016/0022-5193(82)90083-2)
- Roumèjon S, Cannat M (2014) Serpentinization of mantle-derived peridotites at mid-ocean ridges: mesh texture development in the context of tectonic exhumation. *Geochem Geophys Geosyst* 15(6):2354–2379. <https://doi.org/10.1002/2013GC005148> Citations:55. (First published 23 May 2014)
- Russell MJ, Ponce A (2020) Six ‘Must-Have’ minerals for life’s emergence: olivine, pyrrhotite, bridgmanite, serpentine, fougérite and mackinawite. *Life* 10(11):291. <https://doi.org/10.3390/life10110291>
- Russell MJ, Hall AJ, Martin W (2010) Serpentinization as a source of energy at the origin of life. *Geobiology* 8(5):355–371. <https://doi.org/10.1111/j.1472-4669.2010.00249.x>
- Schiller MR (2016) The minimotif synthesis hypothesis for the origin of life. *J Transl Sci* 2(5):289–296. <https://doi.org/10.15761/JTS.1000154> (Published online 19 July 2016)
- Schneider C, Becker S, Okamura H, Crisp A, Amatov T et al (2018) Noncanonical RNA nucleosides as molecular fossils of an early earth-generation by prebiotic methylations and carbamoylations. *Angew Chem Int Ed Engl* 57(20):5943–5946. <https://doi.org/10.1002/anie.201801919>. (Epub 17 April 2018)
- Shimoyama A, Ogasawara R (2002) Dipeptides and diketopiperazines in the Yamato-791198 and Murchison carbonaceous chondrites. *Orig Life Evol Biosph* 32(2):165–179. <https://doi.org/10.1023/a:1016015319112>
- Sousa FL, Thiergart T, Landan G, Nelson-Sathi S, Pereira IAC et al (2013) Early bioenergetic evolution. *Philos Trans R Soc Lond B Biol Sci* 368(1622):20130088. <https://doi.org/10.1098/rstb.2013.0088>. (Print 19 July 2013)
- Takeuchi Y (2020) Y Furukawa, T Kobayashi, T Sekine, N Terada & T Kakegawa Impact-induced amino acid formation on Hadean Earth and Noachian Mars. *Sci Rep* 10:9220
- Thornburg ZR, Bianchi DM, Brier TA, Smith HO, Glass JI et al (2022) Fundamental behaviors emerge from simulations of a living minimal cell. *Cell* 185(2):345–360. <https://doi.org/10.1016/j.cell.2021.12.025>
- Torres de Farias S, José MV (2020) Transfer RNA: The molecular demiurge in the origin of biological systems. *Prog Biophys Mol Biol* 153:28–34. <https://doi.org/10.1016/j.pbiomolbio.2020.02.006>
- Trifonov EN (2004) The triplet code from first principles. *J Biomol Struct Dyn* 22:1–11
- Trivedi M, Saxena D, Ng WK et al (2022) Self-organized lasers from reconfigurable colloidal assemblies. *Nat Phys* 18:939–944. <https://doi.org/10.1038/s41567-022-01656-2>
- Wanjura CC, Gago P, Matsushima T, Blumenfeld R (2019) Structural evolution of granular systems: theory. [arXiv:1904.06549](https://arxiv.org/abs/1904.06549) (Submitted on 13 April 2019)

- Wein T, Sorek R (2022) Bacterial origins of human cell-autonomous innate immune mechanisms. *Nat Rev Immunol* 22:629–638. <https://doi.org/10.1038/s41577-022-00705-4>
- Wieczorek R, Dörr M, Chotera A, Luisi PL, Monnard P-A (2013) Formation of RNA phosphodiester bond by histidine-containing dipeptides. *ChemBioChem* 14(2):217–223. <https://doi.org/10.1002/cbic.201200643>
- Wochner A, Attwater J, Coulson A, Holliger P (2011) Ribozyme-catalyzed transcription of an active ribozyme. *Science* 332(6026):209–212. <https://doi.org/10.1126/science.1200752>
- Wolf YI, Koonin EV (2007) On the origin of the translation system and the genetic code in the RNA world by means of natural selection, exaptation, and subfunctionalization. *Biol Direct* 2:14. <https://doi.org/10.1186/1745-6150-2-14>
- Wołos A, Roszak R, Źądło-Dobrowolska A, Beker W, Mikulak-Klucznik B (2020) Synthetic connectivity, emergence, and self-regeneration in the network of prebiotic chemistry. *Science* 369(6511):eaaw1955. <https://doi.org/10.1126/science.aaw1955>
- Xu J, Chmela V, Green N et al (2020) Selective prebiotic formation of RNA pyrimidine and DNA purine nucleosides. *Nature* 582:60–66. <https://doi.org/10.1038/s41586-020-2330-9>
- Yarus M (1998) Amino acids as RNA ligands: a direct-RNA-template theory for the code's origin. *J Mol Evol* 47(1):109–117

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