Ali G Gharavi

List of Publications by Year
in descending order

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102 papers	12,594 citations	53794 45 h-index	30922 102 g-index
113 all docs	113 docs citations	113 times ranked	20162 citing authors

#	Article	IF	Citations
1	Do research participants share genomic screening results with family members?. Journal of Genetic Counseling, 2022, 31, 447-458.	1.6	12
2	Diagnostic sequencing to support genetically stratified medicine in a tertiary care setting. Genetics in Medicine, 2022, 24, 862-869.	2.4	4
3	GWAS in Mice Maps Susceptibility to HIV-Associated Nephropathy to the Ssbp2 Locus. Journal of the American Society of Nephrology: JASN, 2022, 33, 108-120.	6.1	3
4	Genetics in chronic kidney disease: conclusions from a Kidney Disease: Improving Global Outcomes (KDIGO) Controversies Conference. Kidney International, 2022, 101, 1126-1141.	5.2	46
5	Association of Pathogenic Variants in Hereditary Cancer Genes With Multiple Diseases. JAMA Oncology, 2022, 8, 835.	7.1	25
6	Genome-wide polygenic score to predict chronic kidney disease across ancestries. Nature Medicine, 2022, 28, 1412-1420.	30.7	48
7	Heterozygous loss of WBP11 function causes multiple congenital defects in humans and mice. Human Molecular Genetics, 2021, 29, 3662-3678.	2.9	14
8	COVID-19â€“Associated Glomerular Disease. Journal of the American Society of Nephrology: JASN, 2021, 32, 33-40.	6.1	141
9	Assessing Genetic Risk for IgA Nephropathy. Clinical Journal of the American Society of Nephrology: CJASN, 2021, 16, 182-184.	4.5	4
10	An electronic health record (EHR) log analysis shows limited clinician engagement with unsolicited genetic test results. JAMIA Open, 2021, 4, ooab014.	2.0	5
11	De novo TRIM8 variants impair its protein localization to nuclear bodies and cause developmental delay, epilepsy, and focal segmental glomerulosclerosis. American Journal of Human Genetics, 2021, 108, 357-367.	6.2	14
12	Copy Number Variant Analysis and Genome-wide Association Study Identify Loci with Large Effect for Vesicoureteral Reflux. Journal of the American Society of Nephrology: JASN, 2021, 32, 805-820.	6.1	17
13	Experimental evidence of pathogenic role of IgG autoantibodies in IgA nephropathy. Journal of Autoimmunity, 2021, 118, 102593.	6.5	27
14	Medical records-based chronic kidney disease phenotype for clinical care and â€œbig dataâ€•observational and genetic studies. Npj Digital Medicine, 2021, 4, 70.	10.9	39
15	LIMS1 risk genotype and T cellâ€“mediated rejection in kidney transplant recipients. Nephrology Dialysis Transplantation, 2021, 36, 2120-2129.	0.7	8
16	Cases in Precision Medicine: Genetic Testing to Predict Future Risk for Disease in a Healthy Patient. Annals of Internal Medicine, 2021, 174, 540-547.	3.9	7
17	Medical Records-Based Genetic Studies of the Complement System. Journal of the American Society of Nephrology: JASN, 2021, 32, 2031-2047.	6.1	10
18	Familial Aggregation of CKD: Gene or Environment?. American Journal of Kidney Diseases, 2021, 77, 861-862.	1.9	2

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19	Improving data quality in observational research studies: Report of the Cure Glomerulonephropathy (CureGN) network. Contemporary Clinical Trials Communications, 2021, 22, 100749.	1.1	7
20	Rare loss-of-function variants in type I IFN immunity genes are not associated with severe COVID-19. Journal of Clinical Investigation, 2021, 131, .	8.2	56
21	Quantitative disease risk scores from EHR with applications to clinical risk stratification and genetic studies. Npj Digital Medicine, 2021, 4, 116.	10.9	7
22	Association of rare predicted loss-of-function variants of influenza-related type I IFN genes with critical COVID-19 pneumonia. Reply.. Journal of Clinical Investigation, 2021, 131, .	8.2	20
23	Generalizability of Polygenic Risk Scores for Breast Cancer Among Women With European, African, and Latinx Ancestry. JAMA Network Open, 2021, 4, e2119084.	5.9	31
24	GeneLiFT: A novel test to facilitate rapid screening of genetic literacy in a diverse population undergoing genetic testing. Journal of Genetic Counseling, 2021, 30, 742-754.	1.6	16
25	Longitudinal Outcomes of COVID-19â€“Associated Collapsing Glomerulopathy and Other Podocytopathies. Journal of the American Society of Nephrology: JASN, 2021, 32, 2958-2969.	6.1	31
26	Genetic Architecture of Abdominal Aortic Aneurysm in the Million Veteran Program. Circulation, 2020, 142, 1633-1646.	1.6	78
27	Clinical Genetic Screening in Adult Patients with Kidney Disease. Clinical Journal of the American Society of Nephrology: CJASN, 2020, 15, 1497-1510.	4.5	53
28	Kidney Biopsy Findings in Patients with COVID-19. Journal of the American Society of Nephrology: JASN, 2020, 31, 1959-1968.	6.1	301
29	Dashboards to Facilitate Nephrology Disaster Planning in the COVID-19 Era. Kidney International Reports, 2020, 5, 1298-1302.	0.8	7
30	P0355FAMILY HISTORY OF COMPLEX TRAITS IN THE CUREGN COHORT: ASSOCIATIONS WITH RENAL FUNCTION, COMORBIDITY BURDEN AND DISEASE PROGRESSION. Nephrology Dialysis Transplantation, 2020, 35, .	0.7	0
31	Rare genetic causes of complex kidney and urological diseases. Nature Reviews Nephrology, 2020, 16, 641-656.	9.6	27
32	Mutations of the Transcriptional Corepressor ZMYM2 Cause Syndromic Urinary Tract Malformations. American Journal of Human Genetics, 2020, 107, 727-742.	6.2	25
33	Type IV Collagen Mutations in Familial IgA Nephropathy. Kidney International Reports, 2020, 5, 1075-1078.	0.8	26
34	Pilot Study of Return of Genetic Results to Patients in Adult Nephrology. Clinical Journal of the American Society of Nephrology: CJASN, 2020, 15, 651-664.	4.5	28
35	Genetic testing for kidney disease of unknown etiology. Kidney International, 2020, 98, 590-600.	5.2	46
36	Presentation and Outcomes of Patients with ESKD and COVID-19. Journal of the American Society of Nephrology: JASN, 2020, 31, 1409-1415.	6.1	270

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37	Leukemia Inhibitory Factor Signaling Enhances Production of Galactose-Deficient IgA1 in IgA Nephropathy. Kidney Diseases (Basel, Switzerland), 2020, 6, 168-180.	2.5	26
38	The genetic architecture of membranous nephropathy and its potential to improve non-invasive diagnosis. Nature Communications, 2020, 11, 1600.	12.8	120
39	Persistent Disease Activity in Patients With Long-Standing Glomerular Disease. Kidney International Reports, 2020, 5, 860-871.	0.8	2
40	Acute Kidney Injury Due to Collapsing Glomerulopathy Following COVID-19 Infection. Kidney International Reports, 2020, 5, 940-945.	0.8	182
41	High rate of renal recovery in survivors of COVID-19 associated acute renal failure requiring renal replacement therapy. PLoS ONE, 2020, 15, e0244131.	2.5	46
42	Donorâ€™s APOL1 Risk Genotype and â€œSecond Hitsâ€•Associated With De Novo Collapsing Glomerulopathy in Deceased Donor Kidney Transplant Recipients: A Report of 5 Cases. American Journal of Kidney Diseases, 2019, 73, 134-139.	1.9	45
43	GWAS and enrichment analyses of non-alcoholic fatty liver disease identify new trait-associated genes and pathways across eMERGE Network. BMC Medicine, 2019, 17, 135.	5.5	110
44	Harmonizing Clinical Sequencing and Interpretation for the eMERGE III Network. American Journal of Human Genetics, 2019, 105, 588-605.	6.2	99
45	Genomic Mismatch at LIMS1 Locus and Kidney Allograft Rejection. New England Journal of Medicine, 2019, 380, 1918-1928.	27.0	63
46	Exome-Based Rare-Variant Analyses in CKD. Journal of the American Society of Nephrology: JASN, 2019, 30, 1109-1122.	6.1	40
47	Atlas-CNV: a validated approach to call single-exon CNVs in the eMERGESeq gene panel. Genetics in Medicine, 2019, 21, 2135-2144.	2.4	19
48	Health-related quality of life in glomerular disease. Kidney International, 2019, 95, 1209-1224.	5.2	38
49	Expanding opportunities and emerging challenges: broadening the scope of genetic testing in nephrology. Kidney International, 2019, 95, 743-746.	5.2	8
50	Evaluation of the cost and effectiveness of diverse recruitment methods for a genetic screening study. Genetics in Medicine, 2019, 21, 2371-2380.	2.4	10
51	Precision Medicine in Internal Medicine. Annals of Internal Medicine, 2019, 170, 635.	3.9	12
52	Cases in Precision Medicine: APOL1 and Genetic Testing in the Evaluation of Chronic Kidney Disease and Potential Transplant. Annals of Internal Medicine, 2019, 171, 659.	3.9	13
53	Diagnostic Utility of Exome Sequencing for Kidney Disease. New England Journal of Medicine, 2019, 380, 142-151.	27.0	456
54	Trans-ethnic kidney function association study reveals putative causal genes and effects on kidney-specific disease aetiologies. Nature Communications, 2019, 10, 29.	12.8	113

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55	The copy number variation landscape of congenital anomalies of the kidney and urinary tract. Nature Genetics, 2019, 51, 117-127.	21.4	144
56	The Burden of Candidate Pathogenic Variants for Kidney and Genitourinary Disorders Emerging From Exome Sequencing. Annals of Internal Medicine, 2019, 170, 11.	3.9	60
57	CureGN Study Rationale, Design, and Methods: Establishing a Large Prospective Observational Study of Glomerular Disease. American Journal of Kidney Diseases, 2019, 73, 218-229.	1.9	68
58	The eMERGE genotype set of 83,717 subjects imputed to ~40â€‰million variants genome wide and association with the herpes zoster medical record phenotype. Genetic Epidemiology, 2019, 43, 63-81.	1.3	63
59	Mycophenolate Mofetil in Combination with Steroids for Treatment of C3 Glomerulopathy. Clinical Journal of the American Society of Nephrology: CJASN, 2018, 13, 406-413.	4.5	63
60	Genomic medicine for kidney disease. Nature Reviews Nephrology, 2018, 14, 83-104.	9.6	102
61	Cellular recording devices imprint the history of the cell. Nature Reviews Nephrology, 2018, 14, 477-478.	9.6	0
62	Towards precision nephrology: the opportunities and challenges of genomic medicine. Journal of Nephrology, 2018, 31, 47-60.	2.0	13
63	Serum Response Factor Is Essential for Maintenance of Podocyte Structure and Function. Journal of the American Society of Nephrology: JASN, 2018, 29, 416-422.	6.1	20
64	Ethical Considerations Related to Return of Results from Genomic Medicine Projects: The eMERGE Network (Phase III) Experience. Journal of Personalized Medicine, 2018, 8, 2.	2.5	44
65	Deep Phenotyping on Electronic Health Records Facilitates Genetic Diagnosis by Clinical Exomes. American Journal of Human Genetics, 2018, 103, 58-73.	6.2	99
66	Whole-Exome Sequencing in Adults With Chronic Kidney Disease. Annals of Internal Medicine, 2018, 168, 100.	3.9	154
67	Genetic basis of human congenital anomalies of the kidney and urinary tract. Journal of Clinical Investigation, 2018, 128, 4-15.	8.2	91
68	Genetic Drivers of Kidney Defects in the DiGeorge Syndrome. New England Journal of Medicine, 2017, 376, 742-754.	27.0	120
69	A Dominant Mutation in Nuclear Receptor Interacting Protein 1 Causes Urinary Tract Malformations via Dysregulation of Retinoic Acid Signaling. Journal of the American Society of Nephrology: JASN, 2017, 28, 2364-2376.	6.1	40
70	Genomic Disorders and Neurocognitive Impairment in Pediatric CKD. Journal of the American Society of Nephrology: JASN, 2017, 28, 2303-2309.	6.1	36
71	Exome-wide Association Study Identifies GREB1L Mutations in Congenital Kidney Malformations. American Journal of Human Genetics, 2017, 101, 789-802.	6.2	63
72	Inhibition of STAT3 Signaling Reduces IgA1 Autoantigen Production in IgA Nephropathy. Kidney International Reports, 2017, 2, 1194-1207.	0.8	49

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73	GWAS for serum galactose-deficient IgA1 implicates critical genes of the O-glycosylation pathway. PLoS Genetics, 2017, 13, e1006609.	3.5	92
74	tarSVM: Improving the accuracy of variant calls derived from microfluidic PCR-based targeted next generation sequencing using a support vector machine. BMC Bioinformatics, 2016, 17, 233.	2.6	2
75	Genomeâ€wide association study in mice identifies loci affecting liverâ€related phenotypes including Sel1l influencing serum bile acids. Hepatology, 2016, 63, 1943-1956.	7.3	2
76	Fine Mapping Implicates a Deletion of CFHR1 and CFHR3 in Protection from IgA Nephropathy in Han Chinese. Journal of the American Society of Nephrology: JASN, 2016, 27, 3187-3194.	6.1	63
77	Refinement of the HIVAN1 Susceptibility Locus on Chr. 3A1-A3 via Generation of Sub-Congenic Strains. PLoS ONE, 2016, 11, e0163860.	2.5	3
78	Novel mutations in the inverted formin 2 gene of Chinese families contribute to focal segmental glomerulosclerosis. Kidney International, 2015, 88, 593-604.	5.2	23
79	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
80	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
81	Current Understanding of the Role of Complement in IgA Nephropathy. Journal of the American Society of Nephrology: JASN, 2015, 26, 1503-1512.	6.1	236
82	Mutations in TBX18 Cause Dominant Urinary Tract Malformations via Transcriptional Dysregulation of Ureter Development. American Journal of Human Genetics, 2015, 97, 291-301.	6.2	72
83	Genomic imbalances in pediatric patients with chronic kidney disease. Journal of Clinical Investigation, 2015, 125, 2171-2178.	8.2	68
84	Copy number variation analysis identifies novel CAKUT candidate genes in children with a solitary functioning kidney. Kidney International, 2015, 88, 1402-1410.	5.2	65
85	Variants in Complement Factor H and Complement Factor H-Related Protein Genes, CFHR3 and CFHR1, Affect Complement Activation in IgA Nephropathy. Journal of the American Society of Nephrology: JASN, 2015, 26, 1195-1204.	6.1	124
86	A Panel of Serum Biomarkers Differentiates IgA Nephropathy from Other Renal Diseases. PLoS ONE, 2014, 9, e98081.	2.5	93
87	The emerging role of genomics in the diagnosis and workup of congenital urinary tract defects: a novel deletion syndrome on chromosome 3q13.31-22.1. Pediatric Nephrology, 2014, 29, 257-267.	1.7	15
88	Phenotypic Expansion of DGKE-Associated Diseases. Journal of the American Society of Nephrology: JASN, 2014, 25, 1408-1414.	6.1	59
89	Discovery of new risk loci for IgA nephropathy implicates genes involved in immunity against intestinal pathogens. Nature Genetics, 2014, 46, 1187-1196.	21.4	505
90	Mutations in DSTYK and Dominant Urinary Tract Malformations. New England Journal of Medicine, 2013, 369, 621-629.	27.0	119

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91	Copy-Number Disorders Are a Common Cause of Congenital Kidney Malformations. American Journal of Human Genetics, 2012, 91, 987-997.	6.2	201
92	Genome-wide association study identifies susceptibility loci for IgA nephropathy. Nature Genetics, 2011, 43, 321-327.	21.4	528
93	HNF1B and PAX2 mutations are a common cause of renal hypodysplasia in the CKiD cohort. Pediatric Nephrology, 2011, 26, 897-903.	1.7	114
94	Identification of the Nephropathy-Susceptibility Locus HIVAN4. Journal of the American Society of Nephrology: JASN, 2011, 22, 1497-1504.	6.1	11
95	APOL1 Variants Increase Risk for FSGS and HIVAN but Not IgA Nephropathy. Journal of the American Society of Nephrology: JASN, 2011, 22, 1991-1996.	6.1	110
96	Accelerated development of collapsing glomerulopathy in mice congenic for the HIVAN1 locus. Kidney International, 2009, 75, 366-372.	5.2	31
97	Susceptibility loci for murine HIV-associated nephropathy encode trans-regulators of podocyte gene expression. Journal of Clinical Investigation, 2009, 119, 1178-1188.	8.2	66
98	Aberrant IgA1 Glycosylation Is Inherited in Familial and Sporadic IgA Nephropathy. Journal of the American Society of Nephrology: JASN, 2008, 19, 1008-1014.	6.1	227
99	Genetic Susceptibility, HIV Infection, and the Kidney. Clinical Journal of the American Society of Nephrology: CJASN, 2007, 2, S25-S35.	4.5	22
100	Genetic approaches to human renal agenesis/hypoplasia and dysplasia. Pediatric Nephrology, 2007, 22, 1675-1684.	1.7	99
101	Mapping a locus for susceptibility to HIV-1-associated nephropathy to mouse chromosome 3. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 2488-2493.	7.1	95
102	IgA nephropathy, the most common cause of glomerulonephritis, is linked to 6q22â€“23. Nature Genetics, 2000, 26, 354-357.	21.4	291