Kerstin U Ludwig

List of Publications by Year
in descending order

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83	5,013	136950	102487
papers	citations	32 h-index	66 g-index

89	89	89	7897
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Key susceptibility locus for nonsyndromic cleft lip with or without cleft palate on chromosome 8q24. Nature Genetics, 2009, 41, 473-477.	21.4	415
2	Genome-wide association study identifies two susceptibility loci for nonsyndromic cleft lip with or without cleft palate. Nature Genetics, 2010, 42, 24-26.	21.4	379
3	Swarm Learning for decentralized and confidential clinical machine learning. Nature, 2021, 594, 265-270.	27.8	375
4	Genome-wide Association Study of Alcohol Dependence. Archives of General Psychiatry, 2009, 66, 773.	12.3	354
5	Genome-wide meta-analyses of nonsyndromic cleft lip with or without cleft palate identify six new risk loci. Nature Genetics, 2012, 44, 968-971.	21.4	311
6	Structure-guided multivalent nanobodies block SARS-CoV-2 infection and suppress mutational escape. Science, 2021, 371, .	12.6	304
7	Genome-wide analyses of non-syndromic cleft lip with palate identify 14 novel loci and genetic heterogeneity. Nature Communications, 2017, 8, 14364.	12.8	207
8	Reactive Neutrophil Responses Dependent on the Receptor Tyrosine Kinase c-MET Limit Cancer Immunotherapy. Immunity, 2017, 47, 789-802.e9.	14.3	207
9	Early IFN-Î± signatures and persistent dysfunction are distinguishing features of NK cells in severe COVID-19. Immunity, 2021, 54, 2650-2669.e14.	14.3	145
10	Characterization of a Family with Rare Deletions in CNTNAP5 and DOCK4 Suggests Novel Risk Loci for Autism and Dyslexia. Biological Psychiatry, 2010, 68, 320-328.	1.3	131
11	Breakthroughs in the genetics of orofacial clefting. Trends in Molecular Medicine, 2011, 17, 725-733.	6.7	116
12	A novel microdeletion syndrome involving 5q14.3-q15: clinical and molecular cytogenetic characterization of three patients. European Journal of Human Genetics, 2009, 17, 1592-1599.	2.8	96
13	Sequencing the GRHL3 Coding Region Reveals Rare Truncating Mutations and a Common Susceptibility Variant for Nonsyndromic Cleft Palate. American Journal of Human Genetics, 2016, 98, 755-762.	6.2	92
14	Genetic determination of human facial morphology: links between cleft-lips and normal variation. European Journal of Human Genetics, 2011, 19, 1192-1197.	2.8	89
15	Imputation of Orofacial Clefting Data Identifies Novel Risk Loci and Sheds Light on the Genetic Background of Cleft Lip Â± Cleft Palate and Cleft Palate Only.. Human Molecular Genetics, 2017, 26, ddx012.	2.9	84
16	Genome-wide association scan identifies new variants associated with a cognitive predictor of dyslexia. Translational Psychiatry, 2019, 9, 77.	4.8	82
17	Age-dependent impact of the major common genetic risk factor for COVID-19 on severity and mortality. Journal of Clinical Investigation, 2021, 131, .	8.2	72
18	Dissection of phenotype reveals possible association between schizophrenia and Glutamate Receptor Delta 1 (GRID1) gene promoter. Schizophrenia Research, 2009, 111, 123-130.	2.0	67

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19	Meta-analysis Reveals Genome-Wide Significance at 15q13 for Nonsyndromic Clefting of Both the Lip and the Palate, and Functional Analyses Implicate GREM1 As a Plausible Causative Gene. PLoS Genetics, 2016, 12, e1005914.	3.5	66
20	Genetic analysis of dyslexia candidate genes in the European cross-linguistic NeuroDys cohort. European Journal of Human Genetics, 2014, 22, 675-680.	2.8	59
21	Novel mutations in LRP6 highlight the role of WNT signaling in tooth agenesis. Genetics in Medicine, 2016, 18, 1158-1162.	2.4	58
22	FAF1, a Gene that Is Disrupted in Cleft Palate and Has Conserved Function in Zebrafish. American Journal of Human Genetics, 2011, 88, 150-161.	6.2	57
23	Genome-wide association study reveals new insights into the heritability and genetic correlates of developmental dyslexia. Molecular Psychiatry, 2021, 26, 3004-3017.	7.9	56
24	Compound Heterozygosity of Low-Frequency Promoter Deletions and Rare Loss-of-Function Mutations in TXNL4A Causes Burn-McKeown Syndrome. American Journal of Human Genetics, 2014, 95, 698-707.	6.2	55
25	Genetic risk factors for nonsyndromic cleft lip with or without cleft palate in a Mesoamerican population: Evidence for IRF6 and variants at 8q24 and 10q25. Birth Defects Research Part A: Clinical and Molecular Teratology, 2010, 88, 535-537.	1.6	50
26	Investigation of the DCDC2 intron 2 deletion/compound short tandem repeat polymorphism in a large German dyslexia sample. Psychiatric Genetics, 2008, 18, 310-312.	1.1	46
27	IRF6 gene variants in Central European patients with nonâ€syndromic cleft lip with or without cleft palate. European Journal of Oral Sciences, 2009, 117, 766-769.	1.5	46
28	LAMP-Seq enables sensitive, multiplexed COVID-19 diagnostics using molecular barcoding. Nature Biotechnology, 2021, 39, 1556-1562.	17.5	46
29	Investigating the shared genetics of non-syndromic cleft lip/palate and facial morphology. PLoS Genetics, 2018, 14, e1007501.	3.5	44
30	Investigation of interaction between DCDC2 and KIAA0319 in a large German dyslexia sample. Journal of Neural Transmission, 2008, 115, 1587-1589.	2.8	41
31	Genome-wide Association Study and Meta-Analysis Identify ISL1 as Genome-wide Significant Susceptibility Gene for Bladder Exstrophy. PLoS Genetics, 2015, 11, e1005024.	3.5	41
32	TBK1 and TNFRSF13B mutations and an autoinflammatory disease in a child with lethal COVID-19. Npj Genomic Medicine, 2021, 6, 55.	3.8	38
33	Novel genes and sex differences in COVID-19 severity. Human Molecular Genetics, 2022, 31, 3789-3806.	2.9	38
34	Variation in GRIN2B contributes to weak performance in verbal shortâ€term memory in children with dyslexia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2010, 153B, 503-511.	1.7	37
35	p63 establishes epithelial enhancers at critical craniofacial development genes. Science Advances, 2019, 5, eaaw0946.	10.3	36
36	Replication of novel susceptibility locus for nonsyndromic cleft lip with or without cleft palate on chromosome 8q24 in Estonian and Lithuanian patients. American Journal of Medical Genetics, Part A, 2009, 149A, 2551-2553.	1.2	35

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37	Mapping for dyslexia and related cognitive trait loci provides strong evidence for further risk genes on chromosome 6p21. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2011, 156, 36-43.	1.7	26
38	Nonsyndromic cleft lip with or without cleft palate in arab populations: Genetic analysis of 15 risk loci in a novel caseâ€“control sample recruited in Yemen. Birth Defects Research Part A: Clinical and Molecular Teratology, 2014, 100, 307-313.	1.6	26
39	Non-Syndromic Cleft Lip with or without Cleft Palate: Genome-Wide Association Study in Europeans Identifies a Suggestive Risk Locus at 16p12.1 and Supports SH3PXD2A as a Clefting Susceptibility Gene. Genes, 2019, 10, 1023.	2.4	26
40	Evidence for DNA methylation mediating genetic liability to non-syndromic cleft lip/palate. Epigenomics, 2019, 11, 133-145.	2.1	25
41	Nonsyndromic cleft lip with or without cleft palate: Increased burden of rare variants within Gremlinâ€1, a component of the bone morphogenetic protein 4 pathway. Birth Defects Research Part A: Clinical and Molecular Teratology, 2014, 100, 493-498.	1.6	24
42	Genetics and Neuroscience in Dyslexia: Perspectives for Education and Remediation. Mind, Brain, and Education, 2007, 1, 162-172.	1.9	23
43	Further evidence for genetic variation at the serotonin transporter gene SLC6A4 contributing toward anxiety. Psychiatric Genetics, 2017, 27, 96-102.	1.1	23
44	â€˜Location, Location, Locationâ€™: a spatial approach for rare variant analysis and an application to a study on non-syndromic cleft lip with or without cleft palate. Bioinformatics, 2012, 28, 3027-3033.	4.1	22
45	Common, low-frequency, rare, and ultra-rare coding variants contribute to COVID-19 severity. Human Genetics, 2022, 141, 147-173.	3.8	22
46	Analysis of susceptibility loci for nonsyndromic orofacial clefting in a European trio sample. American Journal of Medical Genetics, Part A, 2013, 161, 2545-2549.	1.2	21
47	Cleft lip/palate and educational attainment: cause, consequence or correlation? A Mendelian randomization study. International Journal of Epidemiology, 2020, 49, 1282-1293.	1.9	21
48	Susceptibility locus for nonâ€syndromic cleft lip with or without cleft palate on chromosome 10q25 confers risk in Estonian patients. European Journal of Oral Sciences, 2010, 118, 317-319.	1.5	19
49	Nonsyndromic cleft lip with or without cleft palate and cancer: Evaluation of a possible common genetic background through the analysis of GWAS data. Genomics Data, 2016, 10, 22-29.	1.3	19
50	Nine newly identified individuals refine the phenotype associated with MYT1L mutations. American Journal of Medical Genetics, Part A, 2020, 182, 1021-1031.	1.2	19
51	Evaluating eight newly identified susceptibility loci for nonsyndromic cleft lip with or without cleft palate in a Mesoamerican population. Birth Defects Research Part A: Clinical and Molecular Teratology, 2014, 100, 43-47.	1.6	16
52	Deletions and loss-of-function variants in TP63 associated with orofacial clefting. European Journal of Human Genetics, 2019, 27, 1101-1112.	2.8	16
53	Resequencing of VAX1 in patients with nonsyndromic cleft lip with or without cleft palate. Birth Defects Research Part A: Clinical and Molecular Teratology, 2012, 94, 925-933.	1.6	14
54	A phenotype map for 14q32.3 terminal deletions. American Journal of Medical Genetics, Part A, 2012, 158A, 695-706.	1.2	14

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55	Msx1 deficiency interacts with hypoxia and induces a morphogenetic regulation during lip development. Development (Cambridge), 2020, 147, .	2.5	14
56	Analysis of sequence data to identify potential risk variants for oral clefts in multiplex families. Molecular Genetics & Genomic Medicine, 2017, 5, 570-579.	1.2	13
57	Exome sequencing in large, multiplex bipolar disorder families from Cuba. PLoS ONE, 2018, 13, e0205895.	2.5	13
58	Genome-wide analysis of parent-of-origin effects in non-syndromic orofacial clefts. European Journal of Human Genetics, 2014, 22, 822-830.	2.8	12
59	Nonsyndromic cleft palate: An association study at GWAS candidate loci in a multiethnic sample. Birth Defects Research, 2018, 110, 871-882.	1.5	11
60	Replication analysis of 15 susceptibility loci for nonsyndromic cleft lip with or without cleft palate in an italian population. Birth Defects Research Part A: Clinical and Molecular Teratology, 2016, 106, 81-87.	1.6	10
61	SUMO1 as a candidate gene for non-syndromic cleft lip with or without cleft palate: No evidence for the involvement of common or rare variants in Central European patients. International Journal of Pediatric Otorhinolaryngology, 2011, 75, 49-52.	1.0	9
62	A post GWAS association study of SNPs associated with cleft lip with or without cleft palate in submucous cleft palate. American Journal of Medical Genetics, Part A, 2015, 167, 670-673.	1.2	9
63	Investigation of dominant and recessive inheritance models in genomeâ€wide association studies data of nonsyndromic cleft lip with or without cleft palate. Birth Defects Research, 2018, 110, 336-341.	1.5	8
64	Integrative approaches generate insights into the architecture of non-syndromic cleft lip Â± cleft palate. Human Genetics and Genomics Advances, 2021, 2, 100038.	1.7	8
65	EvaluatingSKIas a candidate gene for non-syndromic cleft lip with or without cleft palate. European Journal of Oral Sciences, 2012, 120, 373-377.	1.5	6
66	Properties of permutation-based gene tests and controlling type 1 error using a summary statistic based gene test. BMC Genetics, 2013, 14, 108.	2.7	6
67	Further evidence for deletions in 7p14.1 contributing to nonsyndromic cleft lip with or without cleft palate. Birth Defects Research Part A: Clinical and Molecular Teratology, 2016, 106, 767-772.	1.6	6
68	Evaluating shared genetic influences on nonsyndromic cleft lip/palate and oropharyngeal neoplasms. Genetic Epidemiology, 2020, 44, 924-933.	1.3	6
69	Identification of rare variants in KCTD13 at the schizophrenia risk locus 16p11.2. Psychiatric Genetics, 2016, 26, 293-296.	1.1	5
70	Identification of loci of functional relevance to Barrettâ€™s esophagus and esophageal adenocarcinoma: Cross-referencing of expression quantitative trait loci data from disease-relevant tissues with genetic association data. PLoS ONE, 2019, 14, e0227072.	2.5	5
71	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
72	Is It Rare or Common?. Genetic Epidemiology, 2012, 36, 419-429.	1.3	4

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73	The complete mitochondrial genome of the â€˜solar-poweredâ€™ sea slug Plakobranchus cf. ocellatus (Heterobranchia: Panpulmonata: Sacoglossa). Mitochondrial DNA Part B: Resources, 2017, 2, 130-131.	0.4	4
74	First genome-wide association study of esophageal atresia identifies three genetic risk loci at CTNNA3, FOXF1/FOXC2/FOXL1, and HNF1B. Human Genetics and Genomics Advances, 2022, 3, 100093.	1.7	4
75	Genetic predisposition and the variable course of infectious diseases. Deutsches Ärzteblatt International, 2022, , .	0.9	4
76	Molecular Genetic Screening in Patients With ACE Inhibitor/Angiotensin Receptor Blocker-Induced Angioedema to Explore the Role of Hereditary Angioedema Genes. Frontiers in Genetics, 0, 13, .	2.3	4
77	Extending the allelic spectrum at noncoding risk loci of orofacial clefting. Human Mutation, 2021, 42, 1066-1078.	2.5	3
78	Resequencing of <scp>VEGFR3</scp> pathway genes implicate <scp>GJC2</scp> and <scp>FLT4</scp> in the formation of primary congenital chylothorax. American Journal of Medical Genetics, Part A, 2022, 188, 1607-1611.	1.2	3
79	On the analysis of sequence data: testing for disease susceptibility loci using patterns of linkage disequilibrium. Genetic Epidemiology, 2011, 35, 880-886.	1.3	2
80	Die Rolle seltener Varianten bei hÃufigen Krankheiten. Medizinische Genetik, 2019, 31, 212-221.	0.2	1
81	Iron Deficiency Caused by Intestinal Iron Lossâ€”Novel Candidate Genes for Severe Anemia. Genes, 2021, 12, 1869.	2.4	1
82	Combating the SARS-CoV-2 pandemic: How can the field of Human Genetics contribute?. Medizinische Genetik, 2020, 32, 163-167.	0.2	0
83	Allele-specific transcription factor binding in a cellular model of orofacial clefting. Scientific Reports, 2022, 12, 1807.	3.3	0