

Yoshihiro Shimizu

List of Publications by Year in descending order

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74
papers

5,636
citations

201674

27
h-index

98798

67
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all docs

78
docs citations

78
times ranked

6393
citing authors

#	ARTICLE	IF	CITATIONS
1	Versatile and multiplexed mass spectrometry-based absolute quantification with cell-free-synthesized internal standard peptides. <i>Journal of Proteomics</i> , 2022, 251, 104393.	2.4	2
2	<i>In vitro</i> reconstitution of the <i>Escherichia coli</i> 70S ribosome with a full set of recombinant ribosomal proteins. <i>Journal of Biochemistry</i> , 2022, 171, 227-237.	1.7	6
3	Efficient and Precise Protein Synthesis in a Cell-Free System Using a Set of <i>In Vitro</i> Transcribed tRNAs with Nucleotide Modifications. <i>Methods in Molecular Biology</i> , 2022, 2433, 151-168.	0.9	1
4	Cell-Free Synthesis of Human Endothelin Receptors and Its Application to Ribosome Display. <i>Analytical Chemistry</i> , 2022, 94, 3831-3839.	6.5	6
5	Tracking metabolites at single-cell resolution reveals metabolic dynamics during plant mitosis. <i>Plant Physiology</i> , 2022, , .	4.8	3
6	Capillary microsampling-based single-cell metabolomics by mass spectrometry and its applications in medicine and drug discovery. <i>Cancer Biomarkers</i> , 2022, 33, 437-447.	1.7	0
7	A red light-responsive photoswitch for deep tissue optogenetics. <i>Nature Biotechnology</i> , 2022, 40, 1672-1679.	17.5	22
8	Direct infusion nano-electrospray ionization mass spectrometry for therapeutic drug monitoring of ciprofloxacin and its metabolites in human saliva. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2021, 195, 113866.	2.8	4
9	Boundary-Free Ribosome Compartmentalization by Gene Expression on a Surface. <i>ACS Synthetic Biology</i> , 2021, 10, 609-619.	3.8	4
10	Antisense Oligonucleotide Modified with Disulfide Units Induces Efficient Exon Skipping in <i>mdx</i> Myotubes through Enhanced Membrane Permeability and Nucleus Internalization. <i>ChemBioChem</i> , 2021, 22, 3437-3442.	2.6	6
11	Prospects for Comprehensive Analyses of Circulating Tumor Cells in Tumor Biology. <i>Cancers</i> , 2020, 12, 1135.	3.7	16
12	Mass spectrometry-based absolute quantification of amyloid proteins in pathology tissue specimens: Merits and limitations. <i>PLoS ONE</i> , 2020, 15, e0235143.	2.5	8
13	Reconstituted cell-free protein synthesis using <i>in vitro</i> transcribed tRNAs. <i>Communications Biology</i> , 2020, 3, 350.	4.4	39
14	Phosphorothioate Modification of mRNA Accelerates the Rate of Translation Initiation to Provide More Efficient Protein Synthesis. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 17403-17407.	13.8	32
15	Phosphorothioate Modification of mRNA Accelerates the Rate of Translation Initiation to Provide More Efficient Protein Synthesis. <i>Angewandte Chemie</i> , 2020, 132, 17556-17560.	2.0	4
16	Quantification and targeted detection of ciprofloxacin in dosage form and human urine by direct injection nano-electrospray ionization multi-stage mass spectrometry. <i>Microchemical Journal</i> , 2020, 153, 104534.	4.5	9
17	Versatile whole-organ/body staining and imaging based on electrolyte-gel properties of biological tissues. <i>Nature Communications</i> , 2020, 11, 1982.	12.8	134
18	<i>In vitro</i> reconstitution of functional small ribosomal subunit assembly for comprehensive analysis of ribosomal elements in <i>E. coli</i> . <i>Communications Biology</i> , 2020, 3, 142.	4.4	26

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19	Chemically synthesized circular RNAs with phosphoramidate linkages enable rolling circle translation. <i>Chemical Communications</i> , 2020, 56, 6217-6220.	4.1	15
20	Single-Cell Screening of Tamoxifen Abundance and Effect Using Mass Spectrometry and Raman-Spectroscopy. <i>Analytical Chemistry</i> , 2019, 91, 2710-2718.	6.5	27
21	Single-cell metabolomics by mass spectrometry: Advances, challenges, and future applications. <i>TrAC - Trends in Analytical Chemistry</i> , 2019, 120, 115436.	11.4	65
22	Functional and Structural Analysis of Cell-Free Synthesized Membrane Proteins. <i>Biophysical Journal</i> , 2019, 116, 175a.	0.5	0
23	Phosphorogenic and spontaneous formation of tris(bipyridine)ruthenium in peptide scaffolds. <i>Journal of Peptide Science</i> , 2019, 25, e3158.	1.4	1
24	Live single cell mass spectrometry reveals cancer-specific metabolic profiles of circulating tumor cells. <i>Cancer Science</i> , 2019, 110, 697-706.	3.9	90
25	High-resolution crystal structure of peptidyl-tRNA hydrolase from <i>Thermus thermophilus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 226-235.	2.6	2
26	Cell-free synthesis of stable isotope-labeled internal standards for targeted quantitative proteomics. <i>Synthetic and Systems Biotechnology</i> , 2018, 3, 97-104.	3.7	17
27	A three-dimensional single-cell-resolution whole-brain atlas using CUBIC-X expansion microscopy and tissue clearing. <i>Nature Neuroscience</i> , 2018, 21, 625-637.	14.8	234
28	Quantitative Characterization of Translational Riboregulators Using an <i>in Vitro</i> Transcription-Translation System. <i>ACS Synthetic Biology</i> , 2018, 7, 1269-1278.	3.8	16
29	G-Protein Coupled Receptor Protein Synthesis on a Lipid Bilayer Using a Reconstituted Cell-Free Protein Synthesis System. <i>Life</i> , 2018, 8, 54.	2.4	19
30	Reconstitution of 30S ribosomal subunits in vitro using ribosome biogenesis factors. <i>Rna</i> , 2018, 24, 1512-1519.	3.5	22
31	Robustness of a Reconstituted <i>Escherichia coli</i> Protein Translation System Analyzed by Computational Modeling. <i>ACS Synthetic Biology</i> , 2018, 7, 1964-1972.	3.8	17
32	Chemical Landscape for Tissue Clearing Based on Hydrophilic Reagents. <i>Cell Reports</i> , 2018, 24, 2196-2210.e9.	6.4	221
33	Reaction dynamics analysis of a reconstituted <i>Escherichia coli</i> protein translation system by computational modeling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1336-E1344.	7.1	40
34	Mass spectrometry-based absolute quantification reveals rhythmic variation of mouse circadian clock proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3461-7.	7.1	69
35	Mammalian Reverse Genetics without Crossing Reveals Nr3a as a Short-Sleeper Gene. <i>Cell Reports</i> , 2016, 14, 662-677.	6.4	106
36	Integration of a Reconstituted Cell-free Protein-synthesis System on a Glass Microchip. <i>Analytical Sciences</i> , 2015, 31, 67-71.	1.6	8

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37	Biochemical aspects of bacterial strategies for handling the incomplete translation processes. <i>Frontiers in Microbiology</i> , 2014, 5, 170.	3.5	10
38	Whole-Brain Imaging with Single-Cell Resolution Using Chemical Cocktails and Computational Analysis. <i>Cell</i> , 2014, 157, 726-739.	28.9	1,097
39	The PURE System for Protein Production. <i>Methods in Molecular Biology</i> , 2014, 1118, 275-284.	0.9	30
40	Crystallization and preliminary X-ray analysis of peptidyl-tRNA hydrolase from <i>Thermus thermophilus</i> HB8. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 332-335.	0.7	1
41	Structural basis for the substrate recognition and catalysis of peptidyl-tRNA hydrolase. <i>Nucleic Acids Research</i> , 2012, 40, 10521-10531.	14.5	27
42	Crystal structure analysis of the translation factor RF3 (release factor 3). <i>FEBS Letters</i> , 2012, 586, 3705-3709.	2.8	30
43	Robust in vitro affinity maturation strategy based on interface-focused high-throughput mutational scanning. <i>Biochemical and Biophysical Research Communications</i> , 2012, 428, 395-400.	2.1	31
44	ArfA Recruits RF2 into Stalled Ribosomes. <i>Journal of Molecular Biology</i> , 2012, 423, 624-631.	4.2	73
45	Single molecule imaging of the trans-translation entry process via anchoring of the tagged ribosome. <i>Journal of Biochemistry</i> , 2011, 149, 609-618.	1.7	22
46	Crystallization and preliminary X-ray analysis of peptidyl-tRNA hydrolase from <i>Escherichia coli</i> in complex with the acceptor-T ^Ψ C domain of tRNA. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1566-1569.	0.7	9
47	Application of micro-reactor chip technique for millisecond quenching of deuterium incorporation into 70S ribosomal protein complex. <i>International Journal of Mass Spectrometry</i> , 2011, 302, 132-138.	1.5	13
48	A Highly Controllable Reconstituted Cell-Free System -a Breakthrough in Protein Synthesis Research. <i>Current Pharmaceutical Biotechnology</i> , 2010, 11, 267-271.	1.6	52
49	2P128 A study toward the reconstitution of transcription-translation coupled cell-free translation system(The 48th Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuri</i> , 2010, 50, S104-S105.	0.1	1
50	Mg ²⁺ Dependence of 70 S Ribosomal Protein Flexibility Revealed by Hydrogen/Deuterium Exchange and Mass Spectrometry. <i>Journal of Biological Chemistry</i> , 2010, 285, 5646-5652.	3.4	18
51	PURE Technology. <i>Methods in Molecular Biology</i> , 2010, 607, 11-21.	0.9	93
52	Epitope Mapping Using Ribosome Display in a Reconstituted Cell-Free Protein Synthesis System. <i>Journal of Biochemistry</i> , 2009, 145, 693-700.	1.7	21
53	Real-Time Monitoring of Cell-Free Translation on a Quartz-Crystal Microbalance. <i>Journal of the American Chemical Society</i> , 2009, 131, 9326-9332.	13.7	24
54	70S Ribosomes Bind to Shine-Dalgarno Sequences without Required Dissociations. <i>ChemBioChem</i> , 2008, 9, 870-873.	2.6	13

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55	Development of a Minimal Cell-Free Translation System for the Synthesis of Presecretory and Integral Membrane Proteins. <i>Biotechnology Progress</i> , 2008, 21, 1243-1251.	2.6	60
56	Single-molecule imaging of full protein synthesis by immobilized ribosomes. <i>Nucleic Acids Research</i> , 2008, 36, e70-e70.	14.5	41
57	2P-126 Real time imaging of tRNA dynamics with a zero-mode waveguides during translation(The 46th Tj ETQq1 1,0,784314,rgBT /O 0.1	0.1	0
58	Efficient protein selection based on ribosome display system with purified components. <i>Biochemical and Biophysical Research Communications</i> , 2007, 352, 270-276.	2.1	115
59	Ribosomal Protein S1 Is not Essential for the trans-translation Machinery. <i>Journal of Molecular Biology</i> , 2007, 368, 845-852.	4.2	27
60	Elongation Factor Tu Mutants Expand Amino Acid Tolerance of Protein Biosynthesis System. <i>Journal of the American Chemical Society</i> , 2007, 129, 14458-14462.	13.7	98
61	Protein-based peptide-bond formation by aminoacyl-tRNA protein transferase. <i>Nature</i> , 2007, 449, 867-871.	27.8	79
62	Cell-free translation systems for protein engineering. <i>FEBS Journal</i> , 2006, 273, 4133-4140.	4.7	95
63	Crystal structures of leucyl/phenylalanyl-tRNA-protein transferase and its complex with an aminoacyl-tRNA analog. <i>EMBO Journal</i> , 2006, 25, 5942-5950.	7.8	54
64	SmpB Triggers GTP Hydrolysis of Elongation Factor Tu on Ribosomes by Compensating for the Lack of Codon-Anticodon Interaction during Trans-translation Initiation. <i>Journal of Biological Chemistry</i> , 2006, 281, 15987-15996.	3.4	34
65	Esterification of <i>Escherichia coli</i> tRNAs with D-Histidine and D-Lysine by Aminoacyl-tRNA Synthetases. <i>Bioscience, Biotechnology and Biochemistry</i> , 2005, 69, 1040-1041.	1.3	16
66	Protein synthesis by pure translation systems. <i>Methods</i> , 2005, 36, 299-304.	3.8	331
67	Evidence for the Translation Initiation of Leaderless mRNAs by the Intact 70 S Ribosome without Its Dissociation into Subunits in Eubacteria. <i>Journal of Biological Chemistry</i> , 2004, 279, 8539-8546.	3.4	101
68	A Point Mutation in Ribosomal Protein L7/L12 Reduces Its Ability to Form a Compact Dimer Structure and to Assemble into the GTPase Center. <i>Biochemistry</i> , 2003, 42, 4691-4698.	2.5	9
69	A Novel Screening System for Self-mRNA Targeting Proteins. <i>Journal of Biochemistry</i> , 2003, 133, 485-491.	1.7	8
70	PURE Approach for Cell-Free Translation System.. <i>Seibutsu Butsuri</i> , 2003, 43, 9-14.	0.1	0
71	The role of SmpB protein in trans-translation. <i>FEBS Letters</i> , 2002, 514, 74-77.	2.8	57
72	PURE System. , 2002, , 53-60.		0

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73	Cell-free translation reconstituted with purified components. <i>Nature Biotechnology</i> , 2001, 19, 751-755.	17.5	1,647
74	Transfer RNA Synthesis-Coupled Translation and DNA Replication in a Reconstituted Transcription/Translation System. <i>ACS Synthetic Biology</i> , 0, , .	3.8	5