

# Claire D Mcwhite

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1123146/publications.pdf>

Version: 2024-02-01

13  
papers

625  
citations

1040056

9  
h-index

1199594

12  
g-index

17  
all docs

17  
docs citations

17  
times ranked

1357  
citing authors

#	ARTICLE	IF	CITATIONS
1	Integration of over 9,000 mass spectrometry experiments builds a global map of human protein complexes. <i>Molecular Systems Biology</i> , 2017, 13, 932.	7.2	177
2	A Pan-plant Protein Complex Map Reveals Deep Conservation and Novel Assemblies. <i>Cell</i> , 2020, 181, 460-474.e14.	28.9	133
3	Achaete-scute homologue-1 (ASH1) stimulates migration of lung cancer cells through Cdk5/p35 pathway. <i>Molecular Biology of the Cell</i> , 2012, 23, 2856-2866.	2.1	71
4	Towards Consensus Gene Ages. <i>Genome Biology and Evolution</i> , 2016, 8, 1812-1823.	2.5	63
5	Gearing up to handle the mosaic nature of life in the quest for orthologs. <i>Bioinformatics</i> , 2018, 34, 323-329.	4.1	36
6	Sequence amplification via cell passaging creates spurious signals of positive adaptation in influenza virus H3N2 hemagglutinin. <i>Virus Evolution</i> , 2016, 2, vew026.	4.9	35
7	Systematic bacterialization of yeast genes identifies a near-universally swappable pathway. <i>ELife</i> , 2017, 6, .	6.0	32
8	Sensitive detection of proteasomal activation using the Deg-On mammalian synthetic gene circuit. <i>Nature Communications</i> , 2014, 5, 3612.	12.8	24
9	A systematic, label-free method for identifying RNA-associated proteins in vivo provides insights into vertebrate ciliary beating machinery. <i>Developmental Biology</i> , 2020, 467, 108-117.	2.0	22
10	Co-fractionation/mass spectrometry to identify protein complexes. <i>STAR Protocols</i> , 2021, 2, 100370.	1.2	12
11	Influenza passaging annotations: what they tell us and why we should listen. <i>Virus Evolution</i> , 2019, 5, vez016.	4.9	8
12	Applications of comparative evolution to human disease genetics. <i>Current Opinion in Genetics and Development</i> , 2015, 35, 16-24.	3.3	7
13	A yeast selection system for the detection of proteasomal activation. <i>Protein Engineering, Design and Selection</i> , 2018, 31, 437-445.	2.1	0