Paola Sebastiani

List of Publications by Year
in descending order

253 papers	11,114 citations	28190 55 h-index	37111 96 g-index
277 all docs	277 docs citations	277 times ranked	13822 citing authors

#	Article	IF	Citations
1	Airway epithelial gene expression in the diagnostic evaluation of smokers with suspect lung cancer. Nature Medicine, 2007, 13, 361-366.	15.2	507
2	Cluster analysis of gene expression dynamics. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 9121-9126.	3.3	421
3	Fetal hemoglobin in sickle cell anemia. Blood, 2011, 118, 19-27.	0.6	392
4	Genetic Signatures of Exceptional Longevity in Humans. PLoS ONE, 2012, 7, e29848.	1.1	340
5	Implementing Syndromic Surveillance: A Practical Guide Informed by the Early Experience. Journal of the American Medical Informatics Association: JAMIA, 2003, 11, 141-150.	2.2	325
6	Genetic dissection and prognostic modeling of overt stroke in sickle cell anemia. Nature Genetics, 2005, 37, 435-440.	9.4	300
7	Health Span Approximates Life Span Among Many Supercentenarians: Compression of Morbidity at the Approximate Limit of Life Span. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2012, 67A, 395-405.	1.7	292
8	GWAS of Longevity in CHARGE Consortium Confirms APOE and FOXO3 Candidacy. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2015, 70, 110-118.	1.7	250
9	BET bromodomain inhibition as a novel strategy for reactivation of HIV-1. Journal of Leukocyte Biology, 2012, 92, 1147-1154.	1.5	231
10	Genetic modifiers of sickle cell disease. American Journal of Hematology, 2012, 87, 795-803.	2.0	218
11	Reversible and permanent effects of tobacco smoke exposure on airway epithelial gene expression. Genome Biology, 2007, 8, R201.	13.9	217
12	A meta-analysis of genome-wide association studies identifies multiple longevity genes. Nature Communications, 2019, 10, 3669.	5.8	214
13	Fetal hemoglobin in sickle cell anemia: a glass half full?. Blood, 2014, 123, 481-485.	0.6	181
14	Biomarker signatures of aging. Aging Cell, 2017, 16, 329-338.	3.0	178
15	Minimal haplotype tagging. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 9900-9905.	3.3	167
16	Health and function of participants in the Long Life Family Study: A comparison with other cohorts. Aging, 2011, 3, 63-76.	1.4	163
17	A network model to predict the risk of death in sickle cell disease. Blood, 2007, 110, 2727-2735.	0.6	159
18	BCL11A is a major HbF quantitative trait locus in three different populations with Î²-hemoglobinopathies. Blood Cells, Molecules, and Diseases, 2008, 41, 255-258.	0.6	158

#	Article	IF	Citations
19	The Genetics of Extreme Longevity: Lessons from the New England Centenarian Study. Frontiers in Genetics, 2012, 3, 277.	1.1	157
20	Expression of microRNA and their gene targets are dysregulated in preinvasive breast cancer. Breast Cancer Research, 2011, 13, R24.	2.2	156
21	Sickle cell leg ulcers: associations with haemolysis and SNPs in Klotho, TEK and genes of the TGF-beta/BMP pathway. British Journal of Haematology, 2006, 133, 570-578.	1.2	155
22	Fetal hemoglobin in sickle cell anemia: genome-wide association studies suggest a regulatory region in the 5â€² olfactory receptor gene cluster. Blood, 2010, 115, 1815-1822.	0.6	146
23	Novel loci and pathways significantly associated with longevity. Scientific Reports, 2016, 6, 21243.	1.6	145
24	Bayesian Clustering by Dynamics. Machine Learning, 2002, 47, 91-121.	3.4	142
25	A Dynamic Bronchial Airway Gene Expression Signature of Chronic Obstructive Pulmonary Disease and Lung Function Impairment. American Journal of Respiratory and Critical Care Medicine, 2013, 187, 933-942.	2.5	142
26	Prenatal Buprenorphine Versus Methadone Exposure and Neonatal Outcomes: Systematic Review and Meta-Analysis. American Journal of Epidemiology, 2014, 180, 673-686.	1.6	137
27	Disentangling the Roles of Disability and Morbidity in Survival to Exceptional Old Age. Archives of Internal Medicine, 2008, 168, 277.	4.3	123
28	Robust Learning with Missing Data. , 2001, 45, 147-170.		116
29	A 3-bp deletion in the HBS1L-MYB intergenic region on chromosome 6q23 is associated with HbF expression. Blood, 2011, 117, 4935-4945.	0.6	116
30	A Family Longevity Selection Score: Ranking Sibships by Their Longevity, Size, and Availability for Study. American Journal of Epidemiology, 2009, 170, 1555-1562.	1.6	113
31	Similarities and differences between smoking-related gene expression in nasal and bronchial epithelium. Physiological Genomics, 2010, 41, 1-8.	1.0	107
32	Association of klotho, bone morphogenic protein 6, and annexin A2 polymorphisms with sickle cell osteonecrosis. Blood, 2005, 106, 372-375.	0.6	102
33	<i>APOE</i> Alleles and Extreme Human Longevity. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2019, 74, 44-51.	1.7	99
34	Robust Bayes classifiers. Artificial Intelligence, 2001, 125, 209-226.	3.9	98
35	Transcriptional Analysis of Fracture Healing and the Induction of Embryonic Stem Cellâ€"Related Genes. PLoS ONE, 2009, 4, e5393.	1.1	96
36	Genetic Signatures of Exceptional Longevity in Humans. Science, 2010, 329, .	6.0	95

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37	Coherent dispersion criteria for optimal experimental design. Annals of Statistics, 1999, 27, .	1.4	95
38	Four Genome-Wide Association Studies Identify New Extreme Longevity Variants. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2017, 72, 1453-1464.	1.7	91
39	A Prediction Model for Lung Cancer Diagnosis that Integrates Genomic and Clinical Features. Cancer Prevention Research, 2008, 1, 56-64.	0.7	89
40	Uroplakin 3a+ Cells Are a Distinctive Population of Epithelial Progenitors that Contribute to Airway Maintenance and Post-injury Repair. Cell Reports, 2017, 19, 246-254.	2.9	88
41	Statistical Challenges in Functional Genomics. Statistical Science, 2003, 18, 33.	1.6	84
42	Genetic modifiers of the severity of sickle cell anemia identified through a genomeâ€wide association study. American Journal of Hematology, 2010, 85, 29-35.	2.0	83
43	Gene expression in histologically normal epithelium from breast cancer patients and from cancer-free prophylactic mastectomy patients shares a similar profile. British Journal of Cancer, 2010, 102, 1284-1293.	2.9	82
44	RNA Editing Genes Associated with Extreme Old Age in Humans and with Lifespan in C. elegans. PLoS ONE, 2009, 4, e8210.	1.1	81
45	Compression of Morbidity Is Observed Across Cohorts with Exceptional Longevity. Journal of the American Geriatrics Society, 2016, 64, 1583-1591.	1.3	81
46	Meta-analysis of genetic variants associated with human exceptional longevity. Aging, 2013, 5, 653-661.	1.4	75
47	The Transforming Growth Factor-Î² Pathway Is a Common Target of Drugs That Prevent Experimental Diabetic Retinopathy. Diabetes, 2009, 58, 1659-1667.	0.3	74
48	Genome-Wide Association Study of Personality Traits in the Long Life Family Study. Frontiers in Genetics, 2013, 4, 65.	1.1	74
49	Meta-analysis of 2040 sickle cell anemia patients: BCL11A and HBS1L-MYB are the major modifiers of HbF in African Americans. Blood, 2012, 120, 1961-1962.	0.6	73
50	Sickle cell disease in <scp>S</scp>audi <scp>A</scp>rabia: the phenotype in adults with the <scp>A</scp>rabâ€<scp>I</scp>ndian haplotype is not benign. British Journal of Haematology, 2014, 164, 597-604.	1.2	72
51	Genomeâ€wide association studies and the genetic dissection of complex traits. American Journal of Hematology, 2009, 84, 504-515.	2.0	64
52	Families Enriched for Exceptional Longevity also have Increased Health-Span: Findings from the Long Life Family Study. Frontiers in Public Health, 2013, 1, 38.	1.3	63
53	Increasing Sibling Relative Risk of Survival to Older and Older Ages and the Importance of Precise Definitions of â€œAging,â€â€œLife Span,â€and â€œLongevityâ€ Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2016, 71, 340-346.	1.7	62
54	A Bayesian dynamic model for influenza surveillance. Statistics in Medicine, 2006, 25, 1803-1816.	0.8	61

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55	Single nucleotide polymorphisms associated with sporadic brain arteriovenous malformations: where do we stand?. Brain, 2013, 136, 665-681.	3.7	61
56	Sex Differences in Genetic Associations With Longevity. JAMA Network Open, 2018, 1, e181670.	2.8	60
57	Early Dysregulation of Cell Adhesion and Extracellular Matrix Pathways in Breast Cancer Progression. American Journal of Pathology, 2009, 175, 1292-1302.	1.9	59
58	A Genome-Wide Association Study of Total Bilirubin and Cholelithiasis Risk in Sickle Cell Anemia. PLoS ONE, 2012, 7, e34741.	1.1	55
59	Association between wind speed and the occurrence of sickle cell acute painful episodes: results of a caseâ€crossover study. British Journal of Haematology, 2008, 143, 433-438.	1.2	52
60	Extended maternal age at birth of last child and womenâ€™s longevity in the Long Life Family Study. Menopause, 2015, 22, 26-31.	0.8	52
61	Whole Genome Sequences of a Male and Female Supercentenarian, Ages Greater than 114â€‰Years. Frontiers in Genetics, 2011, 2, 90.	1.1	51
62	Fetal hemoglobin in sickle cell anemia: Genetic studies of the Arab-Indian haplotype. Blood Cells, Molecules, and Diseases, 2013, 51, 22-26.	0.6	50
63	DNA methylation modules associate with incident cardiovascular disease and cumulative risk factor exposure. Clinical Epigenetics, 2019, 11, 142.	1.8	46
64	Genetic determinants of haemolysis in sickle cell anaemia. British Journal of Haematology, 2013, 161, 270-278.	1.2	45
65	A Comprehensive, Ethnically Diverse Library of Sickle Cell Disease-Specific Induced Pluripotent Stem Cells. Stem Cell Reports, 2017, 8, 1076-1085.	2.3	45
66	Protein signatures of centenarians and their offspring suggest centenarians age slower than other humans. Aging Cell, 2021, 20, e13290.	3.0	42
67	Clustering by genetic ancestry using genome-wide SNP data. BMC Genetics, 2010, 11, 108.	2.7	40
68	Human longevity and common variations in the <i>LMNA</i> gene: a metaâ€analysis. Aging Cell, 2012, 11, 475-481.	3.0	40
69	Bayesian approaches to reverse engineer cellular systems: a simulation study on nonlinear Gaussian networks. BMC Bioinformatics, 2007, 8, S2.	1.2	38
70	Age and Sex Distributions of Ageâ€Related Biomarker Values in Healthy Older Adults from the Long Life Family Study. Journal of the American Geriatrics Society, 2016, 64, e189-e194.	1.3	38
71	Automated Detection of Influenza Epidemics with Hidden Markov Models. Lecture Notes in Computer Science, 2003, , 521-532.	1.0	38
72	Ancestry of African Americans with sickle cell disease. Blood Cells, Molecules, and Diseases, 2011, 47, 41-45.	0.6	35

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73	Fetal hemoglobin in sickle cell anemia: Bayesian modeling of genetic associations. American Journal of Hematology, 2008, 83, 189-195.	2.0	34
74	Severe sickle cell anemia is associated with increased plasma levels of TNFâ€R1 and VCAMâ€1. American Journal of Hematology, 2011, 86, 220-223.	2.0	34
75	BCL11A enhancer haplotypes and fetal hemoglobin in sickle cell anemia. Blood Cells, Molecules, and Diseases, 2015, 54, 224-230.	0.6	34
76	Factors affecting automated syndromic surveillance. Artificial Intelligence in Medicine, 2005, 34, 269-278.	3.8	32
77	Personality Traits of Centenarians' Offspring. Journal of the American Geriatrics Society, 2009, 57, 683-685.	1.3	32
78	Hypoxic Response Contributes to Altered Gene Expression and Precapillary Pulmonary Hypertension in Patients With Sickle Cell Disease. Circulation, 2014, 129, 1650-1658.	1.6	32
79	Effects of FOXO3 Polymorphisms on Survival to Extreme Longevity in Four Centenarian Studies. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2018, 73, 1439-1447.	1.7	32
80	Imputation of missing genotypes: an empirical evaluation of IMPUTE. BMC Genetics, 2008, 9, 85.	2.7	31
81	A phased SNP-based classification of sickle cell anemia HBB haplotypes. BMC Genomics, 2017, 18, 608.	1.2	31
82	Fetal hemoglobin in sickle cell anemia: Molecular characterization of the unusually high fetal hemoglobin phenotype in African Americans. American Journal of Hematology, 2012, 87, 217-219.	2.0	30
83	Premature expression of a muscle fibrosis axis in chronic HIV infection. Skeletal Muscle, 2012, 2, 10.	1.9	29
84	Naïve Bayesian Classifier and Genetic Risk Score for Genetic Risk Prediction of a Categorical Trait: Not so Different after all!. Frontiers in Genetics, 2012, 3, 26.	1.1	29
85	Transcriptional Profiling of Testosterone-Regulated Genes in the Skeletal Muscle of Human Immunodeficiency Virus-Infected Men Experiencing Weight Loss. Journal of Clinical Endocrinology and Metabolism, 2007, 92, 2793-2802.	1.8	28
86	Bayesian Methods for Multivariate Modeling of Pleiotropic SNP Associations and Genetic Risk Prediction. Frontiers in Genetics, 2012, 3, 176.	1.1	28
87	Prediction of Fetal Hemoglobin in Sickle Cell Anemia Using an Ensemble of Genetic Risk Prediction Models. Circulation: Cardiovascular Genetics, 2014, 7, 110-115.	5.1	27
88	A serum protein signature of <i>APOE</i> genotypes in centenarians. Aging Cell, 2019, 18, e13023.	3.0	27
89	D-optimal designs for generalised linear models with variance proportional to the square of the mean. Biometrika, 1994, 81, 295-304.	1.3	26
90	Gene-expression profiling of HIV-1 infection and perinatal transmission in Botswana. Genes and Immunity, 2006, 7, 298-309.	2.2	26

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91	A hierarchical and modular approach to the discovery of robust associations in genome-wide association studies from pooled DNA samples. BMC Genetics, 2008, 9, 6.	2.7	26
92	Epigenomic Assessment of Cardiovascular Disease Risk and Interactions With Traditional Risk Metrics. Journal of the American Heart Association, 2020, 9, e015299.	1.6	26
93	Bayesian Inference with Missing Data Using Bound and Collapse. Journal of Computational and Graphical Statistics, 2000, 9, 779-800.	0.9	25
94	Limitations and risks of meta-analyses of longevity studies. Mechanisms of Ageing and Development, 2017, 165, 139-146.	2.2	25
95	Telomere length is longer in women with late maternal age. Menopause, 2017, 24, 497-501.	0.8	25
96	Patterns of multi-domain cognitive aging in participants of the Long Life Family Study. GeroScience, 2020, 42, 1335-1350.	2.1	23
97	Biomarker signatures of sickle cell disease severity. Blood Cells, Molecules, and Diseases, 2018, 72, 1-9.	0.6	22
98	Burden of disease variants in participants of the long life family Study. Aging, 2015, 7, 123-132.	1.4	22
99	Age Validation in the Long Life Family Study Through a Linkage to Early-Life Census Records. Journals of Gerontology - Series B Psychological Sciences and Social Sciences, 2013, 68, 580-585.	2.4	21
100	Original Research: A case-control genome-wide association study identifies genetic modifiers of fetal hemoglobin in sickle cell disease. Experimental Biology and Medicine, 2016, 241, 706-718.	1.1	21
101	A note on D-optimal designs for a logistic regression model. Journal of Statistical Planning and Inference, 1997, 59, 359-368.	0.4	20
102	Relationship Between Poor Physical Function, Inflammatory Markers, and Comorbidities in HIV-Infected Women on Antiretroviral Therapy. Journal of Women's Health, 2014, 23, 69-76.	1.5	20
103	The genetics of hemoglobin A_2 regulation in sickle cell anemia. American Journal of Hematology, 2014, 89, 1019-1023.	2.0	20
104	Genetic polymorphism of APOB is associated with diabetes mellitus in sickle cell disease. Human Genetics, 2015, 134, 895-904.	1.8	20
105	Temporal gene expression profiling of the rat knee joint capsule during immobilization-induced joint contractures. BMC Musculoskeletal Disorders, 2015, 16, 125.	0.8	20
106	NIA Long Life Family Study: Objectives, Design, and Heritability of Cross-Sectional and Longitudinal Phenotypes. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2022, 77, 717-727.	1.7	20
107	Differential gene expression in pulmonary artery endothelial cells exposed to sickle cell plasma. Physiological Genomics, 2005, 21, 293-298.	1.0	19
108	Can we use linear Gaussian networks to model dynamic interactions among genes? Results from a simulation study. , 2006, , .		19

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109	Identification of serum biomarkers for aging and anabolic response. Immunity and Ageing, 2011, 8, 5.	1.8	19
110	Personality Factors in the Long Life Family Study. Journals of Gerontology - Series B Psychological Sciences and Social Sciences, 2013, 68, 739-749.	2.4	19
111	Experimental designs for mean and variance estimation in variance components models. Computational Statistics and Data Analysis, 1989, 8, 21-28.	0.7	18
112	Robust Transmission/Disequilibrium Test for Incomplete Family Genotypes. Genetics, 2004, 168, 2329-2337.	1.2	18
113	Bayesian analysis of comparative microarray experiments by model averaging. Bayesian Analysis, 2006, 1, 707.	1.6	18
114	Detection of Significant Groups in Hierarchical Clustering by Resampling. Frontiers in Genetics, 2016, 7, 144.	1.1	18
115	Reduced Prevalence and Incidence of Cognitive Impairment Among Centenarian Offspring. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2019, 74, 108-113.	1.7	18
116	Gene-Gene Interactions and the Pathophysiology of Sickle Cell Disease: Modeling the Effects of SNPs on Sickle Cell-Associated Vasoocclusive Events Using Classification and Regression Trees and Stochastic Gradient Boosting.. Blood, 2005, 106, 3183-3183.	0.6	18
117	Genome-Wide Association Study of Stroke in Sickle Cell Anemia.. Blood, 2009, 114, 1528-1528.	0.6	18
118	Varying Effects of APOE Alleles on Extreme Longevity in European Ethnicities. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2019, 74, S45-S51.	1.7	17
119	Genetic associations with age of menopause in familial longevity. Menopause, 2019, 26, 1204-1212.	0.8	17
120	Profiling your customers using Bayesian networks. SIGKDD Explorations: Newsletter of the Special Interest Group (SIG) on Knowledge Discovery & Data Mining, 2000, 1, 91-96.	3.2	16
121	Learning Bayesian Networks from Correlated Data. Scientific Reports, 2016, 6, 25156.	1.6	16
122	A candidate transacting modulator of fetal hemoglobin gene expression in the Arabâ€"Indian haplotype of sickle cell anemia. American Journal of Hematology, 2016, 91, 1118-1122.	2.0	16
123	Inflammatory signatures distinguish metabolic health in African American women with obesity. PLoS ONE, 2018, 13, e0196755.	1.1	16
124	Evidence for cross-regulated cytokine response in human peripheral blood mononuclear cells exposed to whole gonococcal bacteria in vitro. Microbial Pathogenesis, 2006, 40, 261-270.	1.3	15
125	Evolution and challenges in the design of computational systems for triage assistance. Journal of Biomedical Informatics, 2008, 41, 432-441.	2.5	15
126	Conditional clustering of temporal expression profiles. BMC Bioinformatics, 2008, 9, 147.	1.2	14

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127	Familial Risk for Exceptional Longevity. North American Actuarial Journal, 2016, 20, 57-64.	0.8	14
128	A predictive approach to the Bayesian design problem with application to normal regression models. Biometrika, 1996, 83, 111-125.	1.3	13
129	Homozygosity for a haplotype in the <i>HBG2â€OR51B4</i> region is exclusive to Arabâ€Indian haplotype sickle cell anemia. American Journal of Hematology, 2016, 91, E308-11.	2.0	13
130	Harvard HIV and Aging Workshop: Perspectives and Priorities from Claude D. Pepper Centers and Centers for AIDS Research. AIDS Research and Human Retroviruses, 2019, 35, 999-1012.	0.5	12
131	Effect of longevity genetic variants on the molecular aging rate. GeroScience, 2021, 43, 1237-1251.	2.1	12
132	PleioGRiP: genetic risk prediction with pleiotropy. Bioinformatics, 2013, 29, 1086-1088.	1.8	11
133	Variants of ZBTB7A (LRF) and its Î²-globin gene cluster binding motifs in sickle cell anemia. Blood Cells, Molecules, and Diseases, 2016, 59, 49-51.	0.6	11
134	Heterogeneity of healthy aging: comparing long-lived families across five healthy aging phenotypes of blood pressure, memory, pulmonary function, grip strength, and metabolism. GeroScience, 2019, 41, 383-393.	2.1	11
135	BCL2L1 is associated with Î³-globin gene expression. Blood Advances, 2019, 3, 2995-3001.	2.5	11
136	nf-gwas-pipeline: A Nextflow Genome-Wide Association Study Pipeline. Journal of Open Source Software, 2021, 6, 2957.	2.0	11
137	Parameter Estimation in Bayesian Networks from Incomplete Databases. Intelligent Data Analysis, 1998, 2, 139-160.	0.4	10
138	Genetic determinants of HbF in Saudi Arabian and African Benin haplotype sickle cell anemia. American Journal of Hematology, 2017, 92, E555-E557.	2.0	10
139	Relationships Among Obesity, Type 2 Diabetes, and Plasma Cytokines in African American Women. Obesity, 2017, 25, 1916-1920.	1.5	10
140	Estimating the relative probability of direct transmission between infectious disease patients. International Journal of Epidemiology, 2020, 49, 764-775.	0.9	10
141	Bayesian Selection of Decomposable Models With Incomplete Data. Journal of the American Statistical Association, 2001, 96, 1375-1386.	1.8	9
142	Complex Genetic Models. , 0, , 53-72.		9
143	Assortative Mating by Ethnicity in Longevous Families. Frontiers in Genetics, 2017, 8, 186.	1.1	9
144	First-order optimal designs for non-linear models. Journal of Statistical Planning and Inference, 1998, 74, 177-192.	0.4	8

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145	Building chromosome-wide LD maps. Bioinformatics, 2006, 22, 1933-1934.	1.8	8
146	Genetic studies of fetal hemoglobin in the Arabâ€Indian haplotype sickle cellâ€β^0 thalassemia. American Journal of Hematology, 2013, 88, 531-532.	2.0	8
147	Purpose in Life Among Centenarian Offspring. Journals of Gerontology - Series B Psychological Sciences and Social Sciences, 2020, 75, 308-315.	2.4	8
148	Sequence Learning via Bayesian Clustering by Dynamics. Lecture Notes in Computer Science, 2000, , 11-34.	1.0	8
149	The comparative safety of buprenorphine versus methadone in pregnancyâ€"what about confounding?. Addiction, 2016, 111, 2130-2131.	1.7	7
150	A novel healthy metabolic phenotype developed among a cohort of families enriched for longevity. Metabolism: Clinical and Experimental, 2019, 94, 28-38.	1.5	7
151	Association Between APOE Alleles and Change of Neuropsychological Tests in the Long Life Family Study. Journal of Alzheimer's Disease, 2021, 79, 117-125.	1.2	7
152	Digital Technology Differentiates Graphomotor and Information Processing Speed Patterns of Behavior. Journal of Alzheimer's Disease, 2021, 82, 17-32.	1.2	7
153	Clustering Short Gene Expression Profiles. Lecture Notes in Computer Science, 2006, , 60-68.	1.0	7
154	Cell Type Diversity Statistic: An Entropy-Based Metric to Compare Overall Cell Type Composition Across Samples. Frontiers in Genetics, 2022, 13, 855076.	1.1	7
155	Optimal designs for generalized linear models. Journal of the Italian Statistical Society, 1992, 1, 183-202.	0.1	6
156	Bayesian Inference with Missing Data Using Bound and Collapse. Journal of Computational and Graphical Statistics, 2000, 9, 779.	0.9	6
157	Bayesian Networks. , 2005, , 193-230.		6
158	Bayesian Polynomial Regression Models to Fit Multiple Genetic Models for Quantitative Traits. Bayesian Analysis, 2015, 10, 53-74.	1.6	6
159	A novel healthy blood pressure phenotype in the Long Life Family Study. Journal of Hypertension, 2018, 36, 43-53.	0.3	6
160	CaDrA: A Computational Framework for Performing Candidate Driver Analyses Using Genomic Features. Frontiers in Genetics, 2019, 10, 121.	1.1	6
161	Using Cure Models to Estimate the Serial Interval of Tuberculosis With Limited Follow-up. American Journal of Epidemiology, 2020, 189, 1421-1426.	1.6	6
162	A gene-diet interaction-based score predicts response to dietary fat in the Womenâ€™s Health Initiative. American Journal of Clinical Nutrition, 2020, 111, 893-902.	2.2	6

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163	A Repertoire of Genes Modifying the Risk of Death in Sickle Cell Anemia.. Blood, 2007, 110, 150-150.	0.6	6
164	Clinical and Genetic Variability of Red Blood Cell Hemolysis in Sickle Cell Anemia. Blood, 2011, 118, 1077-1077.	0.6	6
165	On the Derivatives of Matrix Powers. SIAM Journal on Matrix Analysis and Applications, 1996, 17, 640-648.	0.7	5
166	Bayesian estimates of linkage disequilibrium. BMC Genetics, 2007, 8, 36.	2.7	5
167	Prevalence, Incidence, and Risk Factors for Overall, Physical, and Cognitive Independence Among Those From Exceptionally Long-Lived Families: The Long Life Family Study. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2020, 75, 899-905.	1.7	5
168	APOE E2/E2 Is Associated with Slower Rate of Cognitive Decline with Age. Journal of Alzheimer's Disease, 2021, 83, 853-860.	1.2	5
169	HIV-1 burden influences host response to co-infection with Neisseria gonorrhoeae in vitro. International Immunology, 2006, 18, 125-137.	1.8	4
170	Identification of candidate cancer drivers by integrative Epi-DNA and Gene Expression (iEDGE) data analysis. Scientific Reports, 2019, 9, 16904.	1.6	4
171	Studying the Interplay Between Apolipoprotein E and Education on Cognitive Decline in Centenarians Using Bayesian Beta Regression. Frontiers in Genetics, 2020, 11, 606831.	1.1	4
172	Robust Bayesian classification. , 2000, , 445-450.		4
173	Systems Approach to Integrating Preclinical Apolipoprotein E-Knockout Investigations Reveals Novel Etiologic Pathways and Master Atherosclerosis Network in Humans. Arteriosclerosis, Thrombosis, and Vascular Biology, 2022, 42, 35-48.	1.1	4
174	Bayesian Networks. , 2009, , 175-208.		3
175	PopCluster: an algorithm to identify genetic variants with ethnicity-dependent effects. Bioinformatics, 2019, 35, 3046-3054.	1.8	3
176	Slower Decline in Processing Speed Is Associated with Familial Longevity. Gerontology, 2022, 68, 17-29.	1.4	3
177	Genes Associated with Alloimmunization to Blood Group Antigens in Sickle Cell Disease. Blood, 2014, 124, 762-762.	0.6	3
178	Genome-Wide Association Studies Suggest Shared Polymorphisms Are Associated with Severity of Sickle Cell Anemia and Exceptional Longevity.. Blood, 2008, 112, 1446-1446.	0.6	3
179	Distribution of 54 polygenic risk scores for common diseases in long lived individuals and their offspring. GeroScience, 2022, 44, 719-729.	2.1	3
180	Leveraging Observational Cohorts to Study Diet and Nutrition in Older Adults: Opportunities and Obstacles. Advances in Nutrition, 2022, 13, 1652-1668.	2.9	3

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181	Editorial: Methods in Functional Genomics. Machine Learning, 2003, 52, 5-9.	3.4	2
182	Normative selection of Bayesian networks. Journal of Multivariate Analysis, 2005, 93, 340-357.	0.5	2
183	Prediction Models That Include Genetic Data. Circulation: Cardiovascular Genetics, 2010, 3, 1-2.	5.1	2
184	Response: genetic admixture in sickle cell disease. Blood, 2011, 118, 4495-4495.	0.6	2
185	An efficient technique for Bayesian modeling of family data using the BUGS software. Frontiers in Genetics, 2014, 5, 390.	1.1	2
186	Bayesian Clustering of Gene Expression Dynamics. Statistics in the Health Sciences, 2003, , 409-427.	0.2	2
187	A Genome-Wide Association Study of the Alloimmunization Responder Phenotype in Sickle Cell Disease.. Blood, 2009, 114, 2551-2551.	0.6	2
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