

# Arina D Omer

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7820550/publications.pdf>

Version: 2024-02-01

17  
papers

10,680  
citations

840585

11  
h-index

887953

17  
g-index

20  
all docs

20  
docs citations

20  
times ranked

15475  
citing authors

#	ARTICLE	IF	CITATIONS
1	Non-cell-autonomous disruption of nuclear architecture as a potential cause of COVID-19-induced anosmia. <i>Cell</i> , 2022, 185, 1052-1064.e12.	13.5	154
2	Chromosome size affects sequence divergence between species through the interplay of recombination and selection. <i>Evolution; International Journal of Organic Evolution</i> , 2022, 76, 782-798.	1.1	11
3	The Australian dingo is an early offshoot of modern breed dogs. <i>Science Advances</i> , 2022, 8, eabm5944.	4.7	14
4	CTCF loss has limited effects on global genome architecture in <i>Drosophila</i> despite critical regulatory functions. <i>Nature Communications</i> , 2021, 12, 1011.	5.8	60
5	Chromosome-length genome assembly and structural variations of the primal Basenji dog ( <i>Canis lupus</i> ) Tj ETQq1 1,0,784314,rgBT /Overlock I	1.2	22
6	Limited Evidence for Parallel Evolution Among Desert-Adapted <i>Peromyscus</i> Deer Mice. <i>Journal of Heredity</i> , 2021, 112, 286-302.	1.0	14
7	3D genomics across the tree of life reveals condensin II as a determinant of architecture type. <i>Science</i> , 2021, 372, 984-989.	6.0	132
8	The Easter Egg Weevil ( <i>Pachyrhynchus</i> ) genome reveals syntenic patterns in Coleoptera across 200 million years of evolution. <i>PLoS Genetics</i> , 2021, 17, e1009745.	1.5	14
9	The gene-rich genome of the scallop <i>Pecten maximus</i> . <i>GigaScience</i> , 2020, 9, .	3.3	53
10	Canfam_GSD: De novo chromosome-length genome assembly of the German Shepherd Dog ( <i>Canis lupus</i> ) Tj ETQq0,0,0 rgBT /Overlock I	3.3	47
11	The genome sequence of the Eurasian red squirrel, <i>Sciurus vulgaris</i> Linnaeus 1758. <i>Wellcome Open Research</i> , 2020, 5, 18.	0.9	3
12	The genome sequence of the Eurasian river otter, <i>Lutra lutra</i> Linnaeus 1758. <i>Wellcome Open Research</i> , 2020, 5, 33.	0.9	6
13	Topologically Associated Domains Delineate Susceptibility to Somatic Hypermutation. <i>Cell Reports</i> , 2019, 29, 3902-3915.e8.	2.9	33
14	Improved reference genome of <i>Aedes aegypti</i> informs arbovirus vector control. <i>Nature</i> , 2018, 563, 501-507.	13.7	426
15	De novo assembly of the <i>Aedes aegypti</i> genome using Hi-C yields chromosome-length scaffolds. <i>Science</i> , 2017, 356, 92-95.	6.0	1,513
16	Cohesin Loss Eliminates All Loop Domains. <i>Cell</i> , 2017, 171, 305-320.e24.	13.5	1,454
17	A 3D Map of the Human Genome at Kilobase Resolution Reveals Principles of Chromatin Looping. <i>Cell</i> , 2014, 159, 1665-1680.	13.5	6,520