

Ruslan I Sadreyev

List of Publications by Year in descending order

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Version: 2024-02-01

111
papers

8,589
citations

66234

42
h-index

53109

85
g-index

117
all docs

117
docs citations

117
times ranked

16040
citing authors

#	ARTICLE	IF	CITATIONS
1	HERVH-derived lncRNAs negatively regulate chromatin targeting and remodeling mediated by CHD7. <i>Life Science Alliance</i> , 2022, 5, e202101127.	1.3	3
2	Mammalian brain glycoproteins exhibit diminished glycan complexity compared to other tissues. <i>Nature Communications</i> , 2022, 13, 275.	5.8	47
3	Transcriptional regulation of neural stem cell expansion in the adult hippocampus. <i>ELife</i> , 2022, 11, .	2.8	16
4	Bone marrow endothelial dysfunction promotes myeloid cell expansion in cardiovascular disease. , 2022, 1, 28-44.		32
5	DNA replication fork speed underlies cell fate changes and promotes reprogramming. <i>Nature Genetics</i> , 2022, 54, 318-327.	9.4	38
6	The schizophrenia-associated variant in SLC39A8 alters protein glycosylation in the mouse brain. <i>Molecular Psychiatry</i> , 2022, 27, 1405-1415.	4.1	11
7	Human enteric viruses autonomously shape inflammatory bowel disease phenotype through divergent innate immunomodulation. <i>Science Immunology</i> , 2022, 7, eabn6660.	5.6	38
8	Regulation of chromatin accessibility by the histone chaperone CAF-1 sustains lineage fidelity. <i>Nature Communications</i> , 2022, 13, 2350.	5.8	8
9	DEPCOD: a tool to detect and visualize co-evolution of protein domains. <i>Nucleic Acids Research</i> , 2022, , .	6.5	0
10	Phenotypic continuum between Waardenburg syndrome and idiopathic hypogonadotropic hypogonadism in humans with SOX10 variants. <i>Genetics in Medicine</i> , 2021, 23, 629-636.	1.1	9
11	A unique subset of glycolytic tumour-propagating cells drives squamous cell carcinoma. <i>Nature Metabolism</i> , 2021, 3, 182-195.	5.1	17
12	Growth Hormone Releasing Hormone Reduces Plasma Markers of Immune Activation and Hepatic Immune Pathways in Nonalcoholic Fatty Liver Disease. <i>Journal of the Endocrine Society</i> , 2021, 5, A628-A629.	0.1	0
13	Astrocytic interleukin-3 programs microglia and limits Alzheimer's disease. <i>Nature</i> , 2021, 595, 701-706.	13.7	157
14	Dissecting dual roles of MyoD during lineage conversion to mature myocytes and myogenic stem cells. <i>Genes and Development</i> , 2021, 35, 1209-1228.	2.7	20
15	tiRNA signaling via stress-regulated vesicle transfer in the hematopoietic niche. <i>Cell Stem Cell</i> , 2021, 28, 2090-2103.e9.	5.2	20
16	Characterization of the blood microbiota in children with Celiac disease. <i>Current Research in Microbial Sciences</i> , 2021, 2, 100069.	1.4	0
17	Collective regulation of chromatin modifications predicts replication timing during cell cycle. <i>Cell Reports</i> , 2021, 37, 109799.	2.9	20
18	Pilot study of genome-wide differences in DNA methylation among older adults with normal cognition and mild cognitive impairment, with and without neuropsychiatric symptoms. <i>Alzheimer's and Dementia</i> , 2021, 17, .	0.4	2

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19	Low NCOR2 levels in multiple myeloma patients drive multidrug resistance via MYC upregulation. <i>Blood Cancer Journal</i> , 2021, 11, 194.	2.8	5
20	Genome-wide analysis identifies cis-acting elements regulating mRNA polyadenylation and translation during vertebrate oocyte maturation. <i>Rna</i> , 2020, 26, 324-344.	1.6	23
21	Histone Lysine Methylation Dynamics Control EGFR DNA Copy-Number Amplification. <i>Cancer Discovery</i> , 2020, 10, 306-325.	7.7	31
22	A MicroRNA Linking Human Positive Selection and Metabolic Disorders. <i>Cell</i> , 2020, 183, 684-701.e14.	13.5	46
23	The lysine demethylase KDM4A controls the cell-cycle expression of replicative canonical histone genes. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194624.	0.9	7
24	S-phase Enriched Non-coding RNAs Regulate Gene Expression and Cell Cycle Progression. <i>Cell Reports</i> , 2020, 31, 107629.	2.9	11
25	Distinct functions of tissue-resident and circulating memory Th2 cells in allergic airway disease. <i>Journal of Experimental Medicine</i> , 2020, 217, .	4.2	72
26	Liver X receptors are required for thymic resilience and T cell output. <i>Journal of Experimental Medicine</i> , 2020, 217, .	4.2	20
27	Amyloid- β 42/40 ratio drives tau pathology in 3D human neural cell culture models of Alzheimer's disease. <i>Nature Communications</i> , 2020, 11, 1377.	5.8	88
28	A FAK/HDAC5 signaling axis controls osteocyte mechanotransduction. <i>Nature Communications</i> , 2020, 11, 3282.	5.8	57
29	A post-transcriptional program of chemoresistance by AU-rich elements and TTP in quiescent leukemic cells. <i>Genome Biology</i> , 2020, 21, 33.	3.8	22
30	Differential Plasma Protein Regulation and Statin Effects in Human Immunodeficiency Virus (HIV)-Infected and Non-HIV-Infected Patients Utilizing a Proteomics Approach. <i>Journal of Infectious Diseases</i> , 2020, 222, 929-939.	1.9	16
31	The Histone Deacetylase SIRT6 Restrains Transcription Elongation via Promoter-Proximal Pausing. <i>Molecular Cell</i> , 2019, 75, 683-699.e7.	4.5	50
32	The murine IgH locus contains a distinct DNA sequence motif for the chromatin regulatory factor CTCF. <i>Journal of Biological Chemistry</i> , 2019, 294, 13580-13592.	1.6	7
33	Exploiting the Zonulin Mouse Model to Establish the Role of Primary Impaired Gut Barrier Function on Microbiota Composition and Immune Profiles. <i>Frontiers in Immunology</i> , 2019, 10, 2233.	2.2	41
34	Exercise reduces inflammatory cell production and cardiovascular inflammation via instruction of hematopoietic progenitor cells. <i>Nature Medicine</i> , 2019, 25, 1761-1771.	15.2	157
35	Inducible histone K-to-M mutations are dynamic tools to probe the physiological role of site-specific histone methylation in vitro and in vivo. <i>Nature Cell Biology</i> , 2019, 21, 1449-1461.	4.6	40
36	New and Preliminary Evidence on Altered Oral and Gut Microbiota in Individuals with Autism Spectrum Disorder (ASD): Implications for ASD Diagnosis and Subtyping Based on Microbial Biomarkers. <i>Nutrients</i> , 2019, 11, 2128.	1.7	87

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37	The RNA Helicase DDX6 Controls Cellular Plasticity by Modulating P-Body Homeostasis. <i>Cell Stem Cell</i> , 2019, 25, 622-638.e13.	5.2	82
38	Mapping global and local coevolution across 600 species to identify novel homologous recombination repair genes. <i>Genome Research</i> , 2019, 29, 439-448.	2.4	37
39	Single-Cell RNA-seq: Introduction to Bioinformatics Analysis. <i>Current Protocols in Molecular Biology</i> , 2019, 127, e92.	2.9	10
40	Human gut derived-organoids provide model to study gluten response and effects of microbiota-derived molecules in celiac disease. <i>Scientific Reports</i> , 2019, 9, 7029.	1.6	77
41	Mitochondrial Dysfunction in <i>C.Âelegans</i> Activates Mitochondrial Relocalization and Nuclear Hormone Receptor-Dependent Detoxification Genes. <i>Cell Metabolism</i> , 2019, 29, 1182-1191.e4.	7.2	55
42	Exploration of CTCF post-translation modifications uncovers Serine-224 phosphorylation by PLK1 at pericentric regions during the G2/M transition. <i>ELife</i> , 2019, 8, .	2.8	18
43	Salt-inducible kinases dictate parathyroid hormone 1 receptor action in bone development and remodeling. <i>Journal of Clinical Investigation</i> , 2019, 129, 5187-5203.	3.9	28
44	Human Fetal-Derived Enterospheres Provide Insights on Intestinal Development and a Novel Model to Study Necrotizing Enterocolitis (NEC). <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2018, 5, 549-568.	2.3	60
45	An inactivating mutation in the histone deacetylase SIRT6 causes human perinatal lethality. <i>Genes and Development</i> , 2018, 32, 373-388.	2.7	41
46	Nudt21 Controls Cell Fate by Connecting Alternative Polyadenylation to Chromatin Signaling. <i>Cell</i> , 2018, 172, 106-120.e21.	13.5	123
47	Whole Genome Next-Generation Sequencing Mutation Identification in <i>Pseudomonas aeruginosa</i> . <i>Current Protocols in Molecular Biology</i> , 2018, 124, e69.	2.9	1
48	RNA-seq: Basic Bioinformatics Analysis. <i>Current Protocols in Molecular Biology</i> , 2018, 124, e68.	2.9	44
49	Mutant GNAS drives pancreatic tumorigenesis by inducing PKA-mediated SIK suppression and reprogramming lipid metabolism. <i>Nature Cell Biology</i> , 2018, 20, 811-822.	4.6	124
50	The Association of Obesity and Cardiometabolic Traits With IncidentÂHFpEF and HFREF. <i>JACC: Heart Failure</i> , 2018, 6, 701-709.	1.9	254
51	Prospective Isolation of Poised iPSC Intermediates Reveals Principles of Cellular Reprogramming. <i>Cell Stem Cell</i> , 2018, 23, 289-305.e5.	5.2	60
52	Direct Reprogramming of Mouse Fibroblasts into Functional Skeletal Muscle Progenitors. <i>Stem Cell Reports</i> , 2018, 10, 1505-1521.	2.3	74
53	The surveillance of pre-mRNA splicing is an early step in <i>C. elegans</i> RNAi of endogenous genes. <i>Genes and Development</i> , 2018, 32, 670-681.	2.7	27
54	Cell of origin dictates aggression and stem cell number in acute lymphoblastic leukemia. <i>Leukemia</i> , 2018, 32, 1860-1865.	3.3	23

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55	Next-Generation Sequencing for Identification of EMS-Induced Mutations in <i>Caenorhabditis elegans</i> . <i>Current Protocols in Molecular Biology</i> , 2017, 117, 7.29.1-7.29.12.	2.9	19
56	Polycomb Repressive Complex 1 Generates Discrete Compacted Domains that Change during Differentiation. <i>Molecular Cell</i> , 2017, 65, 432-446.e5.	4.5	287
57	T _H 17 Cytokine Responses in Lyme Disease Correlate with <i>Borrelia burgdorferi</i> Antibodies During Early Infection in Patients with Erythema Migrans and with Autoantibodies Late in the Illness in Patients with Antibiotic-Refractory Lyme Arthritis. <i>Clinical Infectious Diseases</i> , 2017, 64, cix002.	2.9	48
58	Mutation of a nucleosome compaction region disrupts Polycomb-mediated axial patterning. <i>Science</i> , 2017, 355, 1081-1084.	6.0	133
59	Maintenance of macrophage transcriptional programs and intestinal homeostasis by epigenetic reader SP140. <i>Science Immunology</i> , 2017, 2, .	5.6	54
60	Macrophages Facilitate Electrical Conduction in the Heart. <i>Cell</i> , 2017, 169, 510-522.e20.	13.5	703
61	Phf8 loss confers resistance to depression-like and anxiety-like behaviors in mice. <i>Nature Communications</i> , 2017, 8, 15142.	5.8	35
62	Widespread changes in nucleosome accessibility without changes in nucleosome occupancy during a rapid transcriptional induction. <i>Genes and Development</i> , 2017, 31, 451-462.	2.7	90
63	DUSP9 Modulates DNA Hypomethylation in Female Mouse Pluripotent Stem Cells. <i>Cell Stem Cell</i> , 2017, 20, 706-719.e7.	5.2	63
64	Genetic Intersection of Tsix and Hedgehog Signaling during the Initiation of X-Chromosome Inactivation. <i>Developmental Cell</i> , 2017, 43, 359-371.e6.	3.1	14
65	TOX Regulates Growth, DNA Repair, and Genomic Instability in T-cell Acute Lymphoblastic Leukemia. <i>Cancer Discovery</i> , 2017, 7, 1336-1353.	7.7	48
66	Polycomb Repressive Complex 2 Methylates Elongin A to Regulate Transcription. <i>Molecular Cell</i> , 2017, 68, 872-884.e6.	4.5	50
67	IRF3 and type I interferons fuel a fatal response to myocardial infarction. <i>Nature Medicine</i> , 2017, 23, 1481-1487.	15.2	358
68	PAR-TERRA directs homologous sex chromosome pairing. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 620-631.	3.6	48
69	HELZ2 Is an IFN Effector Mediating Suppression of Dengue Virus. <i>Frontiers in Microbiology</i> , 2017, 8, 240.	1.5	38
70	IGF2 mRNA binding protein-2 is a tumor promoter that drives cancer proliferation through its client mRNAs IGF2 and HMGA1. <i>ELife</i> , 2017, 6, .	2.8	77
71	Genome-wide identification of autosomal genes with allelic imbalance of chromatin state. <i>PLoS ONE</i> , 2017, 12, e0182568.	1.1	16
72	Shank is a dose-dependent regulator of Cav1 calcium current and CREB target expression. <i>ELife</i> , 2017, 6, .	2.8	16

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73	Osteoblastic Cell-Derived Extracellular Vesicles Transfer Small RNAs That Alter the Physiology of Hematopoietic Cells <i>in Vivo</i> . <i>Blood</i> , 2017, 130, 93-93.	0.6	0
74	Survival in Quiescence Requires the Euchromatic Deployment of Clr4/SUV39H by Argonaute-Associated Small RNAs. <i>Molecular Cell</i> , 2016, 64, 1088-1101.	4.5	27
75	Influence of maternal breast milk ingestion on acquisition of the intestinal microbiome in preterm infants. <i>Microbiome</i> , 2016, 4, 68.	4.9	155
76	A Specialized Mechanism of Translation Mediated by FXR1a-Associated MicroRNP in Cellular Quiescence. <i>Molecular Cell</i> , 2016, 61, 760-773.	4.5	85
77	Single-cell transcriptional analysis of normal, aberrant, and malignant hematopoiesis in zebrafish. <i>Journal of Experimental Medicine</i> , 2016, 213, 979-992.	4.2	69
78	SIRT6 Suppresses Pancreatic Cancer through Control of Lin28b. <i>Cell</i> , 2016, 165, 1401-1415.	13.5	227
79	T Cell Immune Deficiency in <i>zap70</i> Mutant Zebrafish. <i>Molecular and Cellular Biology</i> , 2016, 36, 2868-2876.	1.1	37
80	Sox2 Suppresses Gastric Tumorigenesis in Mice. <i>Cell Reports</i> , 2016, 16, 1929-1941.	2.9	61
81	Inhibition of Dihydroorotate Dehydrogenase Overcomes Differentiation Blockade in Acute Myeloid Leukemia. <i>Cell</i> , 2016, 167, 171-186.e15.	13.5	353
82	CAT7 and cat7l Long Non-coding RNAs Tune Polycomb Repressive Complex 1 Function during Human and Zebrafish Development. <i>Journal of Biological Chemistry</i> , 2016, 291, 19558-19572.	1.6	32
83	Single-cell imaging of normal and malignant cell engraftment into optically clear <i>prkdc</i> -null SCID zebrafish. <i>Journal of Experimental Medicine</i> , 2016, 213, 2575-2589.	4.2	65
84	SIKs control osteocyte responses to parathyroid hormone. <i>Nature Communications</i> , 2016, 7, 13176.	5.8	124
85	Tribbles ortholog NIP1-3 and bZIP transcription factor CEBP-1 regulate a <i>Caenorhabditis elegans</i> intestinal immune surveillance pathway. <i>BMC Biology</i> , 2016, 14, 105.	1.7	35
86	Chromatin topology is coupled to Polycomb group protein subnuclear organization. <i>Nature Communications</i> , 2016, 7, 10291.	5.8	176
87	Inhibiting fungal multidrug resistance by disrupting an activator-Mediator interaction. <i>Nature</i> , 2016, 530, 485-489.	13.7	120
88	Tumor cells can follow distinct evolutionary paths to become resistant to epidermal growth factor receptor inhibition. <i>Nature Medicine</i> , 2016, 22, 262-269.	15.2	768
89	Enhancer regions show high histone H3.3 turnover that changes during differentiation. <i>ELife</i> , 2016, 5, .	2.8	86
90	Using homology relations within a database markedly boosts protein sequence similarity search. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 7003-7008.	3.3	8

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91	Allelic Imbalance Is a Prevalent and Tissue-Specific Feature of the Mouse Transcriptome. <i>Genetics</i> , 2015, 200, 537-549.	1.2	38
92	ATRX Promotes Binding of PRC2 to Xist RNA and Polycomb Targets. <i>FASEB Journal</i> , 2015, 29, 361.3.	0.2	0
93	BRCA1 establishes DNA damage signaling and pericentric heterochromatin of the X chromosome in male meiosis. <i>Journal of Cell Biology</i> , 2014, 205, 663-675.	2.3	74
94	ATRX Directs Binding of PRC2 to Xist RNA and Polycomb Targets. <i>Cell</i> , 2014, 159, 869-883.	13.5	182
95	The Long Noncoding RNAs NEAT1 and MALAT1 Bind Active Chromatin Sites. <i>Molecular Cell</i> , 2014, 55, 791-802.	4.5	578
96	Informatics for Molecular Biologists. <i>Current Protocols in Molecular Biology</i> , 2014, 106, 19.0.1-2.	2.9	0
97	H3K27 modifications define segmental regulatory domains in the <i>Drosophila bithorax</i> complex. <i>ELife</i> , 2014, 3, e02833.	2.8	111
98	Bimodal quantitative relationships between histone modifications for X-linked and autosomal loci. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 6949-6954.	3.3	9
99	X-chromosome hyperactivation in mammals via nonlinear relationships between chromatin states and transcription. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 56-61.	3.6	88
100	Spreading of X chromosome inactivation via a hierarchy of defined Polycomb stations. <i>Genome Research</i> , 2012, 22, 1864-1876.	2.4	143
101	Phenotypic categorization of genetic skin diseases reveals new relations between phenotypes, genes and pathways. <i>Bioinformatics</i> , 2009, 25, 2891-2896.	1.8	5
102	Structure similarity measure with penalty for close non-equivalent residues. <i>Bioinformatics</i> , 2009, 25, 1259-1263.	1.8	17
103	COMPASS server for homology detection: improved statistical accuracy, speed and functionality. <i>Nucleic Acids Research</i> , 2009, 37, W90-W94.	6.5	27
104	Discreteâ€œcontinuous duality of protein structure space. <i>Current Opinion in Structural Biology</i> , 2009, 19, 321-328.	2.6	60
105	Considering scores between unrelated proteins in the search database improves profile comparison. <i>BMC Bioinformatics</i> , 2009, 10, 399.	1.2	1
106	Accurate statistical model of comparison between multiple sequence alignments. <i>Nucleic Acids Research</i> , 2008, 36, 2240-2248.	6.5	19
107	COMPASS server for remote homology inference. <i>Nucleic Acids Research</i> , 2007, 35, W653-W658.	6.5	30
108	Exploring dynamics of protein structure determination and homology-based prediction to estimate the number of superfamilies and folds. , 2006, 6, 6.		23

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109	Quality of alignment comparison by COMPASS improves with inclusion of diverse confident homologs. <i>Bioinformatics</i> , 2004, 20, 818-828.	1.8	28
110	Estimates of statistical significance for comparison of individual positions in multiple sequence alignments. <i>BMC Bioinformatics</i> , 2004, 5, 106.	1.2	8
111	COMPASS: A Tool for Comparison of Multiple Protein Alignments with Assessment of Statistical Significance. <i>Journal of Molecular Biology</i> , 2003, 326, 317-336.	2.0	263