Alex V Kochetov

List of Publications by Year
in descending order

29 papers	914 citations	471509 17 h-index	501196 28 g-index
29 all docs	29 docs citations	29 times ranked	1344 citing authors

#	Article	IF	Citations
1	Abnormal mTOR Activity in Pediatric Autoimmune Neuropsychiatric and MIA-Associated Autism Spectrum Disorders. International Journal of Molecular Sciences, 2022, 23, 967.	4.1	3
2	Do Autism Spectrum and Autoimmune Disorders Share Predisposition Gene Signature Due to mTOR Signaling Pathway Controlling Expression?. International Journal of Molecular Sciences, 2021, 22, 5248.	4.1	7
3	NLR Genes Related Transcript Sets in Potato Cultivars Bearing Genetic Material of Wild Mexican Solanum Species. Agronomy, 2021, 11, 2426.	3.0	2
4	Conversion of hulled into naked barley by Cas endonuclease-mediated knockout of the NUD gene. BMC Plant Biology, 2020, 20, 255.	3.6	33
5	The mechanism of potato resistance to Globodera rostochiensis: comparison of root transcriptomes of resistant and susceptible Solanum phureja genotypes. BMC Plant Biology, 2020, 20, 350.	3.6	5
6	Choice of the Promoter for Tissue and Developmental Stage-Specific Gene Expression. Methods in Molecular Biology, 2020, 2124, 69-106.	0.9	3
7	Genetic control of anthocyanin pigmentation of potato tissues. BMC Genetics, 2019, 20, 27.	2.7	24
8	The mTOR Signaling Pathway Activity and Vitamin D Availability Control the Expression of Most Autism Predisposition Genes. International Journal of Molecular Sciences, 2019, 20, 6332.	4.1	21
9	AltORFev facilitates the prediction of alternative open reading frames in eukaryotic mRNAs. Bioinformatics, 2017, 33, 923-925.	4.1	9
10	Differential expression of NBS-LRR-encoding genes in the root transcriptomes of two Solanum phureja genotypes with contrasting resistance to Globodera rostochiensis. BMC Plant Biology, 2017, 17, 251.	3.6	15
11	Expression of an extracellular ribonuclease gene increases resistance to Cucumber mosaic virus in tobacco. BMC Plant Biology, 2016, 16, 246.	3.6	20
12	mRNA Translational Enhancers as a Tool for Plant Gene Engineering. , 2015, , 187-196.		2
13	The alien replicon: Artificial genetic constructs to direct the synthesis of transmissible selfâ€replicating RNAs. BioEssays, 2014, 36, 1204-1212.	2.5	1
14	Hidden coding potential of eukaryotic genomes: nonAUG started ORFs. Journal of Biomolecular Structure and Dynamics, 2013, 31, 103-114.	3.5	25
15	Extensive Translatome Remodeling during ER Stress Response in Mammalian Cells. PLoS ONE, 2012, 7, e35915.	2.5	32
16	Possible link between the synthesis of GR alpha isoforms and eIF2 alpha phosphorylation state. Medical Hypotheses, 2012, 79, 709-712.	1.5	3
17	Simple database to select promoters for plant transgenesis. Transgenic Research, 2012, 21, 429-437.	2.4	25
18	Alternative translation start sites are conserved in eukaryotic genomes. Nucleic Acids Research, 2011, 39, 567-577.	14.5	133

#	Article	IF	Citations
19	Tandem termination signal in plant mRNAs. Gene, 2011, 481, 1-6.	2.2	4
20	Interrelations between the Nucleotide Context of Human Start AUG Codon, N-end Amino Acids of the Encoded Protein and Initiation of Translation. Journal of Biomolecular Structure and Dynamics, 2010, 27, 611-618.	3.5	22
21	On nucleotide solvent accessibility in RNA structure. Gene, 2010, 463, 41-48.	2.2	10
22	Alternative translation start sites and hidden coding potential of eukaryotic mRNAs. BioEssays, 2008, 30, 683-691.	2.5	163
23	uORFs, reinitiation and alternative translation start sites in human mRNAs. FEBS Letters, 2008, 582, 1293-1297.	2.8	57
24	AUG_hairpin: prediction of a downstream secondary structure influencing the recognition of a translation start site. BMC Bioinformatics, 2007, 8, 318.	2.6	46
25	Protection of transgenic tobacco plants expressing bovine pancreatic ribonuclease against tobacco mosaic virus. Plant Cell Reports, 2007, 26, 1121-1126.	5.6	28
26	The role of alternative translation start sites in the generation of human protein diversity. Molecular Genetics and Genomics, 2005, 273, 491-496.	2.1	61
27	AUG codons at the beginning of protein coding sequences are frequent in eukaryotic mRNAs with a suboptimal start codon context. Bioinformatics, 2005, 21, 837-840.	4.1	44
28	Translational polymorphism as a potential source of plant proteins variety in Arabidopsis thaliana. Bioinformatics, 2004, 20, 445-447.	4.1	19
29	Eukaryotic mRNAs encoding abundant and scarce proteins are statistically dissimilar in many structural features. FEBS Letters, 1998, 440, 351-355.	2.8	97