Giovanni Parmigiani

List of Publications by Year
in descending order

176 papers	16,421 citations	50276 46 h-index	17105 122 g-index
192 all docs	192 docs citations	192 times ranked	24681 citing authors

#	Article	IF	Citations
1	The Genomic Landscapes of Human Breast and Colorectal Cancers. Science, 2007, 318, 1108-1113.	12.6	3,049
2	Meta-Analysis of BRCA1 and BRCA2 Penetrance. Journal of Clinical Oncology, 2007, 25, 1329-1333.	1.6	1,560
3	Heterogeneity of genomic evolution and mutational profiles in multiple myeloma. Nature Communications, 2014, 5, 2997.	12.8	741
4	Determining Carrier Probabilities for Breast Cancerâ€“Susceptibility Genes BRCA1 and BRCA2. American Journal of Human Genetics, 1998, 62, 145-158.	6.2	690
5	The Genetic Landscape of the Childhood Cancer Medulloblastoma. Science, 2011, 331, 435-439.	12.6	652
6	Familial Risk and Heritability of Cancer Among Twins in Nordic Countries. JAMA - Journal of the American Medical Association, 2016, 315, 68.	7.4	648
7	ComBat-seq: batch effect adjustment for RNA-seq count data. NAR Genomics and Bioinformatics, 2020, 2, lqaa078.	3.2	591
8	Detection of Chromosomal Alterations in the Circulation of Cancer Patients with Whole-Genome Sequencing. Science Translational Medicine, 2012, 4, 162ra154.	12.4	557
9	Pathologic Complete Response after Neoadjuvant Chemotherapy and Impact on Breast Cancer Recurrence and Survival: A Comprehensive Meta-analysis. Clinical Cancer Research, 2020, 26, 2838-2848.	7.0	403
10	Integrated genomic analyses identify ARID1A and ARID1B alterations in the childhood cancer neuroblastoma. Nature Genetics, 2013, 45, 12-17.	21.4	374
11	BRCA1 Recruitment to Transcriptional Pause Sites Is Required for R-Loop-Driven DNA Damage Repair. Molecular Cell, 2015, 57, 636-647.	9.7	363
12	Half or more of the somatic mutations in cancers of self-renewing tissues originate prior to tumor initiation. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 1999-2004.	7.1	348
13	Probability of Carrying a Mutation of Breast-Ovarian Cancer Gene BRCA1 Based on Family History. Journal of the National Cancer Institute, 1997, 89, 227-237.	6.3	344
14	Prediction of Germline Mutations and Cancer Risk in the Lynch Syndrome. JAMA - Journal of the American Medical Association, 2006, 296, 1479.	7.4	328
15	Only three driver gene mutations are required for the development of lung and colorectal cancers. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 118-123.	7.1	325
16	Gene Expression Profiling Reveals Reproducible Human Lung Adenocarcinoma Subtypes in Multiple Independent Patient Cohorts. Journal of Clinical Oncology, 2006, 24, 5079-5090.	1.6	263
17	Optimal Sample Size for Multiple Testing. Journal of the American Statistical Association, 2004, 99, 990-1001.	3.1	198
18	A Cross-Study Comparison of Gene Expression Studies for the Molecular Classification of Lung Cancer. Clinical Cancer Research, 2004, 10, 2922-2927.	7.0	196

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19	Risk Prediction for Late-Stage Ovarian Cancer by Meta-analysis of 1525 Patient Samples. Journal of the National Cancer Institute, 2014, 106, .	6.3	184
20	The Predictive Capacity of Personal Genome Sequencing. Science Translational Medicine, 2012, 4, 133ra58.	12.4	168
21	curatedOvarianData: clinically annotated data for the ovarian cancer transcriptome. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat013.	3.0	165
22	Whole-genome sequencing identifies a recurrent functional synonymous mutation in melanoma. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 13481-13486.	7.1	147
23	Systematic Review: Gene Expression Profiling Assays in Early-Stage Breast Cancer. Annals of Internal Medicine, 2008, 148, 358.	3.9	135
24	The role of chemoprevention in modifying the risk of breast cancer in women with atypical breast lesions. Breast Cancer Research and Treatment, 2012, 136, 627-633.	2.5	115
25	Comparative Meta-analysis of Prognostic Gene Signatures for Late-Stage Ovarian Cancer. Journal of the National Cancer Institute, 2014, 106, .	6.3	110
26	Validity of Models for Predicting BRCA1 and BRCA2 Mutations. Annals of Internal Medicine, 2007, 147, 441.	3.9	106
27	Bayesian Adaptive Randomized Trial Design for Patients With Recurrent Glioblastoma. Journal of Clinical Oncology, 2012, 30, 3258-3263.	1.6	104
28	Effect of BRCA1 and BRCA2 on the Association Between Breast Cancer Risk and Family History. Journal of the National Cancer Institute, 1998, 90, 1824-1829.	6.3	102
29	The clinical trials landscape for glioblastoma: is it adequate to develop new treatments?. Neuro-Oncology, 2018, 20, 1034-1043.	1.2	100
30	Penetrance of ATM Gene Mutations in Breast Cancer: A Metaâ€Analysis of Different Measures of Risk. Genetic Epidemiology, 2016, 40, 425-431.	1.3	98
31	DeMix: deconvolution for mixed cancer transcriptomes using raw measured data. Bioinformatics, 2013, 29, 1865-1871.	4.1	97
32	Prediction via Orthogonalized Model Mixing. Journal of the American Statistical Association, 1996, 91, 1197-1208.	3.1	94
33	Consensus on Molecular Subtypes of High-Grade Serous Ovarian Carcinoma. Clinical Cancer Research, 2018, 24, 5037-5047.	7.0	93
34	Stromal and epithelial transcriptional map of initiation progression and metastatic potential of human prostate cancer. Nature Communications, 2017, 8, 420.	12.8	91
35	Bayesian Effect Estimation Accounting for Adjustment Uncertainty. Biometrics, 2012, 68, 661-671.	1.4	84
36	Optimal Design via Curve Fitting of Monte Carlo Experiments. Journal of the American Statistical Association, 1995, 90, 1322-1330.	3.1	76

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37	Cross-study validation for the assessment of prediction algorithms. Bioinformatics, 2014, 30, i105-i112.	4.1	75
38	BayesMendel: an R Environment for Mendelian Risk Prediction. Statistical Applications in Genetics and Molecular Biology, 2004, 3, 1-19.	0.6	74
39	Transcriptome Deconvolution of Heterogeneous Tumor Samples with Immune Infiltration. IScience, 2018, 9, 451-460.	4.1	69
40	Precision Prevention and Early Detection of Cancer: Fundamental Principles. Cancer Discovery, 2018, 8, 803-811.	9.4	62
41	Estimation of sequencing error rates in short reads. BMC Bioinformatics, 2012, 13, 185.	2.6	61
42	Performance of Breast Cancer Risk-Assessment Models in a Large Mammography Cohort. Journal of the National Cancer Institute, 2020, 112, 489-497.	6.3	59
43	Multiomic Analysis of Subtype Evolution and Heterogeneity in High-Grade Serous Ovarian Carcinoma. Cancer Research, 2020, 80, 4335-4345.	0.9	57
44	On Optimal Screening Ages. Journal of the American Statistical Association, 1993, 88, 622-628.	3.1	55
45	Differential and limited expression of mutant alleles in multiple myeloma. Blood, 2014, 124, 3110-3117.	1.4	54
46	Integrating diverse genomic data using gene sets. Genome Biology, 2011, 12, R105.	9.6	52
47	Family History of Breast or Prostate Cancer and Prostate Cancer Risk. Clinical Cancer Research, 2018, 24, 5910-5917.	7.0	52
48	Long intergenic non-coding RNAs have an independent impact on survival in multiple myeloma. Leukemia, 2018, 32, 2626-2635.	7.2	48
49	Cross-study validation and combined analysis of gene expression microarray data. Biostatistics, 2007, 9, 333-354.	1.5	46
50	I-SPY 2 â€" A Glimpse of the Future of Phase 2 Drug Development?. New England Journal of Medicine, 2016, 375, 7-9.	27.0	46
51	Diagnostic Measures for Model Criticism. Journal of the American Statistical Association, 1996, 91, 753-762.	3.1	45
52	Relationship Between Bayesian and Frequentist Sample Size Determination. American Statistician, 2005, 59, 79-87.	1.6	43
53	Adjustment uncertainty in effect estimation. Biometrika, 2008, 95, 635-651.	2.4	42
54	Is Axillary Lymph Node Dissection Indicated for Early-Stage Breast Cancer? A Decision Analysis. Journal of Clinical Oncology, 1999, 17, 1465-1465.	1.6	41

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55	Penetrance of Breast and Ovarian Cancer in Women Who Carry a BRCA1/2 Mutation and Do Not Use Risk-Reducing Salpingo-Oophorectomy: An Updated Meta-Analysis. JNCI Cancer Spectrum, 2020, 4, pkaa029.	2.9	41
56	Bayesian Response-Adaptive Designs for Basket Trials. Biometrics, 2017, 73, 905-915.	1.4	38
57	A Clinical Decision Support Tool to Predict Cancer Risk for Commonly Tested Cancerâ€Related Germline Mutations. Journal of Genetic Counseling, 2018, 27, 1187-1199.	1.6	38
58	Deciphering the chronology of copy number alterations in Multiple Myeloma. Blood Cancer Journal, 2019, 9, 39.	6.2	38
59	Clinical Factors Associated With Gastric Cancer in Individuals With Lynch Syndrome. Clinical Gastroenterology and Hepatology, 2020, 18, 830-837.e1.	4.4	38
60	Biomarker-based adaptive trials for patients with glioblastoma--lessons from I-SPY 2. Neuro-Oncology, 2013, 15, 972-978.	1.2	37
61	Using Machine Learning and Natural Language Processing to Review and Classify the Medical Literature on Cancer Susceptibility Genes. JCO Clinical Cancer Informatics, 2019, 3, 1-9.	2.1	37
62	MÃ¡s-o-menos: a simple sign averaging method for discrimination in genomic data analysis. Bioinformatics, 2014, 30, 3062-3069.	4.1	34
63	Recent Enhancements to the Genetic Risk Prediction Model BRCAPRO. Cancer Informatics, 2015, 14s2, CIN.S17292.	1.9	34
64	Training replicable predictors in multiple studies. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 2578-2583.	7.1	34
65	The Impact of Stroma Admixture on Molecular Subtypes and Prognostic Gene Signatures in Serous Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 509-519.	2.5	34
66	Accounting for uncertainty in confounder and effect modifier selection when estimating average causal effects in generalized linear models. Biometrics, 2015, 71, 654-665.	1.4	33
67	Multi-Study Factor Analysis. Biometrics, 2019, 75, 337-346.	1.4	33
68	Expression Profiling of Archival Tumors for Long-term Health Studies. Clinical Cancer Research, 2012, 18, 6136-6146.	7.0	32
69	Designing Clinical Trials That Accept New Arms: An Example in Metastatic Breast Cancer. Journal of Clinical Oncology, 2017, 35, 3160-3168.	1.6	28
70	Modeling Liquid Association. Biometrics, 2011, 67, 133-141.	1.4	26
71	A Prospective Study of the Association between Physical Activity and Risk of Prostate Cancer Defined by Clinical Features and TMPRSS2:ERG. European Urology, 2019, 76, 33-40.	1.9	26
72	Alternative Splicing Is a Frequent Event and Impacts Clinical Outcome in Myeloma: A Large RNA-Seq Data Analysis of Newly-Diagnosed Myeloma Patients. Blood, 2014, 124, 638-638.	1.4	25

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73	MergeMaid: R Tools for Merging and Cross-Study Validation of Gene Expression Data. Statistical Applications in Genetics and Molecular Biology, 2004, 3, 1-13.	0.6	24
74	Opportunities for the Primary Prevention of Colorectal Cancer in the United States. Cancer Prevention Research, 2012, 5, 138-145.	1.5	24
75	Simplifying clinical use of the genetic risk prediction model BRCAPRO. Breast Cancer Research and Treatment, 2013, 139, 571-579.	2.5	24
76	Bayesian nonparametric cross-study validation of prediction methods. Annals of Applied Statistics, 2015, 9, .	1.1	24
77	High-Dimensional Confounding Adjustment Using Continuous Spike and Slab Priors. Bayesian Analysis, 2019, 14, 805-828.	3.0	24
78	Model Averaged Double Robust Estimation. Biometrics, 2017, 73, 410-421.	1.4	23
79	Leveraging molecular datasets for biomarker-based clinical trial design in glioblastoma. Neuro-Oncology, 2017, 19, 908-917.	1.2	23
80	Comparing Platforms for Messenger RNA Expression Profiling of Archival Formalin-Fixed, Paraffin-Embedded Tissues. Journal of Molecular Diagnostics, 2015, 17, 374-381.	2.8	22
81	Assessing the added value of breast tumor markers in genetic risk prediction model BRCAPRO. Breast Cancer Research and Treatment, 2012, 133, 347-355.	2.5	21
82	Combining progression-free survival and overall survival as a novel composite endpoint for glioblastoma trials. Neuro-Oncology, 2015, 17, 1106-1113.	1.2	21
83	Validation of a Semiautomated Natural Language Processingâ€“Based Procedure for Meta-Analysis of Cancer Susceptibility Gene Penetrance. JCO Clinical Cancer Informatics, 2019, 3, 1-9.	2.1	21
84	Prediction Via Orthogonalized Model Mixing. Journal of the American Statistical Association, 1996, 91, 1197.	3.1	21
85	A Bayesian Hierarchical Approach for Combining Case-Control and Prospective Studies. Biometrics, 1999, 55, 858-866.	1.4	20
86	Bayesian Semiparametric Analysis of Developmental Toxicology Data. Biometrics, 2001, 57, 150-157.	1.4	20
87	Recent BRCAPRO Upgrades Significantly Improve Calibration. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 1689-1695.	2.5	20
88	Continuity of transcriptomes among colorectal cancer subtypes based on meta-analysis. Genome Biology, 2018, 19, 142.	8.8	20
89	A Note on the Residual Entropy Function. Probability in the Engineering and Informational Sciences, 1993, 7, 413-420.	0.8	19
90	Adding experimental arms to platform clinical trials: randomization procedures and interim analyses. Biostatistics, 2018, 19, 199-215.	1.5	19

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91	Modeling and Optimization in Early Detection Programs with a Single Exam. Biometrics, 2002, 58, 30-36.	1.4	18
92	The DoppelgÃnger Effect: Hidden Duplicates in Databases of Transcriptome Profiles. Journal of the National Cancer Institute, 2016, 108, djw146.	6.3	18
93	Genetic Susceptibility and Survival: Application to Breast Cancer. Journal of the American Statistical Association, 2000, 95, 28-42.	3.1	17
94	Penetrance of Colorectal Cancer Among Mismatch Repair Gene Mutation Carriers: A Meta-Analysis. JNCI Cancer Spectrum, 2020, 4, pkaa027.	2.9	17
95	Multiple diseases in carrier probability estimation: Accounting for surviving all cancers other than breast and ovary in BRCAPRO. Statistics in Medicine, 2008, 27, 4532-4548.	1.6	16
96	Frailty Models for Familial Risk With Application to Breast Cancer. Journal of the American Statistical Association, 2013, 108, 1205-1215.	3.1	16
97	The impact of different sources of heterogeneity on loss of accuracy from genomic prediction models. Biostatistics, 2020, 21, 253-268.	1.5	15
98	Diagnostic Measures for Model Criticism. Journal of the American Statistical Association, 1996, 91, 753.	3.1	15
99	Modeling dependent gene expression. Annals of Applied Statistics, 2012, 6, 542-560.	1.1	14
100	Importance of Different Types of Prior Knowledge in Selecting Genomeâ€Wide Findings for Followâ€Up. Genetic Epidemiology, 2013, 37, 205-213.	1.3	14
101	Reassessing risk models for atypical hyperplasia: age may not matter. Breast Cancer Research and Treatment, 2017, 165, 285-291.	2.5	14
102	Providing access to risk prediction tools via the HL7 XML-formatted risk web service. Breast Cancer Research and Treatment, 2013, 140, 187-193.	2.5	13
103	<scp>SNP</scp> Prioritization Using a <scp>B</scp>ayesian Probability of Association. Genetic Epidemiology, 2013, 37, 214-221.	1.3	13
104	A two-stage approach to genetic risk assessment in primary care. Breast Cancer Research and Treatment, 2016, 155, 375-383.	2.5	13
105	Robustifying genomic classifiers to batch effects via ensemble learning. Bioinformatics, 2021, 37, 1521-1527.	4.1	13
106	Modular network construction using eQTL data: an analysis of computational costs and benefits. Frontiers in Genetics, 2014, 5, 40.	2.3	12
107	Minimax, information and ultrapessimism. Theory and Decision, 1992, 33, 241-252.	1.0	11
108	Combining Bayesian experimental designs and frequentist data analyses: motivations and examples. Applied Stochastic Models in Business and Industry, 2017, 33, 302-313.	1.5	11

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109	High-Dose Melphalan Significantly Increases Mutational Burden in Multiple Myeloma Cells at Relapse: Results from a Randomized Study in Multiple Myeloma. Blood, 2020, 136, 4-5.	1.4	11
110	IgM-MM is predominantly a preâ€“germinal center disorder and has a distinct genomic and transcriptomic signature from WM. Blood, 2021, 138, 1980-1985.	1.4	11
111	Validation of Breast Cancer Risk Models by Race/Ethnicity, Family History and Molecular Subtypes. Cancers, 2022, 14, 45.	3.7	11
112	Conjugate analysis of multivariate normal data with incomplete observations. Canadian Journal of Statistics, 2000, 28, 533-550.	0.9	10
113	Calibrated predictions for multivariate competing risks models. Lifetime Data Analysis, 2014, 20, 234-251.	0.9	10
114	RNA-Seq De Novo Assembly of Clonal Immunoglobulin Rearrangements Identifies Interesting Biology and Uncovers Prognostic Features in Multiple Myeloma. Blood, 2016, 128, 195-195.	1.4	10
115	Propensity scores with misclassified treatment assignment: a likelihood-based adjustment. Biostatistics, 2017, 18, 695-710.	1.5	9
116	Designing Follow-Up Times. Journal of the American Statistical Association, 2002, 97, 847-858.	3.1	8
117	Integrative correlation: Properties and relation to canonical correlations. Journal of Multivariate Analysis, 2014, 123, 270-280.	1.0	8
118	Evaluating a 4-marker signature of aggressive prostate cancer using time-dependent AUC. Prostate, 2015, 75, 1926-1933.	2.3	8
119	Multiplex Immunofluorescence in Formalin-Fixed Paraffin-Embedded Tumor Tissue to Identify Single-Cellâ€“Level PI3K Pathway Activation. Clinical Cancer Research, 2020, 26, 5903-5913.	7.0	8
120	On Optimal Screening Ages. Journal of the American Statistical Association, 1993, 88, 622.	3.1	8
121	Cross-Calibration of Stroke Disability Measures. Journal of the American Statistical Association, 2003, 98, 273-281.	3.1	7
122	Assessing the Benefits of Testing for Breast Cancer Susceptibility Genes: A Decision Analysis. Breast Disease, 1998, 10, 115-125.	0.8	6
123	False discovery rates in somatic mutation studies of cancer. Annals of Applied Statistics, 2011, 5, .	1.1	6
124	The penetrance of ductal carcinoma in situ among BRCA1 and BRCA2 mutation carriers. Breast Cancer Research and Treatment, 2013, 137, 315-318.	2.5	6
125	Optimal Bayesian Adaptive Trials When Treatment Efficacy Depends on Biomarkers. Biometrics, 2016, 72, 414-421.	1.4	6
126	A Decisionâ€Theory Approach to Interpretable Set Analysis for Highâ€Dimensional Data. Biometrics, 2013, 69, 614-623.	1.4	5

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127	Frequentist operating characteristics of Bayesian optimal designs via simulation. Statistics in Medicine, 2019, 38, 4026-4039.	1.6	5
128	Multiple Model Evaluation Absent the Gold Standard Through Model Combination. Journal of the American Statistical Association, 2008, 103, 897-909.	3.1	4
129	Hierarchical Bayesian analysis of somatic mutation data in cancer. Annals of Applied Statistics, 2013, 7, .	1.1	4
130	Reclassification of predictions for uncovering subgroup specific improvement. Statistics in Medicine, 2014, 33, 1914-1927.	1.6	4
131	Nonparametric Adjustment for Measurement Error in Time-to-Event Data: Application to Risk Prediction Models. Journal of the American Statistical Association, 2018, 113, 14-25.	3.1	4
132	Identification of a Novel Long Intergenic Noncoding RNA - Linc00936, with Significant Impact on Multiple Myeloma Cell Growth Via mTOR Pathway Inhibition. Blood, 2015, 126, 504-504.	1.4	4
133	Genetic Susceptibility and Survival: Application to Breast Cancer. Journal of the American Statistical Association, 2000, 95, 28.	3.1	4
134	A risk prediction tool for individuals with a family history of breast, ovarian, or pancreatic cancer: BRCAPANCPRO. British Journal of Cancer, 2021, 125, 1712-1717.	6.4	4
135	A dirichlet process elaboration diagnostic for binomial goodness of fit. Test, 1998, 7, 133-145.	1.1	3
136	Rejoinder: Bayesian Effect Estimation Accounting for Adjustment Uncertainty. Biometrics, 2012, 68, 680-686.	1.4	3
137	Reply to B. Freidlin et al. Journal of Clinical Oncology, 2013, 31, 970-971.	1.6	3
138	Misreported Family Histories and Underestimation of Risk. Journal of Clinical Oncology, 2014, 32, 3682-3683.	1.6	3
139	Efficient computation of the joint probability of multiple inherited risk alleles from pedigree data. Genetic Epidemiology, 2018, 42, 528-538.	1.3	3
140	Family history of prostate cancer and the incidence of ERGâ€•and phosphatase and tensin homologâ€defined prostate cancer. International Journal of Cancer, 2020, 146, 2694-2702.	5.1	3
141	Receiver operating characteristic curves with an indeterminacy zone. Pattern Recognition Letters, 2020, 136, 94-100.	4.2	3
142	Estimating the Effects of Fine Particulate Matter on 432 Cardiovascular Diseases Using Multi-Outcome Regression With Tree-Structured Shrinkage. Journal of the American Statistical Association, 2020, 115, 1689-1699.	3.1	3
143	Differentially Expressed and Prognostically Significant Lincrnas May Impact Immune System and Tumor Progression in Multiple Myeloma (MM). Blood, 2015, 126, 2989-2989.	1.4	3
144	Completing the Results of the 2013 Boston Marathon. PLoS ONE, 2014, 9, e93800.	2.5	3

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145	Statistical methods for Mendelian models with multiple genes and cancers. Genetic Epidemiology, 2022, 46, 395-414.	1.3	3
146	Generalized Quantile Treatment Effect: A Flexible Bayesian Approach Using Quantile Ratio Smoothing. Bayesian Analysis, 2015, 10, .	3.0	2
147	Practical implementation of frailty models in Mendelian risk prediction. Genetic Epidemiology, 2020, 44, 564-578.	1.3	2
148	Variation in cancer risk among families with genetic susceptibility. Genetic Epidemiology, 2021, 45, 209-221.	1.3	2
149	Nuclease Activity Is Associated with Genomic Instability As Well As Survival in Myeloma; Underlying Mechanisms and Significance. Blood, 2015, 126, 2420-2420.	1.4	2
150	Redefining Mutational Profiling Using RNA-Seq: Insight into the Functional Mutational Landscape of Multiple Myeloma. Blood, 2015, 126, 837-837.	1.4	2
151	Why tyrosine kinase inhibitor resistance is common in advanced gastrointestinal stromal tumors. F1000Research, 2013, 2, 152.	1.6	2
152	The Multiple Myeloma Genome Project: Development of a Molecular Segmentation Strategy for the Clinical Classification of Multiple Myeloma. Blood, 2016, 128, 196-196.	1.4	2
153	Tree-Weighting for Multi-Study Ensemble Learners. , 2019, , .		2
154	Tree-Weighting for Multi-Study Ensemble Learners. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2020, 25, 451-462.	0.7	2
155	Response to Comments on â€œThe Predictive Capacity of Personal Genome Sequencingâ€• Science Translational Medicine, 2012, 4, .	12.4	1
156	Legacy Genetic Testing Results for Cancer Susceptibility: How Common are Conflicting Classifications in a Large Variant Dataset from Multiple Practices?. Annals of Surgical Oncology, 2020, 27, 2212-2220.	1.5	1
157	Statistical approaches for metaâ€analysis of genetic mutation prevalence. Genetic Epidemiology, 2021, 45, 154-170.	1.3	1
158	Extending models via gradient boosting: An application to Mendelian models. Annals of Applied Statistics, 2021, 15, .	1.1	1
159	Gene Expression Pathways in Prostate Tissue Associated with Vigorous Physical Activity in Prostate Cancer. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 751-756.	2.5	1
160	Frequent Igh Fusion Transcripts with Clinical Impact in Multiple Myeloma. Blood, 2014, 124, 721-721.	1.4	1
161	Functional and Clinical Impact of Splicing Factor Dysregulation in Multiple Myeloma. Blood, 2015, 126, 726-726.	1.4	1
162	The Fusion Gene Landscape in Multiple Myeloma, with Clinical Impact. Blood, 2015, 126, 835-835.	1.4	1

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163	A Detailed Alternate Splicing Landscape in Multiple Myeloma with Significant Potential Biological and Clinical Implications. Blood, 2016, 128, 356-356.	1.4	1
164	Dysregulated Mirnas after Uniform Treatment Predict Outcome of Newly-Diagnosed Multiple Myeloma. Blood, 2019, 134, 4348-4348.	1.4	1
165	Inadequate Sars-Cov-2 Vaccine Effectiveness in Patients with Multiple Myeloma: A Large Nationwide Veterans Affairs Study. Blood, 2021, 138, 400-400.	1.4	1
166	OnionTree XML: A Format to Exchange Gene-Related Probabilities. Journal of Biomolecular Structure and Dynamics, 2011, 29, 417-423.	3.5	0
167	Combinatorial Mixtures of Multiparameter Distributions: An Application to Bivariate Data. International Journal of Biostatistics, 2017, 13, .	0.7	0
168	Integrative factor analysis â€" An unsupervised method for quantifying cross-study consistency of gene expression data. Genomics, 2018, 110, 80-88.	2.9	0
169	covid19census: U.S. and Italy COVID-19 metrics and other epidemiological data. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	3.0	0
170	The Average Baseline BCR-ABL Levels Are Significantly Higher in Patients with Resistance to Dasatinib As First-Line Treatment for Early Chronic Phase Chronic Myeloid Leukemia. Blood, 2012, 120, 4436-4436.	1.4	0
171	Statistical Tools and R Software for Cancer Driver Probabilities. Methods in Molecular Biology, 2014, 1101, 113-134.	0.9	0
172	Bone Marrow Microenvironment Regulates Alternative Splicing Events in Myeloma Cells through Downregulation of RNA Binding Protein Fox2. Blood, 2014, 124, 4714-4714.	1.4	0
173	Genomic Landscape Predictive of Minimal Residual Disease (MRD) in Multiple Myeloma (MM). Blood, 2015, 126, 4212-4212.	1.4	0
174	3' Untranslated Region (UTR) Alterations Are Frequently Targeted By MM-Related Mirnas and Affects the Clinical Outcome. Blood, 2016, 128, 4447-4447.	1.4	0
175	The Landscape of Genome Wide Somatic Alterations Identifies a Good-Risk Group in Newly Diagnosed Multiple Myeloma. Blood, 2019, 134, 3055-3055.	1.4	0
176	Prediction of hereditary cancers using neural networks. Annals of Applied Statistics, 2022, 16, .	1.1	0