

# Anton A Komar

## List of Publications by Year in descending order

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81  
papers

4,936  
citations

109321

35  
h-index

98798

67  
g-index

83  
all docs

83  
docs citations

83  
times ranked

6165  
citing authors

#	ARTICLE	IF	CITATIONS
1	Synonymous codon substitutions affect ribosome traffic and protein folding during in vitro translation. <i>FEBS Letters</i> , 1999, 462, 387-391.	2.8	343
2	Cellular IRES-mediated translation. <i>Cell Cycle</i> , 2011, 10, 229-240.	2.6	336
3	A pause for thought along the co-translational folding pathway. <i>Trends in Biochemical Sciences</i> , 2009, 34, 16-24.	7.5	301
4	Synonymous Codons Direct Cotranslational Folding toward Different Protein Conformations. <i>Molecular Cell</i> , 2016, 61, 341-351.	9.7	297
5	Internal Ribosome Entry Sites in Cellular mRNAs: Mystery of Their Existence. <i>Journal of Biological Chemistry</i> , 2005, 280, 23425-23428.	3.4	236
6	Silent SNPs: impact on gene function and phenotype. <i>Pharmacogenomics</i> , 2007, 8, 1075-1080.	1.3	215
7	Activities of Ligatin and MCT-1/DENR in eukaryotic translation initiation and ribosomal recycling. <i>Genes and Development</i> , 2010, 24, 1787-1801.	5.9	204
8	Curaxins: Anticancer Compounds That Simultaneously Suppress NF- $\kappa$ B and Activate p53 by Targeting FACT. <i>Science Translational Medicine</i> , 2011, 3, 95ra74.	12.4	199
9	GENETICS: SNPs, Silent But Not Invisible. <i>Science</i> , 2007, 315, 466-467.	12.6	193
10	The Zipper Model of Translational Control. <i>Cell</i> , 2003, 113, 519-531.	28.9	185
11	Cotranslational protein folding on the ribosome monitored in real time. <i>Science</i> , 2015, 350, 1104-1107.	12.6	178
12	Whole-genome sequencing identifies a recurrent functional synonymous mutation in melanoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 13481-13486.	7.1	147
13	Cotranslational Folding of Globin. <i>Journal of Biological Chemistry</i> , 1997, 272, 10646-10651.	3.4	135
14	A Unique ISR Program Determines Cellular Responses to Chronic Stress. <i>Molecular Cell</i> , 2017, 68, 885-900.e6.	9.7	135
15	The Yin and Yang of codon usage. <i>Human Molecular Genetics</i> , 2016, 25, R77-R85.	2.9	114
16	Codon and Codon-Pair Usage Tables (CoCoPUTs): Facilitating Genetic Variation Analyses and Recombinant Gene Design. <i>Journal of Molecular Biology</i> , 2019, 431, 2434-2441.	4.2	100
17	L13a Blocks 48S Assembly: Role of a General Initiation Factor in mRNA-Specific Translational Control. <i>Molecular Cell</i> , 2007, 25, 113-126.	9.7	88
18	A new framework for understanding IRES-mediated translation. <i>Gene</i> , 2012, 502, 75-86.	2.2	78

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19	The hnRNA-Binding Proteins hnRNP L and PTB Are Required for Efficient Translation of the Cat-1 Arginine/Lysine Transporter mRNA during Amino Acid Starvation. <i>Molecular and Cellular Biology</i> , 2009, 29, 2899-2912.	2.3	74
20	Genome-Wide Polysome Profiling Reveals an Inflammation-Responsive Posttranscriptional Operon in Gamma Interferon-Activated Monocytes. <i>Molecular and Cellular Biology</i> , 2009, 29, 458-470.	2.3	74
21	Human ribosomal protein L13a is dispensable for canonical ribosome function but indispensable for efficient rRNA methylation. <i>Rna</i> , 2007, 13, 2224-2237.	3.5	69
22	Internal initiation drives the synthesis of Ure2 protein lacking the prion domain and affects [URE3] propagation in yeast cells. <i>EMBO Journal</i> , 2003, 22, 1199-1209.	7.8	68
23	Single synonymous mutation in factor IX alters protein properties and underlies haemophilia B. <i>Journal of Medical Genetics</i> , 2017, 54, 338-345.	3.2	66
24	Characterization of Mammalian eIF2A and Identification of the Yeast Homolog. <i>Journal of Biological Chemistry</i> , 2002, 277, 37079-37087.	3.4	64
25	Characterization of Coding Synonymous and Non-Synonymous Variants in ADAMTS13 Using Ex Vivo and In Silico Approaches. <i>PLoS ONE</i> , 2012, 7, e38864.	2.5	61
26	Requirement of rRNA Methylation for 80S Ribosome Assembly on a Cohort of Cellular Internal Ribosome Entry Sites. <i>Molecular and Cellular Biology</i> , 2011, 31, 4482-4499.	2.3	60
27	Cotranslational heme binding to nascent globin chains. <i>FEBS Letters</i> , 1993, 326, 261-263.	2.8	55
28	Novel Characteristics of the Biological Properties of the Yeast <i>Saccharomyces cerevisiae</i> Eukaryotic Initiation Factor 2A. <i>Journal of Biological Chemistry</i> , 2005, 280, 15601-15611.	3.4	49
29	Exploring Internal Ribosome Entry Sites as Therapeutic Targets. <i>Frontiers in Oncology</i> , 2015, 5, 233.	2.8	48
30	Nonuniform size distribution of nascent globin peptides, evidence for pause localization sites, and a cotranslational protein-folding model. <i>The Protein Journal</i> , 1991, 10, 445-453.	1.1	46
31	Sequence analysis of SARS-CoV-2 genome reveals features important for vaccine design. <i>Scientific Reports</i> , 2020, 10, 15643.	3.3	46
32	Characterization of hibernating ribosomes in mammalian cells. <i>Cell Cycle</i> , 2011, 10, 2691-2702.	2.6	44
33	A Retrospective on eIF2 $\alpha$ and Not the Alpha Subunit of eIF2. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2054.	4.1	43
34	Kinetics of translation of $^{13}\text{C}$ crystallin and its circularly permuted variant in an in vitro cell-free system: possible relations to codon distribution and protein folding. <i>FEBS Letters</i> , 1995, 376, 195-198.	2.8	42
35	Effects of codon optimization on coagulation factor IX translation and structure: Implications for protein and gene therapies. <i>Scientific Reports</i> , 2019, 9, 15449.	3.3	38
36	Birth, life and death of nascent polypeptide chains. <i>Biotechnology Journal</i> , 2011, 6, 623-640.	3.5	37

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37	A Gene-Specific Method for Predicting Hemophilia-Causing Point Mutations. <i>Journal of Molecular Biology</i> , 2013, 425, 4023-4033.	4.2	30
38	The eIF2A knockout mouse. <i>Cell Cycle</i> , 2016, 15, 3115-3120.	2.6	30
39	Salicylates Trigger Protein Synthesis Inhibition in a Protein Kinase R-like Endoplasmic Reticulum Kinase-dependent Manner. <i>Journal of Biological Chemistry</i> , 2007, 282, 10164-10171.	3.4	29
40	Roles of the negatively charged N-terminal extension of <i>Saccharomyces cerevisiae</i> ribosomal protein S5 revealed by characterization of a yeast strain containing human ribosomal protein S5. <i>Rna</i> , 2007, 13, 2116-2128.	3.5	28
41	Yeast strains with N-terminally truncated ribosomal protein S5: implications for the evolution, structure and function of the Rps5/Rps7 proteins. <i>Nucleic Acids Research</i> , 2010, 38, 1261-1272.	14.5	25
42	Unraveling co-translational protein folding: Concepts and methods. <i>Methods</i> , 2018, 137, 71-81.	3.8	25
43	Functions of unconventional mammalian translational GTPases GTPBP1 and GTPBP2. <i>Genes and Development</i> , 2018, 32, 1226-1241.	5.9	25
44	A Small Stem Loop Element Directs Internal Initiation of the URE2 Internal Ribosome Entry Site in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2008, 283, 19011-19025.	3.4	23
45	A Single Synonymous Variant (c.354G>A [p.P118P]) in ADAMTS13 Confers Enhanced Specific Activity. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5734.	4.1	23
46	Role of the uS9/yS16 C-terminal tail in translation initiation and elongation in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2019, 47, 806-823.	14.5	20
47	Gene variants of coagulation related proteins that interact with SARS-CoV-2. <i>PLoS Computational Biology</i> , 2021, 17, e1008805.	3.2	18
48	Rps5-Rps16 communication is essential for efficient translation initiation in yeast <i>S. cerevisiae</i> . <i>Nucleic Acids Research</i> , 2014, 42, 8537-8555.	14.5	14
49	eIF2A knockout mice reveal decreased life span and metabolic syndrome. <i>FASEB Journal</i> , 2021, 35, e21990.	0.5	14
50	Insights into the Mechanism of Ribosomal Incorporation of Mammalian L13a Protein during Ribosome Biogenesis. <i>Molecular and Cellular Biology</i> , 2013, 33, 2829-2842.	2.3	13
51	Properties of the ternary complex formed by yeast eIF4E, p20 and mRNA. <i>Scientific Reports</i> , 2018, 8, 6707.	3.3	13
52	Splicing dysregulation contributes to the pathogenicity of several F9 exonic point variants. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2019, 7, e840.	1.2	13
53	Integrated stress response control of granulosa cell translation and proliferation during normal ovarian follicle development. <i>Molecular Human Reproduction</i> , 2021, 27, .	2.8	11
54	A Code Within a Code: How Codons Fine-Tune Protein Folding in the Cell. <i>Biochemistry (Moscow)</i> , 2021, 86, 976-991.	1.5	9

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55	U6atac snRNA stem-loop interacts with U12 p55 RNA binding protein and is functionally interchangeable with the U12 apical stem-loop III. <i>Scientific Reports</i> , 2016, 6, 31393.	3.3	8
56	The Art of Gene Redesign and Recombinant Protein Production: Approaches and Perspectives. <i>Topics in Medicinal Chemistry</i> , 2016, , 161-177.	0.8	8
57	Conserved structures formed by heterogeneous RNA sequences drive silencing of an inflammation responsive post-transcriptional operon. <i>Nucleic Acids Research</i> , 2017, 45, 12987-13003.	14.5	8
58	A Structurally Conserved RNA Element within SARS-CoV-2 ORF1a RNA and S mRNA Regulates Translation in Response to Viral S Protein-Induced Signaling in Human Lung Cells. <i>Journal of Virology</i> , 2022, 96, JVI0167821.	3.4	8
59	Non-canonical role of cancer-associated mutant SEC23B in the ribosome biogenesis pathway. <i>Human Molecular Genetics</i> , 2018, 27, 3154-3164.	2.9	6
60	Eukaryote-specific extensions in ribosomal proteins of the small subunit: Structure and function. <i>Translation</i> , 2015, 3, e999576.	2.9	5
61	In Silico Evaluation of Cyclophilin Inhibitors as Potential Treatment for SARS-CoV-2. <i>Open Forum Infectious Diseases</i> , 2021, 8, ofab189.	0.9	5
62	Using SecM Arrest Sequence as a Tool to Isolate Ribosome Bound Polypeptides. <i>Journal of Visualized Experiments</i> , 2012, , .	0.3	4
63	The "periodic table" of the genetic code: A new way to look at the code and the decoding process. <i>Translation</i> , 2016, 4, e1234431.	2.9	4
64	Distinct signatures of codon and codon pair usage in 32 primary tumor types in the novel database CancerCoCoPUTs for cancer-specific codon usage. <i>Genome Medicine</i> , 2021, 13, 122.	8.2	4
65	Cell-free Translation: Preparation and Validation of Translation-competent Extracts from <i>Saccharomyces cerevisiae</i> . <i>Bio-protocol</i> , 2021, 11, e4093.	0.4	4
66	Immunotherapy of ovarian cancer with a monoclonal antibody specific for the extracellular domain of anti-Müllerian hormone receptor II. <i>Oncotarget</i> , 2020, 11, 1894-1910.	1.8	4
67	Structural, functional, and immunogenicity implications of <i>F9</i> gene recoding. <i>Blood Advances</i> , 2022, 6, 3932-3944.	5.2	4
68	Aurintricarboxylic acid is a canonical disruptor of the TAZ-TEAD transcriptional complex. <i>PLoS ONE</i> , 2022, 17, e0266143.	2.5	4
69	Communication between RACK1/Asc1 and uS3 (Rps3) is essential for RACK1/Asc1 function in yeast <i>Saccharomyces cerevisiae</i> . <i>Gene</i> , 2019, 706, 69-76.	2.2	3
70	The Murine Genome Contains Two Functional Kininogen Genes Leading to Tissue Specific Expression of High Molecular Weight Kininogen (HK) and Expression of a Novel HK Splice Variant.. <i>Blood</i> , 2004, 104, 3979-3979.	1.4	3
71	Ribosome profiling of HEK293T cells overexpressing codon optimized coagulation factor IX. <i>F1000Research</i> , 2020, 9, 174.	1.6	3
72	Isolation of Ribosome Bound Nascent Polypeptides <i>in vitro</i> to Identify Translational Pause Sites Along mRNA. <i>Journal of Visualized Experiments</i> , 2012, , .	0.3	2

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73	Mutually exclusive amino acid residues of L13a are responsible for its ribosomal incorporation and translational silencing leading to resolution of inflammation. <i>Rna</i> , 2019, 25, 1377-1392.	3.5	2
74	Ribosome profiling of HEK293T cells overexpressing codon optimized coagulation factor IX. <i>F1000Research</i> , 2020, 9, 174.	1.6	2
75	IRES-mediated translation of the pro-apoptotic Bcl2 family member PUMA. <i>Translation</i> , 2013, 1, e24391.	2.9	1
76	From Alpha to Beta â€“ a co-translational way to fold?. <i>Cell Cycle</i> , 2022, 21, 1663-1666.	2.6	1
77	PUM1 mediates the posttranscriptional regulation of human fetal hemoglobin. <i>Blood Advances</i> , 2022, 6, 6016-6022.	5.2	1
78	â€œNakedâ€•FACT is unstable. <i>Cell Cycle</i> , 2013, 12, 2347-2347.	2.6	0
79	Translation Elongation in Eukaryotes. , 2004, , 224-229.		0
80	Ribosomal protein L13a inhibits translation by blocking the formation of 80S complex on the GAIT element containing mRNA: Dependence on the translation initiation factor eIF4G. <i>FASEB Journal</i> , 2006, 20, A108.	0.5	0
81	Protein Synthesis/Degradation: Translation â€“ Components, Initiation, Elongation, Termination, and Regulation. , 2022, , .		0