Ludmila V Prokunina-Olsson

List of Publications by Year
in descending order

131 papers	11,168 citations	81839 39 h-index	30894 102 g-index
143 all docs	143 docs citations	143 times ranked	19104 citing authors

#	Article	IF	Citations
1	A Genome-Wide Association Study of Type 2 Diabetes in Finns Detects Multiple Susceptibility Variants. Science, 2007, 316, 1341-1345.	6.0	2,534
2	From noncoding variant to phenotype via SORT1 at the 1p13 cholesterol locus. Nature, 2010, 466, 714-719.	13.7	1,018
3	A variant upstream of IFNL3 (IL28B) creating a new interferon gene IFNL4 is associated with impaired clearance of hepatitis C virus. Nature Genetics, 2013, 45, 164-171.	9.4	843
4	A regulatory polymorphism in PDCD1 is associated with susceptibility to systemic lupus erythematosus in humans. Nature Genetics, 2002, 32, 666-669.	9.4	694
5	Detectable clonal mosaicism and its relationship to aging and cancer. Nature Genetics, 2012, 44, 651-658.	9.4	519
6	A multi-stage genome-wide association study of bladder cancer identifies multiple susceptibility loci. Nature Genetics, 2010, 42, 978-984.	9.4	493
7	A multistage genome-wide association study in breast cancer identifies two new risk alleles at 1p11.2 and 14q24.1 (RAD51L1). Nature Genetics, 2009, 41, 579-584.	9.4	487
8	Interferons and viruses induce a novel truncated ACE2 isoform and not the full-length SARS-CoV-2 receptor. Nature Genetics, 2020, 52, 1283-1293.	9.4	217
9	Endogenous intrahepatic IFNs and association with IFN-free HCV treatment outcome. Journal of Clinical Investigation, 2014, 124, 3352-3363.	3.9	179
10	COVID-19 and emerging viral infections: The case for interferon lambda. Journal of Experimental Medicine, 2020, 217, .	4.2	177
11	Association of germline variants in the APOBEC3 region with cancer risk and enrichment with APOBEC-signature mutations in tumors. Nature Genetics, 2016, 48, 1330-1338.	9.4	161
12	Analysis of Heritability and Shared Heritability Based on Genome-Wide Association Studies for Thirteen Cancer Types. Journal of the National Cancer Institute, 2015, 107, djv279.	3.0	152
13	Association of the PD-1.3A allele of thePDCD1gene in patients with rheumatoid arthritis negative for rheumatoid factor and the shared epitope. Arthritis and Rheumatism, 2004, 50, 1770-1773.	6.7	146
14	A Functional Variant at a Prostate Cancer Predisposition Locus at 8q24 Is Associated with PVT1 Expression. PLoS Genetics, 2011, 7, e1002165.	1.5	142
15	Genome-wide association study identifies multiple loci associated with bladder cancer risk. Human Molecular Genetics, 2014, 23, 1387-1398.	1.4	137
16	A new haplotype ofPDCD1is associated with rheumatoid arthritis in Hong Kong Chinese. Arthritis and Rheumatism, 2005, 52, 1058-1062.	6.7	131
17	IFN-Î»4: The Paradoxical New Member of the Interferon Lambda Family. Journal of Interferon and Cytokine Research, 2014, 34, 829-838.	0.5	130
18	IL-29 is the dominant type III interferon produced by hepatocytes during acute hepatitis C virus infection. Hepatology, 2012, 56, 2060-2070.	3.6	118

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19	Common Genetic Polymorphisms Modify the Effect of Smoking on Absolute Risk of Bladder Cancer. Cancer Research, 2013, 73, 2211-2220.	0.4	107
20	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	2.6	101
21	Tissue-specific alternative splicing of TCF7L2. Human Molecular Genetics, 2009, 18, 3795-3804.	1.4	100
22	A genome-wide association study of bladder cancer identifies a new susceptibility locus within SLC14A1, a urea transporter gene on chromosome 18q12.3. Human Molecular Genetics, 2011, 20, 4282-4289.	1.4	100
23	A Common Variant Associated with Dyslexia Reduces Expression of the KIAA0319 Gene. PLoS Genetics, 2009, 5, e1000436.	1.5	92
24	APOBEC Mutagenesis and Copy-Number Alterations Are Drivers of Proteogenomic Tumor Evolution and Heterogeneity in Metastatic Thoracic Tumors. Cell Reports, 2019, 26, 2651-2666.e6.	2.9	92
25	Risk alleles for chronic hepatitis B are associated with decreased mRNA expression of HLA-DPA1 and HLA-DPB1 in normal human liver. Genes and Immunity, 2011, 12, 428-433.	2.2	89
26	Weak Induction of Interferon Expression by Severe Acute Respiratory Syndrome Coronavirus 2 Supports Clinical Trials of Interferon-Î» to Treat Early Coronavirus Disease 2019. Clinical Infectious Diseases, 2020, 71, 1410-1412.	2.9	88
27	Selection on a Variant Associated with Improved Viral Clearance Drives Local, Adaptive Pseudogenization of Interferon Lambda 4 (IFNL4). PLoS Genetics, 2014, 10, e1004681.	1.5	87
28	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 2016, 7, 11843.	5.8	86
29	Association of the IFNL4-Î”G Allele With Impaired Spontaneous Clearance of Hepatitis C Virus. Journal of Infectious Diseases, 2014, 209, 350-354.	1.9	81
30	Regulatory SNPs in complex diseases: their identification and functional validation. Expert Reviews in Molecular Medicine, 2004, 6, 1-15.	1.6	79
31	Common genetic variants in the PSCA gene influence gene expression and bladder cancer risk. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 4974-4979.	3.3	79
32	Association of PDCD1 genetic variation with risk and clinical manifestations of systemic lupus erythematosus in a multiethnic cohort. Genes and Immunity, 2007, 8, 279-287.	2.2	76
33	The systemic lupus erythematosus-associatedPDCD1polymorphism PD1.3A in lupus nephritis. Arthritis and Rheumatism, 2004, 50, 327-328.	6.7	75
34	IFNL4-Î”G Genotype Is Associated With Slower Viral Clearance in Hepatitis C, Genotype-1 Patients Treated With Sofosbuvir and Ribavirin. Journal of Infectious Diseases, 2014, 209, 1700-1704.	1.9	74
35	Mapping of the UGT1A locus identifies an uncommon coding variant that affects mRNA expression and protects from bladder cancer. Human Molecular Genetics, 2012, 21, 1918-1930.	1.4	71
36	Comparison of functional variants in IFNL4 and IFNL3 for association with HCV clearance. Journal of Hepatology, 2015, 63, 1103-1110.	1.8	61

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37	IFN-Î»4 Attenuates Antiviral Responses by Enhancing Negative Regulation of IFN Signaling. Journal of Immunology, 2017, 199, 3808-3820.	0.4	55
38	Genetic regulation of OAS1 nonsense-mediated decay underlies association with COVID-19 hospitalization in patients of European and African ancestries. Nature Genetics, 2022, 54, 1103-1116.	9.4	54
39	NOTCH2 in breast cancer: association of SNP rs11249433 with gene expression in ER-positive breast tumors without TP53 mutations. Molecular Cancer, 2010, 9, 113.	7.9	52
40	Genome-wide interaction study of smoking and bladder cancer risk. Carcinogenesis, 2014, 35, 1737-1744.	1.3	50
41	Immune gene expression profiling reveals heterogeneity in luminal breast tumors. Breast Cancer Research, 2019, 21, 147.	2.2	43
42	Alternative Splicing of TCF7L2 Gene in Omental and Subcutaneous Adipose Tissue and Risk of Type 2 Diabetes. PLoS ONE, 2009, 4, e7231.	1.1	41
43	Genome-wide association study identified SNP on 15q24 associated with bladder cancer risk in Japanese population. Human Molecular Genetics, 2015, 24, 1177-1184.	1.4	38
44	Identification of a novel susceptibility locus at 13q34 and refinement of the 20p12.2 region as a multi-signal locus associated with bladder cancer risk in individuals of European ancestry. Human Molecular Genetics, 2016, 25, 1203-1214.	1.4	38
45	Evaluating the Causal Link Between Malaria Infection and Endemic Burkitt Lymphoma in Northern Uganda: A Mendelian Randomization Study. EBioMedicine, 2017, 25, 58-65.	2.7	37
46	IFNL4-Î”G Allele Is Associated with an Interferon Signature in Tumors and Survival of African-American Men with Prostate Cancer. Clinical Cancer Research, 2018, 24, 5471-5481.	3.2	37
47	Genetics of the Human Interferon Lambda Region. Journal of Interferon and Cytokine Research, 2019, 39, 599-608.	0.5	37
48	Common Genetic Variants in miR-1206 (8q24.2) and miR-612 (11q13.3) Affect Biogenesis of Mature miRNA Forms. PLoS ONE, 2012, 7, e47454.	1.1	36
49	Large-Scale Pathway-Based Analysis of Bladder Cancer Genome-Wide Association Data from Five Studies of European Background. PLoS ONE, 2012, 7, e29396.	1.1	36
50	Allelic expression imbalance at high-density lipoprotein cholesterol locus MMAB-MVK. Human Molecular Genetics, 2010, 19, 1921-1929.	1.4	35
51	Modification of Occupational Exposures on Bladder Cancer Risk by Common Genetic Polymorphisms. Journal of the National Cancer Institute, 2015, 107, djv223.	3.0	34
52	APOBEC-mediated Mutagenesis as a Likely Cause of FGFR3 S249C Mutation Over-representation in Bladder Cancer. European Urology, 2019, 76, 9-13.	0.9	34
53	Splicing Diversity of the Human OCLN Gene and Its Biological Significance for Hepatitis C Virus Entry. Journal of Virology, 2010, 84, 6987-6994.	1.5	33
54	Evaluation of a variant in the transcription factor 7â€like 2 (TCF7L2) gene and prostate cancer risk in a populationâ€based study. Prostate, 2008, 68, 740-747.	1.2	32

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55	Expression of Interferon Lambda 4 Is Associated with Reduced Proliferation and Increased Cell Death in Human Hepatic Cells. Journal of Interferon and Cytokine Research, 2015, 35, 888-900.	0.5	31
56	IFNL4-Î”G is associated with prostate cancer among men at increased risk of sexually transmitted infections. Communications Biology, 2018, 1, 191.	2.0	28
57	Refining the Prostate Cancer Genetic Association within the JAZF1 Gene on Chromosome 7p15.2. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 1349-1355.	1.1	26
58	Genetic Variant as a Selection Marker for Antiâ€“Prostate Stem Cell Antigen Immunotherapy of Bladder Cancer. Journal of the National Cancer Institute, 2013, 105, 69-73.	3.0	25
59	No effect of cancer-associated SNP rs6983267 in the 8q24 region on co-expression of MYC and TCF7L2 in normal colon tissue. Molecular Cancer, 2009, 8, 96.	7.9	24
60	Differential urinary specific gravity as a molecular phenotype of the bladder cancer genetic association in the urea transporter gene, SLC14A1. International Journal of Cancer, 2013, 133, 3008-3013.	2.3	24
61	The 19q12 Bladder Cancer GWAS Signal: Association with Cyclin E Function and Aggressive Disease. Cancer Research, 2014, 74, 5808-5818.	0.4	24
62	The IFN-Î»4 Conundrum: When a Good Interferon Goes Bad. Journal of Interferon and Cytokine Research, 2019, 39, 636-641.	0.5	24
63	Genetic signatures of gene flow and malaria-driven natural selection in sub-Saharan populations of the "endemic Burkitt Lymphoma belt". PLoS Genetics, 2019, 15, e1008027.	1.5	23
64	The Association between the Comprehensive Epsteinâ€“Barr Virus Serologic Profile and Endemic Burkitt Lymphoma. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 57-62.	1.1	23
65	Expression analysis of loci associated with type 2 diabetes in human tissues. Diabetologia, 2010, 53, 2334-2339.	2.9	21
66	IL28B rs12979860 Genotype and Spontaneous Clearance of Hepatitis C Virus in a Multi-Ethnic Cohort of Injection Drug Users: Evidence for a Supra-Additive Association. Journal of Infectious Diseases, 2011, 204, 1843-1847.	1.9	21
67	Associations between IgG reactivity to Plasmodium falciparum erythrocyte membrane protein 1 (PfEMP1) antigens and Burkitt lymphoma in Ghana and Uganda case-control studies. EBioMedicine, 2019, 39, 358-368.	2.7	20
68	Evidence for neuroendocrine function of a unique splicing form of TCF7L2 in human brain, islets and gut. Diabetologia, 2010, 53, 712-716.	2.9	19
69	In the Absence of HCV Infection, Interferon Stimulated Gene Expression in Liver Is Not Associated With IL28B Genotype. Gastroenterology, 2010, 139, 1422-1424.	0.6	18
70	No association between a candidate TCF7L2 variant and risk of breast or ovarian cancer. BMC Cancer, 2009, 9, 312.	1.1	16
71	Breast cancer susceptibility risk associations and heterogeneity by E-cadherin tumor tissue expression. Breast Cancer Research and Treatment, 2014, 143, 181-187.	1.1	16
72	Comparative Functional Analysis of 12 Mammalian IFN-Î»4 Orthologs. Journal of Interferon and Cytokine Research, 2016, 36, 30-36.	0.5	16

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73	Decreased Risk for Myocardial Infarction and Lower Tumor Necrosis Factorâ€“Î± Levels in Carriers of Variants of the PDCD1 Gene. Human Immunology, 2006, 67, 700-705.	1.2	13
74	Association of Hepatitis C Virus Infection With CD4/CD8 Ratio in HIV-Positive Women. Journal of Acquired Immune Deficiency Syndromes (1999), 2016, 72, 162-170.	0.9	13
75	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316.	1.1	12
76	Targeted Deep Sequencing of Bladder Tumors Reveals Novel Associations between Cancer Gene Mutations and Mutational Signatures with Major Risk Factors. Clinical Cancer Research, 2021, 27, 3725-3733.	3.2	11
77	APOBEC3B expression in breast cancer cell lines and tumors depends on the estrogen receptor status. Carcinogenesis, 2020, 41, 1030-1037.	1.3	9
78	Vitamin D Status and Virologic Response to HCV Therapy in the HALT-C and VIRAHEP-C Trials. PLoS ONE, 2016, 11, e0166036.	1.1	9
79	Finding genes for SLE: complex interactions and complex populations. Journal of Autoimmunity, 2003, 21, 117-120.	3.0	8
80	Association of donor IFNL4 genotype and non-relapse mortality after unrelated donor myeloablative haematopoietic stem-cell transplantation for acute leukaemia: a retrospective cohort study. Lancet Haematology,the, 2020, 7, e715-e723.	2.2	8
81	IFN-Î»4 is associated with increased risk and earlier occurrence of several common infections in African children. Genes and Immunity, 2021, 22, 44-55.	2.2	8
82	Targeting natural splicing plasticity of APOBEC3B restricts its expression and mutagenic activity. Communications Biology, 2021, 4, 386.	2.0	7
83	Changes in serum hepatitis B surface and e antigen, interferonâ€inducible protein 10, and aminotransferase levels during combination therapy of immuneâ€tolerant chronic hepatitis B. Hepatology, 2022, 76, 775-787.	3.6	7
84	Interferon Lambda 4 Genotype Is Not Associated with Recurrence of Oral or Genital Herpes. PLoS ONE, 2015, 10, e0138827.	1.1	6
85	Metabolic Changes in Chronic Hepatitis C Patients Who Carry IFNL4-Î”G and Achieve Sustained Virologic Response With Direct-Acting Antiviral Therapy. Journal of Infectious Diseases, 2020, 221, 102-109.	1.9	6
86	When the Smoke Clears m6A from a Y Chromosomeâ€“Linked lncRNA, Men Get an Increased Risk of Cancer. Cancer Research, 2020, 80, 2718-2719.	0.4	6
87	Intracellular Accumulation of IFN-Î»4 Induces ER Stress and Results in Anti-Cirrhotic but Pro-HCV Effects. Frontiers in Immunology, 2021, 12, 692263.	2.2	6
88	Fine mapping of 14q24.1 breast cancer susceptibility locus. Human Genetics, 2012, 131, 479-490.	1.8	5
89	Association of IFNL3 and IFNL4 polymorphisms with liverâ€related mortality in a multiracial cohort of HIV/HCVâ€coinfected women. Journal of Viral Hepatitis, 2015, 22, 1055-1060.	1.0	5
90	Meeting Overview: Interferon Lambdaâ€”Disease Impact and Therapeutic Potential. Journal of Interferon and Cytokine Research, 2019, 39, 586-591.	0.5	5

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91	Endemic Burkitt Lymphoma in second-degree relatives in Northern Uganda: in-depth genome-wide analysis suggests clues about genetic susceptibility. Leukemia, 2021, 35, 1209-1213.	3.3	5
92	Disinfection By-Products in Drinking Water and Bladder Cancer: Evaluation of Risk Modification by Common Genetic Polymorphisms in Two Caseâ€“Control Studies. Environmental Health Perspectives, 2022, 130, 57006.	2.8	5
93	Impact of IFNL4 -âˆ†G genotype on sustained virologic response in hepatitis C genotype 1 patients treated with direct-acting antivirals. Diagnostic Microbiology and Infectious Disease, 2018, 92, 34-36.	0.8	4
94	Variation in the Human Leukocyte Antigen system and risk for endemic Burkitt lymphoma in northern Uganda. British Journal of Haematology, 2020, 189, 489-499.	1.2	4
95	Detection of bladder, breast and prostate cancer using serum and tissue miRNA profiling. Genome Biology, 2011, 12, .	13.9	3
96	Prostate stem cell antigen (PSCA) and risk of bladder cancer: linking genotypes to functional mechanisms. Genome Biology, 2011, 12, .	3.8	3
97	Statistical tests for detecting associations with groups of genetic variants: generalization, evaluation, and implementation. European Journal of Human Genetics, 2013, 21, 680-686.	1.4	3
98	Relationship of Genotype for HLA B*57 and IFNL4 With Disease Progression in Female HIV Controllers. Clinical Infectious Diseases, 2017, 65, 1243-1244.	2.9	3
99	Reply to Alexander Yang, Vincent L. Cannataro, Jeffrey P. Townsendâ€™s Letter to the Editor, re: Ming-Jun Shi, Xiang-Yu Meng, Philippe Lamy, et al. APOBEC-mediated Mutagenesis as, a Likely Cause of FGFR3 S249C Mutation Over-representation in Bladder Cancer. Eur Urol 2019, 76:9â€“13. European Urology, 2020, 77, e26-e27.	0.9	3
100	Comparison of somatic mutation landscapes in Chinese versus European breast cancer patients. Human Genetics and Genomics Advances, 2021, 3, 100076.	1.0	3
101	Functional exploration of CCNE1 splicing forms as a possible link to bladder cancer susceptibility. Genome Biology, 2011, 12, .	3.8	2
102	Cancer Sequencing Gets a Little More Personal. Science Translational Medicine, 2010, 2, 20ps8.	5.8	1
103	182. Cytokine, 2013, 63, 286.	1.4	1
104	P1306 COMPARISON OF IFNL4- Î”G AND IFNL3 3â€²UTR rs4803217 GENOTYPES FOR ASSOCIATION WITH HCV TREATMENT RESPONSE. Journal of Hepatology, 2014, 60, S530.	1.8	1
105	Genetics Helps to Find Synergy for Immune Checkpoint and Targeted Combination Therapies. Cancer Research, 2019, 79, 5476-5478.	0.4	1
106	It Takes Two (Genomes) to Cancer: Paired Viral and Host Transcriptome Analysis Provides New Insights about EBV Carcinogenicity. Cancer Research, 2019, 79, 5917-5919.	0.4	1
107	Abstract B051: IFNL4-deltaG allele is associated with an interferon signature in tumors and survival of African-American men with prostate cancer. , 2020, , .		1
108	Abstract 2562: Bladder cancer GWAS signal at 4p16.3 affects response of TMEM129 to chemically-induced endoplasmic reticulum stress. , 2016, , .		1

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109	APOBEC Mutagenesis and Copy Number Alterations are Drivers of Proteogenomic Tumor Evolution and Heterogeneity in Metastatic Thoracic Tumors. SSRN Electronic Journal, 0, , .	0.4	1
110	What makes the hepatitis C virus evolve?. ELife, 2019, 8, .	2.8	1
111	Identification of functional genetic variants associated with prostate cancer through analysis of genome-wide genetic and epigenetic datasets. Genome Biology, 2011, 12, .	13.9	0
112	Whole transcriptome sequencing of normal and tumor bladder tissue samples. Genome Biology, 2011, 12, .	13.9	0
113	An unusual suspect: an uncommon human-specific synonymous coding variant within the UGT1A6 gene explains a GWAS signal and protects against bladder cancer. Genome Biology, 2011, 12, .	3.8	0
114	A novel functional variant in 8q24 is associated with regulation of prostate stem cell antigen (PSCA) gene expression and bladder cancer risk. Genome Biology, 2011, 12, .	3.8	0
115	140. Cytokine, 2014, 70, 62.	1.4	0
116	ID: 87. Cytokine, 2015, 76, 81.	1.4	0
117	Response. Journal of the National Cancer Institute, 2016, 108, djv441.	3.0	0
118	Abstract 861: Diesel engine exhaust is associated withTP53mutations and high-risk non-muscle invasive bladder cancer. , 2021, , .		0
119	Abstract 826: Large-scale genome-wide association study identifies multiple novel germline susceptibility variants associated with bladder cancer risk. , 2021, , .		0
120	Abstract 5126: Allele-specific effect of rs2294008 on mRNA and protein expression of the prostate stem cell antigen (PSCA) in human normal and tumor bladder tissue. , 2012, , .		0
121	Abstract 944: Translational implications of the 19q12 bladder cancer GWAS signal for aggressive bladder cancer. , 2014, , .		0
122	Abstract 4617: An alternatively spliced isoform ofTMEM129shows association with bladder cancer GWAS marker rs798766. , 2015, , .		0
123	Abstract B51: An interferon Î» 4 genotype is linked to a gene expression signature in prostate tumors of African American men. , 2016, , .		0
124	Abstract 2563: Analysis of a novel gene in relation to bladder cancer GWAS signals within the 20p12.2 region. , 2016, , .		0
125	Abstract 4419: Exploration of alternative pathways mediated by IFNL4 and related to cell proliferation and death in a hepatoma cell line. , 2016, , .		0
126	Abstract 598: APOBEC mutagenesis: a link between innate immunity and cancer. , 2017, , .		0

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127	Abstract 1292: Germline genetic, molecular and environmental factors modulate APOBEC mutagenesis in human tumors. , 2017, , .		0
128	Abstract A182: Apobec-mutagenesis drives mutational heterogeneity while copy number alterations drive transcriptomic and proteogenomic heterogeneity in metastatic lung adenocarcinoma and thymic carcinoma. , 2018, , .		0
129	Donor IFNL4 Genotype Is Associated with Transplant-Related Mortality after Unrelated Donor Myeloablative Hematopoietic Cell Transplantation in Patients with Acute Leukemia. Blood, 2018, 132, 968-968.	0.6	0
130	Analysis of Common Infections in Malian Children Under Five: IFNL4-dG Allele Is Associated with Higher Risk and Earlier Episodes of Gastrointestinal Infections. SSRN Electronic Journal, 0, , .	0.4	0
131	Abstract LB-051: Integrative, targeted deep sequencing of bladder tumors reveals novel associations between cancer gene mutations and mutational signatures with major risk factors. , 2019, , .		0