Malik Alawi

List of Publications by Year
in descending order

96 papers	3,942 citations	109321 35 h-index	144013 57 g-index
100 all docs	100 docs citations	100 times ranked	9398 citing authors

#	Article	IF	Citations
1	The landscape of viral associations in human cancers. Nature Genetics, 2020, 52, 320-330.	21.4	261
2	Mutations in KCNH1 and ATP6V1B2 cause Zimmermann-Laband syndrome. Nature Genetics, 2015, 47, 661-667.	21.4	177
3	Tissueâ€specific regulation of cytochrome c by postâ€translational modifications: respiration, the mitochondrial membrane potential, ROS, and apoptosis. FASEB Journal, 2019, 33, 1540-1553.	0.5	159
4	Bromodomain Protein BRD4 Is Required for Estrogen Receptor-Dependent Enhancer Activation and Gene Transcription. Cell Reports, 2014, 8, 460-469.	6.4	149
5	Deep metagenome and metatranscriptome analyses of microbial communities affiliated with an industrial biogas fermenter, a cow rumen, and elephant feces reveal major differences in carbohydrate hydrolysis strategies. Biotechnology for Biofuels, 2016, 9, 121.	6.2	141
6	Presence of atypical porcine pestivirus (APPV) genomes in newborn piglets correlates with congenital tremor. Scientific Reports, 2016, 6, 27735.	3.3	113
7	Metagenome Survey of a Multispecies and Alga-Associated Biofilm Revealed Key Elements of Bacterial-Algal Interactions in Photobioreactors. Applied and Environmental Microbiology, 2013, 79, 6196-6206.	3.1	111
8	Dual Roles of the Transcription Factor Grainyhead-like 2 (GRHL2) in Breast Cancer. Journal of Biological Chemistry, 2013, 288, 22993-23008.	3.4	103
9	Monitoring multiple myeloma by next-generation sequencing of V(D)J rearrangements from circulating myeloma cells and cell-free myeloma DNA. Haematologica, 2017, 102, 1105-1111.	3.5	101
10	Insights into Microalga and Bacteria Interactions of Selected Phycosphere Biofilms Using Metagenomic, Transcriptomic, and Proteomic Approaches. Frontiers in Microbiology, 2017, 8, 1941.	3.5	97
11	Identification of a Novel Hepacivirus in Domestic Cattle from Germany. Journal of Virology, 2015, 89, 7007-7015.	3.4	93
12	Extremophilic nitrite-oxidizing Chloroflexi from Yellowstone hot springs. ISME Journal, 2020, 14, 364-379.	9.8	93
13	Evaluation of Unbiased Next-Generation Sequencing of RNA (RNA-seq) as a Diagnostic Method in Influenza Virus-Positive Respiratory Samples. Journal of Clinical Microbiology, 2015, 53, 2238-2250.	3.9	89
14	Indication of Horizontal DNA Gene Transfer by Extracellular Vesicles. PLoS ONE, 2016, 11, e0163665.	2.5	82
15	The SIRPÎ±â€“CD47 immune checkpoint in NK cells. Journal of Experimental Medicine, 2021, 218, .	8.5	82
16	A Comparative Metagenome Survey of the Fecal Microbiota of a Breast- and a Plant-Fed Asian Elephant Reveals an Unexpectedly High Diversity of Glycoside Hydrolase Family Enzymes. PLoS ONE, 2014, 9, e106707.	2.5	80
17	De novo mutations in mitochondrial DNA of iPSCs produce immunogenic neoepitopes in mice and humans. Nature Biotechnology, 2019, 37, 1137-1144.	17.5	74
18	De Novo Truncating Variants in ASXL2 Are Associated with a Unique and Recognizable Clinical Phenotype. American Journal of Human Genetics, 2016, 99, 991-999.	6.2	68

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19	Pulmonary Targeting of Adeno-associated Viral Vectors by Next-generation Sequencing-guided Screening of Random Capsid Displayed Peptide Libraries. Molecular Therapy, 2016, 24, 1050-1061.	8.2	65
20	Essential control of early B-cell development by Mef2 transcription factors. Blood, 2016, 127, 572-581.	1.4	65
21	A Comprehensive Analysis of Replicating Merkel Cell Polyomavirus Genomes Delineates the Viral Transcription Program and Suggests a Role for mcv-miR-M1 in Episomal Persistence. PLoS Pathogens, 2015, 11, e1004974.	4.7	64
22	Pregnancy-Related Immune Adaptation Promotes the Emergence of Highly Virulent H1N1 Influenza Virus Strains in Allogenically Pregnant Mice. Cell Host and Microbe, 2017, 21, 321-333.	11.0	63
23	Mutations in EBF3 Disturb Transcriptional Profiles and Cause Intellectual Disability, Ataxia, and Facial Dysmorphism. American Journal of Human Genetics, 2017, 100, 117-127.	6.2	62
24	Rapid Metagenomic Diagnostics for Suspected Outbreak of Severe Pneumonia. Emerging Infectious Diseases, 2014, 20, 1072-1075.	4.3	61
25	Epidermal growth factor receptor mutation mediates cross-resistance to panitumumab and cetuximab in gastrointestinal cancer. Oncotarget, 2015, 6, 12035-12047.	1.8	60
26	Mutations in NDUFB11, Encoding a Complex I Component of the Mitochondrial Respiratory Chain, Cause Microphthalmia with Linear Skin Defects Syndrome. American Journal of Human Genetics, 2015, 96, 640-650.	6.2	56
27	Comparative study of whole genome amplification and next generation sequencing performance of single cancer cells. Oncotarget, 2017, 8, 56066-56080.	1.8	56
28	SCNT-Derived ESCs with Mismatched Mitochondria Trigger an Immune Response in Allogeneic Hosts. Cell Stem Cell, 2015, 16, 33-38.	11.1	52
29	A homozygous ATAD1 mutation impairs postsynaptic AMPA receptor trafficking and causes a lethal encephalopathy. Brain, 2018, 141, 651-661.	7.6	52
30	Long-term CD38 saturation by daratumumab interferes with diagnostic myeloma cell detection. Haematologica, 2017, 102, e368-e370.	3.5	48
31	Recovery of the first full-length genome sequence of a parapoxvirus directly from a clinical sample. Scientific Reports, 2017, 7, 3734.	3.3	48
32	Runx1 is essential at two stages of early murine B-cell development. Blood, 2013, 122, 413-423.	1.4	47
33	An AP4B1 frameshift mutation in siblings with intellectual disability and spastic tetraplegia further delineates the AP-4 deficiency syndrome. European Journal of Human Genetics, 2015, 23, 256-259.	2.8	47
34	TDP-43 enhances translation of specific mRNAs linked to neurodegenerative disease. Nucleic Acids Research, 2019, 47, 341-361.	14.5	47
35	Vertically transferred maternal immune cells promote neonatal immunity against early life infections. Nature Communications, 2021, 12, 4706.	12.8	44
36	Deciphering the microRNA signature of pathological cardiac hypertrophy by engineered heart tissue- and sequencing-technology. Journal of Molecular and Cellular Cardiology, 2015, 81, 1-9.	1.9	41

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37	Distinct clonal lineages and within-host diversification shape invasive Staphylococcus epidermidis populations. PLoS Pathogens, 2021, 17, e1009304.	4.7	41
38	Emergence of daptomycin non-susceptibility in colonizing vancomycin-resistant Enterococcus faecium isolates during daptomycin therapy. International Journal of Medical Microbiology, 2015, 305, 902-909.	3.6	40
39	Runx1 downregulates stem cell and megakaryocytic transcription programs that support niche interactions. Blood, 2016, 127, 3369-3381.	1.4	39
40	Versatility of Biofilm Matrix Molecules in Staphylococcus epidermidis Clinical Isolates and Importance of Polysaccharide Intercellular Adhesin Expression during High Shear Stress. MSphere, 2016, 1, .	2.9	39
41	Close Relationship of Ruminant Pestiviruses and Classical Swine Fever Virus. Emerging Infectious Diseases, 2015, 21, 668-672.	4.3	36
42	Mutational landscape reflects the biological continuum of plasma cell dyscrasias. Blood Cancer Journal, 2017, 7, e537-e537.	6.2	32
43	Acute Liver Failure Meets SOPH Syndrome: A Case Report on an Intermediate Phenotype. Pediatrics, 2017, 139, .	2.1	32
44	Immunosuppressive Yersinia Effector YopM Binds DEAD Box Helicase DDX3 to Control Ribosomal S6 Kinase in the Nucleus of Host Cells. PLoS Pathogens, 2016, 12, e1005660.	4.7	31
45	Novel poly-uridine insertion in the 3â€²UTR and E2 amino acid substitutions in a low virulent classical swine fever virus. Veterinary Microbiology, 2017, 201, 103-112.	1.9	29
46	Next-generation sequencing of 32 genes associated with hereditary aortopathies and related disorders of connective tissue in a cohort of 199 patients. Genetics in Medicine, 2019, 21, 1832-1841.	2.4	26
47	High-resolution analysis of Merkel Cell Polyomavirus in Merkel Cell Carcinoma reveals distinct integration patterns and suggests NHEJ and MMBIR as underlying mechanisms. PLoS Pathogens, 2020, 16, e1008562.	4.7	24
48	Molecular profiling of an osseous metastasis in glioblastoma during checkpoint inhibition: potential mechanisms of immune escape. Acta Neuropathologica Communications, 2020, 8, 28.	5.2	24
49	BRD4 promotes p63 and GRHL3 expression downstream of FOXO in mammary epithelial cells. Nucleic Acids Research, 2017, 45, gkw1276.	14.5	22
50	Homozygous HOXB1 lossâ€ofâ€function mutation in a large family with hereditary congenital facial paresis. American Journal of Medical Genetics, Part A, 2016, 170, 1813-1819.	1.2	22
51	Clinical and genetic spectrum of AMPD2-related pontocerebellar hypoplasia type 9. European Journal of Human Genetics, 2018, 26, 695-708.	2.8	22
52	Biallelic MADD variants cause a phenotypic spectrum ranging from developmental delay to a multisystem disorder. Brain, 2020, 143, 2437-2453.	7.6	21
53	Genomic characterization of vulvar squamous cell carcinoma. Gynecologic Oncology, 2020, 158, 547-554.	1.4	21
54	Glioma escape signature and clonal development under immune pressure. Journal of Clinical Investigation, 2020, 130, 5257-5271.	8.2	21

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55	Hypoimmune induced pluripotent stem cellâ€“derived cell therapeutics treat cardiovascular and pulmonary diseases in immunocompetent allogeneic mice. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	20
56	Pegivirus Infection in Domestic Pigs, Germany. Emerging Infectious Diseases, 2016, 22, 1312-1314.	4.3	19
57	Elsahyâ€“Waters syndrome is caused by biallelic mutations in CDH11. American Journal of Medical Genetics, Part A, 2018, 176, 477-482.	1.2	18
58	DAMIAN: an open source bioinformatics tool for fast, systematic and cohort based analysis of microorganisms in diagnostic samples. Scientific Reports, 2019, 9, 16841.	3.3	18
59	The novel RAF1 mutation p.(Gly361Ala) located outside the kinase domain of the CR3 region in two patients with Noonan syndrome, including one with a rare brain tumor. American Journal of Medical Genetics, Part A, 2018, 176, 470-476.	1.2	17
60	Lineage-specific control of TFIIH by MITF determines transcriptional homeostasis and DNA repair. Oncogene, 2019, 38, 3616-3635.	5.9	17
61	A novel multiple joint dislocation syndrome associated with a homozygous nonsense variant in the EXOC6B gene. European Journal of Human Genetics, 2016, 24, 1206-1210.	2.8	16
62	Biallelic and De Novo Variants in DONSON Reveal a Clinical Spectrum of Cell Cycleâ€opathies with Microcephaly, Dwarfism and Skeletal Abnormalities. American Journal of Medical Genetics, Part A, 2019, 179, 2056-2066.	1.2	15
63	A prenatally disrupted airway epithelium orchestrates the fetal origin of asthma in mice. Journal of Allergy and Clinical Immunology, 2020, 145, 1641-1654.	2.9	15
64	Next-generation sequencing of peripheral B-lineage cells pinpoints the circulating clonotypic cell pool in multiple myeloma. Blood, 2014, 123, 3618-3621.	1.4	14
65	Correlation of somatic mutations with outcome after FLAMSAâ€busulfan sequential conditioning and allogeneic stem cell transplantation in patients with myelodysplastic syndromes. European Journal of Haematology, 2016, 97, 288-296.	2.2	14
66	Optimization of design and production strategies for novel adeno-associated viral display peptide libraries. Gene Therapy, 2017, 24, 470-481.	4.5	14
67	Exome sequencing in 38 patients with intracranial aneurysms and subarachnoid hemorrhage. Journal of Neurology, 2020, 267, 2533-2545.	3.6	14
68	Rapid Capture Nextâ€Generation Sequencing in Clinical Diagnostics of Kinase Pathway Aberrations in Bâ€Cell Precursor ALL. Pediatric Blood and Cancer, 2016, 63, 1283-1286.	1.5	11
69	Cellular Importin-Î±3 Expression Dynamics in the Lung Regulate Antiviral Response Pathways against Influenza A Virus Infection. Cell Reports, 2020, 31, 107549.	6.4	11
70	Bi-allelic Pathogenic Variants in HS2ST1 Cause a Syndrome Characterized by Developmental Delay and Corpus Callosum, Skeletal, and Renal Abnormalities. American Journal of Human Genetics, 2020, 107, 1044-1061.	6.2	11
71	Comprehensive profiling of myxopapillary ependymomas identifies a distinct molecular subtype with relapsing disease. Neuro-Oncology, 2022, 24, 1689-1699.	1.2	11
72	Biallelic lossâ€ofâ€function variants in TBC1D2B cause a neurodevelopmental disorder with seizures and gingival overgrowth. Human Mutation, 2020, 41, 1645-1661.	2.5	10

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73	Novel biallelic variants expand the SLC5A6-related phenotypic spectrum. European Journal of Human Genetics, 2022, 30, 439-449.	2.8	10
74	Functional Dissection of an Alternatively Spliced Herpesvirus Gene by Splice Site Mutagenesis. Journal of Virology, 2016, 90, 4626-4636.	3.4	9
75	Biallelic FRA10AC1 variants cause a neurodevelopmental disorder with growth retardation. Brain, 2022, 145, 1551-1563.	7.6	9
76	A transplant â€œimmunomeâ€•screening platform defines a targetable epitope fingerprint of multiple myeloma. Blood, 2016, 127, 3202-3214.	1.4	7
77	Diagnostic potential of extracellular vesicles in meningioma patients. Neuro-Oncology, 2022, 24, 2078-2090.	1.2	6
78	Multiplexed mRNA analysis of brain-derived extracellular vesicles upon experimental stroke in mice reveals increased mRNA content with potential relevance to inflammation and recovery processes. Cellular and Molecular Life Sciences, 2022, 79, .	5.4	6
79	Characterization of novel, recurrent genomic rearrangements as sensitive MRD targets in childhood B-cell precursor ALL. Blood Cancer Journal, 2019, 9, 96.	6.2	5
80	Draft Genome Sequence of the Green Alga Scenedesmus acuminatus SAG 38.81. Microbiology Resource Announcements, 2020, 9, .	0.6	5
81	Deep (Meta)genomics and (Meta)transcriptome Analyses of Fungal and Bacteria Consortia From Aircraft Tanks and Kerosene Identify Key Genes in Fuel and Tank Corrosion. Frontiers in Microbiology, 2021, 12, 722259.	3.5	5
82	Alternative interaction sites in the influenza A virus nucleoprotein mediate viral escape from the importinâ€Î±7 mediated nuclear import pathway. FEBS Journal, 2019, 286, 3374-3388.	4.7	4
83	Differential regulation of extracellular matrix proteins in three recurrent liver metastases of a single patient with colorectal cancer. Clinical and Experimental Metastasis, 2020, 37, 649-656.	3.3	4
84	Biallelic variants in VPS50 cause a neurodevelopmental disorder with neonatal cholestasis. Brain, 2021, 144, 3036-3049.	7.6	4
85	Tâ€lymphocyteâ€“specific knockout of IKKâ€2 or NEMO induces T h 17 cells in an experimental nephrotoxic nephritis mouse model. FASEB Journal, 2019, 33, 2359-2371.	0.5	3
86	Transcriptome Analysis in Vulvar Squamous Cell Cancer. Cancers, 2021, 13, 6372.	3.7	3
87	Cardiofacioneurodevelopmental syndrome: Report of a novel patient and expansion of the phenotype. American Journal of Medical Genetics, Part A, 2022, 188, 2448-2453.	1.2	3
88	Reply: ATAD1 encephalopathy and stiff baby syndrome: a recognizable clinical presentation. Brain, 2018, 141, e50-e50.	7.6	1
89	Deep amoA amplicon sequencing reveals community partitioning within ammonia-oxidizing bacteria in the environmentally dynamic estuary of the River Elbe. Scientific Reports, 2020, 10, 17165.	3.3	1
90	CASSys: an integrated software-system for the interactive analysis of ChIP-seq data. Journal of Integrative Bioinformatics, 2011, 8, 155.	1.5	1

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91	Characterization of IG-MYC-breakpoints and their application for quantitative minimal disease monitoring in high-risk pediatric Burkitt-lymphoma and -leukemia. Leukemia, 0, , .	7.2	1
92	Coinheritance of biallelic SLURP1 and SLC39A4 mutations cause a severe genodermatosis with skin peeling and hair loss all over the body. British Journal of Dermatology, 2018, 179, 1192-1194.	1.5	0
93	ATRT-21. COMPARATIVE INTEGRATIVE ANALYSIS OF PRIMARY AND RELAPSED ATYPICAL TERATOID/RHABDOID TUMORS (AT/RTs). Neuro-Oncology, 2018, 20, i32-i32.	1.2	0
94	Clonal Evolution after Allogeneic Hematopoietic Stem Cell Transplantation: The Case of Myelofibrosis. Biology of Blood and Marrow Transplantation, 2020, 26, e167-e170.	2.0	0
95	EPEN-27. Epigenetic dissection of spinal ependymomas (SP-EPN) separates tumors with and withoutNF2 mutation. Neuro-Oncology, 2022, 24, i44-i45.	1.2	0
96	EPEN-06. Comprehensive profiling of myxopapillary ependymomas identifies a distinct molecular subtype with relapsing disease. Neuro-Oncology, 2022, 24, i39-i39.	1.2	0