

# Kensaku Sakamoto

## List of Publications by Year in descending order

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95  
papers

4,336  
citations

109264  
35  
h-index

114418  
63  
g-index

99  
all docs

99  
docs citations

99  
times ranked

3713  
citing authors

#	ARTICLE	IF	CITATIONS
1	Multistep Engineering of Pyrrolysyl-tRNA Synthetase to Genetically Encode N $\epsilon$ -(o-Azidobenzoyloxycarbonyl) lysine for Site-Specific Protein Modification. <i>Chemistry and Biology</i> , 2008, 15, 1187-1197.	6.2	299
2	Adding l-lysine derivatives to the genetic code of mammalian cells with engineered pyrrolysyl-tRNA synthetases. <i>Biochemical and Biophysical Research Communications</i> , 2008, 371, 818-822.	1.0	245
3	Site-specific incorporation of an unnatural amino acid into proteins in mammalian cells. <i>Nucleic Acids Research</i> , 2002, 30, 4692-4699.	6.5	231
4	Protein photo-cross-linking in mammalian cells by site-specific incorporation of a photoreactive amino acid. <i>Nature Methods</i> , 2005, 2, 201-206.	9.0	223
5	Structural basis for orthogonal tRNA specificities of tyrosyl-tRNA synthetases for genetic code expansion. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 425-432.	3.6	193
6	Codon reassignment in the Escherichia coli genetic code. <i>Nucleic Acids Research</i> , 2010, 38, 8188-8195.	6.5	173
7	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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 9715-9720.	3.3	163
8	Crystal structure of bacterial RNA polymerase bound with a transcription inhibitor protein. <i>Nature</i> , 2010, 468, 978-982.	13.7	140
9	Highly reproductive Escherichia coli cells with no specific assignment to the UAG codon. <i>Scientific Reports</i> , 2015, 5, 9699.	1.6	126
10	Ubiquitin acetylation inhibits polyubiquitin chain elongation. <i>EMBO Reports</i> , 2015, 16, 192-201.	2.0	116
11	Crystal structure of eukaryotic translation initiation factor 2B. <i>Nature</i> , 2016, 531, 122-125.	13.7	103
12	Regioselective Carbon-Carbon Bond Formation in Proteins with Palladium Catalysis; New Protein Chemistry by Organometallic Chemistry. <i>ChemBioChem</i> , 2006, 7, 134-139.	1.3	96
13	Site-Specific Functionalization of Proteins by Organopalladium Reactions. <i>ChemBioChem</i> , 2007, 8, 232-238.	1.3	96
14	State transitions by molecules. <i>BioSystems</i> , 1999, 52, 81-91.	0.9	94
15	Structural Snapshots of the KMSKS Loop Rearrangement for Amino Acid Activation by Bacterial Tyrosyl-tRNA Synthetase. <i>Journal of Molecular Biology</i> , 2005, 346, 105-117.	2.0	92
16	Crystallographic Studies on Multiple Conformational States of Active-site Loops in Pyrrolysyl-tRNA Synthetase. <i>Journal of Molecular Biology</i> , 2008, 378, 634-652.	2.0	88
17	Recognition of Non- $\alpha$ -amino Substrates by Pyrrolysyl-tRNA Synthetase. <i>Journal of Molecular Biology</i> , 2009, 385, 1352-1360.	2.0	78
18	Cation- $\pi$ Interaction in the Polyolefin Cyclization Cascade Uncovered by Incorporating Unnatural Amino Acids into the Catalytic Sites of Squalene Cyclase. <i>Journal of the American Chemical Society</i> , 2006, 128, 13184-13194.	6.6	72

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19	Genetic-code evolution for protein synthesis with non-natural amino acids. Biochemical and Biophysical Research Communications, 2011, 411, 757-761.	1.0	72
20	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
21	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
22	Major Identity Determinants in the "Augmented D Helix" of tRNA <sup>Glu</sup> from <i>Escherichia coli</i> . Journal of Molecular Biology, 1996, 256, 685-700.	2.0	65
23	Genetic Encoding of 3-Iodo-L-Tyrosine in <i>Escherichia coli</i> for Single-Wavelength Anomalous Dispersion Phasing in Protein Crystallography. Structure, 2009, 17, 335-344.	1.6	60
24	Structural basis of interleukin-5 dimer recognition by its $\beta$ receptor. Protein Science, 2012, 21, 850-864.	3.1	57
25	Structural basis for extracellular interactions between calcitonin receptor-like receptor and receptor activity-modifying protein 2 for adrenomedullin-specific binding. Protein Science, 2012, 21, 199-210.	3.1	54
26	Indolmycin Resistance of <i>Streptomyces coelicolor</i> A3(2) by Induced Expression of One of Its Two Tryptophanyl-tRNA Synthetases. Journal of Biological Chemistry, 2002, 277, 23882-23887.	1.6	50
27	Wide-range protein photo-crosslinking achieved by a genetically encoded N $\epsilon$ -(benzyloxycarbonyl)lysine derivative with a diazirinyl moiety. Molecular BioSystems, 2012, 8, 1131.	2.9	50
28	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
29	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
30	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
31	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
32	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
33	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
34	Efficient Decoding of the UAG Triplet as a Full-Fledged Sense Codon Enhances the Growth of a <i>prfA</i> -Deficient Strain of <i>Escherichia coli</i> . Journal of Bacteriology, 2012, 194, 2606-2613.	1.0	36
35	Multiple Site-Specific Installations of N $^{\epsilon}$ -Monomethyl-L-lysine into Histone Proteins by Cell-Based and Cell-Free Protein Synthesis. ChemBioChem, 2014, 15, 1830-1838.	1.3	36
36	A modified uridine in the first position of the anticodon of a minor species of arginine tRNA, the argU gene product, from <i>Escherichia coli</i> . FEBS Journal, 1993, 216, 369-375.	0.2	35

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37	Functional replacement of the endogenous tyrosyl-tRNA synthetase-tRNA <sup>Tyr</sup> pair by the archaeal tyrosine pair in <i>Escherichia coli</i> for genetic code expansion. <i>Nucleic Acids Research</i> , 2010, 38, 3682-3691.	6.5	35
38	Protein stabilization utilizing a redefined codon. <i>Scientific Reports</i> , 2015, 5, 9762.	1.6	35
39	Genetic encoding of non-natural amino acids in <i>Drosophila melanogaster</i> Schneider 2 cells. <i>Protein Science</i> , 2010, 19, 440-448.	3.1	34
40	A reproducible and scalable procedure for preparing bacterial extracts for cell-free protein synthesis. <i>Journal of Biochemistry</i> , 2017, 162, 357-369.	0.9	34
41	JQ1 affects BRD2-dependent and independent transcription regulation without disrupting H4-hyperacetylated chromatin states. <i>Epigenetics</i> , 2018, 13, 410-431.	1.3	32
42	Chemical Synthesis and Properties of Conformationally Fixed Diuridine Monophosphates as Building Blocks of the RNA Turn Motif. <i>Journal of Organic Chemistry</i> , 1998, 63, 1429-1443.	1.7	31
43	Tetrameric Interaction of the Ecto-enzyme CD38 on the Cell Surface Enables Its Catalytic and Raft-Association Activities. <i>Structure</i> , 2012, 20, 1585-1595.	1.6	31
44	Expanded Genetic Code Technologies for Incorporating Modified Lysine at Multiple Sites. <i>ChemBioChem</i> , 2014, 15, 2181-2187.	1.3	29
45	Translation of "rare" Codons in a Cell-free Protein Synthesis System from <i>Escherichia coli</i> . <i>Journal of Structural and Functional Genomics</i> , 2006, 7, 31-36.	1.2	28
46	Transplantation of a tyrosine editing domain into a tyrosyl-tRNA synthetase variant enhances its specificity for a tyrosine analog. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 13298-13303.	3.3	27
47	Genetic Code Expansion of the Silkworm <i>Bombyx mori</i> to Functionalize Silk Fiber. <i>ACS Synthetic Biology</i> , 2018, 7, 801-806.	1.9	26
48	DNA polymerase programmed with a hairpin DNA incorporates a multiple-instruction architecture into molecular computing. <i>BioSystems</i> , 2006, 83, 18-25.	0.9	25
49	Pyrrolysyl-tRNA Synthetase with a Unique Architecture Enhances the Availability of Lysine Derivatives in Synthetic Genetic Codes. <i>Molecules</i> , 2018, 23, 2460.	1.7	25
50	Engineering an Automaturing Transglutaminase with Enhanced Thermostability by Genetic Code Expansion with Two Codon Reassignments. <i>ACS Synthetic Biology</i> , 2018, 7, 2170-2176.	1.9	25
51	Cell-Free Protein Synthesis Using S30 Extracts from <i>Escherichia coli</i> RFzero Strains for Efficient Incorporation of Non-Natural Amino Acids into Proteins. <i>International Journal of Molecular Sciences</i> , 2019, 20, 492.	1.8	25
52	NMR Studies of the Effects of the 5'-Phosphate Group on Conformational Properties of 5-Methylaminomethyluridine Found in the First Position of the Anticodon of <i>Escherichia coli</i> tRNA <sup>Arg</sup> . <i>Biochemistry</i> , 1996, 35, 6533-6538.	1.2	23
53	RNA aptamers that specifically bind to the Ras-binding domain of Raf-1. <i>FEBS Letters</i> , 1998, 441, 322-326.	1.3	22
54	Mechanisms of the inhibition of reverse transcription by unmodified and modified antisense oligonucleotides. <i>FEBS Letters</i> , 1993, 330, 161-164.	1.3	21

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55	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
56	Chemical Synthesis and Conformational Properties of a New Cyclouridylic Acid Having an Ethylene Bridge between the Uracil 5-Position and 5'-Phosphate Group. Journal of Organic Chemistry, 1996, 61, 1500-1504.	1.7	18
57	Hairpin-based state machine and conformational addressing: Design and experiment. Natural Computing, 2005, 4, 103-126.	1.8	18
58	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
59	Extensive Survey of Antibody Invariant Positions for Efficient Chemical Conjugation Using Expanded Genetic Codes. Bioconjugate Chemistry, 2017, 28, 2099-2108.	1.8	15
60	Successive state transitions with I/O interface by molecules. Lecture Notes in Computer Science, 2001, , 17-26.	1.0	14
61	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
62	Structure-based site-directed photo-crosslinking analyses of multimeric cell-adhesive interactions of voltage-gated sodium channel $\alpha$ subunits. Scientific Reports, 2016, 6, 26618.	1.6	13
63	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
64	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
65	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 AGG. Journal of Bacteriology, 2004, 186, 5899-5905.	1.0	11
66	A New Protein Engineering Approach Combining Chemistry and Biology, Part I: Site-Specific Incorporation of 4-Iodo-L-phenylalanine in vitro by Using Misacylated Suppressor tRNA <sup>Phe</sup> . ChemBioChem, 2006, 7, 1577-1581.	1.3	10
67	Incorporation of Halogenated Amino Acids into Antibody Fragments at Multiple Specific Sites Enhances Antigen Binding. ChemBioChem, 2021, 22, 120-123.	1.3	10
68	The two-domain architecture of LAMP2A regulates its interaction with Hsc70. Experimental Cell Research, 2022, 411, 112986.	1.2	10
69	Synthetic Tyrosine tRNA Molecules with Noncanonical Secondary Structures. International Journal of Molecular Sciences, 2019, 20, 92.	1.8	9
70	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
71	Conformational Addressing Using the Hairpin Structure of Single-Strand DNA. Lecture Notes in Computer Science, 2004, , 219-224.	1.0	9
72	Site-Specific Incorporation of Unnatural Amino Acids into Proteins in Mammalian Cells. Methods in Molecular Biology, 2012, 794, 215-228.	0.4	7

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73	Synthesis of Uridylyl (3'â€²-5'â€²) 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
74	Synthesis and properties of conformationally rigid cyclouridylic acid having a covalent bonding linker between the uracil 5-position and the 5'â€²-phosphate group. Tetrahedron Letters, 1995, 36, 9515-9518.	0.7	6
75	Synthesis and Properties of Conformationally Rigid Cyclouridylic Acids Having Covalent Bonding Linkers Between the Uracil 5-Position and the 5'â€²-Phosphate Group. Nucleosides & Nucleotides, 1997, 16, 1023-1032.	0.5	6
76	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
77	Site-specific incorporation of 4-Iodo-L-phenylalanine through opal suppression. Journal of Biochemistry, 2010, 148, 179-187.	0.9	4
78	An integrated computational pipeline for designing high-affinity nanobodies with expanded genetic codes. Briefings in Bioinformatics, 2021, 22, .	3.2	4
79	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
80	Complexity analysis of the SAT engine: DNA algorithms as probabilistic algorithms. Theoretical Computer Science, 2002, 287, 59-71.	0.5	3
81	Dissecting Cell Signaling Pathways with Genetically Encoded 3'â€²-Iodo-L-tyrosine. ChemBioChem, 2011, 12, 387-389.	1.3	3
82	Engineering of Escherichia coli Î²-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
83	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
84	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
85	Biologically-implemented genetic algorithm for protein engineering. , 2009, , .		2
86	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
87	Synthesis Of N-Labeled Peptidyl AMP. Nucleosides, Nucleotides and Nucleic Acids, 2000, 19, 1993-2003.	0.4	1
88	Site-specific Incorporation of 3-Iodo-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
89	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
90	Structural Stability of Halogenated Protein: Fragment Molecular Orbital Study. Journal of Computer Chemistry Japan, 2014, 13, 308-309.	0.0	1

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91	1P065 X-ray structure analyses for iodo-tyrosine incorporated proteins(Proteins-methodology,Poster) Tj ETQq1 1 0.784314 rgBT /Overl	0.0	0
92	Regioselective Carbonâ€“Carbon Bond Formation in Proteins with Palladium Catalysis; New Protein Chemistry by Organometallic Chemistry. ChemBioChem, 2007, 8, 159-159.	1.3	0
93	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 ETQq1 1 0.784314 rgBT /Overl	0.0	0
94	Covalently Capturing Protein Interactions in Living Cells by Site-Specific Incorporation of Photo-Cross-Linkable Amino Acids. , 2017, , 159-181.		0
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