

# Toby James Gibson

## List of Publications by Year in descending order

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Version: 2024-02-01

45  
papers

17,530  
citations

159358

30  
h-index

243296

44  
g-index

46  
all docs

46  
docs citations

46  
times ranked

33397  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Eukaryotic Linear Motif resource: 2022 release. <i>Nucleic Acids Research</i> , 2022, 50, D497-D508.	6.5	144
2	PCARE requires coiled coil, RP62 kinase-binding and EVH1 domain-binding motifs for ciliary expansion. <i>Human Molecular Genetics</i> , 2022, 31, 2560-2570.	1.4	3
3	Divergent Evolution of a Protein-Protein Interaction Revealed through Ancestral Sequence Reconstruction and Resurrection. <i>Molecular Biology and Evolution</i> , 2021, 38, 152-167.	3.5	8
4	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, .	1.6	61
5	PED in 2021: a major update of the protein ensemble database for intrinsically disordered proteins. <i>Nucleic Acids Research</i> , 2021, 49, D404-D411.	6.5	95
6	ELM—the eukaryotic linear motif resource in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D296-D306.	6.5	195
7	Mimicry of Short Linear Motifs by Bacterial Pathogens: A Drugging Opportunity. <i>Trends in Biochemical Sciences</i> , 2020, 45, 526-544.	3.7	33
8	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.	0.4	3
9	CiliaCarta: An integrated and validated compendium of ciliary genes. <i>PLoS ONE</i> , 2019, 14, e0216705.	1.1	104
10	An intrinsically disordered proteins community for ELIXIR. <i>F1000Research</i> , 2019, 8, 1753.	0.8	12
11	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.	1.0	33
12	The eukaryotic linear motif resource — 2018 update. <i>Nucleic Acids Research</i> , 2018, 46, D428-D434.	6.5	183
13	Control of mitotic chromosome condensation by the fission yeast transcription factor Zas1. <i>Journal of Cell Biology</i> , 2018, 217, 2383-2401.	2.3	3
14	Degrans in cancer. <i>Science Signaling</i> , 2017, 10, .	1.6	100
15	Intermolecular base stacking mediates RNA-RNA interaction in a crystal structure of the RNA chaperone Hfq. <i>Scientific Reports</i> , 2017, 7, 9903.	1.6	14
16	CTCF-Mediated Chromatin Loops between Promoter and Gene Body Regulate Alternative Splicing across Individuals. <i>Cell Systems</i> , 2017, 5, 628-637.e6.	2.9	80
17	Exploring Short Linear Motifs Using the ELM Database and Tools. <i>Current Protocols in Bioinformatics</i> , 2017, 58, 8.22.1-8.22.35.	25.8	23
18	The Gene Ontology of eukaryotic cilia and flagella. <i>Cilia</i> , 2017, 6, 10.	1.8	6

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19	Hunting for Cis-Regulatory Elements in Proteins. <i>Cell Systems</i> , 2016, 2, 68-70.	2.9	1
20	An organelle-specific protein landscape identifies novel diseases and molecular mechanisms. <i>Nature Communications</i> , 2016, 7, 11491.	5.8	207
21	ELM 2016 data update and new functionality of the eukaryotic linear motif resource. <i>Nucleic Acids Research</i> , 2016, 44, D294-D300.	6.5	289
22	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.	2.7	58
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.	3.1	172
24	NINL and DZANK1 Co-function in Vesicle Transport and Are Essential for Photoreceptor Development in Zebrafish. <i>PLoS Genetics</i> , 2015, 11, e1005574.	1.5	23
25	Proteome-wide analysis of human disease mutations in short linear motifs: neglected players in cancer?. <i>Molecular BioSystems</i> , 2014, 10, 2626-2642.	2.9	80
26	Asymmetric mRNA localization contributes to fidelity and sensitivity of spatially localized systems. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 833-839.	3.6	57
27	A Million Peptide Motifs for the Molecular Biologist. <i>Molecular Cell</i> , 2014, 55, 161-169.	4.5	429
28	Short Linear Motifs: Ubiquitous and Functionally Diverse Protein Interaction Modules Directing Cell Regulation. <i>Chemical Reviews</i> , 2014, 114, 6733-6778.	23.0	389
29	The transience of transient overexpression. <i>Nature Methods</i> , 2013, 10, 715-721.	9.0	203
30	The switches.ELM Resource: A Compendium of Conditional Regulatory Interaction Interfaces. <i>Science Signaling</i> , 2013, 6, rs7.	1.6	101
31	Linear motifs confer functional diversity onto splice variants. <i>Nucleic Acids Research</i> , 2012, 40, 7123-7131.	6.5	65
32	RACK1 research "ships passing in the night?". <i>FEBS Letters</i> , 2012, 586, 2787-2789.	1.3	40
33	Motif switches: decision-making in cell regulation. <i>Current Opinion in Structural Biology</i> , 2012, 22, 378-385.	2.6	133
34	Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. <i>Molecular Systems Biology</i> , 2011, 7, 539.	3.2	12,778
35	How viruses hijack cell regulation. <i>Trends in Biochemical Sciences</i> , 2011, 36, 159-169.	3.7	339
36	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.	1.6	59

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37	Cell regulation: determined to signal discrete cooperation. Trends in Biochemical Sciences, 2009, 34, 471-482.	3.7	162
38	Multiple Sequence Alignment Using ClustalW and ClustalX. , 2003, 00, 2.3.1.		1
39	The SAND domain structure defines a novel DNA-binding fold in transcriptional regulation. Nature Structural Biology, 2001, 8, 626-633.	9.7	204
40	Gene2EST: a BLAST2 server for searching expressed sequence tag (EST) databases with eukaryotic gene-sized queries. Nucleic Acids Research, 2001, 29, 1272-1277.	6.5	30
41	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. FEBS Letters, 1993, 324, 361-366.	1.3	189
42	Non-muscle and smooth muscle myosin light chain kinases: no end in sight. DNA Sequence, 1993, 3, 333-335.	0.7	5
43	Base sequence discrimination by zinc-finger DNA-binding domains. Nature, 1991, 349, 175-178.	13.7	278
44	Metabolic complexity in the RNA world and implications for the origin of protein synthesis. Journal of Molecular Evolution, 1990, 30, 7-15.	0.8	53
45	DNA-binding domain ancestry. Nature, 1989, 342, 134-134.	13.7	85