

Zoya Ignatova

List of Publications by Year in descending order

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89
papers

4,957
citations

109137

35
h-index

106150

65
g-index

100
all docs

100
docs citations

100
times ranked

6486
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	0.2	1
2	Improving the Robustness of Engineered Bacteria to Nutrient Stress Using Programmed Proteolysis. <i>ACS Synthetic Biology</i> , 2022, 11, 1049-1059.	1.9	9
3	Survival Advantage of Lymphadenectomy in Patients with Ovarian Cancer. <i>Cancer Investigation</i> , 2022, , 1-17.	0.6	0
4	mRNAs sequestered in stress granules recover nearly completely for translation. <i>RNA Biology</i> , 2022, 19, 877-884.	1.5	9
5	Structural Basis for Bacterial Ribosome-Associated Quality Control by RqcH and RqcP. <i>Molecular Cell</i> , 2021, 81, 115-126.e7.	4.5	41
6	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, .	3.3	18
7	Codon Resolution Analysis of Ribosome Profiling Data. <i>Methods in Molecular Biology</i> , 2021, 2252, 251-268.	0.4	5
8	Estimation of peptide elongation times from ribosome profiling spectra. <i>Nucleic Acids Research</i> , 2021, 49, 5124-5142.	6.5	5
9	Repurposing tRNAs for nonsense suppression. <i>Nature Communications</i> , 2021, 12, 3850.	5.8	22
10	smORFer: a modular algorithm to detect small ORFs in prokaryotes. <i>Nucleic Acids Research</i> , 2021, 49, e89-e89.	6.5	16
11	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.	1.5	23
12	Structural basis of ABCF-mediated resistance to pleuromutilin, lincosamide, and streptogramin A antibiotics in Gram-positive pathogens. <i>Nature Communications</i> , 2021, 12, 3577.	5.8	40
13	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.	6.5	11
14	Not4 and Not5 modulate translation elongation by Rps7A ubiquitination, Rli1 moonlighting, and condensates that exclude eIF5A. <i>Cell Reports</i> , 2021, 36, 109633.	2.9	20
15	tRNA overexpression rescues peripheral neuropathy caused by mutations in tRNA synthetase. <i>Science</i> , 2021, 373, 1161-1166.	6.0	59
16	Constraints on error rate revealed by computational study of Gâ€¦U tautomerization in translation. <i>Nucleic Acids Research</i> , 2021, 49, 11823-11833.	6.5	3
17	Characterizing Genetic Parts and Devices Using RNA Sequencing. <i>Methods in Molecular Biology</i> , 2021, 2229, 175-187.	0.4	0
18	Solution Structure and Conformational Flexibility of a Polyketide Synthase Module. <i>Jacs Au</i> , 2021, 1, 2162-2171.	3.6	14

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19	The Effect of Synonymous Single-Nucleotide Polymorphisms on an Atypical Cystic Fibrosis Clinical Presentation. <i>Life</i> , 2021, 11, 14.	1.1	5
20	A rare heterozygous <i>TREM2</i> coding variant identified in familial clustering of dementia affects an intrinsically disordered protein region and function of <i>TREM2</i> . <i>Human Mutation</i> , 2020, 41, 169-181.	1.1	4
21	Expanding the Scope of Orthogonal Translation with Pyrrolysyl-tRNA Synthetases Dedicated to Aromatic Amino Acids. <i>Molecules</i> , 2020, 25, 4418.	1.7	10
22	Germline <i>AGO2</i> mutations impair RNA interference and human neurological development. <i>Nature Communications</i> , 2020, 11, 5797.	5.8	43
23	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.	2.4	5
24	tRNA ^{Arg} -Derived Fragments Can Serve as Arginine Donors for Protein Arginylation. <i>Cell Chemical Biology</i> , 2020, 27, 839-849.e4.	2.5	19
25	eIF3 Associates with 80S Ribosomes to Promote Translation Elongation, Mitochondrial Homeostasis, and Muscle Health. <i>Molecular Cell</i> , 2020, 79, 575-587.e7.	4.5	52
26	Genome-wide effects of the antimicrobial peptide apidaecin on translation termination in bacteria. <i>ELife</i> , 2020, 9, .	2.8	22
27	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.	0.3	4
28	Assessing cell-specific effects of genetic variations using tRNA microarrays. <i>BMC Genomics</i> , 2019, 20, 549.	1.2	16
29	<i>ATF4</i> couples <i>MYC</i> -dependent translational activity to bioenergetic demands during tumour progression. <i>Nature Cell Biology</i> , 2019, 21, 889-899.	4.6	157
30	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.	3.3	22
31	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.	3.3	15
32	Absolute quantification of translational regulation and burden using combined sequencing approaches. <i>Molecular Systems Biology</i> , 2019, 15, e8719.	3.2	61
33	Computational Aminoacyl-tRNA Synthetase Library Design for Photocaged Tyrosine. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2343.	1.8	31
34	Slowing ribosome velocity restores folding and function of mutant <i>CFTR</i> . <i>Journal of Clinical Investigation</i> , 2019, 129, 5236-5253.	3.9	36
35	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.	1.1	3
36	Competition for amino acid flux among translation, growth and detoxification in bacteria. <i>RNA Biology</i> , 2018, 15, 1-4.	1.5	4

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37	The <i>RNA</i> -binding protein Hfq is important for ribosome biogenesis and affects translation fidelity. <i>EMBO Journal</i> , 2018, 37, .	3.5	73
38	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.	1.6	20
39	Structure of a hibernating 100S ribosome reveals an inactive conformation of the ribosomal protein S1. <i>Nature Microbiology</i> , 2018, 3, 1115-1121.	5.9	92
40	Timing during translation matters: synonymous mutations in human pathologies influence protein folding and function. <i>Biochemical Society Transactions</i> , 2018, 46, 937-944.	1.6	36
41	Dynamic m ⁶ A methylation facilitates mRNA triaging to stress granules. <i>Life Science Alliance</i> , 2018, 1, e201800113.	1.3	136
42	Systematic probing of the bacterial RNA structure to reveal new functions. <i>Current Opinion in Microbiology</i> , 2017, 36, 14-19.	2.3	19
43	Growth-Rate Dependent Regulation of tRNA Level and Charging in <i>Bacillus licheniformis</i> . <i>Journal of Molecular Biology</i> , 2017, 429, 3102-3112.	2.0	6
44	Rewiring host activities for synthetic circuit production: a translation view. <i>Biotechnology Letters</i> , 2017, 39, 25-31.	1.1	3
45	Alteration of protein function by a silent polymorphism linked to tRNA abundance. <i>PLoS Biology</i> , 2017, 15, e2000779.	2.6	118
46	Discharging tRNAs: a tug of war between translation and detoxification in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2016, 44, 8324-8334.	6.5	46
47	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.	1.9	106
48	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.	1.6	55
49	An Expanded CAG Repeat in Huntingtin Causes +1 Frameshifting. <i>Journal of Biological Chemistry</i> , 2016, 291, 18505-18513.	1.6	19
50	Probing dimensionality beyond the linear sequence of mRNA. <i>Current Genetics</i> , 2016, 62, 331-334.	0.8	7
51	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.	1.6	82
52	Mapping the non-standardized biases of ribosome profiling. <i>Biological Chemistry</i> , 2016, 397, 23-35.	1.2	50
53	Quantifying the "escapers" among RNA species. <i>Biochemical Society Transactions</i> , 2015, 43, 1215-1220.	1.6	6
54	Tuning innate immunity by translation. <i>Biochemical Society Transactions</i> , 2015, 43, 1247-1252.	1.6	4

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55	Optimization of Translation Profiles Enhances Protein Expression and Solubility. PLoS ONE, 2015, 10, e0127039.	1.1	31
56	Somatic expression of unc-54 and vha-6 mRNAs declines but not pan-neuronal rgef-1 and unc-119 expression in aging Caenorhabditis elegans. Scientific Reports, 2015, 5, 10692.	1.6	11
57	Trade-offs between tRNA abundance and mRNA secondary structure support smoothing of translation elongation rate. Nucleic Acids Research, 2015, 43, 3022-3032.	6.5	111
58	A flexible approach to assess fluorescence decay functions in complex energy transfer systems. BMC Biophysics, 2015, 8, 5.	4.4	2
59	Emerging roles of tRNA in adaptive translation, signalling dynamics and disease. Nature Reviews Genetics, 2015, 16, 98-112.	7.7	439
60	Secondary Structure across the Bacterial Transcriptome Reveals Versatile Roles in mRNA Regulation and Function. PLoS Genetics, 2015, 11, e1005613.	1.5	168
61	Systematic identification of <i>tRNA^{ome}</i> and its dynamics in <i>actococcus lactis</i> . Molecular Microbiology, 2014, 93, 944-956.	1.2	52
62	Stable Polyglutamine Dimers Can Contain β^2 -Hairpins with Interdigitated Side Chains”But Not β^2 -Helices, β^2 -Nanotubes, β^2 -Pseudohelices, or Steric Zippers. Biophysical Journal, 2014, 106, 1721-1728.	0.2	9
63	Depletion of Cognate Charged Transfer RNA Causes Translational Frameshifting within the Expanded CAG Stretch in Huntingtin. Cell Reports, 2013, 3, 148-159.	2.9	60
64	Reversible and Rapid Transfer-RNA Deactivation as a Mechanism of Translational Repression in Stress. PLoS Genetics, 2013, 9, e1003767.	1.5	94
65	Efficient translation initiation dictates codon usage at gene start. Molecular Systems Biology, 2013, 9, 675.	3.2	281
66	FANSe: an accurate algorithm for quantitative mapping of large scale sequencing reads. Nucleic Acids Research, 2012, 40, e83-e83.	6.5	39
67	tRNA concentration fine tunes protein solubility. FEBS Letters, 2012, 586, 3336-3340.	1.3	60
68	Folding at the birth of the nascent chain: coordinating translation with co-translational folding. Current Opinion in Structural Biology, 2011, 21, 25-31.	2.6	162
69	Different sequence signatures in the upstream regions of plant and animal tRNA genes shape distinct modes of regulation. Nucleic Acids Research, 2011, 39, 3331-3339.	6.5	29
70	Improved A. faecalis Penicillin Amidase Mutant Retains the Thermodynamic and pH Stability of the Wild Type Enzyme. Protein Journal, 2010, 29, 181-187.	0.7	2
71	Global and local depletion of ternary complex limits translational elongation. Nucleic Acids Research, 2010, 38, 4778-4787.	6.5	73
72	Silent mutations in sight: co-variations in tRNA abundance as a key to unravel consequences of silent mutations. Molecular BioSystems, 2010, 6, 1767.	2.9	42

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73	Generic Algorithm to Predict the Speed of Translational Elongation: Implications for Protein Biogenesis. PLoS ONE, 2009, 4, e5036.	1.1	78
74	Transient ribosomal attenuation coordinates protein synthesis and co-translational folding. Nature Structural and Molecular Biology, 2009, 16, 274-280.	3.6	493
75	A Method for Direct Measurement of Protein Stability In Vivo. Methods in Molecular Biology, 2009, 490, 165-178.	0.4	4
76	Ca ²⁺ Is a Cofactor Required for Membrane Transport and Maturation and Is a Yield-Determining Factor in High Cell Density Penicillin Amidase Production. Biotechnology Progress, 2008, 21, 432-438.	1.3	20
77	Orthogonal Cross-Seeding: An Approach To Explore Protein Aggregates In Living Cells. Biochemistry, 2008, 47, 4196-4200.	1.2	11
78	Chapter 3 A Fluorescent Window Into Protein Folding and Aggregation in Cells. Methods in Cell Biology, 2008, 89, 59-70.	0.5	4
79	In-cell Aggregation of a Polyglutamine-containing Chimera Is a Multistep Process Initiated by the Flanking Sequence. Journal of Biological Chemistry, 2007, 282, 36736-36743.	1.6	58
80	Effects of Osmolytes on Protein Folding and Aggregation in Cells. Methods in Enzymology, 2007, 428, 355-372.	0.4	57
81	From the test tube to the cell: Exploring the folding and aggregation of a β^2 -clam protein. Biopolymers, 2007, 88, 157-163.	1.2	103
82	Inhibition of protein aggregation in vitro and in vivo by a natural osmoprotectant. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 13357-13361.	3.3	296
83	Extended Polyglutamine Tracts Cause Aggregation and Structural Perturbation of an Adjacent β^2 Barrel Protein. Journal of Biological Chemistry, 2006, 281, 12959-12967.	1.6	55
84	Aggregation of a Slow-Folding Mutant of a β^2 -Clam Protein Proceeds through a Monomeric Nucleus. Biochemistry, 2005, 44, 7266-7274.	1.2	59
85	Pro-sequence and Ca ²⁺ -binding: Implications for Folding and Maturation of Ntn-hydrolase Penicillin Amidase from E.coli. Journal of Molecular Biology, 2005, 348, 999-1014.	2.0	27
86	Monitoring protein stability in vivo. Microbial Cell Factories, 2005, 4, 23.	1.9	16
87	Monitoring protein stability and aggregation in vivo by real-time fluorescent labeling. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 523-528.	3.3	226
88	Fragments of pro-peptide activate mature penicillin amidase of Alcaligenes faecalis. FEBS Journal, 2003, 270, 4721-4728.	0.2	13
89	Unusual Signal Peptide Directs Penicillin Amidase from Escherichia coli to the Tat Translocation Machinery. Biochemical and Biophysical Research Communications, 2002, 291, 146-149.	1.0	77