

David I Heiman

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

62 papers	28,018 citations	61 h-index	67 g-index
67 ext. papers	39,010 ext. citations	27.1 avg, IF	4.56 L-index

#	Paper	IF	Citations
62	PANOPLY: a cloud-based platform for automated and reproducible proteogenomic data analysis. <i>Nature Methods</i> , 2021 , 18, 580-582	21.6	3
61	A proteogenomic portrait of lung squamous cell carcinoma. <i>Cell</i> , 2021 , 184, 4348-4371.e40	56.2	15
60	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. <i>Cell</i> , 2020 , 182, 200-225.e35	56.2	139
59	Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020 , 180, 729-748.e26	56.2	122
58	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020 , 183, 1436-1456.e31	56.2	31
57	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commons Data. <i>Cell Systems</i> , 2019 , 9, 24-34.e10	10.6	64
56	A comprehensive genomic history of extinct and living elephants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E2566-E2574	11.5	86
55	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , 2018 , 173, 400-416.e11	56.2	1072
54	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018 , 173, 371-385.e18	56.2	854
53	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. <i>Cell</i> , 2018 , 173, 291-304.e6	56.2	888
52	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , 2018 , 173, 386-399.e12	56.2	133
51	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018 , 173, 305-320.e10	56.2	166
50	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018 , 173, 338-354.e15	56.2	560
49	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018 , 173, 321-337.e10	56.2	1124
48	Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , 2018 , 173, 355-370.e14	56.2	342
47	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , 2018 , 23, 282-296.e4	10.6	188
46	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018 , 23, 227-238.e3	10.6	235

45	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , 2018 , 23, 194-212.e6	10.6	146
44	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. <i>Cell Reports</i> , 2018 , 23, 297-312.e12	10.6	147
43	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 2018 , 23, 313-326.e5	10.6	295
42	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. <i>Cell Reports</i> , 2018 , 23, 181-193.e7	10.6	366
41	The Immune Landscape of Cancer. <i>Immunity</i> , 2018 , 48, 812-830.e14	32.3	1754
40	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , 2018 , 23, 172-180.e3	10.6	66
39	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , 2018 , 23, 213-226.e3	26.6	56
38	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018 , 23, 239-254.e6	10.6	405
37	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. <i>Cell Reports</i> , 2018 , 23, 255-269.e4	10.6	112
36	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018 , 23, 270-281.e3	10.6	121
35	The Integrated Genomic Landscape of Thymic Epithelial Tumors. <i>Cancer Cell</i> , 2018 , 33, 244-258.e10	24.3	150
34	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018 , 6, 271-281.e7	10.6	320
33	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. <i>Cell Systems</i> , 2018 , 6, 282-300.e2	10.6	159
32	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. <i>Cancer Cell</i> , 2018 , 33, 706-720.e9	24.3	275
31	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018 , 33, 676-689.e3	24.3	377
30	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018 , 33, 721-735.e8	24.3	228
29	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018 , 33, 690-705.e9	24.3	277
28	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018 , 34, 211-224.e6	24.3	327

27	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018 , 23, 3392-3406.10.6	200
26	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- β Superfamily. <i>Cell Systems</i> , 2018 , 7, 422-437.e7	10.6 85
25	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. <i>Cancer Discovery</i> , 2018 , 8, 1548-1565	24.4 258
24	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. <i>Cell Reports</i> , 2018 , 25, 1304-1317.e5	10.6 152
23	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017 , 31, 181-193	24.3 350
22	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017 , 169, 1327-1341.e23	56.2 1125
21	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017 , 31, 411-423	24.3 210
20	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017 , 18, 2780-2794	10.6 247
19	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017 , 32, 204-220.e15	24.3 391
18	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017 , 32, 185-203.e13	24.3 13896
17	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017 , 171, 950-965.e28	56.2 451
16	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016 , 29, 723-736.e13	24.3 324
15	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015 , 372, 2481-98	59.2 1828
14	Contrasting host-pathogen interactions and genome evolution in two generalist and specialist microsporidian pathogens of mosquitoes. <i>Nature Communications</i> , 2015 , 6, 7121	17.4 56
13	Rabbit genome analysis reveals a polygenic basis for phenotypic change during domestication. <i>Science</i> , 2014 , 345, 1074-1079	33.3 246
12	The somatic genomic landscape of glioblastoma. <i>Cell</i> , 2013 , 155, 462-77	56.2 2900
11	Mutational heterogeneity in cancer and the search for new cancer-associated genes. <i>Nature</i> , 2013 , 499, 214-218	50.4 3616
10	Complete genome sequences from three genetically distinct strains reveal high intraspecies genetic diversity in the microsporidian <i>Encephalitozoon cuniculi</i> . <i>Eukaryotic Cell</i> , 2013 , 12, 503-11	43

9	Lifestyle transitions in plant pathogenic <i>Colletotrichum</i> fungi deciphered by genome and transcriptome analyses. <i>Nature Genetics</i> , 2012 , 44, 1060-5	36.3	564
8	Microsporidian genome analysis reveals evolutionary strategies for obligate intracellular growth. <i>Genome Research</i> , 2012 , 22, 2478-88	9.7	191
7	Comparative genome analysis of <i>Trichophyton rubrum</i> and related dermatophytes reveals candidate genes involved in infection. <i>MBio</i> , 2012 , 3, e00259-12	7.8	162
6	Comparative functional genomics of the fission yeasts. <i>Science</i> , 2011 , 332, 930-6	33.3	364
5	The genome of the green anole lizard and a comparative analysis with birds and mammals. <i>Nature</i> , 2011 , 477, 587-91	50.4	478
4	Comparative genomic analysis of human fungal pathogens causing paracoccidioidomycosis. <i>PLoS Genetics</i> , 2011 , 7, e1002345	6	132
3	Comparative genomics yields insights into niche adaptation of plant vascular wilt pathogens. <i>PLoS Pathogens</i> , 2011 , 7, e1002137	7.6	335
2	High-quality draft genome sequences of 28 <i>Enterococcus</i> sp. isolates. <i>Journal of Bacteriology</i> , 2010 , 192, 2469-70	3.5	65
1	Population genomic sequencing of <i>Coccidioides</i> fungi reveals recent hybridization and transposon control. <i>Genome Research</i> , 2010 , 20, 938-46	9.7	140