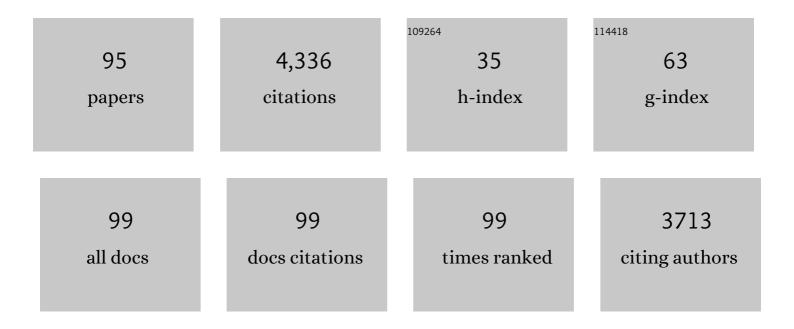
List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	The two-domain architecture of LAMP2A regulates its interaction with Hsc70. Experimental Cell Research, 2022, 411, 112986.	1.2	10
2	Incorporation of Halogenated Amino Acids into Antibody Fragments at Multiple Specific Sites Enhances Antigen Binding. ChemBioChem, 2021, 22, 120-123.	1.3	10
3	An expanded genetic code facilitates antibody chemical conjugation involving the lambda light chain. Biochemical and Biophysical Research Communications, 2021, 546, 35-39.	1.0	3
4	Direct homophilic interaction of LAMP2A with the two-domain architecture revealed by site-directed photo-crosslinks and steric hindrances in mammalian cells. Autophagy, 2021, 17, 4286-4304.	4.3	9
5	An integrated computational pipeline for designing high-affinity nanobodies with expanded genetic codes. Briefings in Bioinformatics, 2021, 22, .	3.2	4
6	Fully Productive Cell-Free Genetic Code Expansion by Structure-Based Engineering of Methanomethylophilus alvus Pyrrolysyl-tRNA Synthetase. ACS Synthetic Biology, 2020, 9, 718-732.	1.9	21
7	Cell-Free Protein Synthesis Using S30 Extracts from Escherichia coli RFzero Strains for Efficient Incorporation of Non-Natural Amino Acids into Proteins. International Journal of Molecular Sciences, 2019, 20, 492.	1.8	25
8	Synthetic Tyrosine tRNA Molecules with Noncanonical Secondary Structures. International Journal of Molecular Sciences, 2019, 20, 92.	1.8	9
9	Structural Basis for Genetic-Code Expansion with Bulky Lysine Derivatives by an Engineered Pyrrolysyl-tRNA Synthetase. Cell Chemical Biology, 2019, 26, 936-949.e13.	2.5	37
10	Variants of the industrially relevant protease KP-43 with suppressed activity under alkaline conditions developed using expanded genetic codes. Biochemistry and Biophysics Reports, 2019, 17, 93-96.	0.7	2
11	Genetic Code Expansion of the Silkworm <i>Bombyx mori</i> to Functionalize Silk Fiber. ACS Synthetic Biology, 2018, 7, 801-806.	1.9	26
12	Pyrrolysyl-tRNA Synthetase with a Unique Architecture Enhances the Availability of Lysine Derivatives in Synthetic Genetic Codes. Molecules, 2018, 23, 2460.	1.7	25
13	Engineering of Escherichia coli β-lactamase TEM-1 variants showing higher activity under acidic conditions than at the neutral pH. Biochemical and Biophysical Research Communications, 2018, 505, 333-337.	1.0	3
14	Engineering an Automaturing Transglutaminase with Enhanced Thermostability by Genetic Code Expansion with Two Codon Reassignments. ACS Synthetic Biology, 2018, 7, 2170-2176.	1.9	25
15	JQ1 affects BRD2-dependent and independent transcription regulation without disrupting H4-hyperacetylated chromatin states. Epigenetics, 2018, 13, 410-431.	1.3	32
16	A reproducible and scalable procedure for preparing bacterial extracts for cell-free protein synthesis. Journal of Biochemistry, 2017, 162, 357-369.	0.9	34
17	Covalently Capturing Protein Interactions in Living Cells by Site-Specific Incorporation of Photo-Cross-Linkable Amino Acids. , 2017, , 159-181.		0
18	Extensive Survey of Antibody Invariant Positions for Efficient Chemical Conjugation Using Expanded Genetic Codes. Bioconjugate Chemistry, 2017, 28, 2099-2108.	1.8	15

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19	Structure-based site-directed photo-crosslinking analyses of multimeric cell-adhesive interactions of voltage-gated sodium channel β subunits. Scientific Reports, 2016, 6, 26618.	1.6	13
20	Adenovirus vector-based incorporation of a photo-cross-linkable amino acid into proteins in human primary cells and cancerous cell lines. Scientific Reports, 2016, 6, 36946.	1.6	12
21	Incorporation of a Doubly Functionalized Synthetic Amino Acid into Proteins for Creating Chemical and Light-Induced Conjugates. Bioconjugate Chemistry, 2016, 27, 198-206.	1.8	37
22	Crystal structure of eukaryotic translation initiation factor 2B. Nature, 2016, 531, 122-125.	13.7	103
23	Intra- and inter-nucleosomal interactions of the histone H4 tail revealed with a human nucleosome core particle with genetically-incorporated H4 tetra-acetylation. Scientific Reports, 2015, 5, 17204.	1.6	67
24	Protein stabilization utilizing a redefined codon. Scientific Reports, 2015, 5, 9762.	1.6	35
25	Highly reproductive Escherichia coli cells with no specific assignment to the UAG codon. Scientific Reports, 2015, 5, 9699.	1.6	126
26	Reassignment of a rare sense codon to a non-canonical amino acid in <i>Escherichia coli</i> . Nucleic Acids Research, 2015, 43, 8111-8122.	6.5	70
27	Ubiquitin acetylation inhibits polyubiquitin chain elongation. EMBO Reports, 2015, 16, 192-201.	2.0	116
28	Multiple Siteâ€Specific Installations of <i>N</i> <sup><i>ε</i></sup> â€Monomethylâ€ <scp>L</scp> â€Lysine in Histone Proteins by Cellâ€Based and Cellâ€Free Protein Synthesis. ChemBioChem, 2014, 15, 1830-1838.	to <sub>1.3</sub>	36
29	Expanded Genetic Code Technologies for Incorporating Modified Lysine at Multiple Sites. ChemBioChem, 2014, 15, 2181-2187.	1.3	29
30	1P088 Multiple site-selective integrations of bulky halogenated tyrosines enhance protein stability(01F. Protein : Engineering,Poster,The 52nd Annual Meeting of the Biophysical Society of) Tj ETQq0 0 0 r	g <b>BT.(</b> Over	loade 10 Tf 50
31	Structural Stability of Halogenated Protein: Fragment Molecular Orbital Study. Journal of Computer Chemistry Japan, 2014, 13, 308-309.	0.0	1
32	Efficient Decoding of the UAG Triplet as a Full-Fledged Sense Codon Enhances the Growth of a <i>prfA</i> -Deficient Strain of Escherichia coli. Journal of Bacteriology, 2012, 194, 2606-2613.	1.0	36
33	Tetrameric Interaction of the Ectoenzyme CD38 on the Cell Surface Enables Its Catalytic and Raft-Association Activities. Structure, 2012, 20, 1585-1595.	1.6	31
34	Wide-range protein photo-crosslinking achieved by a genetically encoded NÎμ-(benzyloxycarbonyl)lysine derivative with a diazirinyl moiety. Molecular BioSystems, 2012, 8, 1131.	2.9	50
35	Site-Specific Incorporation of Unnatural Amino Acids into Proteins in Mammalian Cells. Methods in Molecular Biology, 2012, 794, 215-228.	0.4	7
36	Structural basis for extracellular interactions between calcitonin receptorâ€like receptor and receptor activityâ€modifying protein 2 for adrenomedullinâ€specific binding. Protein Science, 2012, 21, 199-210.	3.1	54

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37	Structural basis of interleukinâ€5 dimer recognition by its α receptor. Protein Science, 2012, 21, 850-864.	3.1	57
38	Crystallographic Study of a Site-Specifically Cross-Linked Protein Complex with a Genetically Incorporated Photoreactive Amino Acid,. Biochemistry, 2011, 50, 250-257.	1.2	48
39	Genetic-code evolution for protein synthesis with non-natural amino acids. Biochemical and Biophysical Research Communications, 2011, 411, 757-761.	1.0	72
40	Genetic Incorporation of a Photo-Crosslinkable Amino Acid Reveals Novel Protein Complexes with GRB2 in Mammalian Cells. Journal of Molecular Biology, 2011, 406, 343-353.	2.0	49
41	Dissecting Cell Signaling Pathways with Genetically Encoded 3â€lodoâ€ <scp>L</scp> â€ŧyrosine. ChemBioChem, 2011, 12, 387-389.	1.3	3
42	Genetic encoding of nonâ€natural amino acids in <i>Drosophila melanogaster</i> Schneider 2 cells. Protein Science, 2010, 19, 440-448.	3.1	34
43	Crystal structure of bacterial RNA polymerase bound with a transcription inhibitor protein. Nature, 2010, 468, 978-982.	13.7	140
44	Functional replacement of the endogenous tyrosyl-tRNA synthetase–tRNATyr pair by the archaeal tyrosine pair in Escherichia coli for genetic code expansion. Nucleic Acids Research, 2010, 38, 3682-3691.	6.5	35
45	Codon reassignment in the Escherichia coli genetic code. Nucleic Acids Research, 2010, 38, 8188-8195.	6.5	173
46	Site-specific incorporation of 4-lodo-l-phenylalanine through opal suppression. Journal of Biochemistry, 2010, 148, 179-187.	0.9	4
47	Biologically-implemented genetic algorithm for protein engineering. , 2009, , .		2
48	Genetic Encoding of 3-lodo-l-Tyrosine in Escherichia coli for Single-Wavelength Anomalous Dispersion Phasing in Protein Crystallography. Structure, 2009, 17, 335-344.	1.6	60
49	Recognition of Non-α-amino Substrates by Pyrrolysyl-tRNA Synthetase. Journal of Molecular Biology, 2009, 385, 1352-1360.	2.0	78
50	Site-specific Incorporation of 3-lodo-L-tyrosine into Proteins and Single-wavelength Anomalous Dispersion Phasing with Soft X-ray in Protein Crystallography. Nihon Kessho Gakkaishi, 2009, 51, 251-257.	0.0	1
51	Multistep Engineering of Pyrrolysyl-tRNA Synthetase to Genetically Encode NÉ›-(o-Azidobenzyloxycarbonyl) lysine for Site-Specific Protein Modification. Chemistry and Biology, 2008, 15, 1187-1197.	6.2	299
52	Crystallographic Studies on Multiple Conformational States of Active-site Loops in Pyrrolysyl-tRNA Synthetase. Journal of Molecular Biology, 2008, 378, 634-652.	2.0	88
53	Adding l-lysine derivatives to the genetic code of mammalian cells with engineered pyrrolysyl-tRNA synthetases. Biochemical and Biophysical Research Communications, 2008, 371, 818-822.	1.0	245
54	Transplantation of a tyrosine editing domain into a tyrosyl-tRNA synthetase variant enhances its specificity for a tyrosine analog. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 13298-13303.	3.3	27

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55	1P065 X-ray structure analyses for iodo-tyrosine incorporated proteins(Proteins-methodology,Poster) Tj ETQq1 1	0,784314	rgBT /Over
56	Site-Specific Functionalization of Proteins by Organopalladium Reactions. ChemBioChem, 2007, 8, 232-238.	1.3	96
57	Regioselective Carbon–Carbon Bond Formation in Proteins with Palladium Catalysis; New Protein Chemistry by Organometallic Chemistry. ChemBioChem, 2007, 8, 159-159.	1.3	Ο
58	Theoretical Basis for Stochastic Optimization Starting from a Single Point in the Search Space Formed by Real DNA Molecules. Transactions of the Japanese Society for Artificial Intelligence, 2007, 22, 405-415.	0.1	1
59	Cationâ~ï€ Interaction in the Polyolefin Cyclization Cascade Uncovered by Incorporating Unnatural Amino Acids into the Catalytic Sites of Squalene Cyclase. Journal of the American Chemical Society, 2006, 128, 13184-13194.	6.6	72
60	Site-specific incorporation of non-natural amino acids into proteins in mammalian cells with an expanded genetic code. Nature Protocols, 2006, 1, 2957-2962.	5.5	41
61	DNA polymerase programmed with a hairpin DNA incorporates a multiple-instruction architecture into molecular computing. BioSystems, 2006, 83, 18-25.	0.9	25
62	Translation of â€~rare' Codons in a Cell-free Protein Synthesis System from Escherichia coli. Journal of Structural and Functional Genomics, 2006, 7, 31-36.	1.2	28
63	Regioselective Carbon-Carbon Bond Formation in Proteins with Palladium Catalysis; New Protein Chemistry by Organometallic Chemistry. ChemBioChem, 2006, 7, 134-139.	1.3	96
64	A New Protein Engineering Approach Combining Chemistry and Biology, Part I; Site-Specific Incorporation of 4-lodo-L-phenylalanine in vitro by Using Misacylated Suppressor tRNAPhe. ChemBioChem, 2006, 7, 1577-1581.	1.3	10
65	Protein photo-cross-linking in mammalian cells by site-specific incorporation of a photoreactive amino acid. Nature Methods, 2005, 2, 201-206.	9.0	223
66	Hairpin-based state machine and conformational addressing: Design and experiment. Natural Computing, 2005, 4, 103-126.	1.8	18
67	Structural basis of nonnatural amino acid recognition by an engineered aminoacyl-tRNA synthetase for genetic code expansion. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1366-1371.	3.3	38
68	Structural Snapshots of the KMSKS Loop Rearrangement for Amino Acid Activation by Bacterial Tyrosyl-tRNA Synthetase. Journal of Molecular Biology, 2005, 346, 105-117.	2.0	92
69	The Escherichia coli argU10(Ts) Phenotype Is Caused by a Reduction in the Cellular Level of the argU tRNA for the Rare Codons AGA and AGC. Journal of Bacteriology, 2004, 186, 5899-5905.	1.0	11
70	Conformational Addressing Using the Hairpin Structure of Single-Strand DNA. Lecture Notes in Computer Science, 2004, , 219-224.	1.0	9
71	Structural basis for orthogonal tRNA specificities of tyrosyl-tRNA synthetases for genetic code expansion. Nature Structural and Molecular Biology, 2003, 10, 425-432.	3.6	193
72	An engineered Escherichia coli tyrosyl-tRNA synthetase for site-specific incorporation of an unnatural amino acid into proteins in eukaryotic translation and its application in a wheat germ cell-free system. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 9715-9720.	3.3	163

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73	Indolmycin Resistance of Streptomyces coelicolor A3(2) by Induced Expression of One of Its Two Tryptophanyl-tRNA Synthetases. Journal of Biological Chemistry, 2002, 277, 23882-23887.	1.6	50
74	Site-specific incorporation of an unnatural amino acid into proteins in mammalian cells. Nucleic Acids Research, 2002, 30, 4692-4699.	6.5	231
75	Solution structure of an RNA fragment with the P7/P9.0 region and the 3???-terminal guanosine of the Tetrahymena group I intron. Rna, 2002, 8, 440-451.	1.6	17
76	Complexity analysis of the SAT engine: DNA algorithms as probabilistic algorithms. Theoretical Computer Science, 2002, 287, 59-71.	0.5	3
77	Shifted positioning of the anticodon nucleotide residues of amber suppressor tRNA species by Escherichia coli arginyl-tRNA synthetase. FEBS Journal, 2001, 268, 6207-6213.	0.2	12
78	Successive state transitions with I/O interface by molecules. Lecture Notes in Computer Science, 2001, , 17-26.	1.0	14
79	Synthesis Of N-Labeled Peptidyl AMP. Nucleosides, Nucleotides and Nucleic Acids, 2000, 19, 1993-2003.	0.4	1
80	State transitions by molecules. BioSystems, 1999, 52, 81-91.	0.9	94
81	RNA aptamers that specifically bind to the Ras-binding domain of Raf-1. FEBS Letters, 1998, 441, 322-326.	1.3	22
82	Chemical Synthesis and Properties of Conformationally Fixed Diuridine Monophosphates as Building Blocks of the RNA Turn Motif. Journal of Organic Chemistry, 1998, 63, 1429-1443.	1.7	31
83	Synthesis and Properties of Conformationally Rigid Cyclouridylic Acids Having Covalent Bonding Linkers Between the Uracil 5-Position and the 5′-Phosphate Group. Nucleosides & Nucleotides, 1997, 16, 1023-1032.	0.5	6
84	Cleavage effect of oligoribonucleotides substituted at the cleavage sites with modified pyrimidine- and purine-nucleosides. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1997, 1354, 211-218.	2.4	5
85	Chemical Synthesis and Conformational Properties of a New Cyclouridylic Acid Having an Ethylene Bridge between the Uracil 5-Position and 5â€~Phosphate Group. Journal of Organic Chemistry, 1996, 61, 1500-1504.	1.7	18
86	NMR Studies of the Effects of the 5â€~-Phosphate Group on Conformational Properties of 5-Methylaminomethyluridine Found in the First Position of the Anticodon ofEscherichia colitRNA4Argâ€. Biochemistry, 1996, 35, 6533-6538.	1.2	23
87	Major Identity Determinants in the "Augmented D Helix" of tRNAClufromEscherichia coli. Journal of Molecular Biology, 1996, 256, 685-700.	2.0	65
88	Synthesis and properties of conformationally rigid cyclouridylic acid having a covalent bonding linker between the uracil 5-position and the 5′-phosphate group. Tetrahedron Letters, 1995, 36, 9515-9518.	0.7	6
89	Characterization of the secondary structure of an oligonucleotide corresponding to the autocleavage site of a precursor RNA from bacteriophage T4. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1994, 1218, 351-356.	2.4	2
90	Chemical Synthesis and Properties of an Interresidually Cyclized Uridylyl(3'-5')uridine as a model of tRNA U-Turn Structure Having a Sharp Bend. Journal of the American Chemical Society, 1994, 116, 4469-4470.	6.6	3

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91	A modified uridine in the first position of the anticodon of a minor species of arginine tRNA, the argU gene product, from Escherichia coli. FEBS Journal, 1993, 216, 369-375.	0.2	35
92	Mechanisms of the inhibition of reverse transcription by unmodified and modified antisense oligonucleotides. FEBS Letters, 1993, 330, 161-164.	1.3	21
93	Synthesis of Uridylyl (3′-5′) Uridine Derivatives Containing 5-(Methylamino-Methyl) Uridine as A Modified Nucleoside Found from <i>E. COLI</i> Minor tRNA <sup>Arg</sup> . Nucleosides & Nucleotides, 1993, 12, 305-321.	0.5	6
94	Cleavage reaction of a synthetic oligoribonucleotide corresponding to the autocleavage site of a precursor RNA from bacteriophage T4. FEBS Letters, 1991, 293, 204-206.	1.3	13
95	Structural Basis for Genetic-Code Expansion with Various Bulky Lysine Derivatives by an Engineered Pyrrolysyl-tRNA Synthetase. SSRN Electronic Journal, 0, , .	0.4	0