Jurg Ott

List of Publications by Year in descending order

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		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	Complement Factor H Polymorphism in Age-Related Macular Degeneration. Science, 2005, 308, 385-389.	12.6	4,018
2	Linkage of a prion protein missense variant to Gerstmannâ€“StrÃussler syndrome. Nature, 1989, 338, 342-345.	27.8	862
3	A Haplotype-Based Haplotype Relative Risk’ Approach to Detecting Allelic Associations. Human Heredity, 1992, 42, 337-346.	0.8	488
4	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
5	Trimming, Weighting, and Grouping SNPs in Human Case-Control Association Studies. Genome Research, 2001, 11, 2115-2119.	5.5	282
6	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
7	Mathematical multi-locus approaches to localizing complex human trait genes. Nature Reviews Genetics, 2003, 4, 701-709.	16.3	251
8	Family-based designs for genome-wide association studies. Nature Reviews Genetics, 2011, 12, 465-474.	16.3	251
9	Exposing the human nude phenotype. Nature, 1999, 398, 473-474.	27.8	247
10	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
11	Dysfunctional nitric oxide signalling increases risk of myocardial infarction. Nature, 2013, 504, 432-436.	27.8	230
12	Genetic linkage analysis in the age of whole-genome sequencing. Nature Reviews Genetics, 2015, 16, 275-284.	16.3	225
13	Additional support for schizophrenia linkage on chromosomes 6 and 8: A multicenter study. , 1996, 67, 580-594.		166
14	TULP1 mutation in two extended Dominican kindreds with autosomal recessive Retinitis pigmentosa. Nature Genetics, 1998, 18, 177-179.	21.4	151
15	Statistical properties of the haplotype relative risk. Genetic Epidemiology, 1989, 6, 127-130.	1.3	150
16	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
17	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
18	PDE3A mutations cause autosomal dominant hypertension with brachydactyly. Nature Genetics, 2015, 47, 647-653.	21.4	146

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19	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
20	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
21	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
22	Chromosomeâ€based method for rapid computer simulation in human genetic linkage analysis. Genetic Epidemiology, 1993, 10, 217-224.	1.3	119
23	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
24	A simple scheme for the analysis of HLA linkages in pedigrees. Annals of Human Genetics, 1978, 42, 255-257.	0.8	84
25	True Pedigree Errors More Frequent Than Apparent Errors for Single Nucleotide Polymorphisms. Human Heredity, 1999, 49, 65-70.	0.8	84
26	Sometimes it's hot, sometimes it's not. Nature Genetics, 1998, 19, 213-214.	21.4	82
27	Relationship Estimation in Affected Sib Pair Analysis of Late-Onset Diseases. European Journal of Human Genetics, 1997, 5, 69-77.	2.8	82
28	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
29	Multi-Locus Nonparametric Linkage Analysis of Complex Trait Loci with Neural Networks. Human Heredity, 1998, 48, 275-284.	0.8	70
30	Linkage probability and its approximate confidence interval under possible heterogeneity. Genetic Epidemiology, 1986, 3, 251-257.	1.3	67
31	Neural network analysis of complex traits. , 1997, 14, 1101-1106.		67
32	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
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	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
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	Prodynorphin gene promoter repeat associated with cocaine/alcohol codependence. Addiction Biology, 2007, 12, 496-502.	2.6	45

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37	Some Classification Procedures for Multivariate Binary Data Using Orthogonal Functions. Journal of the American Statistical Association, 1976, 71, 391-399.	3.1	44
38	Linkage analysis with misclassification at one locus. Clinical Genetics, 1977, 12, 119-124.	2.0	44
39	Genetic dissection of diseases: design and methods. Current Opinion in Genetics and Development, 2004, 14, 229-232.	3.3	43
40	Set Association Analysis of SNP Case-Control and Microarray Data. Journal of Computational Biology, 2003, 10, 569-574.	1.6	41
41	The Effect of Marker Heterozygosity on the Power to Detect Linkage Disequilibrium. Genetics, 1997, 147, 927-930.	2.9	41
42	Estimating distances from the centromere by means of benign ovarian teratomas in man. Annals of Human Genetics, 1976, 40, 191-196.	0.8	40
43	Chromosomes 4q28.3 and 7q31.2 as New Susceptibility Loci for Comitant Strabismus. , 2009, 50, 654.		39
44	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
45	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
46	ASSESSMENT AND MANAGEMENT OF SINGLE NUCLEOTIDE POLYMORPHISM GENOTYPE ERRORS IN GENETIC ASSOCIATION ANALYSIS. , 2000, , 18-29.		37
47	Complex traits on the map. Nature, 1996, 379, 772-773.	27.8	34
48	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
49	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
50	Genetic linkage and complex diseases: A comment. Genetic Epidemiology, 1990, 7, 35-36.	1.3	27
51	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
52	Detecting disease-associated genotype patterns. BMC Bioinformatics, 2009, 10, S75.	2.6	26
53	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
54	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

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55	Power loss for multiallelic transmission/disequilibrium test when errors introduced: GAW11 simulated data. Genetic Epidemiology, 1999, 17, S587-S592.	1.3	24
56	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
57	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
58	Statistical multilocus methods for disequilibrium analysis in complex traits. Human Mutation, 2001, 17, 285-288.	2.5	19
59	Data simulation for GAW9 problems 1 and 2. Genetic Epidemiology, 1995, 12, 561-564.	1.3	17
60	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
61	No Genetic Linkage Detected for Schizophrenia to Xq27â€“q28. British Journal of Psychiatry, 1991, 158, 630-634.	2.8	16
62	Analysis of complex traits using neural networks. Genetic Epidemiology, 1999, 17, S503-7.	1.3	16
63	Issues in Association Analysis: Error Control in Case-Control Association Studies for Disease Gene Discovery. Human Heredity, 2004, 58, 171-174.	0.8	15
64	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
65	Dopamine gene variants in opioid addiction: comparison of dependent patients, nondependent users and healthy controls. Pharmacogenomics, 2018, 19, 95-104.	1.3	15
66	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
67	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
68	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
69	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
70	Linkage analysis in heterogeneous and complex traits. European Child and Adolescent Psychiatry, 1999, 8, S43-S46.	4.7	13
71	Some Classification Procedures for Multivariate Binary Data Using Orthogonal Functions. Journal of the American Statistical Association, 1976, 71, 391.	3.1	13
72	Machine learning approaches to explore digenic inheritance. Trends in Genetics, 2022, 38, 1013-1018.	6.7	13

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73	Beyond Homozygosity Mapping: Family-Control analysis based on Hamming distance for prioritizing variants in exome sequencing. Scientific Reports, 2015, 5, 12028.	3.3	12
74	African-specific variability in the acetylcholine muscarinic receptor M4: association with cocaine and heroin addiction. Pharmacogenomics, 2016, 17, 995-1003.	1.3	12
75	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
76	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
77	Determining informativity of marker typing for genetic counseling in a pedigree. Human Genetics, 1989, 82, 159-162.	3.8	10
78	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
79	Goodness-of-fit tests for locus order in three-point mapping. Genetic Epidemiology, 1987, 4, 51-57.	1.3	8
80	Combining identity by descent and association in genetic case-control studies. BMC Genetics, 2008, 9, 42.	2.7	8
81	Multiple phenotypes in genome-wide genetic mapping studies. Protein and Cell, 2011, 2, 519-522.	11.0	8
82	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
83	VMAT2 gene (SLC18A2) variants associated with a greater risk for developing opioid dependence. Pharmacogenomics, 2019, 20, 331-341.	1.3	8
84	Affective disorders: Evaluation of a three-allele model accounting for clinical heterogeneity. Genetic Epidemiology, 1989, 6, 265-269.	1.3	7
85	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
86	Genome-Wide Conditional Search for Epistatic Disease-Predisposing Variants in Human Association Studies. Human Heredity, 2010, 70, 34-41.	0.8	6
87	Pilot Study on Schizophrenia in Sardinia. Human Heredity, 2010, 70, 92-96.	0.8	6
88	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
89	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
90	Genotype Pattern Mining for Pairs of Interacting Variants Underlying Digenic Traits. Genes, 2021, 12, 1160.	2.4	6

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91	Systematic Removal of Outliers to Reduce Heterogeneity in Case-Control Association Studies. Human Heredity, 2010, 70, 227-231.	0.8	5
92	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
93	Population genetics: past, present, and future. Human Genetics, 2021, 140, 231-240.	3.8	5
94	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
95	The Future of Multilocus Linkage Analysis. Annals of Medicine, 1992, 24, 401-403.	3.8	4
96	A bootstrap approach to estimating power for linkage heterogeneity. Genetic Epidemiology, 1993, 10, 465-470.	1.3	4
97	How do you compute a lod score?. Nature Genetics, 1995, 11, 354-355.	21.4	4
98	Linkage investigation of a large family with Reifenstein's syndrome. Clinical Genetics, 1975, 7, 342-344.	2.0	4
99	Heterozygosity mapping for human dominant trait variants. Human Mutation, 2019, 40, 996-1004.	2.5	4
100	Multilocus association analysis under polygenic models. International Journal of Data Mining and Bioinformatics, 2012, 6, 482.	0.1	3
101	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
102	Note on the prior probability of autosomal linkage. Annals of Human Genetics, 1976, 39, 433-434.	0.8	2
103	Estimating parental relationship in linkage analysis of recessive traits. , 1996, 63, 386-391.		2
104	The combined effects of cardiovascular disease related SNPs on ischemic stroke. Journal of the Neurological Sciences, 2018, 388, 141-145.	0.6	2
105	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
106	Variability of genotype-specific penetrance probabilities in the calculation of risk support intervals. Genetic Epidemiology, 1995, 12, 859-862.	1.3	1
107	Writings on Genetic Linkage in the Annals. Annals of Human Genetics, 2011, 75, 344-347.	0.8	1
108	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

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109	Leveling the Playing Field in Homozygosity Mapping Using Map Distances. Annals of Human Genetics, 2015, 79, 366-372.	0.8	1
110	Further evidence for the association of GAL, GALR1Âand NPY1RÂvariants with opioid dependence. Pharmacogenomics, 2020, 21, 903-917.	1.3	1
111	Shared genomic segment analysis with equivalence testing. Genetic Epidemiology, 2020, 44, 741-747.	1.3	1
112	Maximal Segmental Score Method for Localizing Recessive Disease Variants Based on Sequence Data. Frontiers in Genetics, 2020, 11, 555.	2.3	1
113	Editorial: Multi-Omics Study in Revealing Underlying Pathogenesis of Complex Diseases: A Translational Perspective. Frontiers in Genetics, 2021, 12, 789294.	2.3	1
114	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
115	Introductory Remarks: Genetic Models and Statistical Approaches. Annals of Medicine, 1992, 24, 375-377.	3.8	0
116	Analysis of two-locus traits under heterogeneity for recessive versus dominant inheritance. Genetic Epidemiology, 1997, 14, 1097-1100.	1.3	0
117	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