Steven Lubbe

List of Publications by Year
in descending order

61 papers	7,857 citations	109321 35 h-index	133252 59 g-index
66 all docs	66 docs citations	66 times ranked	11298 citing authors

#	Article	IF	Citations
1	Assessing the relationship between monoallelic PRKN mutations and Parkinsonâ€™s risk. Human Molecular Genetics, 2021, 30, 78-86.	2.9	36
2	Dyshomeostatic modulation of Ca2+-activated K+ channels in a human neuronal model of KCNQ2 encephalopathy. ELife, 2021, 10, .	6.0	23
3	Identification of Candidate Parkinson Disease Genes by Integrating Genome-Wide Association Study, Expression, and Epigenetic Data Sets. JAMA Neurology, 2021, 78, 464.	9.0	95
4	Investigation of Autosomal Genetic Sex Differences in Parkinson's Disease. Annals of Neurology, 2021, 90, 35-42.	5.3	29
5	Identification of sixteen novel candidate genes for late onset Parkinsonâ€™s disease. Molecular Neurodegeneration, 2021, 16, 35.	10.8	41
6	Finding genetically-supported drug targets for Parkinsonâ€™s disease using Mendelian randomization of the druggable genome. Nature Communications, 2021, 12, 7342.	12.8	44
7	The IMAGEN study: a decade of imaging genetics in adolescents. Molecular Psychiatry, 2020, 25, 2648-2671.	7.9	46
8	Penetrance of Parkinson's Disease in LRRK2 p.G2019S Carriers Is Modified by a Polygenic Risk Score. Movement Disorders, 2020, 35, 774-780.	3.9	57
9	Identification of novel risk loci, causal insights, and heritable risk for Parkinson's disease: a meta-analysis of genome-wide association studies. Lancet Neurology, The, 2019, 18, 1091-1102.	10.2	1,414
10	The Genetic Architecture of Parkinson Disease in Spain: Characterizing Populationâ€Specific Risk, Differential Haplotype Structures, and Providing Etiologic Insight. Movement Disorders, 2019, 34, 1851-1863.	3.9	47
11	The endocytic membrane trafficking pathway plays a major role in the risk of Parkinson's disease. Movement Disorders, 2019, 34, 460-468.	3.9	66
12	Frequency and phenotypic spectrum of KMT2B dystonia in childhood: A singleâ€center cohort study. Movement Disorders, 2019, 34, 1516-1527.	3.9	55
13	Recessive mutations in VPS13D cause childhood onset movement disorders. Annals of Neurology, 2018, 83, 1089-1095.	5.3	104
14	LRP10 in Î±-synucleinopathies. Lancet Neurology, The, 2018, 17, 1032.	10.2	15
15	NeuroChip, an updated version of the NeuroX genotyping platform to rapidly screen for variants associated with neurological diseases. Neurobiology of Aging, 2017, 57, 247.e9-247.e13.	3.1	108
16	A PDE10A de novo mutation causes childhoodâ€onset chorea with diurnal fluctuations. Movement Disorders, 2017, 32, 1646-1647.	3.9	13
17	Establishing the role of rare coding variants in known Parkinson's disease risk loci. Neurobiology of Aging, 2017, 59, 220.e11-220.e18.	3.1	15
18	PO184â€…Analysis of copy number variants in familial and sporadic parkinsonâ€™s disease. Journal of Neurology, Neurosurgery and Psychiatry, 2017, 88, A59.4-A60.	1.9	0

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19	Additional rare variant analysis in Parkinsonâ€™s disease cases with and without known pathogenic mutations: evidence for oligogenic inheritance. Human Molecular Genetics, 2016, 25, ddw348.	2.9	48
20	PARKINSON'S FAMILIES PROJECT: RECRUITMENT OF FAMILIAL PD PATIENTS VIA THE BNSU. Journal of Neurology, Neurosurgery and Psychiatry, 2016, 87, e1.20-e1.	1.9	0
21	Is the MC1R variant p.R160W associated with Parkinson's?. Annals of Neurology, 2016, 79, 159-161.	5.3	18
22	Deletions at 22q11.2 in idiopathic Parkinson's disease: a combined analysis of genome-wide association data. Lancet Neurology, The, 2016, 15, 585-596.	10.2	77
23	Loss of VPS13C Function in Autosomal-Recessive Parkinsonism Causes Mitochondrial Dysfunction and Increases PINK1/Parkin-Dependent Mitophagy. American Journal of Human Genetics, 2016, 98, 500-513.	6.2	333
24	Distinct clinical and neuropathological features of G51D SNCA mutation cases compared with SNCA duplication and H50Q mutation. Molecular Neurodegeneration, 2015, 10, 41.	10.8	90
25	Correlated gene expression supports synchronous activity in brain networks. Science, 2015, 348, 1241-1244.	12.6	532
26	EIF4G1 mutations do not cause Parkinson's disease. Neurobiology of Aging, 2015, 36, 2444.e1-2444.e4.	3.1	21
27	Rsu1 regulates ethanol consumption in Drosophila and humans. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E4085-93.	7.1	57
28	NeuroX, a fast and efficient genotyping platform for investigation of neurodegenerative diseases. Neurobiology of Aging, 2015, 36, 1605.e7-1605.e12.	3.1	96
29	Polygenic risk of <scp>P</scp>arkinson disease is correlated with disease age at onset. Annals of Neurology, 2015, 77, 582-591.	5.3	115
30	Genetic risk and age in Parkinson's disease: Continuum not stratum. Movement Disorders, 2015, 30, 850-854.	3.9	71
31	Recent advances in Parkinsonâ€™s disease genetics. Journal of Neurology, 2014, 261, 259-266.	3.6	65
32	Parkinsonâ€™s disease in GTP cyclohydrolase 1 mutation carriers. Brain, 2014, 137, 2480-2492.	7.6	169
33	Cumulative impact of common genetic variants and other risk factors on colorectal cancer risk in 42â€ˆ103 individuals. Gut, 2013, 62, 871-881.	12.1	117
34	Neural Mechanisms of Attention-Deficit/Hyperactivity Disorder Symptoms Are Stratified by MAOA Genotype. Biological Psychiatry, 2013, 74, 607-614.	1.3	54
35	Comprehensive Evaluation of the Impact of 14 Genetic Variants on Colorectal Cancer Phenotype and Risk. American Journal of Epidemiology, 2012, 175, 1-10.	3.4	33
36	The 14q22.2 colorectal cancer variant rs4444235 shows cis-acting regulation of BMP4. Oncogene, 2012, 31, 3777-3784.	5.9	39

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37	Common variation near CDKN1A, POLD3 and SHROOM2 influences colorectal cancer risk. Nature Genetics, 2012, 44, 770-776.	21.4	210
38	Relationship between 16 susceptibility loci and colorectal cancer phenotype in 3146 patients. Carcinogenesis, 2012, 33, 108-112.	2.8	22
39	Evaluation of germline BMP4 mutation as a cause of colorectal cancer. Human Mutation, 2011, 32, E1928-E1938.	2.5	30
40	MLH1-93G > A is a risk factor for MSI colorectal cancer. Carcinogenesis, 2011, 32, 1157-1161.	2.8	32
41	Multiple Common Susceptibility Variants near BMP Pathway Loci GREM1, BMP4, and BMP2 Explain Part of the Missing Heritability of Colorectal Cancer. PLoS Genetics, 2011, 7, e1002105.	3.5	188
42	A large-scale meta-analysis to refine colorectal cancer risk estimates associated with MUTYH variants. British Journal of Cancer, 2010, 103, 1875-1884.	6.4	107
43	A Cancer-associated Aurora A Mutant Is Mislocalized and Misregulated Due to Loss of Interaction with TPX2. Journal of Biological Chemistry, 2009, 284, 33177-33184.	3.4	40
44	Implications of Familial Colorectal Cancer Risk Profiles and Microsatellite Instability Status. Journal of Clinical Oncology, 2009, 27, 2238-2244.	1.6	30
45	The CDH1â€160C>A polymorphism is a risk factor for colorectal cancer. International Journal of Cancer, 2009, 125, 1622-1625.	5.1	26
46	A genome-wide scan of 10â€‰000 gene-centric variants and colorectal cancer risk. European Journal of Human Genetics, 2009, 17, 1507-1514.	2.8	12
47	Clinical Implications of the Colorectal Cancer Risk Associated With MUTYH Mutation. Journal of Clinical Oncology, 2009, 27, 3975-3980.	1.6	194
48	Spectrum of genetic variation at the ABCC6 locus in South Africans: Pseudoxanthoma elasticum patients and healthy individuals. Journal of Dermatological Science, 2009, 54, 198-204.	1.9	10
49	Deciphering the genetics of hereditary non-syndromic colorectal cancer. European Journal of Human Genetics, 2008, 16, 1477-1486.	2.8	31
50	Comprehensive analysis of common mitochondrial DNA variants and colorectal cancer risk. British Journal of Cancer, 2008, 99, 2088-2093.	6.4	36
51	A genome-wide association study identifies colorectal cancer susceptibility loci on chromosomes 10p14 and 8q23.3. Nature Genetics, 2008, 40, 623-630.	21.4	514
52	Common genetic variants at the CRAC1 (HMPS) locus on chromosome 15q13.3 influence colorectal cancer risk. Nature Genetics, 2008, 40, 26-28.	21.4	277
53	Meta-analysis of genome-wide association data identifies four new susceptibility loci for colorectal cancer. Nature Genetics, 2008, 40, 1426-1435.	21.4	498
54	Interleukin-1 receptor antagonist gene polymorphisms are associated with disease severity in Black South Africans with rheumatoid arthritis. Joint Bone Spine, 2008, 75, 422-425.	1.6	13

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55	Refinement of the basis and impact of common 11q23.1 variation to the risk of developing colorectal cancer. Human Molecular Genetics, 2008, 17, 3720-3727.	2.9	61
56	MTHFR C677T has differential influence on risk of MSI and MSS colorectal cancer. Human Molecular Genetics, 2007, 16, 1072-1077.	2.9	28
57	Microsatellite instability indicative of defects in the major mismatch repair genes is rare in patients with B-cell chronic lymphocytic leukemia: Evaluation with disease stage and family history. Leukemia and Lymphoma, 2007, 48, 1320-1322.	1.3	1
58	A genome-wide association study shows that common alleles of SMAD7 influence colorectal cancer risk. Nature Genetics, 2007, 39, 1315-1317.	21.4	463
59	A genome-wide association scan of tag SNPs identifies a susceptibility variant for colorectal cancer at 8q24.21. Nature Genetics, 2007, 39, 984-988.	21.4	754
60	National study of colorectal cancer genetics. British Journal of Cancer, 2007, 97, 1305-1309.	6.4	63
61	Evaluation of NTHL1, NEIL1, NEIL2, MPG, TDG, UNG and SMUG1genes in familial colorectal cancer predisposition. BMC Cancer, 2006, 6, 243.	2.6	69