

# 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	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
2	Structural, functional, and immunogenicity implications of <i>F9</i> gene recoding. <i>Blood Advances</i> , 2022, 6, 3932-3944.	5.2	4
3	Aurintricarboxylic acid is a canonical disruptor of the TAZ-TEAD transcriptional complex. <i>PLoS ONE</i> , 2022, 17, e0266143.	2.5	4
4	From Alpha to Beta â€“ a co-translational way to fold?. <i>Cell Cycle</i> , 2022, 21, 1663-1666.	2.6	1
5	PUM1 mediates the posttranscriptional regulation of human fetal hemoglobin. <i>Blood Advances</i> , 2022, 6, 6016-6022.	5.2	1
6	Protein Synthesis/Degradation: Translation â€“ Components, Initiation, Elongation, Termination, and Regulation. , 2022, , .		0
7	Gene variants of coagulation related proteins that interact with SARS-CoV-2. <i>PLoS Computational Biology</i> , 2021, 17, e1008805.	3.2	18
8	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
9	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
10	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
11	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
12	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
13	eIF2Aâ€™knockout mice reveal decreased life span and metabolic syndrome. <i>FASEB Journal</i> , 2021, 35, e21990.	0.5	14
14	Sequence analysis of SARS-CoV-2 genome reveals features important for vaccine design. <i>Scientific Reports</i> , 2020, 10, 15643.	3.3	46
15	A Retrospective on eIF2Aâ€™ and Not the Alpha Subunit of eIF2. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2054.	4.1	43
16	Ribosome profiling of HEK293T cells overexpressing codon optimized coagulation factor IX. <i>F1000Research</i> , 2020, 9, 174.	1.6	2
17	Immunotherapy of ovarian cancer with a monoclonal antibody specific for the extracellular domain of anti-MÃ¼llerian hormone receptor II. <i>Oncotarget</i> , 2020, 11, 1894-1910.	1.8	4
18	Ribosome profiling of HEK293T cells overexpressing codon optimized coagulation factor IX. <i>F1000Research</i> , 2020, 9, 174.	1.6	3

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19	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
20	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
21	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
22	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
23	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
24	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
25	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
26	Properties of the ternary complex formed by yeast eIF4E, p20 and mRNA. <i>Scientific Reports</i> , 2018, 8, 6707.	3.3	13
27	Unraveling co-translational protein folding: Concepts and methods. <i>Methods</i> , 2018, 137, 71-81.	3.8	25
28	Functions of unconventional mammalian translational GTPases GTPBP1 and GTPBP2. <i>Genes and Development</i> , 2018, 32, 1226-1241.	5.9	25
29	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
30	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
31	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
32	A Unique ISR Program Determines Cellular Responses to Chronic Stress. <i>Molecular Cell</i> , 2017, 68, 885-900.e6.	9.7	135
33	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
34	The eIF2A knockout mouse. <i>Cell Cycle</i> , 2016, 15, 3115-3120.	2.6	30
35	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
36	The Yin and Yang of codon usage. <i>Human Molecular Genetics</i> , 2016, 25, R77-R85.	2.9	114

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37	The Art of Gene Redesign and Recombinant Protein Production: Approaches and Perspectives. Topics in Medicinal Chemistry, 2016, , 161-177.	0.8	8
38	Synonymous Codons Direct Cotranslational Folding toward Different Protein Conformations. Molecular Cell, 2016, 61, 341-351.	9.7	297
39	Exploring Internal Ribosome Entry Sites as Therapeutic Targets. Frontiers in Oncology, 2015, 5, 233.	2.8	48
40	Eukaryote-specific extensions in ribosomal proteins of the small subunit: Structure and function. Translation, 2015, 3, e999576.	2.9	5
41	Cotranslational protein folding on the ribosome monitored in real time. Science, 2015, 350, 1104-1107.	12.6	178
42	Rps5-Rps16 communication is essential for efficient translation initiation in yeast <i>S. cerevisiae</i> . Nucleic Acids Research, 2014, 42, 8537-8555.	14.5	14
43	A Gene-Specific Method for Predicting Hemophilia-Causing Point Mutations. Journal of Molecular Biology, 2013, 425, 4023-4033.	4.2	30
44	Whole-genome sequencing identifies a recurrent functional synonymous mutation in melanoma. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 13481-13486.	7.1	147
45	Insights into the Mechanism of Ribosomal Incorporation of Mammalian L13a Protein during Ribosome Biogenesis. Molecular and Cellular Biology, 2013, 33, 2829-2842.	2.3	13
46	“Naked” FACT is unstable. Cell Cycle, 2013, 12, 2347-2347.	2.6	0
47	IRES-mediated translation of the pro-apoptotic Bcl2 family member PUMA. Translation, 2013, 1, e24391.	2.9	1
48	Isolation of Ribosome Bound Nascent Polypeptides <i>in vitro</i> to Identify Translational Pause Sites Along mRNA. Journal of Visualized Experiments, 2012, , .	0.3	2
49	Using SecM Arrest Sequence as a Tool to Isolate Ribosome Bound Polypeptides. Journal of Visualized Experiments, 2012, , .	0.3	4
50	A new framework for understanding IRES-mediated translation. Gene, 2012, 502, 75-86.	2.2	78
51	Characterization of Coding Synonymous and Non-Synonymous Variants in ADAMTS13 Using Ex Vivo and In Silico Approaches. PLoS ONE, 2012, 7, e38864.	2.5	61
52	Birth, life and death of nascent polypeptide chains. Biotechnology Journal, 2011, 6, 623-640.	3.5	37
53	Curaxins: Anticancer Compounds That Simultaneously Suppress NF- $\kappa$ B and Activate p53 by Targeting FACT. Science Translational Medicine, 2011, 3, 95ra74.	12.4	199
54	Characterization of hibernating ribosomes in mammalian cells. Cell Cycle, 2011, 10, 2691-2702.	2.6	44

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55	Cellular IRES-mediated translation. <i>Cell Cycle</i> , 2011, 10, 229-240.	2.6	336
56	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
57	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
58	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
59	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
60	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
61	A pause for thought along the co-translational folding pathway. <i>Trends in Biochemical Sciences</i> , 2009, 34, 16-24.	7.5	301
62	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
63	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
64	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
65	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
66	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
67	Silent SNPs: impact on gene function and phenotype. <i>Pharmacogenomics</i> , 2007, 8, 1075-1080.	1.3	215
68	GENETICS: SNPs, Silent But Not Invisible. <i>Science</i> , 2007, 315, 466-467.	12.6	193
69	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
70	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
71	Internal Ribosome Entry Sites in Cellular mRNAs: Mystery of Their Existence. <i>Journal of Biological Chemistry</i> , 2005, 280, 23425-23428.	3.4	236
72	Translation Elongation in Eukaryotes. , 2004, , 224-229.		0

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73	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.. Blood, 2004, 104, 3979-3979.	1.4	3
74	Internal initiation drives the synthesis of Ure2 protein lacking the prion domain and affects [URE3] propagation in yeast cells. EMBO Journal, 2003, 22, 1199-1209.	7.8	68
75	The Zipper Model of Translational Control. Cell, 2003, 113, 519-531.	28.9	185
76	Characterization of Mammalian eIF2A and Identification of the Yeast Homolog. Journal of Biological Chemistry, 2002, 277, 37079-37087.	3.4	64
77	Synonymous codon substitutions affect ribosome traffic and protein folding during in vitro translation. FEBS Letters, 1999, 462, 387-391.	2.8	343
78	Cotranslational Folding of Globin. Journal of Biological Chemistry, 1997, 272, 10646-10651.	3.4	135
79	Kinetics of translation of $\hat{I}^{3B}$ crystallin and its circularly permuted variant in an in vitro cell-free system: possible relations to codon distribution and protein folding. FEBS Letters, 1995, 376, 195-198.	2.8	42
80	Cotranslational heme binding to nascent globin chains. FEBS Letters, 1993, 326, 261-263.	2.8	55
81	Nonuniform size distribution of nascent globin peptides, evidence for pause localization sites, and a cotranslational protein-folding model. The Protein Journal, 1991, 10, 445-453.	1.1	46