# Andrew Mungall

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/2828384/publications.pdf

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| 286 | 151,859 | 1457 107 | 660 255 |
|---|---|---|---|
| papers | citations | h-index | g-index |

| 309 | 309 | 309 | 138681 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Initial sequencing and analysis of the human genome. Nature, 2001, 409, 860-921. | 13.7 | 21,074 |
| 2 | Comprehensive molecular portraits of human breast tumours. Nature, 2012, 490, 61-70. | 13.7 | 10,282 |
| 3 | Comprehensive molecular characterization of human colon and rectal cancer. Nature, 2012, 487, 330-337. | 13.7 | 7,168 |
| 4 | The Cancer Genome Atlas Pan-Cancer analysis project. Nature Genetics, 2013, 45, 1113-1120. | 9.4 | 6,265 |
| 5 | Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330. | 13.7 | 5,653 |
| 6 | Comprehensive molecular characterization of gastric adenocarcinoma. Nature, 2014, 513, 202-209. | 13.7 | 5,055 |
| 7 | Comprehensive molecular profiling of lung adenocarcinoma. Nature, 2014, 511, 543-550. | 13.7 | 4,572 |
| 8 | Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074. | 13.9 | 4,139 |
| 9 | Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73. | 13.7 | 4,075 |
| 10 | The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14. | 6.6 | 3,706 |
| 11 | Comprehensive genomic characterization of squamous cell lung cancers. Nature, 2012, 489, 519-525. | 13.7 | 3,483 |
| 12 | Comprehensive genomic characterization of head and neck squamous cell carcinomas. Nature, 2015, 517, 576-582. | 13.7 | 3,209 |
| 13 | Comprehensive molecular characterization of clear cell renal cell carcinoma. Nature, 2013, 499, 43-49. | 13.7 | 2,839 |
| 14 | Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498. | 13.9 | 2,582 |
| 15 | Genomic Classification of Cutaneous Melanoma. Cell, 2015, 161, 1681-1696. | 13.5 | 2,562 |
| 16 | Comprehensive molecular characterization of urothelial bladder carcinoma. Nature, 2014, 507, 315-322. | 13.7 | 2,496 |
| 17 | The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025. | 13.5 | 2,435 |
| 18 | Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690. | 13.5 | 2,318 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11. | 13.5 | 2,277 |
| 20 | Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10. | 13.5 | 2,111 |
| 21 | Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93. | 13.7 | 1,966 |
| 22 | Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23. | 13.5 | 1,794 |
| 23 | Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. Cell, 2017, 171, 540-556.e25. | 13.5 | 1,742 |
| 24 | Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6. | 13.5 | 1,718 |
| 25 | Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. Cell, 2016, 164, 550-563. | 13.5 | 1,695 |
| 26 | Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18. | 13.5 | 1,670 |
| 27 | Somatic mutations altering EZH2 (Tyr641) in follicular and diffuse large B-cell lymphomas of germinal-center origin. Nature Genetics, 2010, 42, 181-185. | 9.4 | 1,504 |
| 28 | Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. Cell, 2015, 163, 506-519. | 13.5 | 1,485 |
| 29 | Integrated genomic characterization of oesophageal carcinoma. Nature, 2017, 541, 169-175. | 13.7 | 1,448 |
| 30 | Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. Nature, 2011, 476, 298-303. | 13.7 | 1,428 |
| 31 | Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-203.e13. | 7.7 | 1,428 |
| 32 | Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15. | 13.5 | 1,417 |
| 33 | Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. Cell, 2014, 158, 929-944. | 13.5 | 1,242 |
| 34 | Integrated genomic and molecular characterization of cervical cancer. Nature, 2017, 543, 378-384. | 13.7 | 1,158 |
| 35 | Mutational Analysis Reveals the Origin and Therapy-Driven Evolution of Recurrent Glioma. Science, 2014, 343, 189-193. | 6.0 | 1,147 |
| 36 | Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. New England Journal of Medicine, 2016, 374, 135-145. | 13.9 | 1,040 |

| # | Article | IF | Citations |
|---|---|---|---|
| 37 | Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6. | 2.9 | 801 |
| 38 | The whole-genome landscape of medulloblastoma subtypes. Nature, 2017, 547, 311-317. | 13.7 | 787 |
| 39 | Subgroup-specific structural variation across 1,000 medulloblastoma genomes. Nature, 2012, 488, 49-56. | 13.7 | 761 |
| 40 | Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3. | 7.7 | 750 |
| 41 | Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28. | 13.5 | 738 |
| 42 | Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. Cell Reports, 2018, 23, 181-193.e7. | 2.9 | 683 |
| 43 | The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. Cancer Cell, 2014, 26, 319-330. | 7.7 | 665 |
| 44 | Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. Cancer Cell, 2017, 32, 204-220.e15. | 7.7 | 642 |
| 45 | Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. Cancer Cell, 2018, 34, 211-224.e6. | 7.7 | 623 |
| 46 | Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14. | 13.5 | 620 |
| 47 | Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7. | 2.9 | 605 |
| 48 | Somatic mutations at EZH2 Y641 act dominantly through a mechanism of selectively altered PRC2 catalytic activity, to increase H3K27 trimethylation. Blood, 2011, 117, 2451-2459. | 0.6 | 556 |
| 49 | Dynamics of genomic clones in breast cancer patient xenografts at single-cell resolution. Nature, 2015, 518, 422-426. | 13.7 | 545 |
| 50 | Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. Cancer Cell, 2017, 31, 181-193. | 7.7 | 532 |
| 51 | The molecular landscape of pediatric acute myeloid leukemia reveals recurrent structural alterations and age-specific mutational interactions. Nature Medicine, 2018, 24, 103-112. | 15.2 | 525 |
| 52 | The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. Cell Reports, 2018, 23, 313-326.e5. | 2.9 | 523 |
| 53 | Mutations in a gene encoding a novel protein tyrosine phosphatase cause progressive myoclonus epilepsy. Nature Genetics, 1998, 20, 171-174. | 9.4 | 499 |
| 54 | Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736. | 7.7 | 482 |

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|---|---|---|---|
| 55 | A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9. | 7.7 | 478 |
| 56 | Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. Cell Reports, 2017, 18, 2780-2794. | 2.9 | 416 |
| 57 | Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3. | 2.9 | 407 |
| 58 | The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149. | 13.5 | 404 |
| 59 | lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. Cancer Cell, 2018, 33, 706-720.e9. | 7.7 | 400 |
| 60 | Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8. | 7.7 | 396 |
| 61 | Assembling the 20 Gb white spruce (Picea glauca) genome from whole-genome shotgun sequencing data. Bioinformatics, 2013, 29, 1492-1497. | 1.8 | 356 |
| 62 | Mutational and structural analysis of diffuse large B-cell lymphoma using whole-genome sequencing. Blood, 2013, 122, 1256-1265. | 0.6 | 349 |
| 63 | Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell Reports, 2018, 23, 282-296.e4. | 2.9 | 333 |
| 64 | Integrated Molecular Characterization of Testicular Germ Cell Tumors. Cell Reports, 2018, 23, 3392-3406. | 2.9 | 324 |
| 65 | Fate mapping of human glioblastoma reveals an invariant stem cell hierarchy. Nature, 2017, 549, 227-232. | 13.7 | 321 |
| 66 | Characterization of HPV and host genome interactions in primary head and neck cancers. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15544-15549. | 3.3 | 317 |
| 67 | Integrated Molecular Characterization of Uterine Carcinosarcoma. Cancer Cell, 2017, 31, 411-423. | 7.7 | 309 |
| 68 | Divergent modes of clonal spread and intraperitoneal mixing in high-grade serous ovarian cancer. Nature Genetics, 2016, 48, 758-767. | 9.4 | 287 |
| 69 | Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. Cell Systems, 2018, 6, 282-300.e2. | 2.9 | 284 |
| 70 | Concurrent CIC mutations, IDH mutations, and 1p/19q loss distinguish oligodendrogliomas from other cancers. Journal of Pathology, 2012, 226, 7-16. | 2.1 | 272 |
| 71 | Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10. | 13.5 | 272 |
| 72 | The Integrated Genomic Landscape of Thymic Epithelial Tumors. Cancer Cell, 2018, 33, 244-258.e10. | 7.7 | 270 |

| # | Article | IF | Citations |
|---|---|---|---|
| 73 | Comparison of human genetic and sequence-based physical maps. Nature, 2001, 409, 951-953. | 13.7 | 267 |
| 74 | Divergent clonal selection dominates medulloblastoma at recurrence. Nature, 2016, 529, 351-357. | 13.7 | 266 |
| 75 | Complete MHC Haplotype Sequencing for Common Disease Gene Mapping. Genome Research, 2004, 14, 1176-1187. | 2.4 | 260 |
| 76 | Double-Hit Gene Expression Signature Defines a Distinct Subgroup of Germinal Center B-Cell-Like Diffuse Large B-Cell Lymphoma. Journal of Clinical Oncology, 2019, 37, 190-201. | 0.8 | 257 |
| 77 | A Children's Oncology Group and TARGET initiative exploring the genetic landscape of Wilms tumor. Nature Genetics, 2017, 49, 1487-1494. | 9.4 | 255 |
| 78 | Mutations in EZH2 Cause Weaver Syndrome. American Journal of Human Genetics, 2012, 90, 110-118. | 2.6 | 253 |
| 79 | Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. Cell Reports, 2018, 23, 194-212.e6. | 2.9 | 245 |
| 80 | Recurrent DGCR8, DROSHA, and SIX Homeodomain Mutations in Favorable Histology Wilms Tumors. Cancer Cell, 2015, 27, 286-297. | 7.7 | 244 |
| 81 | Quiescent Sox2+ Cells Drive Hierarchical Growth and Relapse in Sonic Hedgehog Subgroup Medulloblastoma. Cancer Cell, 2014, 26, 33-47. | 7.7 | 241 |
| 82 | The genetic basis and cell of origin of mixed phenotype acute leukaemia. Nature, 2018, 562, 373-379. | 13.7 | 236 |
| 83 | A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12. | 13.5 | 228 |
| 84 | Genomic consequences of aberrant DNA repair mechanisms stratify ovarian cancer histotypes. Nature Genetics, 2017, 49, 856-865. | 9.4 | 220 |
| 85 | Genomic analyses identify recurrent MEF2D fusions in acute lymphoblastic leukaemia. Nature Communications, 2016, 7, 13331. | 5.8 | 218 |
| 86 | DNA hypomethylation within specific transposable element families associates with tissue-specific enhancer landscape. Nature Genetics, 2013, 45, 836-841. | 9.4 | 207 |
| 87 | Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. Cell Reports, 2018, 23, 297-312.e12. | 2.9 | 205 |
| 88 | Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4. | 2.9 | 204 |
| 89 | Histological Transformation and Progression in Follicular Lymphoma: A Clonal Evolution Study. PLoS Medicine, 2016, 13, e1002197. | 3.9 | 185 |
| 90 | Systematic Analysis of Splice-Site-Creating Mutations in Cancer. Cell Reports, 2018, 23, 270-281.e3. | 2.9 | 177 |

| # | Article | IF | Citations |
|---|---|---|---|
| 91 | Genome-wide discovery of somatic coding and noncoding mutations in pediatric endemic and sporadic Burkitt lymphoma. Blood, 2019, 133, 1313-1324. | 0.6 | 172 |
| 92 | Dissociation of solid tumor tissues with cold active protease for single-cell RNA-seq minimizes conserved collagenase-associated stress responses. Genome Biology, 2019, 20, 210. | 3.8 | 171 |
| 93 | Conservation of the H19 noncoding RNA and H19-IGF2 imprinting mechanism in therians. Nature Genetics, 2008, 40, 971-976. | 9.4 | 169 |
| 94 | The Evolution of the DLK1-DIO3 Imprinted Domain in Mammals. PLoS Biology, 2008, 6, e135. | 2.6 | 162 |
| 95 | Clonal Decomposition and DNA Replication States Defined by Scaled Single-Cell Genome Sequencing. Cell, 2019, 179, 1207-1221.e22. | 13.5 | 162 |
| 96 | Homologous Recombination Deficiency and Platinum-Based Therapy Outcomes in Advanced Breast Cancer. Clinical Cancer Research, 2017, 23, 7521-7530. | 3.2 | 144 |
| 97 | Analysis of FOXO1 mutations in diffuse large B-cell lymphoma. Blood, 2013, 121, 3666-3674. | 0.6 | 139 |
| 98 | A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF-Î² Superfamily. Cell Systems, 2018, 7, 422-437.e7. | 2.9 | 134 |
| 99 | Recurrent targets of aberrant somatic hypermutation in lymphoma. Oncotarget, 2012, 3, 1308-1319. | 0.8 | 127 |
| 100 | Cyclin D3 is a target gene of t(6;14)(p21.1;q32.3) of mature B-cell malignancies. Blood, 2001, 98, 2837-2844. | 0.6 | 125 |
| 101 | Large-scale profiling of microRNAs for The Cancer Genome Atlas. Nucleic Acids Research, 2016, 44, e3-e3. | 6.5 | 125 |
| 102 | The E3 ubiquitin ligase UBR5 is recurrently mutated in mantle cell lymphoma. Blood, 2013, 121, 3161-3164. | 0.6 | 124 |
| 103 | NRG1 Gene Fusions Are Recurrent, Clinically Actionable Gene Rearrangements in KRAS Wild-Type Pancreatic Ductal Adenocarcinoma. Clinical Cancer Research, 2019, 25, 4674-4681. | 3.2 | 121 |
| 104 | Altered Gene Expression along the Glycolysisâ€“Cholesterol Synthesis Axis Is Associated with Outcome in Pancreatic Cancer. Clinical Cancer Research, 2020, 26, 135-146. | 3.2 | 121 |
| 105 | Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. Cell Reports, 2018, 23, 172-180.e3. | 2.9 | 119 |
| 106 | Spatial heterogeneity in medulloblastoma. Nature Genetics, 2017, 49, 780-788. | 9.4 | 112 |
| 107 | Comprehensive miRNA sequence analysis reveals survival differences in diffuse large B-cell lymphoma patients. Genome Biology, 2015, 16, 18. | 3.8 | 107 |
| 108 | Genome-Wide Profiles of Extra-cranial Malignant Rhabdoid Tumors Reveal Heterogeneity and Dysregulated Developmental Pathways. Cancer Cell, 2016, 29, 394-406. | 7.7 | 105 |

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|---|---|---|---|
| 109 | Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commonsâ€™ Data. Cell Systems, 2019, 9, 24-34.e10. | 2.9 | 103 |
| 110 | Pan-cancer analysis of advanced patient tumors reveals interactions between therapy and genomic landscapes. Nature Cancer, 2020, 1, 452-468. | 5.7 | 103 |
| 111 | Genome-wide discovery of somatic regulatory variants in diffuse large B-cell lymphoma. Nature Communications, 2018, 9, 4001. | 5.8 | 102 |
| 112 | Integrative genomic analysis identifies key pathogenic mechanisms in primary mediastinal large B-cell lymphoma. Blood, 2019, 134, 802-813. | 0.6 | 96 |
| 113 | Lessons learned from the application of whole-genome analysis to the treatment of patients with advanced cancers. Journal of Physical Education and Sports Management, 2015, 1, a000570. | 0.5 | 92 |
| 114 | Analysis of Normal Human Mammary Epigenomes Reveals Cell-Specific Active Enhancer States and Associated Transcription Factor Networks. Cell Reports, 2016, 17, 2060-2074. | 2.9 | 90 |
| 115 | The North American bullfrog draft genome provides insight into hormonal regulation of long noncoding RNA. Nature Communications, 2017, 8, 1433. | 5.8 | 86 |
| 116 | Successful targeting of the NRG1 pathway indicates novel treatment strategy for metastatic cancer. Annals of Oncology, 2017, 28, 3092-3097. | 0.6 | 83 |
| 117 | Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. Cell Reports, 2018, 23, 213-226.e3. | 2.9 | 83 |
| 118 | Significance of TP53 Mutation in Wilms Tumors with Diffuse Anaplasia: A Report from the Children's Oncology Group. Clinical Cancer Research, 2016, 22, 5582-5591. | 3.2 | 82 |
| 119 | Cloning and characterization of the common fragile site FRA6F harboring a replicative senescence gene and frequently deleted in human tumors. Oncogene, 2002, 21, 7266-7276. | 2.6 | 79 |
| 120 | High-resolution architecture and partner genes of MYC rearrangements in lymphoma with DLBCL morphology. Blood Advances, 2018, 2, 2755-2765. | 2.5 | 74 |
| 121 | Identification and Analyses of Extra-Cranial and Cranial Rhabdoid Tumor Molecular Subgroups Reveal Tumors with Cytotoxic T Cell Infiltration. Cell Reports, 2019, 29, 2338-2354.e7. | 2.9 | 74 |
| 122 | Clonal fitness inferred from time-series modelling of single-cell cancer genomes. Nature, 2021, 595, 585-590. | 13.7 | 71 |
| 123 | A transgenic mouse model demonstrating the oncogenic role of mutations in the polycomb-group gene EZH2 in lymphomagenesis. Blood, 2014, 123, 3914-3924. | 0.6 | 69 |
| 124 | Vanin genes are clustered (human 6q22-24 and mouse 10A2B1) and encode isoforms of pantetheinase ectoenzymes. Immunogenetics, 2001, 53, 296-306. | 1.2 | 68 |
| 125 | Application of a Neural Network Whole Transcriptomeâ€“Based Pan-Cancer Method for Diagnosis of Primary and Metastatic Cancers. JAMA Network Open, 2019, 2, e192597. | 2.8 | 67 |
| 126 | Replication Timing of Human Chromosome 6. Cell Cycle, 2005, 4, 172-176. | 1.3 | 66 |

| # | Article | IF | Citations |
|---|---|---|---|
| 127 | MLLT1 YEATS domain mutations in clinically distinctive Favourable Histology Wilms tumours. Nature Communications, 2015, 6, 10013. | 5.8 | 64 |
| 128 | A somatic reference standard for cancer genome sequencing. Scientific Reports, 2016, 6, 24607. | 1.6 | 64 |
| 129 | Ocular developmental abnormalities and glaucoma associated with interstitial 6p25 duplications and deletions. Investigative Ophthalmology and Visual Science, 2002, 43, 1843-9. | 3.3 | 63 |
| 130 | TBL1XR1/TP63: a novel recurrent gene fusion in B-cell non-Hodgkin lymphoma. Blood, 2012, 119, 4949-4952. | 0.6 | 60 |
| 131 | Assessment of Capture and Amplicon-Based Approaches for the Development of a Targeted Next-Generation Sequencing Pipeline to Personalize Lymphoma Management. Journal of Molecular Diagnostics, 2018, 20, 203-214. | 1.2 | 58 |
| 132 | Complete genomic landscape of a recurring sporadic parathyroid carcinoma. Journal of Pathology, 2013, 230, 249-260. | 2.1 | 57 |
| 133 | Epigenetic and transcriptional determinants of the human breast. Nature Communications, 2015, 6, 6351. | 5.8 | 56 |
| 134 | The genomic and transcriptomic landscape of anaplastic thyroid cancer: implications for therapy. BMC Cancer, 2015, 15, 984. | 1.1 | 55 |
| 135 | BreakFusion: targeted assembly-based identification of gene fusions in whole transcriptome paired-end sequencing data. Bioinformatics, 2012, 28, 1923-1924. | 1.8 | 54 |
| 136 | The Organization of the Î³-Glutamyl Transferase Genes and Other Low Copy Repeats in Human Chromosomeâ€‰22q11. Genome Research, 1997, 7, 522-531. | 2.4 | 53 |
| 137 | High-resolution structural genomics reveals new therapeutic vulnerabilities in glioblastoma. Genome Research, 2019, 29, 1211-1222. | 2.4 | 52 |
| 138 | High resolution analysis of follicular lymphoma genomes reveals somatic recurrent sites of copyâ€neutral loss of heterozygosity and copy number alterations that target single genes. Genes Chromosomes and Cancer, 2010, 49, 669-681. | 1.5 | 51 |
| 139 | Sources of erroneous sequences and artifact chimeric reads in next generation sequencing of genomic DNA from formalin-fixed paraffin-embedded samples. Nucleic Acids Research, 2019, 47, e12-e12. | 6.5 | 50 |
| 140 | Genome and Transcriptome Biomarkers of Response to Immune Checkpoint Inhibitors in Advanced Solid Tumors. Clinical Cancer Research, 2021, 27, 202-212. | 3.2 | 50 |
| 141 | miR-509-3p is clinically significant and strongly attenuates cellular migration and multi-cellular spheroids in ovarian cancer. Oncotarget, 2016, 7, 25930-25948. | 0.8 | 49 |
| 142 | CSF3R mutations have a high degree of overlap with CEBPA mutations in pediatric AML. Blood, 2016, 127, 3094-3098. | 0.6 | 49 |
| 143 | MicroRNA Expression-Based Model Indicates Event-Free Survival in Pediatric Acute Myeloid Leukemia. Journal of Clinical Oncology, 2017, 35, 3964-3977. | 0.8 | 49 |
| 144 | A clinical transcriptome approach to patient stratification and therapy selection in acute myeloid leukemia. Nature Communications, 2021, 12, 2474. | 5.8 | 49 |

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|---|---|---|---|
| 145 | Recurrent genomic rearrangements in primary testicular lymphoma. Journal of Pathology, 2015, 236, 136-141. | 2.1 | 47 |
| 146 | Comprehensive characterization of programmed death ligand structural rearrangements in B-cell non-Hodgkin lymphomas. Blood, 2016, 128, 1206-1213. | 0.6 | 47 |
| 147 | The transcriptional landscape of Shh medulloblastoma. Nature Communications, 2021, 12, 1749. | 5.8 | 47 |
| 148 | TMEM30A loss-of-function mutations drive lymphomagenesis and confer therapeutically exploitable vulnerability in B-cell lymphoma. Nature Medicine, 2020, 26, 577-588. | 15.2 | 46 |
| 149 | Pyruvate Kinase Inhibits Proliferation during Postnatal Cerebellar Neurogenesis and Suppresses Medulloblastoma Formation. Cancer Research, 2017, 77, 3217-3230. | 0.4 | 45 |
| 150 | Coding and noncoding drivers of mantle cell lymphoma identified through exome and genome sequencing. Blood, 2020, 136, 572-584. | 0.6 | 44 |
| 151 | Comprehensive genomic profiling of glioblastoma tumors, BTICs, and xenografts reveals stability and adaptation to growth environments. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 19098-19108. | 3.3 | 42 |
| 152 | Improved structural variant interpretation for hereditary cancer susceptibility using long-read sequencing. Genetics in Medicine, 2020, 22, 1892-1897. | 1.1 | 42 |
| 153 | The Genomic Structure and Promoter Region of the Human Parkin Gene. Biochemical and Biophysical Research Communications, 2001, 286, 863-868. | 1.0 | 41 |
| 154 | An Exon Splice Enhancer Primes IGF2:IGF2R Binding Site Structure and Function Evolution. Science, 2012, 338, 1209-1213. | 6.0 | 40 |
| 155 | Analysis of Ugandan cervical carcinomas identifies human papillomavirus cladeâ€“specific epigenome and transcriptome landscapes. Nature Genetics, 2020, 52, 800-810. | 9.4 | 40 |
| 156 | Identification of candidate tumor-suppressor genes in 6q27 by combined deletion mapping and electronic expression profiling in lymphoid neoplasms. Genes Chromosomes and Cancer, 2003, 37, 421-426. | 1.5 | 39 |
| 157 | Response to angiotensin blockade with irbesartan in a patient with metastatic colorectal cancer. Annals of Oncology, 2016, 27, 801-806. | 0.6 | 39 |
| 158 | The Genome of the Beluga Whale (Delphinapterus leucas). Genes, 2017, 8, 378. | 1.0 | 39 |
| 159 | The evolution of imprinting: chromosomal mapping of orthologues of mammalian imprinted domains in monotreme and marsupial mammals. BMC Evolutionary Biology, 2007, 7, 157. | 3.2 | 38 |
| 160 | A novel mechanistic spectrum underlies glaucoma-associated chromosome 6p25 copy number variation. Human Molecular Genetics, 2008, 17, 3446-3458. | 1.4 | 38 |
| 161 | Whole-Genome Sequencing in Cancer. Cold Spring Harbor Perspectives in Medicine, 2019, 9, a034579. | 2.9 | 38 |
| 162 | Opposing Effects of CREBBP Mutations Govern the Phenotype of Rubinstein-Taybi Syndrome and Adult SHH Medulloblastoma. Developmental Cell, 2018, 44, 709-724.e6. | 3.1 | 35 |

| # | Article | IF | Citations |
|---|---|---|---|
| 163 | The Genome of the North American Brown Bear or Grizzly: Ursus arctos ssp. horribilis. Genes, 2018, 9, 598. | 1.0 | 34 |
| 164 | Base excision repair deficiency signatures implicate germline and somatic MUTYH aberrations in pancreatic ductal adenocarcinoma and breast cancer oncogenesis. Journal of Physical Education and Sports Management, 2019, 5, a003681. | 0.5 | 33 |
| 165 | Investigation of PD-L1 Biomarker Testing Methods for PD-1 Axis Inhibition in Non-squamous Nonâ€“small Cell Lung Cancer. Journal of Histochemistry and Cytochemistry, 2016, 64, 587-600. | 1.3 | 30 |
| 166 | Molecular characterization of metastatic pancreatic neuroendocrine tumors (PNETs) using whole-genome and transcriptome sequencing. Journal of Physical Education and Sports Management, 2018, 4, a002329. | 0.5 | 30 |
| 167 | A Clinically Validated Diagnostic Second-Generation Sequencing Assay for Detection of Hereditary BRCA1 and BRCA2 Mutations. Journal of Molecular Diagnostics, 2013, 15, 796-809. | 1.2 | 29 |
| 168 | Intratumoral Genetic and Functional Heterogeneity in Pediatric Glioblastoma. Cancer Research, 2019, 79, 2111-2123. | 0.4 | 28 |
| 169 | Physical and transcript map of the region between D6S264 and D6S149 on chromosome 6q27, the minimal region of allele loss in sporadic epithelial ovarian cancer. Oncogene, 2002, 21, 387-399. | 2.6 | 26 |
| 170 | Cloning and characterization of two overlapping genes in a subregion at 6q21 involved in replicative senescence and schizophrenia. Gene, 2000, 252, 217-225. | 1.0 | 24 |
| 171 | The Genome of the Northern Sea Otter (Enhydra lutris kenyoni). Genes, 2017, 8, 379. | 1.0 | 24 |
| 172 | Subtype-Discordant Pancreatic Ductal Adenocarcinoma Tumors Show Intermediate Clinical and Molecular Characteristics. Clinical Cancer Research, 2021, 27, 150-157. | 3.2 | 24 |
| 173 | Mapping the human T cell repertoire to recurrent driver mutations in MYD88 and EZH2 in lymphoma. OncoImmunology, 2017, 6, e1321184. | 2.1 | 23 |
| 174 | MAVIS: merging, annotation, validation, and illustration of structural variants. Bioinformatics, 2019, 35, 515-517. | 1.8 | 22 |
| 175 | The human homologue of unc-93 maps to chromosome 6q27 - characterisation and analysis in sporadic epithelial ovarian cancer. BMC Genetics, 2002, 3, 20. | 2.7 | 21 |
| 176 | RhoGAP domain-containing fusions and PPAPDC1A fusions are recurrent and prognostic in diffuse gastric cancer. Nature Communications, 2018, 9, 4439. | 5.8 | 21 |
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