Jurg Ott

List of Publications by Year in descending order

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Version: 2024-02-01

		87888	30087
117	11,266	38	103
papers	citations	h-index	g-index

162	162	162	11417
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Analyses of polymorphisms of intron 2 of OPRK1 (kappa-opioid receptor gene) in association with opioid and cocaine dependence diagnoses in an African-American population. Neuroscience Letters, 2022, 768, 136364.	2.1	7
2	Machine learning approaches to explore digenic inheritance. Trends in Genetics, 2022, 38, 1013-1018.	6.7	13
3	Population genetics: past, present, and future. Human Genetics, 2021, 140, 231-240.	3.8	5
4	Genotype Pattern Mining for Pairs of Interacting Variants Underlying Digenic Traits. Genes, 2021, 12, 1160.	2.4	6
5	Editorial: Multi-Omics Study in Revealing Underlying Pathogenesis of Complex Diseases: A Translational Perspective. Frontiers in Genetics, 2021, 12, 789294.	2.3	1
6	Polymorphisms in Stress-Related Genes Are Associated with Reduced Cocaine Abuse and Longer Retention in Methadone Maintenance Treatment for Opioid Use Disorder. European Addiction Research, 2021, 27, 198-205.	2.4	1
7	Further evidence for the association of GAL, GALR1Âand NPY1RÂvariants with opioid dependence. Pharmacogenomics, 2020, 21, 903-917.	1.3	1
8	Shared genomic segment analysis with equivalence testing. Genetic Epidemiology, 2020, 44, 741-747.	1.3	1
9	Variants of opioid genes and response to treatment of opioid use disorder with buprenorphine-naloxone versus extended-release naltrexone in Caucasians. American Journal of Drug and Alcohol Abuse, 2020, 46, 761-768.	2.1	3
10	Maximal Segmental Score Method for Localizing Recessive Disease Variants Based on Sequence Data. Frontiers in Genetics, 2020, 11, 555.	2.3	1
11	A Novel Locus and Candidate Gene for Familial Developmental Dyslexia on Chromosome 4q. Zeitschrift FÃœr Kinder- Und Jugendpsychiatrie Und Psychotherapie, 2020, 48, 478-489.	0.7	5
12	A 3â€™ UTR SNP rs885863, a cis-eQTL for the circadian gene VIPR2 and lincRNA 689, is associated with opioid addiction. PLoS ONE, 2019, 14, e0224399.	2.5	8
13	VMAT2 gene (SLC18A2) variants associated with a greater risk for developing opioid dependence. Pharmacogenomics, 2019, 20, 331-341.	1.3	8
14	Heterozygosity mapping for human dominant trait variants. Human Mutation, 2019, 40, 996-1004.	2.5	4
15	Association of variants of prodynorphin promoter 68-bp repeats in caucasians with opioid dependence diagnosis: Effect on age trajectory of heroin use. Neuroscience Letters, 2019, 704, 100-105.	2.1	5
16	A novel association of rs13334070 in the RPGRIP1L gene with adiposity factors discovered by joint linkage and linkage disequilibrium analysis in Iranian pedigrees: Tehran Cardiometabolic Genetic Study (TCGS). Genetic Epidemiology, 2019, 43, 342-351.	1.3	6
17	The combined effects of cardiovascular disease related SNPs on ischemic stroke. Journal of the Neurological Sciences, 2018, 388, 141-145.	0.6	2
18	Dopamine gene variants in opioid addiction: comparison of dependent patients, nondependent users and healthy controls. Pharmacogenomics, 2018, 19, 95-104.	1.3	15

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19	Re-evaluation of the KMSK scales, rapid dimensional measures of self-exposure to specific drugs: Gender-specific features. Drug and Alcohol Dependence, 2018, 190, 179-187.	3.2	15
20	To aggregate or not, that is the question. A commentary on single-nucleotide variant proportion in genes: a new concept to explore major depression based on DNA sequencing data. Journal of Human Genetics, 2017, 62, 523-523.	2.3	0
21	HDR-del: A tool based on Hamming distance for prioritizing pathogenic chromosomal deletions in exome sequencing. Human Mutation, 2017, 38, 1796-1800.	2.5	6
22	Variants of opioid system genes are associated with non-dependent opioid use and heroin dependence. Drug and Alcohol Dependence, 2016, 168, 164-169.	3.2	14
23	African-specific variability in the acetylcholine muscarinic receptor M4: association with cocaine and heroin addiction. Pharmacogenomics, 2016, 17, 995-1003.	1.3	12
24	HDR: a statistical two-step approach successfully identifies disease genes in autosomal recessive families. Journal of Human Genetics, 2016, 61, 959-963.	2.3	11
25	Glutamatergic and GABAergic susceptibility loci for heroin and cocaine addiction in subjects of African and European ancestry. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2016, 64, 118-123.	4.8	17
26	Beyond Homozygosity Mapping: Family-Control analysis based on Hamming distance for prioritizing variants in exome sequencing. Scientific Reports, 2015, 5, 12028.	3.3	12
27	Leveling the Playing Field in Homozygosity Mapping Using Map Distances. Annals of Human Genetics, 2015, 79, 366-372.	0.8	1
28	Common Regulatory Variants of CYFIP1 Contribute to Susceptibility for Autism Spectrum Disorder (ASD) and Classical Autism. Annals of Human Genetics, 2015, 79, 329-340.	0.8	37
29	Synaptic Plasticity and Signal Transduction Gene Polymorphisms and Vulnerability to Drug Addictions in Populations of European or African Ancestry. CNS Neuroscience and Therapeutics, 2015, 21, 898-904.	3.9	21
30	PDE3A mutations cause autosomal dominant hypertension with brachydactyly. Nature Genetics, 2015, 47, 647-653.	21.4	146
31	Genetic linkage analysis in the age of whole-genome sequencing. Nature Reviews Genetics, 2015, 16, 275-284.	16.3	225
32	Susceptibility loci for heroin and cocaine addiction in the serotonergic and adrenergic pathways in populations of different ancestry. Pharmacogenomics, 2015, 16, 1329-1342.	1.3	15
33	Genome-wide association scan in north Indians reveals three novel HLA-independent risk loci for ulcerative colitis. Gut, 2015, 64, 571-579.	12.1	58
34	AprioriGWAS, a New Pattern Mining Strategy for Detecting Genetic Variants Associated with Disease through Interaction Effects. PLoS Computational Biology, 2014, 10, e1003627.	3.2	30
35	Drug Addiction and Stress-Response Genetic Variability: Association Study in African Americans. Annals of Human Genetics, 2014, 78, 290-298.	0.8	55
36	Dysfunctional nitric oxide signalling increases risk of myocardial infarction. Nature, 2013, 504, 432-436.	27.8	230

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37	Challenging False Discovery Rate: A Partition Test Based on p Values in Human Case-Control Association Studies. Human Heredity, 2012, 74, 45-50.	0.8	9
38	Multilocus association analysis under polygenic models. International Journal of Data Mining and Bioinformatics, 2012, 6, 482.	0.1	3
39	Writings on Genetic Linkage in the Annals. Annals of Human Genetics, 2011, 75, 344-347.	0.8	1
40	Family-based designs for genome-wide association studies. Nature Reviews Genetics, 2011, 12, 465-474.	16.3	251
41	William Allan Award Address: On the Role and Soul of a Statistical Geneticist. American Journal of Human Genetics, 2011, 88, 264-268.	6.2	1
42	Multiple phenotypes in genome-wide genetic mapping studies. Protein and Cell, 2011, 2, 519-522.	11.0	8
43	Associations of Six Single Nucleotide Polymorphisms in Obesity-Related Genes With BMI and Risk of Obesity in Chinese Children. Diabetes, 2010, 59, 3085-3089.	0.6	94
44	Genome-Wide Conditional Search for Epistatic Disease-Predisposing Variants in Human Association Studies. Human Heredity, 2010, 70, 34-41.	0.8	6
45	Pilot Study on Schizophrenia in Sardinia. Human Heredity, 2010, 70, 92-96.	0.8	6
46	Systematic Removal of Outliers to Reduce Heterogeneity in Case-Control Association Studies. Human Heredity, 2010, 70, 227-231.	0.8	5
47	Genome-wide examination of genetic variants associated with response to platinum-based chemotherapy in patients with small-cell lung cancer. Pharmacogenetics and Genomics, 2010, 20, 389-395.	1.5	26
48	Chromosomes 4q28.3 and 7q31.2 as New Susceptibility Loci for Comitant Strabismus. , 2009, 50, 654.		39
49	Detecting disease-associated genotype patterns. BMC Bioinformatics, 2009, 10, S75.	2.6	26
50	Combining identity by descent and association in genetic case-control studies. BMC Genetics, 2008, 9, 42.	2.7	8
51	ABCB1 (MDR1) genetic variants are associated with methadone doses required for effective treatment of heroin dependence. Human Molecular Genetics, 2008, 17, 2219-2227.	2.9	150
52	Collapsing SNP Genotypes in Case-Control Genome-Wide Association Studies Increases the Type I Error Rate and Power. Statistical Applications in Genetics and Molecular Biology, 2008, 7, Article23.	0.6	14
53	Prodynorphin gene promoter repeat associated with cocaine/alcohol codependence. Addiction Biology, 2007, 12, 496-502.	2.6	45
54	Complement Factor H Polymorphism in Age-Related Macular Degeneration. Science, 2005, 308, 385-389.	12.6	4,018

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55	Issues in Association Analysis: Error Control in Case-Control Association Studies for Disease Gene Discovery. Human Heredity, 2004, 58, 171-174.	0.8	15
56	A transmission disequilibrium test for general pedigrees that is robust to the presence of random genotyping errors and any number of untyped parents. European Journal of Human Genetics, 2004, 12, 752-761.	2.8	57
57	Genetic dissection of diseases: design and methods. Current Opinion in Genetics and Development, 2004, 14, 229-232.	3.3	43
58	Mathematical multi-locus approaches to localizing complex human trait genes. Nature Reviews Genetics, 2003, 4, 701-709.	16.3	251
59	Set Association Analysis of SNP Case-Control and Microarray Data. Journal of Computational Biology, 2003, 10, 569-574.	1.6	41
60	Power and Sample Size Calculations for Case-Control Genetic Association Tests when Errors Are Present: Application to Single Nucleotide Polymorphisms. Human Heredity, 2002, 54, 22-33.	0.8	269
61	Further evidence for linkage of Gilles de la Tourette syndrome (GTS) susceptibility loci on chromosomes 2p11, 8q22 and 11q23-24 in South African Afrikaners. American Journal of Medical Genetics Part A, 2001, 105, 163-167.	2.4	71
62	A Transmission/Disequilibrium Test That Allows for Genotyping Errors in the Analysis of Single-Nucleotide Polymorphism Data. American Journal of Human Genetics, 2001, 69, 371-380.	6.2	147
63	Trimming, Weighting, and Grouping SNPs in Human Case-Control Association Studies. Genome Research, 2001, 11, 2115-2119.	5.5	282
64	Statistical multilocus methods for disequilibrium analysis in complex traits. Human Mutation, 2001, 17, 285-288.	2.5	19
65	Fine mapping of a gene responsible for regulating dietary cholesterol absorption; founder effects underlie cases of phytosterolaemia in multiple communities. European Journal of Human Genetics, 2001, 9, 375-384.	2.8	38
66	ASSESSMENT AND MANAGEMENT OF SINGLE NUCLEOTIDE POLYMORPHISM GENOTYPE ERRORS IN GENETIC ASSOCIATION ANALYSIS. , 2000, , 18-29.		37
67	Analysis of complex traits using neural networks. Genetic Epidemiology, 1999, 17, S503-7.	1.3	16
68	Exposing the human nude phenotype. Nature, 1999, 398, 473-474.	27.8	247
69	Linkage analysis in heterogeneous and complex traits. European Child and Adolescent Psychiatry, 1999, 8, S43-S46.	4.7	13
70	True Pedigree Errors More Frequent Than Apparent Errors for Single Nucleotide Polymorphisms. Human Heredity, 1999, 49, 65-70.	0.8	84
71	Power loss for multiallelic transmission/disequilibrium test when errors introduced: GAW11 simulated data. Genetic Epidemiology, 1999, 17, S587-S592.	1.3	24
72	TULP1 mutation in two extended Dominican kindreds with autosomal recessive Retinitis pigmentosa. Nature Genetics, 1998, 18, 177-179.	21.4	151

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73	Sometimes it's hot, sometimes it's not. Nature Genetics, 1998, 19, 213-214.	21.4	82
74	Multi-Locus Nonparametric Linkage Analysis of Complex Trait Loci with Neural Networks. Human Heredity, 1998, 48, 275-284.	0.8	70
75	Analysis of two-locus traits under heterogeneity for recessive versus dominant inheritance. Genetic Epidemiology, 1997, 14, 1097-1100.	1.3	0
76	Neural network analysis of complex traits. , 1997, 14, 1101-1106.		67
77	The Effect of Marker Heterozygosity on the Power to Detect Linkage Disequilibrium. Genetics, 1997, 147, 927-930.	2.9	41
78	Relationship Estimation in Affected Sib Pair Analysis of Late-Onset Diseases. European Journal of Human Genetics, 1997, 5, 69-77.	2.8	82
79	Estimating parental relationship in linkage analysis of recessive traits. , 1996, 63, 386-391.		2
80	Additional support for schizophrenia linkage on chromosomes 6 and 8: A multicenter study. , 1996, 67, 580-594.		166
81	Complex traits on the map. Nature, 1996, 379, 772-773.	27.8	34
82	Schizophrenia: A genome scan targets chromosomes 3p and 8p as potential sites of susceptibility genes. American Journal of Medical Genetics Part A, 1995, 60, 252-260.	2.4	243
83	Failure to find a chromosome 18 pericentric linkage in families with schizophrenia. American Journal of Medical Genetics Part A, 1995, 60, 532-534.	2.4	20
84	Data simulation for GAW9 problems 1 and 2. Genetic Epidemiology, 1995, 12, 561-564.	1.3	17
85	Variability of genotype-specific penetrance probabilities in the calculation of risk support intervals. Genetic Epidemiology, 1995, 12, 859-862.	1.3	1
86	How do you compute a lod score?. Nature Genetics, 1995, 11, 354-355.	21.4	4
87	Identification of a locus, distinct from RDS-peripherin, for autosomal recessive retinitis pigmentosa on chromosome 6p. Human Molecular Genetics, 1994, 3, 1401-1403.	2.9	129
88	Linkage analysis of a candidate locus (HLA) in autosomal dominant sacral defect with anterior meningocele. American Journal of Medical Genetics Part A, 1994, 52, 1-4.	2.4	13
89	Sequential strategy to identify a susceptibility gene for schizophrenia: Report of potential linkage on chromosome 22q12â€q13.1: Part 1. American Journal of Medical Genetics Part A, 1994, 54, 36-43.	2.4	356
90	Follow-up of a report of a potential linkage for schizophrenia on chromosome 22q12-q13.1: Part 2. American Journal of Medical Genetics Part A, 1994, 54, 44-50.	2.4	145

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91	Search for linkage to schizophrenia on the X and Y chromosomes. American Journal of Medical Genetics Part A, 1994, 54, 113-121.	2.4	66
92	Chromosomeâ€based method for rapid computer simulation in human genetic linkage analysis. Genetic Epidemiology, 1993, 10, 217-224.	1.3	119
93	Two new approaches toward linkage heterogeneity of FAD: Two-locus models and age of onset as a discriminator. Genetic Epidemiology, 1993, 10, 455-459.	1.3	1
94	A bootstrap approach to estimating power for linkage heterogeneity. Genetic Epidemiology, 1993, 10, 465-470.	1.3	4
95	A novel polylocus method for linkage analysis using the lod-score or affected sib-pair method. Genetic Epidemiology, 1993, 10, 477-482.	1.3	32
96	Introductory Remarks: Genetic Models and Statistical Approaches. Annals of Medicine, 1992, 24, 375-377.	3.8	0
97	The Future of Multilocus Linkage Analysis. Annals of Medicine, 1992, 24, 401-403.	3.8	4
98	A Haplotype-Based Haplotype Relative Risk’ Approach to Detecting Allelic Associations. Human Heredity, 1992, 42, 337-346.	0.8	488
99	Spastic paraplegia with iron deposits in the basal ganglia: A new X-linked mental retardation syndrome. American Journal of Medical Genetics Part A, 1992, 43, 479-490.	2.4	24
100	Guidelines for human linkage maps An International System for Human Linkage Maps (ISLM, 1990). Annals of Human Genetics, 1991, 55, 1-6.	0.8	27
101	No Genetic Linkage Detected for Schizophrenia to Xq27â€“q28. British Journal of Psychiatry, 1991, 158, 630-634.	2.8	16
102	Genetic linkage and complex diseases: A comment. Genetic Epidemiology, 1990, 7, 35-36.	1.3	27
103	Measuring the inflation of the lod score due to its maximization over model parameter values in human linkage analysis. Genetic Epidemiology, 1990, 7, 237-243.	1.3	127
104	Statistical properties of the haplotype relative risk. Genetic Epidemiology, 1989, 6, 127-130.	1.3	150
105	Affective disorders: Evaluation of a three-allele model accounting for clinical heterogeneity. Genetic Epidemiology, 1989, 6, 265-269.	1.3	7
106	Determining informativity of marker typing for genetic counseling in a pedigree. Human Genetics, 1989, 82, 159-162.	3.8	10
107	Linkage of a prion protein missense variant to Gerstmannâ€“StrÃussler syndrome. Nature, 1989, 338, 342-345.	27.8	862
108	Goodness-of-fit tests for locus order in three-point mapping. Genetic Epidemiology, 1987, 4, 51-57.	1.3	8

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109	Linkage probability and its approximate confidence interval under possible heterogeneity. Genetic Epidemiology, 1986, 3, 251-257.	1.3	67
110	A simple scheme for the analysis of HLA linkages in pedigrees. Annals of Human Genetics, 1978, 42, 255-257.	0.8	84
111	Linkage analysis with misclassification at one locus. Clinical Genetics, 1977, 12, 119-124.	2.0	44
112	Note on the prior probability of autosomal linkage. Annals of Human Genetics, 1976, 39, 433-434.	0.8	2
113	Estimating distances from the centromere by means of benign ovarian teratomas in man. Annals of Human Genetics, 1976, 40, 191-196.	0.8	40
114	Some Classification Procedures for Multivariate Binary Data Using Orthogonal Functions. Journal of the American Statistical Association, 1976, 71, 391-399.	3.1	44
115	Some Classification Procedures for Multivariate Binary Data Using Orthogonal Functions. Journal of the American Statistical Association, 1976, 71, 391.	3.1	13
116	Linkage investigation of a large family with Reifenstein's syndrome. Clinical Genetics, 1975, 7, 342-344.	2.0	4
117	Nachweis natÃ¼rlicher reproduktiver Isolation zwischen zwischen Sorex gemellus sp. n. und Sorex araneus Linnaeus 1758 in der Schweiz (Mammalia, Insectivora). Revue Suisse De Zoologie, 1968, 75, 53-75.	0.3	12