

Lilia M Iakoucheva

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

59
papers

13,063
citations

38
h-index

66
g-index

66
ext. papers

15,172
ext. citations

17.3
avg, IF

5.78
L-index

#	Paper	IF	Citations
59	Autism-linked Cullin3 germline haploinsufficiency impacts cytoskeletal dynamics and cortical neurogenesis through RhoA signaling. <i>Molecular Psychiatry</i> , 2021 , 26, 3586-3613	15.1	1
58	Full-length isoform transcriptome of the developing human brain provides further insights into autism. <i>Cell Reports</i> , 2021 , 36, 109631	10.6	2
57	Cortical organoids model early brain development disrupted by 16p11.2 copy number variants in autism. <i>Molecular Psychiatry</i> , 2021 ,	15.1	6
56	Prioritizing de novo autism risk variants with calibrated gene- and variant-scoring models. <i>Human Genetics</i> , 2021 , 1	6.3	0
55	Inferring the molecular and phenotypic impact of amino acid variants with MutPred2. <i>Nature Communications</i> , 2020 , 11, 5918	17.4	84
54	Getting to the Cores of Autism. <i>Cell</i> , 2019 , 178, 1287-1298	56.2	91
53	Oligogenic Effects of 16p11.2 Copy-Number Variation on Craniofacial Development. <i>Cell Reports</i> , 2019 , 28, 3320-3328.e4	10.6	16
52	Pathogenicity and functional impact of non-frameshifting insertion/deletion variation in the human genome. <i>PLoS Computational Biology</i> , 2019 , 15, e1007112	5	15
51	Paternally inherited cis-regulatory structural variants are associated with autism. <i>Science</i> , 2018 , 360, 327-331	33.3	106
50	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. <i>Science</i> , 2018 , 362,	33.3	434
49	Comprehensive Analyses of Tissue-Specific Networks with Implications to Psychiatric Diseases. <i>Methods in Molecular Biology</i> , 2017 , 1613, 371-402	1.4	4
48	When loss-of-function is loss of function: assessing mutational signatures and impact of loss-of-function genetic variants. <i>Bioinformatics</i> , 2017 , 33, i389-i398	7.2	23
47	Frequency and Complexity of De Novo Structural Mutation in Autism. <i>American Journal of Human Genetics</i> , 2016 , 98, 667-79	11	61
46	Widespread Expansion of Protein Interaction Capabilities by Alternative Splicing. <i>Cell</i> , 2016 , 164, 805-1756.2	56.2	308
45	Spatiotemporal 16p11.2 protein network implicates cortical late mid-fetal brain development and KCTD13-Cul3-RhoA pathway in psychiatric diseases. <i>Neuron</i> , 2015 , 85, 742-54	13.9	94
44	Predicted disorder-to-order transition mutations in IB β disrupt function. <i>Physical Chemistry Chemical Physics</i> , 2014 , 16, 6480-5	3.6	16
43	Pathological unfoldomics of uncontrolled chaos: intrinsically disordered proteins and human diseases. <i>Chemical Reviews</i> , 2014 , 114, 6844-79	68.1	186

42	A proteome-scale map of the human interactome network. <i>Cell</i> , 2014 , 159, 1212-1226	56.2	898
41	Protein interaction network of alternatively spliced isoforms from brain links genetic risk factors for autism. <i>Nature Communications</i> , 2014 , 5, 3650	17.4	101
40	Whole-genome sequencing in autism identifies hot spots for de novo germline mutation. <i>Cell</i> , 2012 , 151, 1431-42	56.2	392
39	A Protein Domain-Based Interactome Network for <i>C. elegans</i> Early Embryogenesis. <i>Cell</i> , 2012 , 151, 1633-1644	56.2	3
38	Protein Disorder and Human Genetic Disease 2012 ,		2
37	Disease mutations in disordered regions--exception to the rule?. <i>Molecular BioSystems</i> , 2012 , 8, 27-32		64
36	Disease-associated mutations disrupt functionally important regions of intrinsic protein disorder. <i>PLoS Computational Biology</i> , 2012 , 8, e1002709	5	95
35	Duplications of the neuropeptide receptor gene VIPR2 confer significant risk for schizophrenia. <i>Nature</i> , 2011 , 471, 499-503	50.4	257
34	Mapping copy number variation by population-scale genome sequencing. <i>Nature</i> , 2011 , 470, 59-65	50.4	833
33	Graphlet kernels for prediction of functional residues in protein structures. <i>Journal of Computational Biology</i> , 2010 , 17, 55-72	1.7	36
32	Loss of post-translational modification sites in disease. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2010 , 337-47	1.3	47
31	Identification, analysis, and prediction of protein ubiquitination sites. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010 , 78, 365-80	4.2	424
30	Unfoldomics of human diseases: linking protein intrinsic disorder with diseases. <i>BMC Genomics</i> , 2009 , 10 Suppl 1, S7	4.5	199
29	Microduplications of 16p11.2 are associated with schizophrenia. <i>Nature Genetics</i> , 2009 , 41, 1223-7	36.3	550
28	Prioritizing Disease Genes and Understanding Disease Pathways 2009 , 239-256		
27	RNA association or phosphorylation of the RS domain prevents aggregation of RS domain-containing proteins. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2008 , 1780, 214-25	4	29
26	A protein domain-based interactome network for <i>C. elegans</i> early embryogenesis. <i>Cell</i> , 2008 , 134, 534-545	56.2	161
25	Functional anthology of intrinsic disorder. 2. Cellular components, domains, technical terms, developmental processes, and coding sequence diversities correlated with long disordered regions. <i>Journal of Proteome Research</i> , 2007 , 6, 1899-916	5.6	215

24	Intrinsic disorder and functional proteomics. <i>Biophysical Journal</i> , 2007 , 92, 1439-56	2.9	571
23	Functional anthology of intrinsic disorder. 1. Biological processes and functions of proteins with long disordered regions. <i>Journal of Proteome Research</i> , 2007 , 6, 1882-98	5.6	455
22	Functional anthology of intrinsic disorder. 3. Ligands, post-translational modifications, and diseases associated with intrinsically disordered proteins. <i>Journal of Proteome Research</i> , 2007 , 6, 1917-32	5.6	322
21	Prediction of intrinsic disorder and its use in functional proteomics. <i>Methods in Molecular Biology</i> , 2007 , 408, 69-92	1.4	32
20	Serine/arginine-rich splicing factors belong to a class of intrinsically disordered proteins. <i>Nucleic Acids Research</i> , 2006 , 34, 305-12	20.1	87
19	Intrinsic disorder is a common feature of hub proteins from four eukaryotic interactomes. <i>PLoS Computational Biology</i> , 2006 , 2, e100	5	435
18	Two Sample Logo: a graphical representation of the differences between two sets of sequence alignments. <i>Bioinformatics</i> , 2006 , 22, 1536-7	7.2	336
17	Flexible nets. The roles of intrinsic disorder in protein interaction networks. <i>FEBS Journal</i> , 2005 , 272, 5129-48	5.7	895
16	DisProt: a database of protein disorder. <i>Bioinformatics</i> , 2005 , 21, 137-40	7.2	205
15	Combining prediction, computation and experiment for the characterization of protein disorder. <i>Current Opinion in Structural Biology</i> , 2004 , 14, 570-6	8.1	113
14	The importance of intrinsic disorder for protein phosphorylation. <i>Nucleic Acids Research</i> , 2004 , 32, 1037-40	10.1	1043
13	Order, disorder, and flexibility: prediction from protein sequence. <i>Structure</i> , 2003 , 11, 1316-7	5.2	49
12	Intrinsic disorder and protein function. <i>Biochemistry</i> , 2002 , 41, 6573-82	3.2	1462
11	Equilibrium and stop-flow kinetic studies of fluorescently labeled DNA substrates with DNA repair proteins XPA and replication protein A. <i>Biochemistry</i> , 2002 , 41, 131-43	3.2	22
10	Intrinsic disorder in cell-signaling and cancer-associated proteins. <i>Journal of Molecular Biology</i> , 2002 , 323, 573-84	6.5	967
9	Aberrant mobility phenomena of the DNA repair protein XPA. <i>Protein Science</i> , 2001 , 10, 1353-62	6.3	61
8	Identification of intrinsic order and disorder in the DNA repair protein XPA. <i>Protein Science</i> , 2001 , 10, 560-71	6.3	101
7	Single-molecule conformational dynamics of fluctuating noncovalent DNA-protein interactions in DNA damage recognition. <i>Journal of the American Chemical Society</i> , 2001 , 123, 9184-5	16.4	42

6	Nucleotide excision repair in oocyte nuclear extracts from <i>Xenopus laevis</i> . <i>Methods</i> , 2000 , 22, 188-93	4.6	5
5	Extended X-ray absorption fine structure evidence for a single metal binding domain in <i>Xenopus laevis</i> nucleotide excision repair protein XPA. <i>Biochemical and Biophysical Research Communications</i> , 1999 , 254, 109-13	3.4	12
4	Oligogenic Effects of 16p11.2 Copy Number Variation on Craniofacial Development. <i>SSRN Electronic Journal</i> ,	1	1
3	Paternally inherited noncoding structural variants contribute to autism		7
2	MutPred2: inferring the molecular and phenotypic impact of amino acid variants		79
1	Cortical Organoids Model Early Brain Development Disrupted by 16p11.2 Copy Number Variants in Autism		2