

# Mohsen Hooshyar

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6113860/publications.pdf>

Version: 2024-02-01

25  
papers

360  
citations

933447

10  
h-index

940533

16  
g-index

26  
all docs

26  
docs citations

26  
times ranked

597  
citing authors

#	ARTICLE	IF	CITATIONS
1	Discovery and identification of genes involved in DNA damage repair in yeast. <i>Gene</i> , 2022, , 146549.	2.2	2
2	Actin-Related Protein 6 (Arp6) Influences Double-Strand Break Repair in Yeast. <i>Applied Microbiology</i> , 2021, 1, 225-238.	1.6	0
3	The conserved Tpk1 regulates non-homologous end joining double-strand break repair by phosphorylation of Nej1, a homolog of the human XLF. <i>Nucleic Acids Research</i> , 2021, 49, 8145-8160.	14.5	4
4	Lithium Chloride Sensitivity in Yeast and Regulation of Translation. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5730.	4.1	8
5	Deletion of yeast TPK1 reduces the efficiency of non-homologous end joining DNA repair. <i>Biochemical and Biophysical Research Communications</i> , 2020, 533, 899-904.	2.1	4
6	Sensitivity of yeast to lithium chloride connects the activity of YTA6 and YPR096C to translation of structured mRNAs. <i>PLoS ONE</i> , 2020, 15, e0235033.	2.5	9
7	Title is missing!. , 2020, 15, e0235033.		0
8	Title is missing!. , 2020, 15, e0235033.		0
9	Title is missing!. , 2020, 15, e0235033.		0
10	Title is missing!. , 2020, 15, e0235033.		0
11	Title is missing!. , 2020, 15, e0235033.		0
12	Title is missing!. , 2020, 15, e0235033.		0
13	Title is missing!. , 2020, 15, e0235033.		0
14	Title is missing!. , 2020, 15, e0235033.		0
15	In Silico Engineering of Synthetic Binding Proteins from Random Amino Acid Sequences. <i>IScience</i> , 2019, 11, 375-387.	4.1	10
16	Uncharacterized ORF HUR1 influences the efficiency of non-homologous end-joining repair in <i>Saccharomyces cerevisiae</i> . <i>Gene</i> , 2018, 639, 128-136.	2.2	19
17	Global landscape of cell envelope protein complexes in <i>Escherichia coli</i> . <i>Nature Biotechnology</i> , 2018, 36, 103-112.	17.5	110
18	Designing anti-Zika virus peptides derived from predicted human-Zika virus protein-protein interactions. <i>Computational Biology and Chemistry</i> , 2017, 71, 180-187.	2.3	20

#	ARTICLE	IF	CITATIONS
19	Evolution of protein-protein interaction networks in yeast. PLoS ONE, 2017, 12, e0171920.	2.5	24
20	The sensitivity of the yeast, <i>Saccharomyces cerevisiae</i> , to acetic acid is influenced by <i>DOM34</i> and <i>RPL36A</i> . PeerJ, 2017, 5, e4037.	2.0	15
21	Conditional Epistatic Interaction Maps Reveal Global Functional Rewiring of Genome Integrity Pathways in <i>Escherichia coli</i> . Cell Reports, 2016, 14, 648-661.	6.4	34
22	Spindle Checkpoint Factors Bub1 and Bub2 Promote DNA Double-Strand Break Repair by Nonhomologous End Joining. Molecular and Cellular Biology, 2015, 35, 2448-2463.	2.3	21
23	Efficient prediction of human protein-protein interactions at a global scale. BMC Bioinformatics, 2014, 15, 383.	2.6	32
24	Phosphatase Complex Pph3/Psy2 Is Involved in Regulation of Efficient Non-Homologous End-Joining Pathway in the Yeast <i>Saccharomyces cerevisiae</i> . PLoS ONE, 2014, 9, e87248.	2.5	20
25	Recent advances in protein-protein interaction prediction: experimental and computational methods. Expert Opinion on Drug Discovery, 2011, 6, 921-935.	5.0	26