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2016- Present	Professor, Henan Normal University
2023	Visiting Professor, Albert-Ludwigs-Universität Freiburg
2016	Collaborative Professor, Scripps Research Institute, USA
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Research Interests:

Unnatural base pairs (UBPs), Nucleic acid modification, Sequencing, Synthetic biology

Selected Publications:

1. Wang HL#, Tie WC#, Zhu WY#, Wang SY, Zhang RZ, Duan JL, Ye BY, Zhu AL, **Li LJ***, Recognition and Sequencing of Mutagenic DNA Adduct at Single-Base Resolution Through Unnatural Base Pair, ***Advanced Science* 2024**, DOI: 10.1002/advs.202404622

2. Wang HL[#], Zhu WY[#], Wang C, Li XH, Wang LY, Huo BB, Mei H, Zhu AL, Zhang GS, **Li LJ.***, Locating, Tracing, and Sequencing Multiple Expanded Genetic Letters in Complex DNA Context via a Bridge-Base Approach, ***Nucleic Acids Res.* 2023**, 51, e52

3. Zhu WY[#], Wang HL[#], Li XH, Tie WH, Huo BB, Zhu AL; **Li LJ.***, Amplification, Enrichment, and Sequencing of Mutagenic Methylated DNA Adduct through Specifically Pairing with Unnatural Nucleobases, ***J. Am. Chem. Soc.*** 2022, 144, 20165-20170

4. Zhu AL[#], Li X[#], Bai L[#], Zhu G, Guo Y, Lin J, Cui Y, Tian G, Zhang L, Wang J, **Li DX***, **Li LJ.***, Biomimetic α-selective Ribosylation Enables Two-step Modular Synthesis of Biologically Important ADP-ribosylated peptides, ***Nat. Commun.*** 2020, 11, 5600.

5. Feldman, AW, Dien, VT, Karadeema, RJ. Fischer, EC, You Y, Chen JS, **Li LJ,* Romesberg EF***, Optimization of Replication, Transcription, and Translation in a Semi-Synthetic Organism, ***J. Am. Chem. Soc.*** 2019, 141, 10644-10653.

Mining Unnatural Base Pairs form DNA Damage and Its Applications

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Abstract

Although unnatural base pairs (UBPs) have great potentials in extended genetic alphabet, functional nucleic acid materials, semi synthetic organisms (SSO), etc., the known skeletons of UBPs are rare, and the synthetical access of them are costly, which limited their further applications. Herein, I would like to introduce our latest advances in mining the ***inexpensive*** unnatural base pairs (UBPs) from DNA damage and its biotechnological applications (***Advanced Science* 2024**, DOI: 10.1002/advs.202404622). Our novel approach poses the damaged nucleobases, e. g ethenodeoxycytidine (εC) in the DNA template, and then unveils the suitable pairing partner of them via primer extension, elongation, and kinetic assays. The low sequence dependence for amplification and its capacity for enhancing lesions are tested. From the new definite pair, we can recognize, amply, enrich, and sequence the real biological samples bearing εC DNA lesions vitro and in vivo at single-base resolution. Furthermore, such kind of UBPs show 99.96% fidelity in Polymerase Chain Reaction (PCR), 99% selectivity for transcriptions, and can be smoothly incorporated into tRNA and mRNA. We anticipate that these features, together with the simple, inexpensive synthesis of these UBPs, will render a useful platform for advancing more extensive UBPs-based technology.

1. Wang HL#, Tie WC#, Zhu WY#, Wang SY, Zhang RZ, Duan JL, Ye BY, Zhu AL, **Li LJ***, Recognition and Sequencing of Mutagenic DNA Adduct at Single-Base Resolution Through Unnatural Base Pair, ***Advanced Science* 2024**, DOI: 10.1002/advs.202404622