Nelson B Freimer

List of Publications by Year
in descending order

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133 papers	28,649 citations	23567 58 h-index	14208 128 g-index
160 all docs	160 docs citations	160 times ranked	35752 citing authors

#	Article	IF	Citations
1	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	21.4	2,641
2	Variance component model to account for sample structure in genome-wide association studies. Nature Genetics, 2010, 42, 348-354.	21.4	2,287
3	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	21.4	2,067
4	Replicating genotypeâ€“phenotype associations. Nature, 2007, 447, 655-660.	27.8	1,509
5	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	21.4	1,191
6	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	12.6	1,085
7	A gene encoding a liver-specific ABC transporter is mutated in progressive familial intrahepatic cholestasis. Nature Genetics, 1998, 20, 233-238.	21.4	968
8	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	27.8	929
9	Genome-wide association meta-analysis in 269,867 individuals identifies new genetic and functional links to intelligence. Nature Genetics, 2018, 50, 912-919.	21.4	893
10	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35.	21.4	838
11	A gene encoding a P-type ATPase mutated in two forms of hereditary cholestasis. Nature Genetics, 1998, 18, 219-224.	21.4	710
12	Reconstructing Native American population history. Nature, 2012, 488, 370-374.	27.8	699
13	The ENIGMA Consortium: large-scale collaborative analyses of neuroimaging and genetic data. Brain Imaging and Behavior, 2014, 8, 153-182.	2.1	696
14	Genome-wide association analysis of metabolic traits in a birth cohort from a founder population. Nature Genetics, 2009, 41, 35-46.	21.4	676
15	Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. Nature Genetics, 2021, 53, 817-829.	21.4	629
16	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. Cell, 2018, 173, 1705-1715.e16.	28.9	623
17	Identification of common variants associated with human hippocampal and intracranial volumes. Nature Genetics, 2012, 44, 552-561.	21.4	594
18	Genome-wide association study identifies multiple loci influencing human serum metabolite levels. Nature Genetics, 2012, 44, 269-276.	21.4	516

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19	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	12.8	484
20	Genome Scan Meta-Analysis of Schizophrenia and Bipolar Disorder, Part III: Bipolar Disorder. American Journal of Human Genetics, 2003, 73, 49-62.	6.2	400
21	Rare loss-of-function variants in SETD1A are associated with schizophrenia and developmental disorders. Nature Neuroscience, 2016, 19, 571-577.	14.8	388
22	The Human Phenome Project. Nature Genetics, 2003, 34, 15-21.	21.4	356
23	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. PLoS Genetics, 2014, 10, e1004494.	3.5	351
24	Rare coding variants in ten genes confer substantial risk for schizophrenia. Nature, 2022, 604, 509-516.	27.8	326
25	Genome screening by searching for shared segments: mapping a gene for benign recurrent intrahepatic cholestasis. Nature Genetics, 1994, 8, 380-386.	21.4	315
26	Genetic mapping using haplotype, association and linkage methods suggests a locus for severe bipolar disorder (BPI) at 18q22-q23. Nature Genetics, 1996, 12, 436-441.	21.4	246
27	Interrogating the Genetic Determinants of Touretteâ€™s Syndrome and Other Tic Disorders Through Genome-Wide Association Studies. American Journal of Psychiatry, 2019, 176, 217-227.	7.2	242
28	Partitioning the Heritability of Tourette Syndrome and Obsessive Compulsive Disorder Reveals Differences in Genetic Architecture. PLoS Genetics, 2013, 9, e1003864.	3.5	241
29	Magnitude and distribution of linkage disequilibrium in population isolates and implications for genome-wide association studies. Nature Genetics, 2006, 38, 556-560.	21.4	227
30	Endophenotypes for psychiatric disorders: ready for primetime?. Trends in Genetics, 2006, 22, 306-313.	6.7	193
31	Exome sequencing of Finnish isolates enhances rare-variant association power. Nature, 2019, 572, 323-328.	27.8	161
32	Genetic demography of Antioquia (Colombia) and the Central Valley of Costa Rica. Human Genetics, 2003, 112, 534-541.	3.8	160
33	De Novo Coding Variants Are Strongly Associated with Tourette Disorder. Neuron, 2017, 94, 486-499.e9.	8.1	155
34	The use of pedigree, sib-pair and association studies of common diseases for genetic mapping and epidemiology. Nature Genetics, 2004, 36, 1045-1051.	21.4	144
35	Deletion of TOP3Î², a component of FMRP-containing mRNPs, contributes to neurodevelopmental disorders. Nature Neuroscience, 2013, 16, 1228-1237.	14.8	144
36	False Discovery Rate in Linkage and Association Genome Screens for Complex Disorders. Genetics, 2003, 164, 829-833.	2.9	138

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37	Rare Copy Number Variants in NRXN1 and CNTN6 Increase Risk for Tourette Syndrome. Neuron, 2017, 94, 1101-1111.e7.	8.1	137
38	The Genetics of the Mood Disorder Spectrum: Genome-wide Association Analyses of More Than 185,000 Cases and 439,000 Controls. Biological Psychiatry, 2020, 88, 169-184.	1.3	137
39	The Genome-wide Patterns of Variation Expose Significant Substructure in a Founder Population. American Journal of Human Genetics, 2008, 83, 787-794.	6.2	132
40	Whole genome sequencing in psychiatric disorders: the WGSPD consortium. Nature Neuroscience, 2017, 20, 1661-1668.	14.8	122
41	Cognitive ontologies for neuropsychiatric phenomics research. Cognitive Neuropsychiatry, 2009, 14, 419-450.	1.3	120
42	Systems Biology of the Vervet Monkey. ILAR Journal, 2013, 54, 122-143.	1.8	120
43	Genetic architecture of human plasma lipidome and its link to cardiovascular disease. Nature Communications, 2019, 10, 4329.	12.8	120
44	The genome of the vervet (Chlorocebus aethiops sabaeus). Genome Research, 2015, 25, 1921-1933.	5.5	114
45	Copy Number Variation in Obsessive-Compulsive Disorder and Tourette Syndrome: A Cross-Disorder Study. Journal of the American Academy of Child and Adolescent Psychiatry, 2014, 53, 910-919.	0.5	111
46	Ancient hybridization and strong adaptation to viruses across African vervet monkey populations. Nature Genetics, 2017, 49, 1705-1713.	21.4	107
47	Large-Scale Cognitive GWAS Meta-Analysis Reveals Tissue-Specific Neural Expression and Potential Nootropic Drug Targets. Cell Reports, 2017, 21, 2597-2613.	6.4	103
48	SIVagm Infection in Wild African Green Monkeys from South Africa: Epidemiology, Natural History, and Evolutionary Considerations. PLoS Pathogens, 2013, 9, e1003011.	4.7	96
49	De Novo Sequence and Copy Number Variants Are Strongly Associated with Tourette Disorder and Implicate Cell Polarity in Pathogenesis. Cell Reports, 2018, 24, 3441-3454.e12.	6.4	91
50	Multisystem Component Phenotypes of Bipolar Disorder for Genetic Investigations of Extended Pedigrees. JAMA Psychiatry, 2014, 71, 375.	11.0	87
51	Pleiotropic Meta-Analysis of Cognition, Education, and Schizophrenia Differentiates Roles of Early Neurodevelopmental and Adult Synaptic Pathways. American Journal of Human Genetics, 2019, 105, 334-350.	6.2	86
52	Factors Associated with Siman Immunodeficiency Virus Transmission in a Natural African Nonhuman Primate Host in the Wild. Journal of Virology, 2014, 88, 5687-5705.	3.4	77
53	Genetic contributions to circadian activity rhythm and sleep pattern phenotypes in pedigrees segregating for severe bipolar disorder. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E754-61.	7.1	77
54	The genome-wide distribution of background linkage disequilibrium in a population isolate. Human Molecular Genetics, 2001, 10, 545-551.	2.9	72

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55	Identification of brain transcriptional variation reproduced in peripheral blood: an approach for mapping brain expression traits. Human Molecular Genetics, 2009, 18, 4415-4427.	2.9	72
56	Guidelines for association studies in Human Molecular Genetics. Human Molecular Genetics, 2005, 14, 2481-2483.	2.9	70
57	Use of linkage disequilibrium approaches to map genes for bipolar disorder in the Costa Rican population. American Journal of Medical Genetics Part A, 1996, 67, 244-253.	2.4	69
58	Variants in common diseases. Nature, 2007, 445, 828-829.	27.8	66
59	Exome sequencing in bipolar disorder identifies AKAP11 as a risk gene shared with schizophrenia. Nature Genetics, 2022, 54, 541-547.	21.4	65
60	Genomewide Linkage Disequilibrium Mapping of Severe Bipolar Disorder in a Population Isolate. American Journal of Human Genetics, 2002, 71, 565-574.	6.2	63
61	Genome-wide association studies of metabolites in Finnish men identify disease-relevant loci. Nature Communications, 2022, 13, 1644.	12.8	63
62	Assessing the Feasibility of Linkage Disequilibrium Methods for Mapping Complex Traits: An Initial Screen for Bipolar Disorder Loci on Chromosome 18. American Journal of Human Genetics, 1999, 64, 1670-1678.	6.2	61
63	Sex-Dependent Shared and Nonshared Genetic Architecture Across Mood and Psychotic Disorders. Biological Psychiatry, 2022, 91, 102-117.	1.3	61
64	Identifying Heritable Brain Phenotypes in an Extended Pedigree of Vervet Monkeys. Journal of Neuroscience, 2009, 29, 2867-2875.	3.6	60
65	Polygenic Hyperlipidemias and Coronary Artery Disease Risk. Circulation Genomic and Precision Medicine, 2020, 13, e002725.	3.6	60
66	Genetic variation and gene expression across multiple tissues and developmental stages in a nonhuman primate. Nature Genetics, 2017, 49, 1714-1721.	21.4	57
67	A genetic linkage map of the vervet monkey (Chlorocebus aethiops sabaeus). Mammalian Genome, 2007, 18, 347-360.	2.2	55
68	Morphological variation in the genus Chlorocebus: Ecogeographic and anthropogenically mediated variation in body mass, postcranial morphology, and growth. American Journal of Physical Anthropology, 2018, 166, 682-707.	2.1	55
69	Association analysis of candidate genes for neuropsychiatric disease: the perpetual campaign. Trends in Genetics, 2002, 18, 307-312.	6.7	51
70	A quantitative trait locus for variation in dopamine metabolism mapped in a primate model using reference sequences from related species. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 15811-15816.	7.1	51
71	A non-human primate system for large-scale genetic studies of complex traits. Human Molecular Genetics, 2012, 21, 3307-3316.	2.9	51
72	Evidence for Genetic Overlap Between Schizophrenia and Age at First Birth in Women. JAMA Psychiatry, 2016, 73, 497.	11.0	51

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73	Re-sequencing Expands Our Understanding of the Phenotypic Impact of Variants at GWAS Loci. PLoS Genetics, 2014, 10, e1004147.	3.5	50
74	Seroprevalence of Zika Virus in Wild African Green Monkeys and Baboons. MSphere, 2017, 2, .	2.9	50
75	A web-based brain atlas of the vervet monkey, Chlorocebus aethiops. NeuroImage, 2011, 54, 1872-1880.	4.2	49
76	The Contribution of GWAS Loci in Familial Dyslipidemias. PLoS Genetics, 2016, 12, e1006078.	3.5	48
77	Zoonotic Potential of Simian Arteriviruses. Journal of Virology, 2016, 90, 630-635.	3.4	48
78	Understanding the Hidden Complexity of Latin American Population Isolates. American Journal of Human Genetics, 2018, 103, 707-726.	6.2	48
79	Local Virus Extinctions following a Host Population Bottleneck. Journal of Virology, 2015, 89, 8152-8161.	3.4	46
80	Linkage Analysis of a Complex Pedigree with Severe Bipolar Disorder, Using a Markov Chain Monte Carlo Method. American Journal of Human Genetics, 2001, 68, 1061-1064.	6.2	45
81	Why genetic investigation of psychiatric disorders is so difficult. Current Opinion in Genetics and Development, 2004, 14, 280-286.	3.3	45
82	Sequencing strategies and characterization of 721 vervet monkey genomes for future genetic analyses of medically relevant traits. BMC Biology, 2015, 13, 41.	3.8	45
83	Neurodegenerative disease biomarkers AÎ²_{1â€“40}, AÎ²_{1â€“42}, tau, and pâ€tau₁₈₁ in the vervet monkey cerebrospinal fluid: RelationÂto normal aging, genetic influences, and cerebral amyloid angiopathy. Brain and Behavior, 2018, 8, e00903.	2.2	45
84	Understanding the Genetic Basis of Mood Disorders: Where Do We Stand?. American Journal of Human Genetics, 1997, 60, 1283-1288.	6.2	42
85	Convergent linkage evidence from two Latin-American population isolates supports the presence of a susceptibility locus for bipolar disorder in 5q31â€“34. Human Molecular Genetics, 2006, 15, 3146-3153.	2.9	40
86	Benign recurrent intrahepatic cholestasis (BRIC): evidence of genetic heterogeneity and delimitation of the BRIC locus to a 7-cM interval between D18S69 and D18S64. Human Genetics, 1997, 100, 382-387.	3.8	39
87	The static allometry of sexual and nonsexual traits in vervet monkeys. Biological Journal of the Linnean Society, 2015, 114, 527-537.	1.6	38
88	Genetic studies of neuropsychiatric disorders in Costa Rica: a model for the use of isolated populations. Psychiatric Genetics, 2004, 14, 13-23.	1.1	37
89	Genome screening for linkage disequilibrium in a Costa Rican sample of patients with bipolar-I disorder: A follow-up study on chromosome 18. American Journal of Medical Genetics Part A, 2001, 105, 207-213.	2.4	35
90	Localized population divergence of vervet monkeys (Chlorocebus spp.) in South Africa: Evidence from mt<scp>DNA</scp>. American Journal of Physical Anthropology, 2016, 159, 17-30.	2.1	35

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91	Brain structureâ€“function associations in multi-generational families genetically enriched for bipolar disorder. Brain, 2015, 138, 2087-2102.	7.6	33
92	Expanding on population studies. Nature Genetics, 1997, 17, 371-373.	21.4	32
93	Synaptic processes and immune-related pathways implicated in Tourette syndrome. Translational Psychiatry, 2021, 11, 56.	4.8	31
94	Tag SNPs chosen from HapMap perform well in several population isolates. Genetic Epidemiology, 2007, 31, 189-194.	1.3	30
95	Genetic mapping using haplotype and model-free linkage analysis supports previous evidence for a locus predisposing to severe bipolar disorder at 5q31-33. , 2004, 125B, 83-86.		26
96	Arteriviruses, Pegiviruses, and Lentiviruses Are Common among Wild African Monkeys. Journal of Virology, 2016, 90, 6724-6737.	3.4	26
97	Contribution of common and rare variants to bipolar disorder susceptibility in extended pedigrees from population isolates. Translational Psychiatry, 2020, 10, 74.	4.8	25
98	Microsatellites: Evolution and Mutational Processes. Novartis Foundation Symposium, 1996, 197, 51-72.	1.1	25
99	Coronary Artery Disease Risk and Lipidomic Profiles Are Similar in Hyperlipidemias With Family History and Populationâ€Ascertained Hyperlipidemias. Journal of the American Heart Association, 2019, 8, e012415.	3.7	24
100	Distinct and shared contributions of diagnosis and symptom domains to cognitive performance in severe mental illness in the Paisa population: a case-control study. Lancet Psychiatry,the, 2020, 7, 411-419.	7.4	24
101	Evidence of linkage to psychosis on chromosome 5q33-34 in pedigrees ascertained for bipolar disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2007, 144B, 74-78.	1.7	22
102	Roadmap for a precision-medicine initiative in the Nordic region. Nature Genetics, 2019, 51, 924-930.	21.4	22
103	Association of structural variation with cardiometabolic traits in Finns. American Journal of Human Genetics, 2021, 108, 583-596.	6.2	22
104	ACE2 and TMPRSS2 variation in savanna monkeys (Chlorocebus spp.): Potential risk for zoonotic/anthroponotic transmission of SARS-CoV-2 and a potential model for functional studies. PLoS ONE, 2020, 15, e0235106.	2.5	21
105	Neurocognitive Phenotypes and Genetic Dissection of Disorders of Brain and Behavior. Neuron, 2010, 68, 218-230.	8.1	20
106	Characterisation of age and polarity at onset in bipolar disorder. British Journal of Psychiatry, 2021, 219, 659-669.	2.8	20
107	Results of a SNP genome screen in a large Costa Rican pedigree segregating for severe bipolar disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2006, 141B, 367-373.	1.7	19
108	Epigenetic clock and methylation studies in vervet monkeys. GeroScience, 2022, 44, 699-717.	4.6	18

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109	ForestQC: Quality control on genetic variants from next-generation sequencing data using random forest. PLoS Computational Biology, 2019, 15, e1007556.	3.2	17
110	Molecular Population Genetics of the Northern Elephant Seal Mirounga angustirostris. Journal of Heredity, 2017, 108, 618-627.	2.4	16
111	Multivariate Pattern Analysis of Genotypeâ€“Phenotype Relationships in Schizophrenia. Schizophrenia Bulletin, 2018, 44, 1045-1052.	4.3	15
112	Integrating behavioural health tracking in human genetics research. Nature Reviews Genetics, 2019, 20, 129-130.	16.3	13
113	Methodological Issues in Molecular Genetic Studies of Mental Disorders. Annual Review of Clinical Psychology, 2009, 5, 49-69.	12.3	12
114	Extensions of Multiple-Group Item Response Theory Alignment: Application to Psychiatric Phenotypes in an International Genomics Consortium. Educational and Psychological Measurement, 2020, 80, 870-909.	2.4	12
115	Identifying nootropic drug targets via large-scale cognitive GWAS and transcriptomics. Neuropsychopharmacology, 2021, 46, 1788-1801.	5.4	12
116	Shifts in microbial diversity, composition, and functionality in the gut and genital microbiome during a natural SIV infection in vervet monkeys. Microbiome, 2020, 8, 154.	11.1	11
117	Diversity matters: opportunities in the study of the genetics of psychotic disorders in low- and middle-income countries in Latin America. Revista Brasileira De Psiquiatria, 2021, 43, 631-637.	1.7	10
118	Memory systems in schizophrenia: Modularity is preserved but deficits are generalized. Schizophrenia Research, 2015, 168, 223-230.	2.0	7
119	Mitochondrial genome copy number measured by DNA sequencing in human blood is strongly associated with metabolic traits via cell-type composition differences. Human Genomics, 2021, 15, 34.	2.9	7
120	Genetic analysis of activity, brain and behavioral associations in extended families with heavy genetic loading for bipolar disorder. Psychological Medicine, 2021, 51, 494-502.	4.5	6
121	Characterization of Expression Quantitative Trait Loci in Pedigrees from Colombia and Costa Rica Ascertained for Bipolar Disorder. PLoS Genetics, 2016, 12, e1006046.	3.5	4
122	Genome-wide mapping of brain phenotypes in extended pedigrees with strong genetic loading for bipolar disorder. Molecular Psychiatry, 2021, 26, 5229-5238.	7.9	4
123	Cognitive phenomics. , 2009, , 271-282.		3
124	Populationâ€based identityâ€byâ€descent mapping combined with exome sequencing to detect rare risk variants for schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 223-231.	1.7	2
125	Immunosuppressive effect and global dysregulation of blood transcriptome in response to psychosocial stress in vervet monkeys (Chlorocebus sabaeus). Scientific Reports, 2020, 10, 3459.	3.3	2
126	Reducing policing in mental health crises: A vision for university campuses. Journal of American College Health, 2021, , 1-4.	1.5	1

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127	Use of linkage disequilibrium approaches to map genes for bipolar disorder in the Costa Rican population. American Journal of Medical Genetics Part A, 1996, 67, 244-253.	2.4	1
128	Pathogens & strain diversity: Is sex disruptive?. Nature Medicine, 1996, 2, 401-403.	30.7	0
129	Insight into bile duct differentiation takes (notched) wings. Hepatology, 1998, 27, 298-298.	7.3	0
130	Differences in the commonly used genotype imputation algorithms and their imputation accuracy estimates. , 2018, , .		0
131	Population Genetic Structure of Vervet Monkeys in South Africa. , 2019, , 101-106.		0
132	Causes of Variation in the Static Allometry of Morphological Structures: A Case Study with Vervet Monkeys. , 2019, , 224-232.		0
133	Bruins-in-Genomics: Evaluation of the impact of a UCLA undergraduate summer program in computational biology on participating students. PLoS ONE, 2022, 17, e0268861.	2.5	0