

# Ignaty Leshchiner

## List of Publications by Year in descending order

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Version: 2024-02-01

61  
papers

13,051  
citations

117625

34  
h-index

123424

61  
g-index

75  
all docs

75  
docs citations

75  
times ranked

25306  
citing authors

#	ARTICLE	IF	CITATIONS
1	Combined tumor and immune signals from genomes or transcriptomes predict outcomes of checkpoint inhibition in melanoma. <i>Cell Reports Medicine</i> , 2022, 3, 100500.	6.5	13
2	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. <i>Cell</i> , 2021, 184, 2239-2254.e39.	28.9	260
3	Longitudinal Single-Cell Dynamics of Chromatin Accessibility and Mitochondrial Mutations in Chronic Lymphocytic Leukemia Mirror Disease History. <i>Cancer Discovery</i> , 2021, 11, 3048-3063.	9.4	31
4	Parallel Genomic Alterations of Antigen and Payload Targets Mediate Polyclonal Acquired Clinical Resistance to Sacituzumab Govitecan in Triple-Negative Breast Cancer. <i>Cancer Discovery</i> , 2021, 11, 2436-2445.	9.4	69
5	Molecular features of exceptional response to neoadjuvant anti-androgen therapy in high-risk localized prostate cancer. <i>Cell Reports</i> , 2021, 36, 109665.	6.4	24
6	The RNA helicase Ddx21 controls Vegfc-driven developmental lymphangiogenesis by balancing endothelial cell ribosome biogenesis and p53 function. <i>Nature Cell Biology</i> , 2021, 23, 1136-1147.	10.3	17
7	The cationic amino acid exporter Slc7a7 is induced and vital in tissue macrophages with sustained efferocytic activity. <i>Journal of Cell Science</i> , 2020, 133, .	2.0	8
8	Distinct evolutionary paths in chronic lymphocytic leukemia during resistance to the graft-versus-leukemia effect. <i>Science Translational Medicine</i> , 2020, 12, .	12.4	17
9	The evolutionary history of 2,658 cancers. <i>Nature</i> , 2020, 578, 122-128.	27.8	690
10	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. <i>Cell</i> , 2020, 181, 236-249.	28.9	334
11	Butler enables rapid cloud-based analysis of thousands of human genomes. <i>Nature Biotechnology</i> , 2020, 38, 288-292.	17.5	11
12	Genomic Profiling of Smoldering Multiple Myeloma Identifies Patients at a High Risk of Disease Progression. <i>Journal of Clinical Oncology</i> , 2020, 38, 2380-2389.	1.6	110
13	Mutations in RABL3 alter KRAS prenylation and are associated with hereditary pancreatic cancer. <i>Nature Genetics</i> , 2019, 51, 1308-1314.	21.4	47
14	Liquid versus tissue biopsy for detecting acquired resistance and tumor heterogeneity in gastrointestinal cancers. <i>Nature Medicine</i> , 2019, 25, 1415-1421.	30.7	359
15	Mitochondrial Reprogramming Underlies Resistance to BCL-2 Inhibition in Lymphoid Malignancies. <i>Cancer Cell</i> , 2019, 36, 369-384.e13.	16.8	224
16	A Murine Model of Chronic Lymphocytic Leukemia Based on B Cell-Restricted Expression of Sf3b1 Mutation and Atm Deletion. <i>Cancer Cell</i> , 2019, 35, 283-296.e5.	16.8	71
17	Tfap2a is a novel gatekeeper of nephron differentiation during kidney development. <i>Development (Cambridge)</i> , 2019, 146, .	2.5	41
18	Growth dynamics in naturally progressing chronic lymphocytic leukaemia. <i>Nature</i> , 2019, 570, 474-479.	27.8	86

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19	T Cell Determinants of Response and Resistance to PD-1 Blockade in Richter's Transformation. <i>Blood</i> , 2019, 134, 680-680.	1.4	1
20	MCL-1 and PKA/AMPK Axis Fuel Venetoclax Resistance in Lymphoid Cancers. <i>Blood</i> , 2019, 134, 1284-1284.	1.4	3
21	Distinct Evolutionary Patterns in Chronic Lymphocytic Leukemia (CLL) during Resistance to Graft-Versus-Leukemia (GvL). <i>Blood</i> , 2019, 134, 516-516.	1.4	0
22	Distinct mutational signatures characterize concurrent loss of polymerase proofreading and mismatch repair. <i>Nature Communications</i> , 2018, 9, 1746.	12.8	142
23	Molecular subtypes of diffuse large B cell lymphoma are associated with distinct pathogenic mechanisms and outcomes. <i>Nature Medicine</i> , 2018, 24, 679-690.	30.7	1,224
24	Heterogeneity and Coexistence of T790M and T790 Wild-Type Resistant Subclones Drive Mixed Response to Third-Generation Epidermal Growth Factor Receptor Inhibitors in Lung Cancer. <i>JCO Precision Oncology</i> , 2018, 2018, 1-15.	3.0	17
25	Comment on "DNA damage is a pervasive cause of sequencing errors, directly confounding variant identification". <i>Science</i> , 2018, 361, .	12.6	2
26	Widespread Chromosomal Losses and Mitochondrial DNA Alterations as Genetic Drivers in H <sub>1</sub> /4rthle Cell Carcinoma. <i>Cancer Cell</i> , 2018, 34, 242-255.e5.	16.8	185
27	An integrated clinical program and crowdsourcing strategy for genomic sequencing and Mendelian disease gene discovery. <i>Npj Genomic Medicine</i> , 2018, 3, 21.	3.8	24
28	Activating MAPK Pathway Mutations Mediate Primary Resistance to PI3K Inhibitors in Chronic Lymphocytic Leukemia (CLL). <i>Blood</i> , 2018, 132, 587-587.	1.4	43
29	Genetic Determinants of Venetoclax Resistance in Lymphoid Malignancies. <i>Blood</i> , 2018, 132, 893-893.	1.4	4
30	Clonal and Single Cell Dynamics of Resistance to Graft-Versus-Leukemia (GvL) in Chronic Lymphocytic Leukemia (CLL). <i>Blood</i> , 2018, 132, 820-820.	1.4	0
31	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017, 31, 181-193.	16.8	532
32	The zebrafish kidney mutant zeppelin reveals that <i>brca2/fancd1</i> is essential for pronephros development. <i>Developmental Biology</i> , 2017, 428, 148-163.	2.0	38
33	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017, 31, 411-423.	16.8	309
34	Polyclonal Secondary <i>FGFR2</i> Mutations Drive Acquired Resistance to FGFR Inhibition in Patients with <i>FGFR2</i> Fusion-Positive Cholangiocarcinoma. <i>Cancer Discovery</i> , 2017, 7, 252-263.	9.4	384
35	A mutational signature reveals alterations underlying deficient homologous recombination repair in breast cancer. <i>Nature Genetics</i> , 2017, 49, 1476-1486.	21.4	427
36	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017, 32, 185-203.e13.	16.8	1,428

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37	Scalable whole-exome sequencing of cell-free DNA reveals high concordance with metastatic tumors. <i>Nature Communications</i> , 2017, 8, 1324.	12.8	584
38	Resolving the phylogenetic origin of glioblastoma via multifocal genomic analysis of pre-treatment and treatment-resistant autopsy specimens. <i>Npj Precision Oncology</i> , 2017, 1, 33.	5.4	27
39	The evolutionary landscape of chronic lymphocytic leukemia treated with ibrutinib targeted therapy. <i>Nature Communications</i> , 2017, 8, 2185.	12.8	148
40	An argument for early genomic sequencing in atypical cases: a <i>WISP3</i> variant leads to diagnosis of progressive pseudorheumatoid arthropathy of childhood. <i>Rheumatology</i> , 2016, 55, kev367.	1.9	6
41	Loss of function mutation in <i>LOX</i> causes thoracic aortic aneurysm and dissection in humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8759-8764.	7.1	144
42	Molecular Mechanisms of Resistance to First- and Second-Generation ALK Inhibitors in <i>ALK</i> -Rearranged Lung Cancer. <i>Cancer Discovery</i> , 2016, 6, 1118-1133.	9.4	919
43	Resensitization to Crizotinib by the Lorlatinib <i>ALK</i> Resistance Mutation L1198F. <i>New England Journal of Medicine</i> , 2016, 374, 54-61.	27.0	433
44	The Landscape of Dynamic Genetic Changes in Ibrutinib-Treated CLL. <i>Blood</i> , 2016, 128, 188-188.	1.4	3
45	Inherited <i>CHST11/MIR3922</i> deletion is associated with a novel recessive syndrome presenting with skeletal malformation and malignant lymphoproliferative disease. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2015, 3, 413-423.	1.2	11
46	Paired exome analysis of Barrett's esophagus and adenocarcinoma. <i>Nature Genetics</i> , 2015, 47, 1047-1055.	21.4	310
47	The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015, 163, 1011-1025.	28.9	2,435
48	Comprehensive assessment of cancer missense mutation clustering in protein structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E5486-95.	7.1	195
49	Summarizing polygenic risks for complex diseases in a clinical whole-genome report. <i>Genetics in Medicine</i> , 2015, 17, 536-544.	2.4	34
50	An international effort towards developing standards for best practices in analysis, interpretation and reporting of clinical genome sequencing results in the CLARITY Challenge. <i>Genome Biology</i> , 2014, 15, R53.	9.6	101
51	Synthesis and physical behavior of amphiphilic dendrimers with layered organization of hydrophilic and hydrophobic blocks. <i>Colloid and Polymer Science</i> , 2013, 291, 927-936.	2.1	5
52	Rapid identification of kidney cyst mutations by whole exome sequencing in zebrafish. <i>Development (Cambridge)</i> , 2013, 140, 4445-4451.	2.5	43
53	Specific temperature-induced perturbations of secondary mRNA structures are associated with the cold-adapted temperature-sensitive phenotype of influenza A virus. <i>RNA Biology</i> , 2012, 9, 1266-1274.	3.1	17
54	Bithiophenesilane-Based Dendronized Polymers: Facile Synthesis and Properties of Novel Highly Branched Organosilicon Macromolecular Structures. <i>Macromolecules</i> , 2012, 45, 2014-2024.	4.8	35

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55	Synthesis of Carbosilane Dendrimers with Variable Distance between Branching Nodes. <i>Macromolecules</i> , 2012, 45, 8796-8804.	4.8	18
56	Mutation mapping and identification by whole-genome sequencing. <i>Genome Research</i> , 2012, 22, 1541-1548.	5.5	126
57	Combinatorial Approach to Determine Functional Group Effects on Lipidoid-Mediated siRNA Delivery. <i>Bioconjugate Chemistry</i> , 2010, 21, 1448-1454.	3.6	64
58	Structure of carbosilane amphiphilic liquid-crystalline codendrimers in bulk and in thin (Langmuir) films. <i>Russian Chemical Bulletin</i> , 2008, 57, 2101-2110.	1.5	2
59	Liquid Crystal Codendrimers with a Statistical Distribution of Phenolic and Mesogenic Groups: Behavior as Langmuir and Langmuir-Blodgett Films. <i>Langmuir</i> , 2008, 24, 11082-11088.	3.5	12
60	Detection of Explosives using nanofibrous membranes. , 2008, , .		1
61	Organized Monolayers of Carbosilane Dendrimers with Mesogenic Terminal Groups. <i>Macromolecules</i> , 2005, 38, 8028-8035.	4.8	23