

# Arshan Nasir

## List of Publications by Year in descending order

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Version: 2024-02-01

56  
papers

1,439  
citations

331259

21  
h-index

360668

35  
g-index

59  
all docs

59  
docs citations

59  
times ranked

1372  
citing authors

#	ARTICLE	IF	CITATIONS
1	A phylogenomic data-driven exploration of viral origins and evolution. <i>Science Advances</i> , 2015, 1, e1500527.	4.7	158
2	Lokiarchaea are close relatives of Euryarchaeota, not bridging the gap between prokaryotes and eukaryotes. <i>PLoS Genetics</i> , 2017, 13, e1006810.	1.5	136
3	Giant viruses coexisted with the cellular ancestors and represent a distinct supergroup along with superkingdoms Archaea, Bacteria and Eukarya. <i>BMC Evolutionary Biology</i> , 2012, 12, 156.	3.2	110
4	Asgard archaea do not close the debate about the universal tree of life topology. <i>PLoS Genetics</i> , 2018, 14, e1007215.	1.5	80
5	Global Patterns of Protein Domain Gain and Loss in Superkingdoms. <i>PLoS Computational Biology</i> , 2014, 10, e1003452.	1.5	65
6	Horizontal gene transfer in human-associated microorganisms inferred by phylogenetic reconstruction and reconciliation. <i>Scientific Reports</i> , 2019, 9, 5953.	1.6	55
7	Investigating the Concept and Origin of Viruses. <i>Trends in Microbiology</i> , 2020, 28, 959-967.	3.5	47
8	HGTtree: database of horizontally transferred genes determined by tree reconciliation. <i>Nucleic Acids Research</i> , 2016, 44, D610-D619.	6.5	45
9	Ancestrality and Mosaicism of Giant Viruses Supporting the Definition of the Fourth TRUC of Microbes. <i>Frontiers in Microbiology</i> , 2018, 9, 2668.	1.5	44
10	The distribution and impact of viral lineages in domains of life. <i>Frontiers in Microbiology</i> , 2014, 5, 194.	1.5	42
11	Rooting Phylogenies and the Tree of Life While Minimizing Ad Hoc and Auxiliary Assumptions. <i>Evolutionary Bioinformatics</i> , 2018, 14, 117693431880510.	0.6	40
12	Viral evolution. <i>Mobile Genetic Elements</i> , 2012, 2, 247-252.	1.8	35
13	Benefits of using molecular structure and abundance in phylogenomic analysis. <i>Frontiers in Genetics</i> , 2012, 3, 172.	1.1	32
14	Phylogenetic Tracings of Proteome Size Support the Gradual Accretion of Protein Structural Domains and the Early Origin of Viruses from Primordial Cells. <i>Frontiers in Microbiology</i> , 2017, 8, 1178.	1.5	32
15	Untangling the origin of viruses and their impact on cellular evolution. <i>Annals of the New York Academy of Sciences</i> , 2015, 1341, 61-74.	1.8	30
16	A General Framework of Persistence Strategies for Biological Systems Helps Explain Domains of Life. <i>Frontiers in Genetics</i> , 2013, 4, 16.	1.1	27
17	Archaea: The First Domain of Diversified Life. <i>Archaea</i> , 2014, 2014, 1-26.	2.3	27
18	A Tree of Cellular Life Inferred from a Genomic Census of Molecular Functions. <i>Journal of Molecular Evolution</i> , 2014, 79, 240-262.	0.8	25

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19	Arguments Reinforcing the Three-Domain View of Diversified Cellular Life. <i>Archaea</i> , 2016, 2016, 1-11.	2.3	25
20	Lokiarchaeota: eukaryote-like missing links from microbial dark matter?. <i>Trends in Microbiology</i> , 2015, 23, 448-450.	3.5	24
21	Do Viruses Exchange Genes across Superkingdoms of Life?. <i>Frontiers in Microbiology</i> , 2017, 8, 2110.	1.5	23
22	Annotation of Protein Domains Reveals Remarkable Conservation in the Functional Make up of Proteomes Across Superkingdoms. <i>Genes</i> , 2011, 2, 869-911.	1.0	22
23	Long-term evolution of viruses: A Janus-faced balance. <i>BioEssays</i> , 2017, 39, 1700026.	1.2	22
24	A Phylogenomic Census of Molecular Functions Identifies Modern Thermophilic Archaea as the Most Ancient Form of Cellular Life. <i>Archaea</i> , 2014, 2014, 1-15.	2.3	21
25	Complete genome of <i>Kangiella geojedonensis</i> KCTC 23420T, putative evidence for recent genome reduction in marine environments. <i>Marine Genomics</i> , 2015, 24, 215-217.	0.4	21
26	Identification of Capsid/Coat Related Protein Folds and Their Utility for Virus Classification. <i>Frontiers in Microbiology</i> , 2017, 8, 380.	1.5	21
27	The origin and evolution of viruses inferred from fold family structure. <i>Archives of Virology</i> , 2020, 165, 2177-2191.	0.9	20
28	Environmental exposure pathway analysis of trace elements and autism risk in Pakistani children population. <i>Science of the Total Environment</i> , 2020, 712, 136471.	3.9	18
29	Comparative Analysis of Proteomes and Functionomes Provides Insights into Origins of Cellular Diversification. <i>Archaea</i> , 2013, 2013, 1-13.	2.3	17
30	The importance of using realistic evolutionary models for retrodicting proteomes. <i>Biochimie</i> , 2014, 99, 129-137.	1.3	17
31	Initial Sequencing and Characterization of the Gastrointestinal and Oral Microbiota in Urban Pakistani Adults. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 409.	1.8	12
32	A Preliminary List of Horizontally Transferred Genes in Prokaryotes Determined by Tree Reconstruction and Reconciliation. <i>Frontiers in Genetics</i> , 2017, 8, 112.	1.1	11
33	Bacterial Origin and Reductive Evolution of the CPR Group. <i>Genome Biology and Evolution</i> , 2020, 12, 103-121.	1.1	11
34	Complete genome of the marine bacterium <i>Wenzhouxiangella marina</i> KCTC 42284T. <i>Marine Genomics</i> , 2015, 24, 277-280.	0.4	10
35	CLUSTOM-CLOUD: In-Memory Data Grid-Based Software for Clustering 16S rRNA Sequence Data in the Cloud Environment. <i>PLoS ONE</i> , 2016, 11, e0151064.	1.1	9
36	Complete genome of <i>Streptomyces hygrosopicus</i> subsp. <i>limoneus</i> KCTC 1717 (=KCCM 11405), a soil bacterium producing validamycin and diverse secondary metabolites. <i>Journal of Biotechnology</i> , 2016, 219, 1-2.	1.9	8

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37	Order and polarity in character state transformation models that root the tree of life. <i>Biochimie</i> , 2018, 149, 135-136.	1.3	8
38	What Should Health Departments Do with HIV Sequence Data?. <i>Viruses</i> , 2020, 12, 1018.	1.5	8
39	The tree of life describes a tripartite cellular world. <i>BioEssays</i> , 2021, 43, 2000343.	1.2	8
40	Large Evolutionary Rate Heterogeneity among and within HIV-1 Subtypes and CRFs. <i>Viruses</i> , 2021, 13, 1689.	1.5	8
41	Complete genome of biodegradable plastics-decomposing <i>Roseateles depolymerans</i> KCTC 42856T (=61AT). <i>Journal of Biotechnology</i> , 2016, 220, 47-48.	1.9	7
42	The Compressed Vocabulary of the Proteins of Archaea. , 2017, , 147-174.		7
43	Computational analysis reveals abundance of potential glycoproteins in Archaea, Bacteria and Eukarya. <i>Bioinformatics</i> , 2011, 6, 352-355.	0.2	7
44	Testing Empirical Support for Evolutionary Models that Root the Tree of Life. <i>Journal of Molecular Evolution</i> , 2019, 87, 131-142.	0.8	6
45	Complete genome of <i>Pseudoalteromonas phenolica</i> KCTC 12086T (= O-BC30T), a marine bacterium producing polybrominated aromatic compounds. <i>Journal of Biotechnology</i> , 2016, 218, 23-24.	1.9	4
46	Characterization of the Gastrointestinal and Reproductive Tract Microbiota in Fertile and Infertile Pakistani Couples. <i>Biology</i> , 2022, 11, 40.	1.3	4
47	Complete genome of a metabolically-diverse marine bacterium <i>Shewanella japonica</i> KCTC 22435 T. <i>Marine Genomics</i> , 2017, 35, 39-42.	0.4	3
48	Editorial: Viruses, Genetic Exchange, and the Tree of Life. <i>Frontiers in Microbiology</i> , 2019, 10, 2782.	1.5	3
49	Complete genome of <i>Polaromonas vacuolata</i> KCTC 22033T isolated from beneath Antarctic Sea ice. <i>Marine Genomics</i> , 2021, 55, 100790.	0.4	3
50	Comparative analysis of organophosphate degrading enzymes from diverse species. <i>Bioinformatics</i> , 2010, 5, 67-72.	0.2	3
51	Complete Genome Sequence of Nitrotriacetate-Degrading <i>Aminobacter aminovorans</i> KCTC 2477. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
52	Analysis of glycosylation motifs and glycosyltransferases in Bacteria and Archaea. <i>Bioinformatics</i> , 2011, 6, 191-195.	0.2	2
53	Complete genome of brown algal polysaccharides-degrading <i>Pseudoalteromonas issachenkonii</i> KCTC 12958T (=KMM 3549T). <i>Journal of Biotechnology</i> , 2016, 219, 86-87.	1.9	1
54	The functional make up of proteomes is remarkably conserved. , 2011, , .		0

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55	Editorial: Viruses, Genetic Exchange, and the Tree of Life. , 2020, , .		0
56	Woese's Three Domains of Cellular Life. , 2022, , 7304-7306.		0