

Yungki Park

List of Publications by Year in descending order

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582
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#	ARTICLE	IF	CITATIONS
1	Functional mechanisms of MYRF DNA-binding domain mutations implicated in birth defects. <i>Journal of Biological Chemistry</i> , 2021, 296, 100612.	3.4	9
2	Identifying oligodendrocyte enhancers governing <i>Plp1</i> expression. <i>Human Molecular Genetics</i> , 2021, 30, 2225-2239.	2.9	14
3	PRC2 Acts as a Critical Timer That Drives Oligodendrocyte Fate over Astrocyte Identity by Repressing the Notch Pathway. <i>Cell Reports</i> , 2020, 32, 108147.	6.4	20
4	Broadening our understanding of the genetics of Juvenile Idiopathic Arthritis (JIA): Interrogation of three dimensional chromatin structures and genetic regulatory elements within JIA-associated risk loci. <i>PLoS ONE</i> , 2020, 15, e0235857.	2.5	5
5	Functional mechanism and pathogenic potential of MYRF ICA domain mutations implicated in birth defects. <i>Scientific Reports</i> , 2020, 10, 814.	3.3	11
6	A principled strategy for mapping enhancers to genes. <i>Scientific Reports</i> , 2019, 9, 11043.	3.3	14
7	Molecular mechanism for the multiple sclerosis risk variant rs17594362. <i>Human Molecular Genetics</i> , 2019, 28, 3600-3609.	2.9	5
8	Elucidating the transactivation domain of the pleiotropic transcription factor Myrf. <i>Scientific Reports</i> , 2018, 8, 13075.	3.3	11
9	Homo-trimerization is essential for the transcription factor function of Myrf for oligodendrocyte differentiation. <i>Nucleic Acids Research</i> , 2017, 45, 5112-5125.	14.5	38
10	A Bacteriophage Tailspike Domain Promotes Self-Cleavage of a Human Membrane-Bound Transcription Factor, the Myelin Regulatory Factor MYRF. <i>PLoS Biology</i> , 2013, 11, e1001624.	5.6	59
11	Flaws in evaluation schemes for pair-input computational predictions. <i>Nature Methods</i> , 2012, 9, 1134-1136.	19.0	157
12	Statistical analysis and exposure status classification of transmembrane beta barrel residues. <i>Computational Biology and Chemistry</i> , 2011, 35, 96-107.	2.3	6
13	PREDICTION OF THE EXPOSURE STATUS OF TRANSMEMBRANE BETA BARREL RESIDUES FROM PROTEIN SEQUENCE. <i>Journal of Bioinformatics and Computational Biology</i> , 2011, 09, 43-65.	0.8	9
14	Assembly of transmembrane helices of simple polytopic membrane proteins from sequence conservation patterns. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 895-905.	2.6	15
15	Novel scoring function for modeling structures of oligomers of transmembrane α -helices. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 57, 577-585.	2.6	22