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	23567 58 h-index	14208 128 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. Biological Psychiatry, 2022, 91, 102-117.	1.3	61
2	Epigenetic clock and methylation studies in vervet monkeys. GeroScience, 2022, 44, 699-717.	4.6	18
3	Genome-wide association studies of metabolites in Finnish men identify disease-relevant loci. Nature Communications, 2022, 13, 1644.	12.8	63
4	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	27.8	929
5	Rare coding variants in ten genes confer substantial risk for schizophrenia. Nature, 2022, 604, 509-516.	27.8	326
6	Exome sequencing in bipolar disorder identifies AKAP11 as a risk gene shared with schizophrenia. Nature Genetics, 2022, 54, 541-547.	21.4	65
7	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
8	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
9	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
10	Synaptic processes and immune-related pathways implicated in Tourette syndrome. Translational Psychiatry, 2021, 11, 56.	4.8	31
11	Association of structural variation with cardiometabolic traits in Finns. American Journal of Human Genetics, 2021, 108, 583-596.	6.2	22
12	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
13	Identifying nootropic drug targets via large-scale cognitive GWAS and transcriptomics. Neuropsychopharmacology, 2021, 46, 1788-1801.	5.4	12
14	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
15	Characterisation of age and polarity at onset in bipolar disorder. British Journal of Psychiatry, 2021, 219, 659-669.	2.8	20
16	Reducing policing in mental health crises: A vision for university campuses. Journal of American College Health, 2021, , 1-4.	1.5	1
17	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
18	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

#	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. Lancet Psychiatry,the, 2020, 7, 411-419.	7.4	24
20	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
21	Polygenic Hyperlipidemias and Coronary Artery Disease Risk. Circulation Genomic and Precision Medicine, 2020, 13, e002725.	3.6	60
22	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
23	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
24	Contribution of common and rare variants to bipolar disorder susceptibility in extended pedigrees from population isolates. Translational Psychiatry, 2020, 10, 74.	4.8	25
25	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
26	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
27	Exome sequencing of Finnish isolates enhances rare-variant association power. Nature, 2019, 572, 323-328.	27.8	161
28	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
29	Genetic architecture of human plasma lipidome and its link to cardiovascular disease. Nature Communications, 2019, 10, 4329.	12.8	120
30	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	21.4	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. American Journal of Psychiatry, 2019, 176, 217-227.	7.2	242
34	Roadmap for a precision-medicine initiative in the Nordic region. Nature Genetics, 2019, 51, 924-930.	21.4	22
35	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
36	ForestQC: Quality control on genetic variants from next-generation sequencing data using random forest. PLoS Computational Biology, 2019, 15, e1007556.	3.2	17

#	Article	IF	Citations
37	Integrating behavioural health tracking in human genetics research. Nature Reviews Genetics, 2019, 20, 129-130.	16.3	13
38	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
39	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
40	Multivariate Pattern Analysis of Genotypeâ€“Phenotype Relationships in Schizophrenia. Schizophrenia Bulletin, 2018, 44, 1045-1052.	4.3	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. Cell Reports, 2018, 24, 3441-3454.e12.	6.4	91
43	Understanding the Hidden Complexity of Latin American Population Isolates. American Journal of Human Genetics, 2018, 103, 707-726.	6.2	48
44	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	12.8	484
45	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
46	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	12.6	1,085
47	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. Cell, 2018, 173, 1705-1715.e16.	28.9	623
48	De Novo Coding Variants Are Strongly Associated with Tourette Disorder. Neuron, 2017, 94, 486-499.e9.	8.1	155
49	Rare Copy Number Variants in NRXN1 and CNTN6 Increase Risk for Tourette Syndrome. Neuron, 2017, 94, 1101-1111.e7.	8.1	137
50	Seroprevalence of Zika Virus in Wild African Green Monkeys and Baboons. MSphere, 2017, 2, .	2.9	50
51	Ancient hybridization and strong adaptation to viruses across African vervet monkey populations. Nature Genetics, 2017, 49, 1705-1713.	21.4	107
52	Genetic variation and gene expression across multiple tissues and developmental stages in a nonhuman primate. Nature Genetics, 2017, 49, 1714-1721.	21.4	57
53	Molecular Population Genetics of the Northern Elephant Seal Mirounga angustirostris. Journal of Heredity, 2017, 108, 618-627.	2.4	16
54	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

#	Article	IF	Citations
55	Whole genome sequencing in psychiatric disorders: the WGSPD consortium. Nature Neuroscience, 2017, 20, 1661-1668.	14.8	122
56	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
57	The Contribution of GWAS Loci in Familial Dyslipidemias. PLoS Genetics, 2016, 12, e1006078.	3.5	48
58	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
59	Arteriviruses, Pegiviruses, and Lentiviruses Are Common among Wild African Monkeys. Journal of Virology, 2016, 90, 6724-6737.	3.4	26
60	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
61	Zoonotic Potential of Simian Arteriviruses. Journal of Virology, 2016, 90, 630-635.	3.4	48
62	Evidence for Genetic Overlap Between Schizophrenia and Age at First Birth in Women. JAMA Psychiatry, 2016, 73, 497.	11.0	51
63	Rare loss-of-function variants in SETD1A are associated with schizophrenia and developmental disorders. Nature Neuroscience, 2016, 19, 571-577.	14.8	388
64	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
65	The static allometry of sexual and nonsexual traits in vervet monkeys. Biological Journal of the Linnean Society, 2015, 114, 527-537.	1.6	38
66	Local Virus Extinctions following a Host Population Bottleneck. Journal of Virology, 2015, 89, 8152-8161.	3.4	46
67	Brain structureâ€“function associations in multi-generational families genetically enriched for bipolar disorder. Brain, 2015, 138, 2087-2102.	7.6	33
68	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
69	Memory systems in schizophrenia: Modularity is preserved but deficits are generalized. Schizophrenia Research, 2015, 168, 223-230.	2.0	7
70	The genome of the vervet (Chlorocebus aethiops sabaeus). Genome Research, 2015, 25, 1921-1933.	5.5	114
71	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
72	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. PLoS Genetics, 2014, 10, e1004494.	3.5	351

#	Article	IF	Citations
73	Multisystem Component Phenotypes of Bipolar Disorder for Genetic Investigations of Extended Pedigrees. JAMA Psychiatry, 2014, 71, 375.	11.0	87
74	Re-sequencing Expands Our Understanding of the Phenotypic Impact of Variants at GWAS Loci. PLoS Genetics, 2014, 10, e1004147.	3.5	50
75	The ENIGMA Consortium: large-scale collaborative analyses of neuroimaging and genetic data. Brain Imaging and Behavior, 2014, 8, 153-182.	2.1	696
76	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
77	Deletion of TOP3Î², a component of FMRP-containing mRNPs, contributes to neurodevelopmental disorders. Nature Neuroscience, 2013, 16, 1228-1237.	14.8	144
78	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	21.4	2,641
79	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	21.4	2,067
80	SIVagm Infection in Wild African Green Monkeys from South Africa: Epidemiology, Natural History, and Evolutionary Considerations. PLoS Pathogens, 2013, 9, e1003011.	4.7	96
81	Partitioning the Heritability of Tourette Syndrome and Obsessive Compulsive Disorder Reveals Differences in Genetic Architecture. PLoS Genetics, 2013, 9, e1003864.	3.5	241
82	Systems Biology of the Vervet Monkey. ILAR Journal, 2013, 54, 122-143.	1.8	120
83	A non-human primate system for large-scale genetic studies of complex traits. Human Molecular Genetics, 2012, 21, 3307-3316.	2.9	51
84	Identification of common variants associated with human hippocampal and intracranial volumes. Nature Genetics, 2012, 44, 552-561.	21.4	594
85	Genome-wide association study identifies multiple loci influencing human serum metabolite levels. Nature Genetics, 2012, 44, 269-276.	21.4	516
86	Reconstructing Native American population history. Nature, 2012, 488, 370-374.	27.8	699
87	A web-based brain atlas of the vervet monkey, Chlorocebus aethiops. NeuroImage, 2011, 54, 1872-1880.	4.2	49
88	Variance component model to account for sample structure in genome-wide association studies. Nature Genetics, 2010, 42, 348-354.	21.4	2,287
89	Neurocognitive Phenotypes and Genetic Dissection of Disorders of Brain and Behavior. Neuron, 2010, 68, 218-230.	8.1	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. Human Molecular Genetics, 2009, 18, 4415-4427.	2.9	72
92	Identifying Heritable Brain Phenotypes in an Extended Pedigree of Vervet Monkeys. Journal of Neuroscience, 2009, 29, 2867-2875.	3.6	60
93	Genome-wide association analysis of metabolic traits in a birth cohort from a founder population. Nature Genetics, 2009, 41, 35-46.	21.4	676
94	Cognitive ontologies for neuropsychiatric phenomics research. Cognitive Neuropsychiatry, 2009, 14, 419-450.	1.3	120
95	Methodological Issues in Molecular Genetic Studies of Mental Disorders. Annual Review of Clinical Psychology, 2009, 5, 49-69.	12.3	12
96	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
97	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
98	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
99	Tag SNPs chosen from HapMap perform well in several population isolates. Genetic Epidemiology, 2007, 31, 189-194.	1.3	30
100	Replicating genotypeâ€“phenotype associations. Nature, 2007, 447, 655-660.	27.8	1,509
101	Variants in common diseases. Nature, 2007, 445, 828-829.	27.8	66
102	A genetic linkage map of the vervet monkey (Chlorocebus aethiops sabaeus). Mammalian Genome, 2007, 18, 347-360.	2.2	55
103	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
104	Endophenotypes for psychiatric disorders: ready for primetime?. Trends in Genetics, 2006, 22, 306-313.	6.7	193
105	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
106	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
107	Guidelines for association studies in Human Molecular Genetics. Human Molecular Genetics, 2005, 14, 2481-2483.	2.9	70
108	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

#	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.	3.3	45
111	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
112	Genetic demography of Antioquia (Colombia) and the Central Valley of Costa Rica. Human Genetics, 2003, 112, 534-541.	3.8	160
113	The Human Phenome Project. Nature Genetics, 2003, 34, 15-21.	21.4	356
114	Genome Scan Meta-Analysis of Schizophrenia and Bipolar Disorder, Part III: Bipolar Disorder. American Journal of Human Genetics, 2003, 73, 49-62.	6.2	400
115	False Discovery Rate in Linkage and Association Genome Screens for Complex Disorders. Genetics, 2003, 164, 829-833.	2.9	138
116	Genomewide Linkage Disequilibrium Mapping of Severe Bipolar Disorder in a Population Isolate. American Journal of Human Genetics, 2002, 71, 565-574.	6.2	63
117	Association analysis of candidate genes for neuropsychiatric disease: the perpetual campaign. Trends in Genetics, 2002, 18, 307-312.	6.7	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.	6.2	45
120	The genome-wide distribution of background linkage disequilibrium in a population isolate. Human Molecular Genetics, 2001, 10, 545-551.	2.9	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.	6.2	61
122	A gene encoding a liver-specific ABC transporter is mutated in progressive familial intrahepatic cholestasis. Nature Genetics, 1998, 20, 233-238.	21.4	968
123	A gene encoding a P-type ATPase mutated in two forms of hereditary cholestasis. Nature Genetics, 1998, 18, 219-224.	21.4	710
124	Insight into bile duct differentiation takes (notched) wings. Hepatology, 1998, 27, 298-298.	7.3	0
125	Understanding the Genetic Basis of Mood Disorders: Where Do We Stand?. American Journal of Human Genetics, 1997, 60, 1283-1288.	6.2	42
126	Expanding on population studies. Nature Genetics, 1997, 17, 371-373.	21.4	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. Human Genetics, 1997, 100, 382-387.	3.8	39
128	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
129	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
130	Pathogens & strain diversity: Is sex disruptive?. Nature Medicine, 1996, 2, 401-403.	30.7	0
131	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
132	Microsatellites: Evolution and Mutational Processes. Novartis Foundation Symposium, 1996, 197, 51-72.	1.1	25
133	Genome screening by searching for shared segments: mapping a gene for benign recurrent intrahepatic cholestasis. Nature Genetics, 1994, 8, 380-386.	21.4	315