

Zoya Ignatova

List of Publications by Year in descending order

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89
papers

4,957
citations

109321

35
h-index

102487

66
g-index

100
all docs

100
docs citations

100
times ranked

6486
citing authors

#	ARTICLE	IF	CITATIONS
1	Transient ribosomal attenuation coordinates protein synthesis and co-translational folding. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 274-280.	8.2	493
2	Emerging roles of tRNA in adaptive translation, signalling dynamics and disease. <i>Nature Reviews Genetics</i> , 2015, 16, 98-112.	16.3	439
3	Inhibition of protein aggregation in vitro and in vivo by a natural osmoprotectant. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 13357-13361.	7.1	296
4	Efficient translation initiation dictates codon usage at gene start. <i>Molecular Systems Biology</i> , 2013, 9, 675.	7.2	281
5	Monitoring protein stability and aggregation in vivo by real-time fluorescent labeling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 523-528.	7.1	226
6	Secondary Structure across the Bacterial Transcriptome Reveals Versatile Roles in mRNA Regulation and Function. <i>PLoS Genetics</i> , 2015, 11, e1005613.	3.5	168
7	Folding at the birth of the nascent chain: coordinating translation with co-translational folding. <i>Current Opinion in Structural Biology</i> , 2011, 21, 25-31.	5.7	162
8	ATF4 couples MYC-dependent translational activity to bioenergetic demands during tumour progression. <i>Nature Cell Biology</i> , 2019, 21, 889-899.	10.3	157
9	Dynamic m ⁶ A methylation facilitates mRNA triaging to stress granules. <i>Life Science Alliance</i> , 2018, 1, e201800113.	2.8	136
10	Alteration of protein function by a silent polymorphism linked to tRNA abundance. <i>PLoS Biology</i> , 2017, 15, e2000779.	5.6	118
11	Trade-offs between tRNA abundance and mRNA secondary structure support smoothing of translation elongation rate. <i>Nucleic Acids Research</i> , 2015, 43, 3022-3032.	14.5	111
12	A Minimal Model of Ribosome Allocation Dynamics Captures Trade-offs in Expression between Endogenous and Synthetic Genes. <i>ACS Synthetic Biology</i> , 2016, 5, 710-720.	3.8	106
13	From the test tube to the cell: Exploring the folding and aggregation of a $\hat{1}^2$ -clam protein. <i>Biopolymers</i> , 2007, 88, 157-163.	2.4	103
14	Reversible and Rapid Transfer-RNA Deactivation as a Mechanism of Translational Repression in Stress. <i>PLoS Genetics</i> , 2013, 9, e1003767.	3.5	94
15	Structure of a hibernating 100S ribosome reveals an inactive conformation of the ribosomal protein S1. <i>Nature Microbiology</i> , 2018, 3, 1115-1121.	13.3	92
16	Bacteria differently regulate mRNA abundance to specifically respond to various stresses. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2016, 374, 20150069.	3.4	82
17	Generic Algorithm to Predict the Speed of Translational Elongation: Implications for Protein Biogenesis. <i>PLoS ONE</i> , 2009, 4, e5036.	2.5	78
18	Unusual Signal Peptide Directs Penicillin Amidase from <i>Escherichia coli</i> to the Tat Translocation Machinery. <i>Biochemical and Biophysical Research Communications</i> , 2002, 291, 146-149.	2.1	77

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19	Global and local depletion of ternary complex limits translational elongation. <i>Nucleic Acids Research</i> , 2010, 38, 4778-4787.	14.5	73
20	The <i>RNA</i> -binding protein Hfq is important for ribosome biogenesis and affects translation fidelity. <i>EMBO Journal</i> , 2018, 37, .	7.8	73
21	Absolute quantification of translational regulation and burden using combined sequencing approaches. <i>Molecular Systems Biology</i> , 2019, 15, e8719.	7.2	61
22	tRNA concentration fine tunes protein solubility. <i>FEBS Letters</i> , 2012, 586, 3336-3340.	2.8	60
23	Depletion of Cognate Charged Transfer RNA Causes Translational Frameshifting within the Expanded CAG Stretch in Huntingtin. <i>Cell Reports</i> , 2013, 3, 148-159.	6.4	60
24	Aggregation of a Slow-Folding Mutant of a β -Clam Protein Proceeds through a Monomeric Nucleus. <i>Biochemistry</i> , 2005, 44, 7266-7274.	2.5	59
25	tRNA overexpression rescues peripheral neuropathy caused by mutations in tRNA synthetase. <i>Science</i> , 2021, 373, 1161-1166.	12.6	59
26	In-cell Aggregation of a Polyglutamine-containing Chimera Is a Multistep Process Initiated by the Flanking Sequence. <i>Journal of Biological Chemistry</i> , 2007, 282, 36736-36743.	3.4	58
27	Effects of Osmolytes on Protein Folding and Aggregation in Cells. <i>Methods in Enzymology</i> , 2007, 428, 355-372.	1.0	57
28	Extended Polyglutamine Tracts Cause Aggregation and Structural Perturbation of an Adjacent β Barrel Protein. <i>Journal of Biological Chemistry</i> , 2006, 281, 12959-12967.	3.4	55
29	Insights into the adaptive response of <i>Arabidopsis thaliana</i> to prolonged thermal stress by ribosomal profiling and RNA-Seq. <i>BMC Plant Biology</i> , 2016, 16, 221.	3.6	55
30	Systematic identification of <i>tRNA^{ome}</i> and its dynamics in <i>actococcus lactis</i> . <i>Molecular Microbiology</i> , 2014, 93, 944-956.	2.5	52
31	eIF3 Associates with 80S Ribosomes to Promote Translation Elongation, Mitochondrial Homeostasis, and Muscle Health. <i>Molecular Cell</i> , 2020, 79, 575-587.e7.	9.7	52
32	Mapping the non-standardized biases of ribosome profiling. <i>Biological Chemistry</i> , 2016, 397, 23-35.	2.5	50
33	Discharging tRNAs: a tug of war between translation and detoxification in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2016, 44, 8324-8334.	14.5	46
34	Germline AGO2 mutations impair RNA interference and human neurological development. <i>Nature Communications</i> , 2020, 11, 5797.	12.8	43
35	Silent mutations in sight: co-variations in tRNA abundance as a key to unravel consequences of silent mutations. <i>Molecular BioSystems</i> , 2010, 6, 1767.	2.9	42
36	Structural Basis for Bacterial Ribosome-Associated Quality Control by RqcH and RqcP. <i>Molecular Cell</i> , 2021, 81, 115-126.e7.	9.7	41

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37	Structural basis of ABCF-mediated resistance to pleuromutilin, lincosamide, and streptogramin A antibiotics in Gram-positive pathogens. <i>Nature Communications</i> , 2021, 12, 3577.	12.8	40
38	FANSe: an accurate algorithm for quantitative mapping of large scale sequencing reads. <i>Nucleic Acids Research</i> , 2012, 40, e83-e83.	14.5	39
39	Timing during translation matters: synonymous mutations in human pathologies influence protein folding and function. <i>Biochemical Society Transactions</i> , 2018, 46, 937-944.	3.4	36
40	Slowing ribosome velocity restores folding and function of mutant CFTR. <i>Journal of Clinical Investigation</i> , 2019, 129, 5236-5253.	8.2	36
41	Optimization of Translation Profiles Enhances Protein Expression and Solubility. <i>PLoS ONE</i> , 2015, 10, e0127039.	2.5	31
42	Computational Aminoacyl-tRNA Synthetase Library Design for Photocaged Tyrosine. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2343.	4.1	31
43	Different sequence signatures in the upstream regions of plant and animal tRNA genes shape distinct modes of regulation. <i>Nucleic Acids Research</i> , 2011, 39, 3331-3339.	14.5	29
44	Pro-sequence and Ca ²⁺ -binding: Implications for Folding and Maturation of Ntn-hydrolase Penicillin Amidase from <i>E.coli</i> . <i>Journal of Molecular Biology</i> , 2005, 348, 999-1014.	4.2	27
45	Towards the characterization of the hidden world of small proteins in <i>Staphylococcus aureus</i> , a proteogenomics approach. <i>PLoS Genetics</i> , 2021, 17, e1009585.	3.5	23
46	Invariable stoichiometry of ribosomal proteins in mouse brain tissues with aging. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 22567-22572.	7.1	22
47	Repurposing tRNAs for nonsense suppression. <i>Nature Communications</i> , 2021, 12, 3850.	12.8	22
48	Genome-wide effects of the antimicrobial peptide apidaecin on translation termination in bacteria. <i>ELife</i> , 2020, 9, .	6.0	22
49	Ca ²⁺ Is a Cofactor Required for Membrane Transport and Maturation and Is a Yield-Determining Factor in High Cell Density Penicillin Amidase Production. <i>Biotechnology Progress</i> , 2008, 21, 432-438.	2.6	20
50	Examining tRNA 3' ends in <i>Escherichia coli</i> : teamwork between CCA-adding enzyme, RNase T, and RNase R. <i>Rna</i> , 2018, 24, 361-370.	3.5	20
51	Not4 and Not5 modulate translation elongation by Rps7A ubiquitination, Rli1 moonlighting, and condensates that exclude eIF5A. <i>Cell Reports</i> , 2021, 36, 109633.	6.4	20
52	An Expanded CAG Repeat in Huntingtin Causes +1 Frameshifting. <i>Journal of Biological Chemistry</i> , 2016, 291, 18505-18513.	3.4	19
53	Systematic probing of the bacterial RNA structurome to reveal new functions. <i>Current Opinion in Microbiology</i> , 2017, 36, 14-19.	5.1	19
54	tRNAArg-Derived Fragments Can Serve as Arginine Donors for Protein Arginylation. <i>Cell Chemical Biology</i> , 2020, 27, 839-849.e4.	5.2	19

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55	Positive epistasis between disease-causing missense mutations and silent polymorphism with effect on mRNA translation velocity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	18
56	Monitoring protein stability in vivo. <i>Microbial Cell Factories</i> , 2005, 4, 23.	4.0	16
57	Assessing cell-specific effects of genetic variations using tRNA microarrays. <i>BMC Genomics</i> , 2019, 20, 549.	2.8	16
58	smORFer: a modular algorithm to detect small ORFs in prokaryotes. <i>Nucleic Acids Research</i> , 2021, 49, e89-e89.	14.5	16
59	Polymerase III transcription is necessary for T cell priming by dendritic cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 22721-22729.	7.1	15
60	Solution Structure and Conformational Flexibility of a Polyketide Synthase Module. <i>Jacs Au</i> , 2021, 1, 2162-2171.	7.9	14
61	Fragments of pro-peptide activate mature penicillin amidase of <i>Alcaligenes faecalis</i> . <i>FEBS Journal</i> , 2003, 270, 4721-4728.	0.2	13
62	Orthogonal Cross-Seeding: An Approach To Explore Protein Aggregates In Living Cells. <i>Biochemistry</i> , 2008, 47, 4196-4200.	2.5	11
63	Somatic expression of <i>unc-54</i> and <i>vha-6</i> mRNAs declines but not pan-neuronal <i>rgef-1</i> and <i>unc-119</i> expression in aging <i>Caenorhabditis elegans</i> . <i>Scientific Reports</i> , 2015, 5, 10692.	3.3	11
64	RqcH and RqcP catalyze processive poly-alanine synthesis in a reconstituted ribosome-associated quality control system. <i>Nucleic Acids Research</i> , 2021, 49, 8355-8369.	14.5	11
65	Expanding the Scope of Orthogonal Translation with Pyrrolysyl-tRNA Synthetases Dedicated to Aromatic Amino Acids. <i>Molecules</i> , 2020, 25, 4418.	3.8	10
66	Stable Polyglutamine Dimers Can Contain β -Hairpins with Interdigitated Side Chainsâ€”But Not α -Helices, β -Nanotubes, β -Pseudohelices, or Steric Zippers. <i>Biophysical Journal</i> , 2014, 106, 1721-1728.	0.5	9
67	Improving the Robustness of Engineered Bacteria to Nutrient Stress Using Programmed Proteolysis. <i>ACS Synthetic Biology</i> , 2022, 11, 1049-1059.	3.8	9
68	mRNAs sequestered in stress granules recover nearly completely for translation. <i>RNA Biology</i> , 2022, 19, 877-884.	3.1	9
69	Probing dimensionality beyond the linear sequence of mRNA. <i>Current Genetics</i> , 2016, 62, 331-334.	1.7	7
70	Quantifying the "escapers"™ among RNA species. <i>Biochemical Society Transactions</i> , 2015, 43, 1215-1220.	3.4	6
71	Growth-Rate Dependent Regulation of tRNA Level and Charging in <i>Bacillus licheniformis</i> . <i>Journal of Molecular Biology</i> , 2017, 429, 3102-3112.	4.2	6
72	Fine-tuning the metabolic rewiring and adaptation of translational machinery during an epithelial-mesenchymal transition in breast cancer cells. <i>Cancer & Metabolism</i> , 2020, 8, 8.	5.0	5

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73	Codon Resolution Analysis of Ribosome Profiling Data. <i>Methods in Molecular Biology</i> , 2021, 2252, 251-268.	0.9	5
74	Estimation of peptide elongation times from ribosome profiling spectra. <i>Nucleic Acids Research</i> , 2021, 49, 5124-5142.	14.5	5
75	The Effect of Synonymous Single-Nucleotide Polymorphisms on an Atypical Cystic Fibrosis Clinical Presentation. <i>Life</i> , 2021, 11, 14.	2.4	5
76	Chapter 3 A Fluorescent Window Into Protein Folding and Aggregation in Cells. <i>Methods in Cell Biology</i> , 2008, 89, 59-70.	1.1	4
77	A Method for Direct Measurement of Protein Stability In Vivo. <i>Methods in Molecular Biology</i> , 2009, 490, 165-178.	0.9	4
78	Tuning innate immunity by translation. <i>Biochemical Society Transactions</i> , 2015, 43, 1247-1252.	3.4	4
79	Competition for amino acid flux among translation, growth and detoxification in bacteria. <i>RNA Biology</i> , 2018, 15, 1-4.	3.1	4
80	A rare heterozygous <i>TREM2</i> coding variant identified in familial clustering of dementia affects an intrinsically disordered protein region and function of TREM2. <i>Human Mutation</i> , 2020, 41, 169-181.	2.5	4
81	Global assessment of the integrated stress response in CF patient-derived airway and intestinal tissues. <i>Journal of Cystic Fibrosis</i> , 2020, 19, 1021-1026.	0.7	4
82	Rewiring host activities for synthetic circuit production: a translation view. <i>Biotechnology Letters</i> , 2017, 39, 25-31.	2.2	3
83	Constraints on error rate revealed by computational study of Gâ€¦U tautomerization in translation. <i>Nucleic Acids Research</i> , 2021, 49, 11823-11833.	14.5	3
84	A Novel <i>Caenorhabditis Elegans</i> Proteinopathy Model Shows Changes in mRNA Translational Frameshifting During Aging. <i>Cellular Physiology and Biochemistry</i> , 2019, 52, 970-983.	1.6	3
85	Improved <i>A. faecalis</i> Penicillin Amidase Mutant Retains the Thermodynamic and pH Stability of the Wild Type Enzyme. <i>Protein Journal</i> , 2010, 29, 181-187.	1.6	2
86	A flexible approach to assess fluorescence decay functions in complex energy transfer systems. <i>BMC Biophysics</i> , 2015, 8, 5.	4.4	2
87	Immunoprecipitation Assay to Quantify the Amount of tRNAs associated with Their Interacting Proteins in Tissue and Cell Culture. <i>Bio-protocol</i> , 2022, 12, e4335.	0.4	1
88	Characterizing Genetic Parts and Devices Using RNA Sequencing. <i>Methods in Molecular Biology</i> , 2021, 2229, 175-187.	0.9	0
89	Survival Advantage of Lymphadenectomy in Patients with Ovarian Cancer. <i>Cancer Investigation</i> , 2022, , 1-17.	1.3	0