

Nelson B Freimer

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8897976/publications.pdf>

Version: 2024-02-01

133
papers

28,649
citations

23500

58
h-index

14702

127
g-index

160
all docs

160
docs citations

160
times ranked

35752
citing authors

#	ARTICLE	IF	CITATIONS
1	Sex-Dependent Shared and Nonshared Genetic Architecture Across Mood and Psychotic Disorders. <i>Biological Psychiatry</i> , 2022, 91, 102-117.	0.7	61
2	Epigenetic clock and methylation studies in vervet monkeys. <i>GeroScience</i> , 2022, 44, 699-717.	2.1	18
3	Genome-wide association studies of metabolites in Finnish men identify disease-relevant loci. <i>Nature Communications</i> , 2022, 13, 1644.	5.8	63
4	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. <i>Nature</i> , 2022, 604, 502-508.	13.7	929
5	Rare coding variants in ten genes confer substantial risk for schizophrenia. <i>Nature</i> , 2022, 604, 509-516.	13.7	326
6	Exome sequencing in bipolar disorder identifies AKAP11 as a risk gene shared with schizophrenia. <i>Nature Genetics</i> , 2022, 54, 541-547.	9.4	65
7	Bruins-in-Genomics: Evaluation of the impact of a UCLA undergraduate summer program in computational biology on participating students. <i>PLoS ONE</i> , 2022, 17, e0268861.	1.1	0
8	Genome-wide mapping of brain phenotypes in extended pedigrees with strong genetic loading for bipolar disorder. <i>Molecular Psychiatry</i> , 2021, 26, 5229-5238.	4.1	4
9	Genetic analysis of activity, brain and behavioral associations in extended families with heavy genetic loading for bipolar disorder. <i>Psychological Medicine</i> , 2021, 51, 494-502.	2.7	6
10	Synaptic processes and immune-related pathways implicated in Tourette syndrome. <i>Translational Psychiatry</i> , 2021, 11, 56.	2.4	31
11	Association of structural variation with cardiometabolic traits in Finns. <i>American Journal of Human Genetics</i> , 2021, 108, 583-596.	2.6	22
12	Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. <i>Nature Genetics</i> , 2021, 53, 817-829.	9.4	629
13	Identifying nootropic drug targets via large-scale cognitive GWAS and transcriptomics. <i>Neuropsychopharmacology</i> , 2021, 46, 1788-1801.	2.8	12
14	Mitochondrial genome copy number measured by DNA sequencing in human blood is strongly associated with metabolic traits via cell-type composition differences. <i>Human Genomics</i> , 2021, 15, 34.	1.4	7
15	Characterisation of age and polarity at onset in bipolar disorder. <i>British Journal of Psychiatry</i> , 2021, 219, 659-669.	1.7	20
16	Reducing policing in mental health crises: A vision for university campuses. <i>Journal of American College Health</i> , 2021, , 1-4.	0.8	1
17	Diversity matters: opportunities in the study of the genetics of psychotic disorders in low- and middle-income countries in Latin America. <i>Revista Brasileira De Psiquiatria</i> , 2021, 43, 631-637.	0.9	10
18	The Genetics of the Mood Disorder Spectrum: Genome-wide Association Analyses of More Than 185,000 Cases and 439,000 Controls. <i>Biological Psychiatry</i> , 2020, 88, 169-184.	0.7	137

#	ARTICLE	IF	CITATIONS
19	Distinct and shared contributions of diagnosis and symptom domains to cognitive performance in severe mental illness in the Paisa population: a case-control study. <i>Lancet Psychiatry</i> , 2020, 7, 411-419.	3.7	24
20	Shifts in microbial diversity, composition, and functionality in the gut and genital microbiome during a natural SIV infection in vervet monkeys. <i>Microbiome</i> , 2020, 8, 154.	4.9	11
21	Polygenic Hyperlipidemias and Coronary Artery Disease Risk. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002725.	1.6	60
22	ACE2 and TMPRSS2 variation in savanna monkeys (<i>Chlorocebus</i> spp.): Potential risk for zoonotic/anthroponotic transmission of SARS-CoV-2 and a potential model for functional studies. <i>PLoS ONE</i> , 2020, 15, e0235106.	1.1	21
23	Extensions of Multiple-Group Item Response Theory Alignment: Application to Psychiatric Phenotypes in an International Genomics Consortium. <i>Educational and Psychological Measurement</i> , 2020, 80, 870-909.	1.2	12
24	Contribution of common and rare variants to bipolar disorder susceptibility in extended pedigrees from population isolates. <i>Translational Psychiatry</i> , 2020, 10, 74.	2.4	25
25	Immunosuppressive effect and global dysregulation of blood transcriptome in response to psychosocial stress in vervet monkeys (<i>Chlorocebus sabaeus</i>). <i>Scientific Reports</i> , 2020, 10, 3459.	1.6	2
26	Pleiotropic Meta-Analysis of Cognition, Education, and Schizophrenia Differentiates Roles of Early Neurodevelopmental and Adult Synaptic Pathways. <i>American Journal of Human Genetics</i> , 2019, 105, 334-350.	2.6	86
27	Exome sequencing of Finnish isolates enhances rare-variant association power. <i>Nature</i> , 2019, 572, 323-328.	13.7	161
28	Coronary Artery Disease Risk and Lipidomic Profiles Are Similar in Hyperlipidemias With Family History and Population-Ascertained Hyperlipidemias. <i>Journal of the American Heart Association</i> , 2019, 8, e012415.	1.6	24
29	Genetic architecture of human plasma lipidome and its link to cardiovascular disease. <i>Nature Communications</i> , 2019, 10, 4329.	5.8	120
30	Genome-wide association study identifies 30 loci associated with bipolar disorder. <i>Nature Genetics</i> , 2019, 51, 793-803.	9.4	1,191
31	Population Genetic Structure of Vervet Monkeys in South Africa. , 2019, , 101-106.		0
32	Causes of Variation in the Static Allometry of Morphological Structures: A Case Study with Vervet Monkeys. , 2019, , 224-232.		0
33	Interrogating the Genetic Determinants of Tourette's Syndrome and Other Tic Disorders Through Genome-Wide Association Studies. <i>American Journal of Psychiatry</i> , 2019, 176, 217-227.	4.0	242
34	Roadmap for a precision-medicine initiative in the Nordic region. <i>Nature Genetics</i> , 2019, 51, 924-930.	9.4	22
35	Population-based identity-by-descent mapping combined with exome sequencing to detect rare risk variants for schizophrenia. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2019, 180, 223-231.	1.1	2
36	ForestQC: Quality control on genetic variants from next-generation sequencing data using random forest. <i>PLoS Computational Biology</i> , 2019, 15, e1007556.	1.5	17

#	ARTICLE	IF	CITATIONS
37	Integrating behavioural health tracking in human genetics research. <i>Nature Reviews Genetics</i> , 2019, 20, 129-130.	7.7	13
38	Neurodegenerative disease biomarkers A β ₄₀ , A β ₄₂ , tau, and p-tau ₁₈₁ in the vervet monkey cerebrospinal fluid: Relation to normal aging, genetic influences, and cerebral amyloid angiopathy. <i>Brain and Behavior</i> , 2018, 8, e00903.	1.0	45
39	Morphological variation in the genus <i>Chlorocebus</i> : Ecogeographic and anthropogenically mediated variation in body mass, postcranial morphology, and growth. <i>American Journal of Physical Anthropology</i> , 2018, 166, 682-707.	2.1	55
40	Multivariate Pattern Analysis of Genotype-Phenotype Relationships in Schizophrenia. <i>Schizophrenia Bulletin</i> , 2018, 44, 1045-1052.	2.3	15
41	Differences in the commonly used genotype imputation algorithms and their imputation accuracy estimates. , 2018, , .		0
42	De Novo Sequence and Copy Number Variants Are Strongly Associated with Tourette Disorder and Implicate Cell Polarity in Pathogenesis. <i>Cell Reports</i> , 2018, 24, 3441-3454.e12.	2.9	91
43	Understanding the Hidden Complexity of Latin American Population Isolates. <i>American Journal of Human Genetics</i> , 2018, 103, 707-726.	2.6	48
44	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. <i>Nature Communications</i> , 2018, 9, 2098.	5.8	484
45	Genome-wide association meta-analysis in 269,867 individuals identifies new genetic and functional links to intelligence. <i>Nature Genetics</i> , 2018, 50, 912-919.	9.4	893
46	Analysis of shared heritability in common disorders of the brain. <i>Science</i> , 2018, 360, .	6.0	1,085
47	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. <i>Cell</i> , 2018, 173, 1705-1715.e16.	13.5	623
48	De Novo Coding Variants Are Strongly Associated with Tourette Disorder. <i>Neuron</i> , 2017, 94, 486-499.e9.	3.8	155
49	Rare Copy Number Variants in NRXN1 and CNTN6 Increase Risk for Tourette Syndrome. <i>Neuron</i> , 2017, 94, 1101-1111.e7.	3.8	137
50	Seroprevalence of Zika Virus in Wild African Green Monkeys and Baboons. <i>MSphere</i> , 2017, 2, .	1.3	50
51	Ancient hybridization and strong adaptation to viruses across African vervet monkey populations. <i>Nature Genetics</i> , 2017, 49, 1705-1713.	9.4	107
52	Genetic variation and gene expression across multiple tissues and developmental stages in a nonhuman primate. <i>Nature Genetics</i> , 2017, 49, 1714-1721.	9.4	57
53	Molecular Population Genetics of the Northern Elephant Seal <i>Mirounga angustirostris</i> . <i>Journal of Heredity</i> , 2017, 108, 618-627.	1.0	16
54	Large-Scale Cognitive GWAS Meta-Analysis Reveals Tissue-Specific Neural Expression and Potential Nootropic Drug Targets. <i>Cell Reports</i> , 2017, 21, 2597-2613.	2.9	103

#	ARTICLE	IF	CITATIONS
55	Whole genome sequencing in psychiatric disorders: the WGSPD consortium. <i>Nature Neuroscience</i> , 2017, 20, 1661-1668.	7.1	122
56	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. <i>Nature Genetics</i> , 2017, 49, 27-35.	9.4	838
57	The Contribution of GWAS Loci in Familial Dyslipidemias. <i>PLoS Genetics</i> , 2016, 12, e1006078.	1.5	48
58	Characterization of Expression Quantitative Trait Loci in Pedigrees from Colombia and Costa Rica Ascertained for Bipolar Disorder. <i>PLoS Genetics</i> , 2016, 12, e1006046.	1.5	4
59	Arteriviruses, Pegiviruses, and Lentiviruses Are Common among Wild African Monkeys. <i>Journal of Virology</i> , 2016, 90, 6724-6737.	1.5	26
60	Localized population divergence of vervet monkeys (<i>Chlorocebus</i> spp.) in South Africa: Evidence from mtDNA. <i>American Journal of Physical Anthropology</i> , 2016, 159, 17-30.	2.1	35
61	Zoonotic Potential of Simian Arteriviruses. <i>Journal of Virology</i> , 2016, 90, 630-635.	1.5	48
62	Evidence for Genetic Overlap Between Schizophrenia and Age at First Birth in Women. <i>JAMA Psychiatry</i> , 2016, 73, 497.	6.0	51
63	Rare loss-of-function variants in SETD1A are associated with schizophrenia and developmental disorders. <i>Nature Neuroscience</i> , 2016, 19, 571-577.	7.1	388
64	Genetic contributions to circadian activity rhythm and sleep pattern phenotypes in pedigrees segregating for severe bipolar disorder. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E754-61.	3.3	77
65	The static allometry of sexual and nonsexual traits in vervet monkeys. <i>Biological Journal of the Linnean Society</i> , 2015, 114, 527-537.	0.7	38
66	Local Virus Extinctions following a Host Population Bottleneck. <i>Journal of Virology</i> , 2015, 89, 8152-8161.	1.5	46
67	Brain structure-function associations in multi-generational families genetically enriched for bipolar disorder. <i>Brain</i> , 2015, 138, 2087-2102.	3.7	33
68	Sequencing strategies and characterization of 721 vervet monkey genomes for future genetic analyses of medically relevant traits. <i>BMC Biology</i> , 2015, 13, 41.	1.7	45
69	Memory systems in schizophrenia: Modularity is preserved but deficits are generalized. <i>Schizophrenia Research</i> , 2015, 168, 223-230.	1.1	7
70	The genome of the vervet (<i>Chlorocebus aethiops sabaeus</i>). <i>Genome Research</i> , 2015, 25, 1921-1933.	2.4	114
71	Factors Associated with Simian Immunodeficiency Virus Transmission in a Natural African Nonhuman Primate Host in the Wild. <i>Journal of Virology</i> , 2014, 88, 5687-5705.	1.5	77
72	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. <i>PLoS Genetics</i> , 2014, 10, e1004494.	1.5	351

#	ARTICLE	IF	CITATIONS
73	Multisystem Component Phenotypes of Bipolar Disorder for Genetic Investigations of Extended Pedigrees. <i>JAMA Psychiatry</i> , 2014, 71, 375.	6.0	87
74	Re-sequencing Expands Our Understanding of the Phenotypic Impact of Variants at GWAS Loci. <i>PLoS Genetics</i> , 2014, 10, e1004147.	1.5	50
75	The ENIGMA Consortium: large-scale collaborative analyses of neuroimaging and genetic data. <i>Brain Imaging and Behavior</i> , 2014, 8, 153-182.	1.1	696
76	Copy Number Variation in Obsessive-Compulsive Disorder and Tourette Syndrome: A Cross-Disorder Study. <i>Journal of the American Academy of Child and Adolescent Psychiatry</i> , 2014, 53, 910-919.	0.3	111
77	Deletion of TOP3 β , a component of FMRP-containing mRNPs, contributes to neurodevelopmental disorders. <i>Nature Neuroscience</i> , 2013, 16, 1228-1237.	7.1	144
78	Discovery and refinement of loci associated with lipid levels. <i>Nature Genetics</i> , 2013, 45, 1274-1283.	9.4	2,641
79	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. <i>Nature Genetics</i> , 2013, 45, 984-994.	9.4	2,067
80	SIVagm Infection in Wild African Green Monkeys from South Africa: Epidemiology, Natural History, and Evolutionary Considerations. <i>PLoS Pathogens</i> , 2013, 9, e1003011.	2.1	96
81	Partitioning the Heritability of Tourette Syndrome and Obsessive Compulsive Disorder Reveals Differences in Genetic Architecture. <i>PLoS Genetics</i> , 2013, 9, e1003864.	1.5	241
82	Systems Biology of the Vervet Monkey. <i>ILAR Journal</i> , 2013, 54, 122-143.	1.8	120
83	A non-human primate system for large-scale genetic studies of complex traits. <i>Human Molecular Genetics</i> , 2012, 21, 3307-3316.	1.4	51
84	Identification of common variants associated with human hippocampal and intracranial volumes. <i>Nature Genetics</i> , 2012, 44, 552-561.	9.4	594
85	Genome-wide association study identifies multiple loci influencing human serum metabolite levels. <i>Nature Genetics</i> , 2012, 44, 269-276.	9.4	516
86	Reconstructing Native American population history. <i>Nature</i> , 2012, 488, 370-374.	13.7	699
87	A web-based brain atlas of the vervet monkey, <i>Chlorocebus aethiops</i> . <i>NeuroImage</i> , 2011, 54, 1872-1880.	2.1	49
88	Variance component model to account for sample structure in genome-wide association studies. <i>Nature Genetics</i> , 2010, 42, 348-354.	9.4	2,287
89	Neurocognitive Phenotypes and Genetic Dissection of Disorders of Brain and Behavior. <i>Neuron</i> , 2010, 68, 218-230.	3.8	20
90	Cognitive phenomics. , 2009, , 271-282.		3

#	ARTICLE	IF	CITATIONS
91	Identification of brain transcriptional variation reproduced in peripheral blood: an approach for mapping brain expression traits. <i>Human Molecular Genetics</i> , 2009, 18, 4415-4427.	1.4	72
92	Identifying Heritable Brain Phenotypes in an Extended Pedigree of Vervet Monkeys. <i>Journal of Neuroscience</i> , 2009, 29, 2867-2875.	1.7	60
93	Genome-wide association analysis of metabolic traits in a birth cohort from a founder population. <i>Nature Genetics</i> , 2009, 41, 35-46.	9.4	676
94	Cognitive ontologies for neuropsychiatric phenomics research. <i>Cognitive Neuropsychiatry</i> , 2009, 14, 419-450.	0.7	120
95	Methodological Issues in Molecular Genetic Studies of Mental Disorders. <i>Annual Review of Clinical Psychology</i> , 2009, 5, 49-69.	6.3	12
96	The Genome-wide Patterns of Variation Expose Significant Substructure in a Founder Population. <i>American Journal of Human Genetics</i> , 2008, 83, 787-794.	2.6	132
97	A quantitative trait locus for variation in dopamine metabolism mapped in a primate model using reference sequences from related species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 15811-15816.	3.3	51
98	Evidence of linkage to psychosis on chromosome 5q33-34 in pedigrees ascertained for bipolar disorder. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2007, 144B, 74-78.	1.1	22
99	Tag SNPs chosen from HapMap perform well in several population isolates. <i>Genetic Epidemiology</i> , 2007, 31, 189-194.	0.6	30
100	Replicating genotype-phenotype associations. <i>Nature</i> , 2007, 447, 655-660.	13.7	1,509
101	Variants in common diseases. <i>Nature</i> , 2007, 445, 828-829.	13.7	66
102	A genetic linkage map of the vervet monkey (<i>Chlorocebus aethiops sabaues</i>). <i>Mammalian Genome</i> , 2007, 18, 347-360.	1.0	55
103	Magnitude and distribution of linkage disequilibrium in population isolates and implications for genome-wide association studies. <i>Nature Genetics</i> , 2006, 38, 556-560.	9.4	227
104	Endophenotypes for psychiatric disorders: ready for primetime?. <i>Trends in Genetics</i> , 2006, 22, 306-313.	2.9	193
105	Results of a SNP genome screen in a large Costa Rican pedigree segregating for severe bipolar disorder. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2006, 141B, 367-373.	1.1	19
106	Convergent linkage evidence from two Latin-American population isolates supports the presence of a susceptibility locus for bipolar disorder in 5q31-34. <i>Human Molecular Genetics</i> , 2006, 15, 3146-3153.	1.4	40
107	Guidelines for association studies in Human Molecular Genetics. <i>Human Molecular Genetics</i> , 2005, 14, 2481-2483.	1.4	70
108	The use of pedigree, sib-pair and association studies of common diseases for genetic mapping and epidemiology. <i>Nature Genetics</i> , 2004, 36, 1045-1051.	9.4	144

#	ARTICLE	IF	CITATIONS
109	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
110	Why genetic investigation of psychiatric disorders is so difficult. Current Opinion in Genetics and Development, 2004, 14, 280-286.	1.5	45
111	Genetic studies of neuropsychiatric disorders in Costa Rica: a model for the use of isolated populations. Psychiatric Genetics, 2004, 14, 13-23.	0.6	37
112	Genetic demography of Antioquia (Colombia) and the Central Valley of Costa Rica. Human Genetics, 2003, 112, 534-541.	1.8	160
113	The Human Phenome Project. Nature Genetics, 2003, 34, 15-21.	9.4	356
114	Genome Scan Meta-Analysis of Schizophrenia and Bipolar Disorder, Part III: Bipolar Disorder. American Journal of Human Genetics, 2003, 73, 49-62.	2.6	400
115	False Discovery Rate in Linkage and Association Genome Screens for Complex Disorders. Genetics, 2003, 164, 829-833.	1.2	138
116	Genomewide Linkage Disequilibrium Mapping of Severe Bipolar Disorder in a Population Isolate. American Journal of Human Genetics, 2002, 71, 565-574.	2.6	63
117	Association analysis of candidate genes for neuropsychiatric disease: the perpetual campaign. Trends in Genetics, 2002, 18, 307-312.	2.9	51
118	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
119	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.	2.6	45
120	The genome-wide distribution of background linkage disequilibrium in a population isolate. Human Molecular Genetics, 2001, 10, 545-551.	1.4	72
121	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.	2.6	61
122	A gene encoding a liver-specific ABC transporter is mutated in progressive familial intrahepatic cholestasis. Nature Genetics, 1998, 20, 233-238.	9.4	968
123	A gene encoding a P-type ATPase mutated in two forms of hereditary cholestasis. Nature Genetics, 1998, 18, 219-224.	9.4	710
124	Insight into bile duct differentiation takes (notched) wings. Hepatology, 1998, 27, 298-298.	3.6	0
125	Understanding the Genetic Basis of Mood Disorders: Where Do We Stand?. American Journal of Human Genetics, 1997, 60, 1283-1288.	2.6	42
126	Expanding on population studies. Nature Genetics, 1997, 17, 371-373.	9.4	32

#	ARTICLE	IF	CITATIONS
127	Benign recurrent intrahepatic cholestasis (BRIC): evidence of genetic heterogeneity and delimitation of the BRIC locus to a 7-cM interval between D18S69 and D18S64. <i>Human Genetics</i> , 1997, 100, 382-387.	1.8	39
128	Use of linkage disequilibrium approaches to map genes for bipolar disorder in the Costa Rican population. <i>American Journal of Medical Genetics Part A</i> , 1996, 67, 244-253.	2.4	69
129	Genetic mapping using haplotype, association and linkage methods suggests a locus for severe bipolar disorder (BPI) at 18q22-q23. <i>Nature Genetics</i> , 1996, 12, 436-441.	9.4	246
130	Pathogens & strain diversity: Is sex disruptive?. <i>Nature Medicine</i> , 1996, 2, 401-403.	15.2	0
131	Use of linkage disequilibrium approaches to map genes for bipolar disorder in the Costa Rican population. , 1996, 67, 244.		1
132	Microsatellites: Evolution and Mutational Processes. <i>Novartis Foundation Symposium</i> , 1996, 197, 51-72.	1.2	25
133	Genome screening by searching for shared segments: mapping a gene for benign recurrent intrahepatic cholestasis. <i>Nature Genetics</i> , 1994, 8, 380-386.	9.4	315