

Toby James Gibson

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/7495483/toby-james-gibson-publications-by-year.pdf>

Version: 2024-04-26

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

44
papers

11,928
citations

29
h-index

46
g-index

46
ext. papers

15,435
ext. citations

13.8
avg, IF

5.98
L-index

#	Paper	IF	Citations
44	The Eukaryotic Linear Motif resource: 2022 release. <i>Nucleic Acids Research</i> , 2021 ,	20.1	10
43	Divergent Evolution of a Protein-Protein Interaction Revealed through Ancestral Sequence Reconstruction and Resurrection. <i>Molecular Biology and Evolution</i> , 2021 , 38, 152-167	8.3	2
42	Short linear motif candidates in the cell entry system used by SARS-CoV-2 and their potential therapeutic implications. <i>Science Signaling</i> , 2021 , 14,	8.8	31
41	PED in 2021: a major update of the protein ensemble database for intrinsically disordered proteins. <i>Nucleic Acids Research</i> , 2021 , 49, D404-D411	20.1	31
40	Mimicry of Short Linear Motifs by Bacterial Pathogens: A Drugging Opportunity. <i>Trends in Biochemical Sciences</i> , 2020 , 45, 526-544	10.3	15
39	ELM-the eukaryotic linear motif resource in 2020. <i>Nucleic Acids Research</i> , 2020 , 48, D296-D306	20.1	110
38	How to Annotate and Submit a Short Linear Motif to the Eukaryotic Linear Motif Resource. <i>Methods in Molecular Biology</i> , 2020 , 2141, 73-102	1.4	1
37	CiliaCarta: An integrated and validated compendium of ciliary genes. <i>PLoS ONE</i> , 2019 , 14, e0216705	3.7	47
36	An intrinsically disordered proteins community for ELIXIR. <i>F1000Research</i> , 2019 , 8,	3.6	7
35	Short linear motif core and flanking regions modulate retinoblastoma protein binding affinity and specificity. <i>Protein Engineering, Design and Selection</i> , 2018 , 31, 69-77	1.9	15
34	The eukaryotic linear motif resource - 2018 update. <i>Nucleic Acids Research</i> , 2018 , 46, D428-D434	20.1	129
33	Control of mitotic chromosome condensation by the fission yeast transcription factor Zas1. <i>Journal of Cell Biology</i> , 2018 , 217, 2383-2401	7.3	3
32	Degrans in cancer. <i>Science Signaling</i> , 2017 , 10,	8.8	58
31	The Gene Ontology of eukaryotic cilia and flagella. <i>Cilia</i> , 2017 , 6, 10	5.5	3
30	Intermolecular base stacking mediates RNA-RNA interaction in a crystal structure of the RNA chaperone Hfq. <i>Scientific Reports</i> , 2017 , 7, 9903	4.9	6
29	CTCF-Mediated Chromatin Loops between Promoter and Gene Body Regulate Alternative Splicing across Individuals. <i>Cell Systems</i> , 2017 , 5, 628-637.e6	10.6	43
28	Exploring Short Linear Motifs Using the ELM Database and Tools. <i>Current Protocols in Bioinformatics</i> , 2017 , 58, 8.22.1-8.22.35	24.2	18

27	An organelle-specific protein landscape identifies novel diseases and molecular mechanisms. <i>Nature Communications</i> , 2016 , 7, 11491	17.4	134
26	ELM 2016--data update and new functionality of the eukaryotic linear motif resource. <i>Nucleic Acids Research</i> , 2016 , 44, D294-300	20.1	222
25	Hunting for Cis-Regulatory Elements in Proteins. <i>Cell Systems</i> , 2016 , 2, 68-70	10.6	1
24	Experimental detection of short regulatory motifs in eukaryotic proteins: tips for good practice as well as for bad. <i>Cell Communication and Signaling</i> , 2015 , 13, 42	7.5	44
23	The ABBA motif binds APC/C activators and is shared by APC/C substrates and regulators. <i>Developmental Cell</i> , 2015 , 32, 358-372	10.2	109
22	NINL and DZANK1 Co-function in Vesicle Transport and Are Essential for Photoreceptor Development in Zebrafish. <i>PLoS Genetics</i> , 2015 , 11, e1005574	6	16
21	Proteome-wide analysis of human disease mutations in short linear motifs: neglected players in cancer?. <i>Molecular BioSystems</i> , 2014 , 10, 2626-42		62
20	Asymmetric mRNA localization contributes to fidelity and sensitivity of spatially localized systems. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 833-9	17.6	48
19	A million peptide motifs for the molecular biologist. <i>Molecular Cell</i> , 2014 , 55, 161-9	17.6	310
18	Short linear motifs: ubiquitous and functionally diverse protein interaction modules directing cell regulation. <i>Chemical Reviews</i> , 2014 , 114, 6733-78	68.1	254
17	The transience of transient overexpression. <i>Nature Methods</i> , 2013 , 10, 715-21	21.6	140
16	The switches.ELM resource: a compendium of conditional regulatory interaction interfaces. <i>Science Signaling</i> , 2013 , 6, rs7	8.8	83
15	Motif switches: decision-making in cell regulation. <i>Current Opinion in Structural Biology</i> , 2012 , 22, 378-858.1		107
14	RACK1 research - ships passing in the night?. <i>FEBS Letters</i> , 2012 , 586, 2787-9	3.8	34
13	Linear motifs confer functional diversity onto splice variants. <i>Nucleic Acids Research</i> , 2012 , 40, 7123-31	20.1	54
12	Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. <i>Molecular Systems Biology</i> , 2011 , 7, 539	12.2	8587
11	How viruses hijack cell regulation. <i>Trends in Biochemical Sciences</i> , 2011 , 36, 159-69	10.3	260
10	Dimerization and protein binding specificity of the U2AF homology motif of the splicing factor Puf60. <i>Journal of Biological Chemistry</i> , 2009 , 284, 630-639	5.4	49

9	Cell regulation: determined to signal discrete cooperation. <i>Trends in Biochemical Sciences</i> , 2009 , 34, 471-82.3	132
8	Multiple Sequence Alignment Using ClustalW and ClustalX 2003 , 00, 2.3.1	1
7	The SAND domain structure defines a novel DNA-binding fold in transcriptional regulation. <i>Nature Structural Biology</i> , 2001 , 8, 626-33	167
6	Gene2EST: a BLAST2 server for searching expressed sequence tag (EST) databases with eukaryotic gene-sized queries. <i>Nucleic Acids Research</i> , 2001 , 29, 1272-7	20.1 24
5	Non-muscle and smooth muscle myosin light chain kinases: no end in sight. <i>DNA Sequence</i> , 1993 , 3, 333-5	5
4	The KH domain occurs in a diverse set of RNA-binding proteins that include the antiterminator NusA and is probably involved in binding to nucleic acid. <i>FEBS Letters</i> , 1993 , 324, 361-6	3.8 174
3	Base sequence discrimination by zinc-finger DNA-binding domains. <i>Nature</i> , 1991 , 349, 175-8	50.4 265
2	Metabolic complexity in the RNA world and implications for the origin of protein synthesis. <i>Journal of Molecular Evolution</i> , 1990 , 30, 7-15	3.1 47
1	DNA-binding domain ancestry. <i>Nature</i> , 1989 , 342, 134	50.4 70