

# Naser Ansari-Pour

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7616144/publications.pdf>

Version: 2024-02-01

31  
papers

1,041  
citations

623188

14  
h-index

476904

29  
g-index

37  
all docs

37  
docs citations

37  
times ranked

2503  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mosaic PPM1D mutations are associated with predisposition to breast and ovarian cancer. <i>Nature</i> , 2013, 493, 406-410.	13.7	218
2	Why, When and How to Adjust Your P Values?. <i>Cell Journal</i> , 2019, 20, 604-607.	0.2	207
3	Multiple cereblon genetic changes are associated with acquired resistance to lenalidomide or pomalidomide in multiple myeloma. <i>Blood</i> , 2021, 137, 232-237.	0.6	90
4	Genomic and evolutionary classification of lung cancer in never smokers. <i>Nature Genetics</i> , 2021, 53, 1348-1359.	9.4	81
5	The Essentiality of Reporting Hardy-Weinberg Equilibrium Calculations in Population-Based Genetic Association Studies. <i>Cell Journal</i> , 2015, 17, 187-92.	0.2	66
6	Isoform-Level Gene Expression Profiles of Human Y Chromosome Azoospermia Factor Genes and Their X Chromosome Paralogs in the Testicular Tissue of Non-Obstructive Azoospermia Patients. <i>Journal of Proteome Research</i> , 2015, 14, 3595-3605.	1.8	35
7	A logic-based dynamic modeling approach to explicate the evolution of the central dogma of molecular biology. <i>PLoS ONE</i> , 2017, 12, e0189922.	1.1	33
8	A sperm-specific proteome-scale metabolic network model identifies non-glycolytic genes for energy deficiency in asthenozoospermia. <i>Systems Biology in Reproductive Medicine</i> , 2017, 63, 100-112.	1.0	32
9	Evidence from Y-chromosome analysis for a late exclusively eastern expansion of the Bantu-speaking people. <i>European Journal of Human Genetics</i> , 2013, 21, 423-429.	1.4	29
10	Multi-site clonality analysis uncovers pervasive heterogeneity across melanoma metastases. <i>Nature Communications</i> , 2020, 11, 4306.	5.8	26
11	<i>IRF6</i> Is a Marker of Severity in Nonsyndromic Cleft Lip/Palate. <i>Journal of Dental Research</i> , 2015, 94, 226S-232S.	2.5	22
12	Whole-genome analysis of Nigerian patients with breast cancer reveals ethnic-driven somatic evolution and distinct genomic subtypes. <i>Nature Communications</i> , 2021, 12, 6946.	5.8	22
13	Systems Biomedicine of Rabies Delineates the Affected Signaling Pathways. <i>Frontiers in Microbiology</i> , 2016, 7, 1688.	1.5	21
14	The Genetic Legacy of Zoroastrianism in Iran and India: Insights into Population Structure, Gene Flow, and Selection. <i>American Journal of Human Genetics</i> , 2017, 101, 353-368.	2.6	19
15	Testis-Specific Y-Centric Protein-Protein Interaction Network Provides Clues to the Etiology of Severe Spermatogenic Failure. <i>Journal of Proteome Research</i> , 2016, 15, 1011-1022.	1.8	15
16	Palenque de San Basilio in Colombia: genetic data support an oral history of a paternal ancestry in Congo. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20152980.	1.2	14
17	Identification of a missense variant in <i>CLDN2</i> in obstructive azoospermia. <i>Journal of Human Genetics</i> , 2019, 64, 1023-1032.	1.1	14
18	GTA: a game theoretic approach to identifying cancer subnetwork markers. <i>Molecular BioSystems</i> , 2016, 12, 818-825.	2.9	11

#	ARTICLE	IF	CITATIONS
19	Re-evaluating experimental validation in the Big Data Era: a conceptual argument. <i>Genome Biology</i> , 2021, 22, 71.	3.8	10
20	Label-free discrimination of single nucleotide changes in DNA by reflectometric interference Fourier transform spectroscopy. <i>Colloids and Surfaces B: Biointerfaces</i> , 2019, 181, 714-720.	2.5	9
21	Genetic legacy of state centralization in the Kuba Kingdom of the Democratic Republic of the Congo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 593-598.	3.3	9
22	Can We Assume the Gene Expression Profile as a Proxy for Signaling Network Activity?. <i>Biomolecules</i> , 2020, 10, 850.	1.8	8
23	Systems genetics of nonsyndromic orofacial clefting provides insights into its complex aetiology. <i>European Journal of Human Genetics</i> , 2019, 27, 226-234.	1.4	7
24	Myeloma Genome Project Panel is a Comprehensive Targeted Genomics Panel for Molecular Profiling of Patients with Multiple Myeloma. <i>Clinical Cancer Research</i> , 2022, 28, 2854-2864.	3.2	6
25	Contrasting exome constancy and regulatory region variation in the gene encoding CYP3A4. <i>Pharmacogenetics and Genomics</i> , 2016, 26, 255-270.	0.7	5
26	Group-based pharmacogenetic prediction: is it feasible and do current NHS England ethnic classifications provide appropriate data?. <i>Pharmacogenomics Journal</i> , 2021, 21, 47-59.	0.9	3
27	Optimization of Porous Silicon Conditions for DNA-based Biosensing via Reflectometric Interference Spectroscopy. <i>Cell Journal</i> , 2019, 20, 584-591.	0.2	3
28	A novel gene-wide haplotype at the macrophage migration inhibitory factor (MIF) locus is associated with endometrioma. <i>European Journal of Obstetrics, Gynecology and Reproductive Biology</i> , 2020, 247, 6-9.	0.5	2
29	Loss of COP9 Signalosome Gene-Containing 2q Region Is Associated with Lenalidomide and Pomalidomide Resistance in Myeloma Patients. <i>Blood</i> , 2021, 138, 458-458.	0.6	1
30	A Clinically Validated Targeted Capture Panel to Identify Translocations, Copy Number Abnormalities, and Mutations in Multiple Myeloma. <i>Blood</i> , 2021, 138, 2676-2676.	0.6	1
31	Association of MSY haplotype background with nonobstructive azoospermia is AZFa-dependent: A case-control study. <i>Andrologia</i> , 2021, 53, e13946.	1.0	0