Ruslan I Sadreyev

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	HERVH-derived IncRNAs negatively regulate chromatin targeting and remodeling mediated by CHD7. Life Science Alliance, 2022, 5, e202101127.	2.8	3
2	Mammalian brain glycoproteins exhibit diminished glycan complexity compared to other tissues. Nature Communications, 2022, 13, 275.	12.8	47
3	Transcriptional regulation of neural stem cell expansion in the adult hippocampus. ELife, 2022, 11, .	6.0	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. Nature Genetics, 2022, 54, 318-327.	21.4	38
6	The schizophrenia-associated variant in SLC39A8 alters protein glycosylation in the mouse brain. Molecular Psychiatry, 2022, 27, 1405-1415.	7.9	11
7	Human enteric viruses autonomously shape inflammatory bowel disease phenotype through divergent innate immunomodulation. Science Immunology, 2022, 7, eabn6660.	11.9	38
8	Regulation of chromatin accessibility by the histone chaperone CAF-1 sustains lineage fidelity. Nature Communications, 2022, 13, 2350.	12.8	8
9	DEPCOD: a tool to detect and visualize co-evolution of protein domains. Nucleic Acids Research, 2022,	14.5	0
10	Phenotypic continuum between Waardenburg syndrome and idiopathic hypogonadotropic hypogonadism in humans with SOX10 variants. Genetics in Medicine, 2021, 23, 629-636.	2.4	9
11	A unique subset of glycolytic tumour-propagating cells drives squamous cell carcinoma. Nature Metabolism, 2021, 3, 182-195.	11.9	17
12	Growth Hormone Releasing Hormone Reduces Plasma Markers of Immune Activation and Hepatic Immune Pathways in Nonalcoholic Fatty Liver Disease. Journal of the Endocrine Society, 2021, 5, A628-A629.	0.2	0
13	Astrocytic interleukin-3 programs microglia and limits Alzheimer's disease. Nature, 2021, 595, 701-706.	27.8	157
14	Dissecting dual roles of MyoD during lineage conversion to mature myocytes and myogenic stem cells. Genes and Development, 2021, 35, 1209-1228.	5.9	20
15	tiRNA signaling via stress-regulated vesicle transfer in the hematopoietic niche. Cell Stem Cell, 2021, 28, 2090-2103.e9.	11.1	20
16	Characterization of the blood microbiota in children with Celiac disease. Current Research in Microbial Sciences, 2021, 2, 100069.	2.3	0
17	Collective regulation of chromatin modifications predicts replication timing during cell cycle. Cell Reports, 2021, 37, 109799.	6.4	20
18	Pilot study of genomeâ€wide differences in DNA methylation among older adults with normal cognition and mild cognitive impairment, with and without neuropsychiatric symptoms. Alzheimer's and Dementia, 2021, 17, .	0.8	2

Ruslan I Sadreyev

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19	Low NCOR2 levels in multiple myeloma patients drive multidrug resistance via MYC upregulation. Blood Cancer Journal, 2021, 11, 194.	6.2	5
20	Genome-wide analysis identifies <i>cis</i> -acting elements regulating mRNA polyadenylation and translation during vertebrate oocyte maturation. Rna, 2020, 26, 324-344.	3.5	23
21	Histone Lysine Methylation Dynamics Control <i>EGFR</i> DNA Copy-Number Amplification. Cancer Discovery, 2020, 10, 306-325.	9.4	31
22	A MicroRNA Linking Human Positive Selection and Metabolic Disorders. Cell, 2020, 183, 684-701.e14.	28.9	46
23	The lysine demethylase KDM4A controls the cell-cycle expression of replicative canonical histone genes. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2020, 1863, 194624.	1.9	7
24	S-phase Enriched Non-coding RNAs Regulate Gene Expression and Cell Cycle Progression. Cell Reports, 2020, 31, 107629.	6.4	11
25	Distinct functions of tissue-resident and circulating memory Th2 cells in allergic airway disease. Journal of Experimental Medicine, 2020, 217, .	8.5	72
26	Liver X receptors are required for thymic resilience and T cell output. Journal of Experimental Medicine, 2020, 217, .	8.5	20
27	Amyloid-β42/40 ratio drives tau pathology in 3D human neural cell culture models of Alzheimer's disease. Nature Communications, 2020, 11, 1377.	12.8	88
28	A FAK/HDAC5 signaling axis controls osteocyte mechanotransduction. Nature Communications, 2020, 11, 3282.	12.8	57
29	A post-transcriptional program of chemoresistance by AU-rich elements and TTP in quiescent leukemic cells. Genome Biology, 2020, 21, 33.	8.8	22
30	Differential Plasma Protein Regulation and Statin Effects in Human Immunodeficiency Virus (HIV)-Infected and Non-HIV-Infected Patients Utilizing a Proteomics Approach. Journal of Infectious Diseases, 2020, 222, 929-939.	4.0	16
31	The Histone Deacetylase SIRT6 Restrains Transcription Elongation via Promoter-Proximal Pausing. Molecular Cell, 2019, 75, 683-699.e7.	9.7	50
32	The murine IgH locus contains a distinct DNA sequence motif for the chromatin regulatory factor CTCF. Journal of Biological Chemistry, 2019, 294, 13580-13592.	3.4	7
33	Exploiting the Zonulin Mouse Model to Establish the Role of Primary Impaired Gut Barrier Function on Microbiota Composition and Immune Profiles. Frontiers in Immunology, 2019, 10, 2233.	4.8	41
34	Exercise reduces inflammatory cell production and cardiovascular inflammation via instruction of hematopoietic progenitor cells. Nature Medicine, 2019, 25, 1761-1771.	30.7	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. Nature Cell Biology, 2019, 21, 1449-1461.	10.3	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. Nutrients, 2019, 11, 2128.	4.1	87

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37	The RNA Helicase DDX6 Controls Cellular Plasticity by Modulating P-Body Homeostasis. Cell Stem Cell, 2019, 25, 622-638.e13.	11.1	82
38	Mapping global and local coevolution across 600 species to identify novel homologous recombination repair genes. Genome Research, 2019, 29, 439-448.	5.5	37
39	Singleâ€Cell RNAâ€seq: Introduction to Bioinformatics Analysis. Current Protocols in Molecular Biology, 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. Scientific Reports, 2019, 9, 7029.	3.3	77
41	Mitochondrial Dysfunction in C.Âelegans Activates Mitochondrial Relocalization and Nuclear Hormone Receptor-Dependent Detoxification Genes. Cell Metabolism, 2019, 29, 1182-1191.e4.	16.2	55
42	Exploration of CTCF post-translation modifications uncovers Serine-224 phosphorylation by PLK1 at pericentric regions during the G2/M transition. ELife, 2019, 8, .	6.0	18
43	Salt-inducible kinases dictate parathyroid hormone 1 receptor action in bone development and remodeling. Journal of Clinical Investigation, 2019, 129, 5187-5203.	8.2	28
44	Human Fetal-Derived Enterospheres Provide Insights on Intestinal Development and a Novel Model to Study Necrotizing Enterocolitis (NEC). Cellular and Molecular Gastroenterology and Hepatology, 2018, 5, 549-568.	4.5	60
45	An inactivating mutation in the histone deacetylase SIRT6 causes human perinatal lethality. Genes and Development, 2018, 32, 373-388.	5.9	41
46	Nudt21 Controls Cell Fate by Connecting Alternative Polyadenylation to Chromatin Signaling. Cell, 2018, 172, 106-120.e21.	28.9	123
47	Whole Genome Nextâ€Generation Sequencing Mutation Identification in <i>Pseudomonas aeruginosa</i> . Current Protocols in Molecular Biology, 2018, 124, e69.	2.9	1
48	RNAâ€seq: Basic Bioinformatics Analysis. Current Protocols in Molecular Biology, 2018, 124, e68.	2.9	44
49	Mutant GNAS drives pancreatic tumourigenesis by inducing PKA-mediated SIK suppression and reprogramming lipid metabolism. Nature Cell Biology, 2018, 20, 811-822.	10.3	124
50	The Association of Obesity and Cardiometabolic Traits With IncidentÂHFpEF and HFrEF. JACC: Heart Failure, 2018, 6, 701-709.	4.1	254
51	Prospective Isolation of Poised iPSC Intermediates Reveals Principles of Cellular Reprogramming. Cell Stem Cell, 2018, 23, 289-305.e5.	11.1	60
52	Direct Reprogramming of Mouse Fibroblasts into Functional Skeletal Muscle Progenitors. Stem Cell Reports, 2018, 10, 1505-1521.	4.8	74
53	The surveillance of pre-mRNA splicing is an early step in <i>C. elegans</i> RNAi of endogenous genes. Genes and Development, 2018, 32, 670-681.	5.9	27
54	Cell of origin dictates aggression and stem cell number in acute lymphoblastic leukemia. Leukemia, 2018, 32, 1860-1865.	7.2	23

4

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55	Nextâ€Generation Sequencing for Identification of EMSâ€Induced Mutations in <i>Caenorhabditis elegans</i> . Current Protocols in Molecular Biology, 2017, 117, 7.29.1-7.29.12.	2.9	19
56	Polycomb Repressive Complex 1 Generates Discrete Compacted Domains that Change during Differentiation. Molecular Cell, 2017, 65, 432-446.e5.	9.7	287
57	T _H 17 Cytokine Responses in Lyme Disease Correlate with <i>Borreliaburgdorferi</i> Antibodies During Early Infection in Patients with Erythema Migrans and with Autoantibodies Late in the Illness in Patients with Antibiotic-Refractory Lyme Arthritis. Clinical Infectious Diseases, 2017, 64, cix002.	5.8	48
58	Mutation of a nucleosome compaction region disrupts Polycomb-mediated axial patterning. Science, 2017, 355, 1081-1084.	12.6	133
59	Maintenance of macrophage transcriptional programs and intestinal homeostasis by epigenetic reader SP140. Science Immunology, 2017, 2, .	11.9	54
60	Macrophages Facilitate Electrical Conduction in the Heart. Cell, 2017, 169, 510-522.e20.	28.9	703
61	Phf8 loss confers resistance to depression-like and anxiety-like behaviors in mice. Nature Communications, 2017, 8, 15142.	12.8	35
62	Widespread changes in nucleosome accessibility without changes in nucleosome occupancy during a rapid transcriptional induction. Genes and Development, 2017, 31, 451-462.	5.9	90
63	DUSP9 Modulates DNA Hypomethylation in Female Mouse Pluripotent Stem Cells. Cell Stem Cell, 2017, 20, 706-719.e7.	11.1	63
64	Genetic Intersection of Tsix and Hedgehog Signaling during the Initiation of X-Chromosome Inactivation. Developmental Cell, 2017, 43, 359-371.e6.	7.0	14
65	TOX Regulates Growth, DNA Repair, and Genomic Instability in T-cell Acute Lymphoblastic Leukemia. Cancer Discovery, 2017, 7, 1336-1353.	9.4	48
66	Polycomb Repressive Complex 2 Methylates Elongin A to Regulate Transcription. Molecular Cell, 2017, 68, 872-884.e6.	9.7	50
67	IRF3 and type I interferons fuel a fatal response to myocardial infarction. Nature Medicine, 2017, 23, 1481-1487.	30.7	358
68	PAR-TERRA directs homologous sex chromosome pairing. Nature Structural and Molecular Biology, 2017, 24, 620-631.	8.2	48
69	HELZ2 Is an IFN Effector Mediating Suppression of Dengue Virus. Frontiers in Microbiology, 2017, 8, 240.	3.5	38
70	IGF2 mRNA binding protein-2 is a tumor promoter that drives cancer proliferation through its client mRNAs IGF2 and HMGA1. ELife, 2017, 6, .	6.0	77
71	Genome-wide identification of autosomal genes with allelic imbalance of chromatin state. PLoS ONE, 2017, 12, e0182568.	2.5	16
72	Shank is a dose-dependent regulator of Cav1 calcium current and CREB target expression. ELife, 2017, 6,	6.0	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> . Blood, 2017, 130, 93-93.	1.4	0
74	Survival in Quiescence Requires the Euchromatic Deployment of Clr4/SUV39H by Argonaute-Associated Small RNAs. Molecular Cell, 2016, 64, 1088-1101.	9.7	27
75	Influence of maternal breast milk ingestion on acquisition of the intestinal microbiome in preterm infants. Microbiome, 2016, 4, 68.	11.1	155
76	A Specialized Mechanism of Translation Mediated by FXR1a-Associated MicroRNP in Cellular Quiescence. Molecular Cell, 2016, 61, 760-773.	9.7	85
77	Single-cell transcriptional analysis of normal, aberrant, and malignant hematopoiesis in zebrafish. Journal of Experimental Medicine, 2016, 213, 979-992.	8.5	69
78	SIRT6 Suppresses Pancreatic Cancer through Control of Lin28b. Cell, 2016, 165, 1401-1415.	28.9	227
79	T Cell Immune Deficiency in <i>zap70</i> Mutant Zebrafish. Molecular and Cellular Biology, 2016, 36, 2868-2876.	2.3	37
80	Sox2 Suppresses Gastric Tumorigenesis in Mice. Cell Reports, 2016, 16, 1929-1941.	6.4	61
81	Inhibition of Dihydroorotate Dehydrogenase Overcomes Differentiation Blockade in Acute Myeloid Leukemia. Cell, 2016, 167, 171-186.e15.	28.9	353
82	CAT7 and cat7l Long Non-coding RNAs Tune Polycomb Repressive Complex 1 Function during Human and Zebrafish Development. Journal of Biological Chemistry, 2016, 291, 19558-19572.	3.4	32
83	Single-cell imaging of normal and malignant cell engraftment into optically clear <i>prkdc</i> -null SCID zebrafish. Journal of Experimental Medicine, 2016, 213, 2575-2589.	8.5	65
84	SIKs control osteocyte responses to parathyroid hormone. Nature Communications, 2016, 7, 13176.	12.8	124
85	Tribbles ortholog NIPI-3 and bZIP transcription factor CEBP-1 regulate a Caenorhabditis elegans intestinal immune surveillance pathway. BMC Biology, 2016, 14, 105.	3.8	35
86	Chromatin topology is coupled to Polycomb group protein subnuclear organization. Nature Communications, 2016, 7, 10291.	12.8	176
87	Inhibiting fungal multidrug resistance by disrupting an activator–Mediator interaction. Nature, 2016, 530, 485-489.	27.8	120
88	Tumor cells can follow distinct evolutionary paths to become resistant to epidermal growth factor receptor inhibition. Nature Medicine, 2016, 22, 262-269.	30.7	768
89	Enhancer regions show high histone H3.3 turnover that changes during differentiation. ELife, 2016, 5, .	6.0	86
90	Using homology relations within a database markedly boosts protein sequence similarity search. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7003-7008.	7.1	8

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91	Allelic Imbalance Is a Prevalent and Tissue-Specific Feature of the Mouse Transcriptome. Genetics, 2015, 200, 537-549.	2.9	38
92	ATRX Promotes Binding of PRC2 to Xist RNA and Polycomb Targets. FASEB Journal, 2015, 29, 361.3.	0.5	0
93	BRCA1 establishes DNA damage signaling and pericentric heterochromatin of the X chromosome in male meiosis. Journal of Cell Biology, 2014, 205, 663-675.	5.2	74
94	ATRX Directs Binding of PRC2 to Xist RNA and Polycomb Targets. Cell, 2014, 159, 869-883.	28.9	182
95	The Long Noncoding RNAs NEAT1 and MALAT1 Bind Active Chromatin Sites. Molecular Cell, 2014, 55, 791-802.	9.7	578
96	Informatics for Molecular Biologists. Current Protocols in Molecular Biology, 2014, 106, 19.0.1-2.	2.9	0
97	H3K27 modifications define segmental regulatory domains in the Drosophila bithorax complex. ELife, 2014, 3, e02833.	6.0	111
98	Bimodal quantitative relationships between histone modifications for X-linked and autosomal loci. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6949-6954.	7.1	9
99	X-chromosome hyperactivation in mammals via nonlinear relationships between chromatin states and transcription. Nature Structural and Molecular Biology, 2012, 19, 56-61.	8.2	88
100	Spreading of X chromosome inactivation via a hierarchy of defined Polycomb stations. Genome Research, 2012, 22, 1864-1876.	5.5	143
101	Phenotypic categorization of genetic skin diseases reveals new relations between phenotypes, genes and pathways. Bioinformatics, 2009, 25, 2891-2896.	4.1	5
102	Structure similarity measure with penalty for close non-equivalent residues. Bioinformatics, 2009, 25, 1259-1263.	4.1	17
103	COMPASS server for homology detection: improved statistical accuracy, speed and functionality. Nucleic Acids Research, 2009, 37, W90-W94.	14.5	27
104	Discrete–continuous duality of protein structure space. Current Opinion in Structural Biology, 2009, 19, 321-328.	5.7	60
105	Considering scores between unrelated proteins in the search database improves profile comparison. BMC Bioinformatics, 2009, 10, 399.	2.6	1
106	Accurate statistical model of comparison between multiple sequence alignments. Nucleic Acids Research, 2008, 36, 2240-2248.	14.5	19
107	COMPASS server for remote homology inference. Nucleic Acids Research, 2007, 35, W653-W658.	14.5	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. Bioinformatics, 2004, 20, 818-828.	4.1	28
110	Estimates of statistical significance for comparison of individual positions in multiple sequence alignments. BMC Bioinformatics, 2004, 5, 106.	2.6	8
111	COMPASS: A Tool for Comparison of Multiple Protein Alignments with Assessment of Statistical Significance. Journal of Molecular Biology, 2003, 326, 317-336.	4.2	263