

# Norman E Davey

## List of Publications by Year in descending order

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Version: 2024-02-01

58  
papers

9,032  
citations

66234

42  
h-index

133063

59  
g-index

71  
all docs

71  
docs citations

71  
times ranked

13441  
citing authors

#	ARTICLE	IF	CITATIONS
1	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. <i>Nucleic Acids Research</i> , 2022, 50, D480-D487.	6.5	117
2	The Eukaryotic Linear Motif resource: 2022 release. <i>Nucleic Acids Research</i> , 2022, 50, D497-D508.	6.5	144
3	Proteome-scale mapping of binding sites in the unstructured regions of the human proteome. <i>Molecular Systems Biology</i> , 2022, 18, e10584.	3.2	33
4	ProP-PD for proteome-wide motif-mediated interaction discovery. <i>Trends in Biochemical Sciences</i> , 2022, 47, 547-548.	3.7	11
5	MobiDB: intrinsically disordered proteins in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D361-D367.	6.5	183
6	Large scale discovery of coronavirus-host factor protein interaction motifs reveals SARS-CoV-2 specific mechanisms and vulnerabilities. <i>Nature Communications</i> , 2021, 12, 6761.	5.8	47
7	ELM—the eukaryotic linear motif resource in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D296-D306.	6.5	195
8	DisProt: intrinsic protein disorder annotation in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D269-D276.	6.5	141
9	Comprehensive Analysis of G1 Cyclin Docking Motif Sequences that Control CDK Regulatory Potency In Vivo. <i>Current Biology</i> , 2020, 30, 4454-4466.e5.	1.8	21
10	Phosphorylation-dependent substrate selectivity of protein kinase B (AKT1). <i>Journal of Biological Chemistry</i> , 2020, 295, 8120-8134.	1.6	35
11	Systematic Discovery of Short Linear Motifs Decodes Calcineurin Phosphatase Signaling. <i>Molecular Cell</i> , 2020, 79, 342-358.e12.	4.5	51
12	PP1 and PP2A Use Opposite Phospho-dependencies to Control Distinct Processes at the Kinetochore. <i>Cell Reports</i> , 2019, 28, 2206-2219.e8.	2.9	43
13	A Consensus Binding Motif for the PP4 Protein Phosphatase. <i>Molecular Cell</i> , 2019, 76, 953-964.e6.	4.5	59
14	SIRT3 controls brown fat thermogenesis by deacetylation regulation of pathways upstream of UCP1. <i>Molecular Metabolism</i> , 2019, 25, 35-49.	3.0	30
15	The functional importance of structure in unstructured protein regions. <i>Current Opinion in Structural Biology</i> , 2019, 56, 155-163.	2.6	77
16	An intrinsically disordered proteins community for ELIXIR. <i>F1000Research</i> , 2019, 8, 1753.	0.8	12
17	The Ebola Virus Nucleoprotein Recruits the Host PP2A-B56 Phosphatase to Activate Transcriptional Support Activity of VP30. <i>Molecular Cell</i> , 2018, 69, 136-145.e6.	4.5	76
18	The eukaryotic linear motif resource — 2018 update. <i>Nucleic Acids Research</i> , 2018, 46, D428-D434.	6.5	183

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19	A Screen for Candidate Targets of Lysine Polyphosphorylation Uncovers a Conserved Network Implicated in Ribosome Biogenesis. <i>Cell Reports</i> , 2018, 22, 3427-3439.	2.9	61
20	MobiDB 3.0: more annotations for intrinsic disorder, conformational diversity and interactions in proteins. <i>Nucleic Acids Research</i> , 2018, 46, D471-D476.	6.5	190
21	PSSMSearch: a server for modeling, visualization, proteome-wide discovery and annotation of protein motif specificity determinants. <i>Nucleic Acids Research</i> , 2018, 46, W235-W241.	6.5	54
22	DisProt 7.0: a major update of the database of disordered proteins. <i>Nucleic Acids Research</i> , 2017, 45, D219-D227.	6.5	242
23	Peptigram: A Web-Based Application for Peptidomics Data Visualization. <i>Journal of Proteome Research</i> , 2017, 16, 712-719.	1.8	73
24	Discovery of short linear motif-mediated interactions through phage display of intrinsically disordered regions of the human proteome. <i>FEBS Journal</i> , 2017, 284, 485-498.	2.2	81
25	SLIMSearch: a framework for proteome-wide discovery and annotation of functional modules in intrinsically disordered regions. <i>Nucleic Acids Research</i> , 2017, 45, W464-W469.	6.5	87
26	The Mitotic Checkpoint Complex Requires an Evolutionary Conserved Cassette to Bind and Inhibit Active APC/C. <i>Molecular Cell</i> , 2016, 64, 1144-1153.	4.5	43
27	Building a Regulatory Network with Short Linear Sequence Motifs: Lessons from the Degrons of the Anaphase-Promoting Complex. <i>Molecular Cell</i> , 2016, 64, 12-23.	4.5	132
28	A Conserved Motif Provides Binding Specificity to the PP2A-B56 Phosphatase. <i>Molecular Cell</i> , 2016, 63, 686-695.	4.5	235
29	ProViz—a web-based visualization tool to investigate the functional and evolutionary features of protein sequences. <i>Nucleic Acids Research</i> , 2016, 44, W11-W15.	6.5	68
30	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
31	Short linear motifs — ex nihilo evolution of protein regulation. <i>Cell Communication and Signaling</i> , 2015, 13, 43.	2.7	171
32	Motif co-regulation and co-operativity are common mechanisms in transcriptional, post-transcriptional and post-translational regulation. <i>Cell Communication and Signaling</i> , 2015, 13, 45.	2.7	21
33	Acetylome Profiling Reveals Overlap in the Regulation of Diverse Processes by Sirtuins, Gcn5, and Esa1. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 162-176.	2.5	59
34	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
35	The HIV Mutation Browser: A Resource for Human Immunodeficiency Virus Mutagenesis and Polymorphism Data. <i>PLoS Computational Biology</i> , 2014, 10, e1003951.	1.5	25
36	The eukaryotic linear motif resource ELM: 10 years and counting. <i>Nucleic Acids Research</i> , 2014, 42, D259-D266.	6.5	260

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37	Multiple mechanisms determine the order of APC/C substrate degradation in mitosis. <i>Journal of Cell Biology</i> , 2014, 207, 23-39.	2.3	68
38	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
39	A Million Peptide Motifs for the Molecular Biologist. <i>Molecular Cell</i> , 2014, 55, 161-169.	4.5	429
40	Short Linear Motifs: Ubiquitous and Functionally Diverse Protein Interaction Modules Directing Cell Regulation. <i>Chemical Reviews</i> , 2014, 114, 6733-6778.	23.0	389
41	The switches.ELM Resource: A Compendium of Conditional Regulatory Interaction Interfaces. <i>Science Signaling</i> , 2013, 6, rs7.	1.6	101
42	ELM—the database of eukaryotic linear motifs. <i>Nucleic Acids Research</i> , 2012, 40, D242-D251.	6.5	290
43	Linear motifs confer functional diversity onto splice variants. <i>Nucleic Acids Research</i> , 2012, 40, 7123-7131.	6.5	65
44	SLiMPrints: conservation-based discovery of functional motif fingerprints in intrinsically disordered protein regions. <i>Nucleic Acids Research</i> , 2012, 40, 10628-10641.	6.5	92
45	Attributes of short linear motifs. <i>Molecular BioSystems</i> , 2012, 8, 268-281.	2.9	502
46	Insights into RNA Biology from an Atlas of Mammalian mRNA-Binding Proteins. <i>Cell</i> , 2012, 149, 1393-1406.	13.5	1,765
47	A Proteome-wide Screen for Mammalian SxIP Motif-Containing Microtubule Plus-End Tracking Proteins. <i>Current Biology</i> , 2012, 22, 1800-1807.	1.8	192
48	Interactome-wide prediction of short, disordered protein interaction motifs in humans. <i>Molecular BioSystems</i> , 2012, 8, 282-295.	2.9	30
49	Motif switches: decision-making in cell regulation. <i>Current Opinion in Structural Biology</i> , 2012, 22, 378-385.	2.6	133
50	How viruses hijack cell regulation. <i>Trends in Biochemical Sciences</i> , 2011, 36, 159-169.	3.7	339
51	SLiMSearch 2.0: biological context for short linear motifs in proteins. <i>Nucleic Acids Research</i> , 2011, 39, W56-W60.	6.5	68
52	Computational identification and analysis of protein short linear motifs. <i>Frontiers in Bioscience - Landmark</i> , 2010, 15, 801.	3.0	34
53	ELM: the status of the 2010 eukaryotic linear motif resource. <i>Nucleic Acids Research</i> , 2010, 38, D167-D180.	6.5	217
54	SLiMFinder: a web server to find novel, significantly over-represented, short protein motifs. <i>Nucleic Acids Research</i> , 2010, 38, W534-W539.	6.5	64

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55	Masking residues using context-specific evolutionary conservation significantly improves short linear motif discovery. <i>Bioinformatics</i> , 2009, 25, 443-450.	1.8	60
56	CompariMotif: quick and easy comparisons of sequence motifs. <i>Bioinformatics</i> , 2008, 24, 1307-1309.	1.8	47
57	The SLiMDisc server: short, linear motif discovery in proteins. <i>Nucleic Acids Research</i> , 2007, 35, W455-W459.	6.5	51
58	SLiMFinder: A Probabilistic Method for Identifying Over-Represented, Convergently Evolved, Short Linear Motifs in Proteins. <i>PLoS ONE</i> , 2007, 2, e967.	1.1	143