

# Yoshihiro Shimizu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8855923/publications.pdf>

Version: 2024-02-01

74  
papers

5,636  
citations

201674

27  
h-index

98798

67  
g-index

78  
all docs

78  
docs citations

78  
times ranked

6393  
citing authors

#	ARTICLE	IF	CITATIONS
1	Cell-free translation reconstituted with purified components. <i>Nature Biotechnology</i> , 2001, 19, 751-755.	17.5	1,647
2	Whole-Brain Imaging with Single-Cell Resolution Using Chemical Cocktails and Computational Analysis. <i>Cell</i> , 2014, 157, 726-739.	28.9	1,097
3	Protein synthesis by pure translation systems. <i>Methods</i> , 2005, 36, 299-304.	3.8	331
4	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
5	Chemical Landscape for Tissue Clearing Based on Hydrophilic Reagents. <i>Cell Reports</i> , 2018, 24, 2196-2210.e9.	6.4	221
6	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
7	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
8	Mammalian Reverse Genetics without Crossing Reveals Nr3a as a Short-Sleeper Gene. <i>Cell Reports</i> , 2016, 14, 662-677.	6.4	106
9	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
10	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
11	Cell-free translation systems for protein engineering. <i>FEBS Journal</i> , 2006, 273, 4133-4140.	4.7	95
12	PURE Technology. <i>Methods in Molecular Biology</i> , 2010, 607, 11-21.	0.9	93
13	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
14	Protein-based peptide-bond formation by aminoacyl-tRNA protein transferase. <i>Nature</i> , 2007, 449, 867-871.	27.8	79
15	ArfA Recruits RF2 into Stalled Ribosomes. <i>Journal of Molecular Biology</i> , 2012, 423, 624-631.	4.2	73
16	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
17	Single-cell metabolomics by mass spectrometry: Advances, challenges, and future applications. <i>TrAC - Trends in Analytical Chemistry</i> , 2019, 120, 115436.	11.4	65
18	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

#	ARTICLE	IF	CITATIONS
19	The role of SmpB protein intrans-translation. FEBS Letters, 2002, 514, 74-77.	2.8	57
20	Crystal structures of leucyl/phenylalanyl-tRNA-protein transferase and its complex with an aminoacyl-tRNA analog. EMBO Journal, 2006, 25, 5942-5950.	7.8	54
21	A Highly Controllable Reconstituted Cell-Free System -a Breakthrough in Protein Synthesis Research. Current Pharmaceutical Biotechnology, 2010, 11, 267-271.	1.6	52
22	Single-molecule imaging of full protein synthesis by immobilized ribosomes. Nucleic Acids Research, 2008, 36, e70-e70.	14.5	41
23	Reaction dynamics analysis of a reconstituted <i>Escherichia coli</i> protein translation system by computational modeling. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1336-E1344.	7.1	40
24	Reconstituted cell-free protein synthesis using in vitro transcribed tRNAs. Communications Biology, 2020, 3, 350.	4.4	39
25	SmpB Triggers GTP Hydrolysis of Elongation Factor Tu on Ribosomes by Compensating for the Lack of Codon-Anticodon Interaction during Trans-translation Initiation. Journal of Biological Chemistry, 2006, 281, 15987-15996.	3.4	34
26	Phosphorothioate Modification of mRNA Accelerates the Rate of Translation Initiation to Provide More Efficient Protein Synthesis. Angewandte Chemie - International Edition, 2020, 59, 17403-17407.	13.8	32
27	Robust in vitro affinity maturation strategy based on interface-focused high-throughput mutational scanning. Biochemical and Biophysical Research Communications, 2012, 428, 395-400.	2.1	31
28	Crystal structure analysis of the translation factor RF3 (release factor 3). FEBS Letters, 2012, 586, 3705-3709.	2.8	30
29	The PURE System for Protein Production. Methods in Molecular Biology, 2014, 1118, 275-284.	0.9	30
30	Ribosomal Protein S1 Is not Essential for the trans-translation Machinery. Journal of Molecular Biology, 2007, 368, 845-852.	4.2	27
31	Structural basis for the substrate recognition and catalysis of peptidyl-tRNA hydrolase. Nucleic Acids Research, 2012, 40, 10521-10531.	14.5	27
32	Single-Cell Screening of Tamoxifen Abundance and Effect Using Mass Spectrometry and Raman-Spectroscopy. Analytical Chemistry, 2019, 91, 2710-2718.	6.5	27
33	In vitro reconstitution of functional small ribosomal subunit assembly for comprehensive analysis of ribosomal elements in E. coli. Communications Biology, 2020, 3, 142.	4.4	26
34	Real-Time Monitoring of Cell-Free Translation on a Quartz-Crystal Microbalance. Journal of the American Chemical Society, 2009, 131, 9326-9332.	13.7	24
35	Single molecule imaging of the trans-translation entry process via anchoring of the tagged ribosome. Journal of Biochemistry, 2011, 149, 609-618.	1.7	22
36	Reconstitution of 30S ribosomal subunits in vitro using ribosome biogenesis factors. Rna, 2018, 24, 1512-1519.	3.5	22

#	ARTICLE	IF	CITATIONS
37	A red light-responsive photoswitch for deep tissue optogenetics. <i>Nature Biotechnology</i> , 2022, 40, 1672-1679.	17.5	22
38	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
39	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
40	Mg <sup>2+</sup> 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
41	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
42	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
43	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
44	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
45	Prospects for Comprehensive Analyses of Circulating Tumor Cells in Tumor Biology. <i>Cancers</i> , 2020, 12, 1135.	3.7	16
46	Chemically synthesized circular RNAs with phosphoramidate linkages enable rolling circle translation. <i>Chemical Communications</i> , 2020, 56, 6217-6220.	4.1	15
47	70S Ribosomes Bind to Shine-Dalgarno Sequences without Required Dissociations. <i>ChemBioChem</i> , 2008, 9, 870-873.	2.6	13
48	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
49	Biochemical aspects of bacterial strategies for handling the incomplete translation processes. <i>Frontiers in Microbiology</i> , 2014, 5, 170.	3.5	10
50	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
51	Crystallization and preliminary X-ray analysis of peptidyl-tRNA hydrolase from <i>Escherichia coli</i> in complex with the acceptor-T <sup>1</sup> C domain of tRNA. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1566-1569.	0.7	9
52	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
53	A Novel Screening System for Self-mRNA Targeting Proteins. <i>Journal of Biochemistry</i> , 2003, 133, 485-491.	1.7	8
54	Integration of a Reconstituted Cell-free Protein-synthesis System on a Glass Microchip. <i>Analytical Sciences</i> , 2015, 31, 67-71.	1.6	8

#	ARTICLE	IF	CITATIONS
55	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
56	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
57	<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
58	Cell-Free Synthesis of Human Endothelin Receptors and Its Application to Ribosome Display. <i>Analytical Chemistry</i> , 2022, 94, 3831-3839.	6.5	6
59	Transfer RNA Synthesis-Coupled Translation and DNA Replication in a Reconstituted Transcription/Translation System. <i>ACS Synthetic Biology</i> , 0, , .	3.8	5
60	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
61	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
62	Boundary-Free Ribosome Compartmentalization by Gene Expression on a Surface. <i>ACS Synthetic Biology</i> , 2021, 10, 609-619.	3.8	4
63	Tracking metabolites at single-cell resolution reveals metabolic dynamics during plant mitosis. <i>Plant Physiology</i> , 2022, , .	4.8	3
64	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
65	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
66	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
67	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
68	Phosphorogenic and spontaneous formation of tris(bipyridine)ruthenium in peptide scaffolds. <i>Journal of Peptide Science</i> , 2019, 25, e3158.	1.4	1
69	Efficient and Precise Protein Synthesis in a Cell-Free System Using a Set of In Vitro Transcribed tRNAs with Nucleotide Modifications. <i>Methods in Molecular Biology</i> , 2022, 2433, 151-168.	0.9	1
70	2P-126 Real time imaging of tRNA dynamics with a zero-mode waveguides during translation(The 46th Tj ETQq0 0,0,rgBT /Oyerlock 10	0.1	0
71	Functional and Structural Analysis of Cell-Free Synthesized Membrane Proteins. <i>Biophysical Journal</i> , 2019, 116, 175a.	0.5	0
72	PURE System. , 2002, , 53-60.		0

#	ARTICLE	IF	CITATIONS
73	PURE Approach for Cell-Free Translation System.. Seibutsu Butsuri, 2003, 43, 9-14.	0.1	0
74	Capillary microsampling-based single-cell metabolomics by mass spectrometry and its applications in medicine and drug discovery. Cancer Biomarkers, 2022, 33, 437-447.	1.7	0