

# Pedro R Romero

## List of Publications by Year in descending order

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45  
papers

11,790  
citations

159585

30  
h-index

302126

39  
g-index

47  
all docs

47  
docs citations

47  
times ranked

14582  
citing authors

#	ARTICLE	IF	CITATIONS
1	BioMagResBank (BMRB) as a Resource for Structural Biology. <i>Methods in Molecular Biology</i> , 2020, 2112, 187-218.	0.9	35
2	When Should FAIR Begin?. , 2019, , .		1
3	NMR-STAR: comprehensive ontology for representing, archiving and exchanging data from nuclear magnetic resonance spectroscopic experiments. <i>Journal of Biomolecular NMR</i> , 2019, 73, 5-9.	2.8	32
4	Protein Data Bank: the single global archive for 3D macromolecular structure data. <i>Nucleic Acids Research</i> , 2019, 47, D520-D528.	14.5	671
5	An intrinsically disordered proteins community for ELIXIR. <i>F1000Research</i> , 2019, 8, 1753.	1.6	12
6	NMRbox: A Resource for Biomolecular NMR Computation. <i>Biophysical Journal</i> , 2017, 112, 1529-1534.	0.5	336
7	Increasing rigor in NMR-based metabolomics through validated and open source tools. <i>Current Opinion in Biotechnology</i> , 2017, 43, 56-61.	6.6	20
8	Improving protein order-disorder classification using charge-hydrophathy plots. <i>BMC Bioinformatics</i> , 2014, 15, S4.	2.6	63
9	An assignment of intrinsically disordered regions of proteins based on NMR structures. <i>Journal of Structural Biology</i> , 2013, 181, 29-36.	2.8	26
10	Exploring the binding diversity of intrinsically disordered proteins involved in one-to-many binding. <i>Protein Science</i> , 2013, 22, 258-273.	7.6	155
11	Stochastic machines as a colocalization mechanism for scaffold protein function. <i>FEBS Letters</i> , 2013, 587, 1587-1591.	2.8	40
12	D2P2: database of disordered protein predictions. <i>Nucleic Acids Research</i> , 2012, 41, D508-D516.	14.5	570
13	The HumanCyc Pathway-Genome Database and Pathway Tools Software as Tools for Imaging and Analyzing Metabolomics Data. <i>Methods in Pharmacology and Toxicology</i> , 2012, , 419-438.	0.2	1
14	Secondary Structure, a Missing Component of Sequence-Based Minimotif Definitions. <i>PLoS ONE</i> , 2012, 7, e49957.	2.5	7
15	Intrinsic protein disorder and protein-protein interactions. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2012, , 116-27.	0.7	42
16	Subclassifying disordered proteins by the CH-CDF plot method. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2012, , 128-39.	0.7	30
17	SUBCLASSIFYING DISORDERED PROTEINS BY THE CH-CDF PLOT METHOD. , 2011, , .		36
18	INTRINSIC PROTEIN DISORDER AND PROTEIN-PROTEIN INTERACTIONS. , 2011, , .		32

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19	Toxicogenomics and cancer risk assessment: A framework for key event analysis and dose-response assessment for nongenotoxic carcinogens. <i>Regulatory Toxicology and Pharmacology</i> , 2010, 58, 369-381.	2.7	31
20	Overlapping Genes Produce Proteins with Unusual Sequence Properties and Offer Insight into De Novo Protein Creation. <i>Journal of Virology</i> , 2009, 83, 10719-10736.	3.4	161
21	Intrinsic disorder in Viral Proteins Genome-Linked: experimental and predictive analyses. <i>Virology Journal</i> , 2009, 6, 23.	3.4	80
22	Intrinsic Disorder and the Evolution of Viral Overlapping Genes. <i>Biophysical Journal</i> , 2009, 96, 221a.	0.5	0
23	The unfoldomics decade: an update on intrinsically disordered proteins. <i>BMC Genomics</i> , 2008, 9, S1.	2.8	485
24	Intrinsically Disordered Proteins: An Update. , 2007, , .		1
25	Mining $\alpha$ -Helix-Forming Molecular Recognition Features with Cross Species Sequence Alignments. <i>Biochemistry</i> , 2007, 46, 13468-13477.	2.5	300
26	Intrinsic Disorder in the Protein Data Bank. <i>Journal of Biomolecular Structure and Dynamics</i> , 2007, 24, 325-341.	3.5	140
27	Conservation of Intrinsic Disorder in Protein Domains and Families: II. Functions of Conserved Disorder. <i>Journal of Proteome Research</i> , 2006, 5, 888-898.	3.7	126
28	Conservation of Intrinsic Disorder in Protein Domains and Families: I. A Database of Conserved Predicted Disordered Regions. <i>Journal of Proteome Research</i> , 2006, 5, 879-887.	3.7	124
29	Rational drug design via intrinsically disordered protein. <i>Trends in Biotechnology</i> , 2006, 24, 435-442.	9.3	225
30	Evidence supporting predicted metabolic pathways for <i>Vibrio cholerae</i> : gene expression data and clinical tests. <i>Nucleic Acids Research</i> , 2006, 34, 2438-2444.	14.5	27
31	Alternative splicing in concert with protein intrinsic disorder enables increased functional diversity in multicellular organisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 8390-8395.	7.1	428
32	Flexible nets. The roles of intrinsic disorder in protein interaction networks. <i>FEBS Journal</i> , 2005, 272, 5129-5148.	4.7	1,052
33	Coupled Folding and Binding with $\alpha$ -Helix-Forming Molecular Recognition Elements. <i>Biochemistry</i> , 2005, 44, 12454-12470.	2.5	593
34	Transcriptional Profiling of <i>Caulobacter crescentus</i> during Growth on Complex and Minimal Media. <i>Journal of Bacteriology</i> , 2004, 186, 1448-1461.	2.2	129
35	Combining prediction, computation and experiment for the characterization of protein disorder. <i>Current Opinion in Structural Biology</i> , 2004, 14, 570-576.	5.7	125
36	Natively Disordered Proteins. <i>Applied Bioinformatics</i> , 2004, 3, 105-113.	1.6	133

#	ARTICLE	IF	CITATIONS
37	Computational prediction of human metabolic pathways from the complete human genome. <i>Genome Biology</i> , 2004, 6, R2.	9.6	462
38	PseudoCyc, A Pathway-Genome Database for <i>Pseudomonas aeruginosa</i> . <i>Journal of Molecular Microbiology and Biotechnology</i> , 2003, 5, 230-239.	1.0	38
39	The Pathway Tools software. <i>Bioinformatics</i> , 2002, 18, S225-S232.	4.1	603
40	Intrinsically disordered protein. <i>Journal of Molecular Graphics and Modelling</i> , 2001, 19, 26-59.	2.4	2,005
41	Sequence complexity of disordered protein. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 42, 38-48.	2.6	1,547
42	The Genome of the Natural Genetic Engineer <i>Agrobacterium tumefaciens</i> C58. <i>Science</i> , 2001, 294, 2317-2323.	12.6	741
43	Sequence complexity of disordered protein. , 2001, 42, 38.		19
44	Intelligent Data Analysis for Protein Disorder Prediction. <i>Artificial Intelligence Review</i> , 2000, 14, 447-484.	15.7	29
45	Folding minimal sequences: the lower bound for sequence complexity of globular proteins. <i>FEBS Letters</i> , 1999, 462, 363-367.	2.8	64