

The BioPlex Network: A Systematic Exploration of the H

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Structural in silico dissection of the collagen V interactome to identify genotypeâ€“phenotype correlations in classic Ehlersâ€“Danlos Syndrome (EDS). <i>FEBS Letters</i> , 2015, 589, 3871-3878.	1.3	11
2	Illuminating Spatial and Temporal Organization of Protein Interaction Networks by Mass Spectrometry-Based Proteomics. <i>Frontiers in Genetics</i> , 2015, 6, 344.	1.1	16
3	Golgi Fragmentation in ALS Motor Neurons. New Mechanisms Targeting Microtubules, Tethers, and Transport Vesicles. <i>Frontiers in Neuroscience</i> , 2015, 9, 448.	1.4	60
4	Forward Individualized Medicine from Personal Genomes to Interactomes. <i>Frontiers in Physiology</i> , 2015, 6, 364.	1.3	15
5	Hypothesis: NDL proteins function in stress responses by regulating microtubule organization. <i>Frontiers in Plant Science</i> , 2015, 6, 947.	1.7	16
6	Identifying communities from multiplex biological networks. <i>PeerJ</i> , 2015, 3, e1525.	0.9	57
7	Gene essentiality and synthetic lethality in haploid human cells. <i>Science</i> , 2015, 350, 1092-1096.	6.0	773
8	A Scalable Genome-Editing-Based Approach for Mapping Multiprotein Complexes in Human Cells. <i>Cell Reports</i> , 2015, 13, 621-633.	2.9	93
10	Bioinformatics Approaches for Predicting Kinaseâ€“Substrate Relationships. , 2016, , .		0
11	Multi-OMICs and Genome Editing Perspectives on Liver Cancer Signaling Networks. <i>BioMed Research International</i> , 2016, 2016, 1-14.	0.9	7
12	Akt1-Inhibitor of DNA binding2 is essential for growth cone formation and axon growth and promotes central nervous system axon regeneration. <i>ELife</i> , 2016, 5, .	2.8	27
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16	Shedding light on the expansion and diversification of the Cdc48 protein family during the rise of the eukaryotic cell. <i>BMC Evolutionary Biology</i> , 2016, 16, 215.	3.2	15
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18	Understanding the roles of intrinsic disorder in subunits of hemoglobin and the disease process of sickle cell anemia. <i>Intrinsically Disordered Proteins</i> , 2016, 4, e1248273.	1.9	8
19	Salivary and pellicle proteome: A datamining analysis. <i>Scientific Reports</i> , 2016, 6, 38882.	1.6	24

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21	Proteomics to study DNA-bound and chromatin-associated gene regulatory complexes. <i>Human Molecular Genetics</i> , 2016, 25, R106-R114.	1.4	59
22	Structure of the RBM7-ZCCHC8 core of the NEXT complex reveals connections to splicing factors. <i>Nature Communications</i> , 2016, 7, 13573.	5.8	38
23	The Borg family of Cdc42 effector proteins Cdc42EP1-5. <i>Biochemical Society Transactions</i> , 2016, 44, 1709-1716.	1.6	45
24	Dissecting the Keap1/Nrf2 pathway through proteomics. <i>Current Opinion in Toxicology</i> , 2016, 1, 118-124.	2.6	9
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