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	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
2	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
3	Allele-specific transcription factor binding in a cellular model of orofacial clefting. Scientific Reports, 2022, 12, 1807.	3.3	0
4	Common, low-frequency, rare, and ultra-rare coding variants contribute to COVID-19 severity. Human Genetics, 2022, 141, 147-173.	3.8	22
5	Genetic predisposition and the variable course of infectious diseases. Deutsches Ärzteblatt International, 2022, , .	0.9	4
6	Novel genes and sex differences in COVID-19 severity. Human Molecular Genetics, 2022, 31, 3789-3806.	2.9	38
7	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
8	Structure-guided multivalent nanobodies block SARS-CoV-2 infection and suppress mutational escape. Science, 2021, 371, .	12.6	304
9	Swarm Learning for decentralized and confidential clinical machine learning. Nature, 2021, 594, 265-270.	27.8	375
10	Extending the allelic spectrum at noncoding risk loci of orofacial clefting. Human Mutation, 2021, 42, 1066-1078.	2.5	3
11	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
12	LAMP-Seq enables sensitive, multiplexed COVID-19 diagnostics using molecular barcoding. Nature Biotechnology, 2021, 39, 1556-1562.	17.5	46
13	TBK1 and TNFRSF13B mutations and an autoinflammatory disease in a child with lethal COVID-19. Npj Genomic Medicine, 2021, 6, 55.	3.8	38
14	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
15	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
16	Iron Deficiency Caused by Intestinal Iron Lossâ€"Novel Candidate Genes for Severe Anemia. Genes, 2021, 12, 1869.	2.4	1
17	Evaluating shared genetic influences on nonsyndromic cleft lip/palate and oropharyngeal neoplasms. Genetic Epidemiology, 2020, 44, 924-933.	1.3	6
18	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

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19	Msx1 deficiency interacts with hypoxia and induces a morphogenetic regulation during lip development. Development (Cambridge), 2020, 147, .	2.5	14
20	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
21	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
22	Combating the SARS-CoV-2 pandemic: How can the field of Human Genetics contribute?. Medizinische Genetik, 2020, 32, 163-167.	0.2	0
23	Die Rolle seltener Varianten bei hÃufigen Krankheiten. Medizinische Genetik, 2019, 31, 212-221.	0.2	1
24	p63 establishes epithelial enhancers at critical craniofacial development genes. Science Advances, 2019, 5, eaaw0946.	10.3	36
25	Deletions and loss-of-function variants in TP63 associated with orofacial clefting. European Journal of Human Genetics, 2019, 27, 1101-1112.	2.8	16
26	Genome-wide association scan identifies new variants associated with a cognitive predictor of dyslexia. Translational Psychiatry, 2019, 9, 77.	4.8	82
27	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
28	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
29	Evidence for DNA methylation mediating genetic liability to non-syndromic cleft lip/palate. Epigenomics, 2019, 11, 133-145.	2.1	25
30	Nonsyndromic cleft palate: An association study at GWAS candidate loci in a multiethnic sample. Birth Defects Research, 2018, 110, 871-882.	1.5	11
31	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
32	Exome sequencing in large, multiplex bipolar disorder families from Cuba. PLoS ONE, 2018, 13, e0205895.	2.5	13
33	Investigating the shared genetics of non-syndromic cleft lip/palate and facial morphology. PLoS Genetics, 2018, 14, e1007501.	3.5	44
34	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
35	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
36	Further evidence for genetic variation at the serotonin transporter gene SLC6A4 contributing toward anxiety. Psychiatric Genetics, 2017, 27, 96-102.	1.1	23

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37	Reactive Neutrophil Responses Dependent on the Receptor Tyrosine Kinase c-MET Limit Cancer Immunotherapy. Immunity, 2017, 47, 789-802.e9.	14.3	207
38	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
39	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
40	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
41	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
42	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
43	Identification of rare variants in KCTD13 at the schizophrenia risk locus 16p11.2. Psychiatric Genetics, 2016, 26, 293-296.	1.1	5
44	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
45	Novel mutations in LRP6 highlight the role of WNT signaling in tooth agenesis. Genetics in Medicine, 2016, 18, 1158-1162.	2.4	58
46	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
47	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
48	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
49	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
50	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
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	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
53	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
54	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

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55	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
56	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
57	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
58	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
59	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
60	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
61	Is It Rare or Common?. Genetic Epidemiology, 2012, 36, 419-429.	1.3	4
62	A phenotype map for 14q32.3 terminal deletions. American Journal of Medical Genetics, Part A, 2012, 158A, 695-706.	1.2	14
63	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
64	Breakthroughs in the genetics of orofacial clefting. Trends in Molecular Medicine, 2011, 17, 725-733.	6.7	116
65	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
66	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
67	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
68	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
69	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
70	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
71	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
72	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

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73	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
74	Genome-wide Association Study of Alcohol Dependence. Archives of General Psychiatry, 2009, 66, 773.	12.3	354
75	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
76	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
77	Key susceptibility locus for nonsyndromic cleft lip with or without cleft palate on chromosome 8q24. Nature Genetics, 2009, 41, 473-477.	21.4	415
78	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
79	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
80	Investigation of interaction between DCDC2 and KIAA0319 in a large German dyslexia sample. Journal of Neural Transmission, 2008, 115, 1587-1589.	2.8	41
81	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
82	Genetics and Neuroscience in Dyslexia: Perspectives for Education and Remediation. Mind, Brain, and Education, 2007, 1, 162-172.	1.9	23
83	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