

Erich E Wanker

List of Publications by Year in descending order

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76
papers

14,802
citations

66234

42
h-index

71532

76
g-index

80
all docs

80
docs citations

80
times ranked

17759
citing authors

#	ARTICLE	IF	CITATIONS
1	A Human Protein-Protein Interaction Network: A Resource for Annotating the Proteome. <i>Cell</i> , 2005, 122, 957-968.	13.5	2,169
2	Formation of Neuronal Intranuclear Inclusions Underlies the Neurological Dysfunction in Mice Transgenic for the HD Mutation. <i>Cell</i> , 1997, 90, 537-548.	13.5	2,105
3	EGCG redirects amyloidogenic polypeptides into unstructured, off-pathway oligomers. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 558-566.	3.6	1,249
4	Huntingtin-Encoded Polyglutamine Expansions Form Amyloid-like Protein Aggregates In Vitro and In Vivo. <i>Cell</i> , 1997, 90, 549-558.	13.5	1,224
5	EGCG remodels mature β -synuclein and amyloid- β fibrils and reduces cellular toxicity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 7710-7715.	3.3	888
6	An empirical framework for binary interactome mapping. <i>Nature Methods</i> , 2009, 6, 83-90.	9.0	800
7	Accumulation of Mutant Huntingtin Fragments in Aggresome-like Inclusion Bodies as a Result of Insufficient Protein Degradation. <i>Molecular Biology of the Cell</i> , 2001, 12, 1393-1407.	0.9	583
8	The hunt for huntingtin function: interaction partners tell many different stories. <i>Trends in Biochemical Sciences</i> , 2003, 28, 425-433.	3.7	456
9	Small-molecule conversion of toxic oligomers to nontoxic β -sheet-rich amyloid fibrils. <i>Nature Chemical Biology</i> , 2012, 8, 93-101.	3.9	400
10	A Protein Interaction Network Links GIT1, an Enhancer of Huntingtin Aggregation, to Huntington's Disease. <i>Molecular Cell</i> , 2004, 15, 853-865.	4.5	398
11	Green tea (β -epigallocatechin-gallate) modulates early events in huntingtin misfolding and reduces toxicity in Huntington's disease models. <i>Human Molecular Genetics</i> , 2006, 15, 2743-2751.	1.4	357
12	A Directed Protein Interaction Network for Investigating Intracellular Signal Transduction. <i>Science Signaling</i> , 2011, 4, rs8.	1.6	313
13	HIPPIE: Integrating Protein Interaction Networks with Experiment Based Quality Scores. <i>PLoS ONE</i> , 2012, 7, e31826.	1.1	297
14	[24] Membrane filter assay for detection of amyloid-like polyglutamine-containing protein aggregates. <i>Methods in Enzymology</i> , 1999, 309, 375-386.	0.4	217
15	SH3GL3 Associates with the Huntingtin Exon 1 Protein and Promotes the Formation of PolyIn-Containing Protein Aggregates. <i>Molecular Cell</i> , 1998, 2, 427-436.	4.5	208
16	Identification of benzothiazoles as potential polyglutamine aggregation inhibitors of Huntington's disease by using an automated filter retardation assay. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 16400-16406.	3.3	199
17	The green tea polyphenol (β -epigallocatechin gallate) prevents the aggregation of tau protein into toxic oligomers at substoichiometric ratios. <i>FEBS Letters</i> , 2015, 589, 77-83.	1.3	172
18	Evolution and function of CAG/polyglutamine repeats in protein-protein interaction networks. <i>Nucleic Acids Research</i> , 2012, 40, 4273-4287.	6.5	166

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19	An arginine/lysine-rich motif is crucial for VCP/p97-mediated modulation of ataxin-3 fibrillogenesis. <i>EMBO Journal</i> , 2006, 25, 1547-1558.	3.5	142
20	Protein Aggregation and Pathogenesis of Huntingtons Disease: Mechanisms and Correlations. <i>Biological Chemistry</i> , 2000, 381, 937-942.	1.2	134
21	Human iPSC-Derived Neural Progenitors Are an Effective Drug Discovery Model for Neurological mtDNA Disorders. <i>Cell Stem Cell</i> , 2017, 20, 659-674.e9.	5.2	126
22	Mutant Huntingtin Promotes the Fibrillogenesis of Wild-type Huntingtin. <i>Journal of Biological Chemistry</i> , 2003, 278, 41452-41461.	1.6	107
23	Ataxin-3 is transported into the nucleus and associates with the nuclear matrix. <i>Human Molecular Genetics</i> , 1998, 7, 991-997.	1.4	104
24	The value of high quality protein-protein interaction networks for systems biology. <i>Current Opinion in Chemical Biology</i> , 2006, 10, 551-558.	2.8	100
25	A Y2H-seq approach defines the human protein methyltransferase interactome. <i>Nature Methods</i> , 2013, 10, 339-342.	9.0	99
26	Amyloid- β (1-42) Aggregation Initiates Its Cellular Uptake and Cytotoxicity. <i>Journal of Biological Chemistry</i> , 2016, 291, 19590-19606.	1.6	91
27	Quantitative Interaction Proteomics of Neurodegenerative Disease Proteins. <i>Cell Reports</i> , 2015, 11, 1134-1146.	2.9	88
28	Translation of HTT mRNA with expanded CAG repeats is regulated by the MID1-PP2A protein complex. <i>Nature Communications</i> , 2013, 4, 1511.	5.8	84
29	Epigallocatechin-3-gallate: a useful, effective and safe clinical approach for targeted prevention and individualised treatment of neurological diseases?. <i>EPMA Journal</i> , 2013, 4, 5.	3.3	80
30	The pathobiology of perturbed mutant huntingtin protein-protein interactions in Huntington's disease. <i>Journal of Neurochemistry</i> , 2019, 151, 507-519.	2.1	70
31	Interactome Mapping Provides a Network of Neurodegenerative Disease Proteins and Uncovers Widespread Protein Aggregation in Affected Brains. <i>Cell Reports</i> , 2020, 32, 108050.	2.9	64
32	Metformin reverses early cortical network dysfunction and behavior changes in Huntington's disease. <i>ELife</i> , 2018, 7, .	2.8	64
33	Detection of Alpha-Rod Protein Repeats Using a Neural Network and Application to Huntingtin. <i>PLoS Computational Biology</i> , 2009, 5, e1000304.	1.5	59
34	Modulation of human IAPP fibrillation: cosolutes, crowders and chaperones. <i>Physical Chemistry Chemical Physics</i> , 2015, 17, 8338-8348.	1.3	59
35	UniHI 4: new tools for query, analysis and visualization of the human protein-protein interactome. <i>Nucleic Acids Research</i> , 2009, 37, D657-D660.	6.5	58
36	The palmitoyl acyltransferase HIP14 shares a high proportion of interactors with huntingtin: implications for a role in the pathogenesis of Huntington's disease. <i>Human Molecular Genetics</i> , 2014, 23, 4142-4160.	1.4	58

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37	Maximizing binary interactome mapping with a minimal number of assays. <i>Nature Communications</i> , 2019, 10, 3907.	5.8	57
38	Defective metabolic programming impairs early neuronal morphogenesis in neural cultures and an organoid model of Leigh syndrome. <i>Nature Communications</i> , 2021, 12, 1929.	5.8	55
39	mHTT Seeding Activity: A Marker of Disease Progression and Neurotoxicity in Models of Huntington's Disease. <i>Molecular Cell</i> , 2018, 71, 675-688.e6.	4.5	50
40	Inhibition of Huntingtin Exon-1 Aggregation by the Molecular Tweezer CLR01. <i>Journal of the American Chemical Society</i> , 2017, 139, 5640-5643.	6.6	49
41	Identification of VCP/p97, Carboxyl Terminus of Hsp70-interacting Protein (CHIP), and Amphiphysin II Interaction Partners Using Membrane-based Human Proteome Arrays. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 234-244.	2.5	48
42	Prion-like proteins sequester and suppress the toxicity of huntingtin exon 1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 12085-12090.	3.3	47
43	Phosphorylation-regulated axonal dependent transport of syntaxin 1 is mediated by a Kinesin-1 adapter. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5862-5867.	3.3	44
44	An integer programming framework for inferring disease complexes from network data. <i>Bioinformatics</i> , 2016, 32, i271-i277.	1.8	44
45	Multiplex approaches in protein microarray technology. <i>Expert Review of Proteomics</i> , 2005, 2, 499-510.	1.3	39
46	Aggregation of polyQ-extended proteins is promoted by interaction with their natural coiled-coil partners. <i>BioEssays</i> , 2013, 35, 503-507.	1.2	39
47	Mixing A ¹² (1-40) and A ¹² (1-42) peptides generates unique amyloid fibrils. <i>Chemical Communications</i> , 2020, 56, 8830-8833.	2.2	39
48	Aggregation of Full-length Immunoglobulin Light Chains from Systemic Light Chain Amyloidosis (AL) Patients Is Remodeled by Epigallocatechin-3-gallate. <i>Journal of Biological Chemistry</i> , 2017, 292, 2328-2344.	1.6	37
49	Quantitative interaction mapping reveals an extended UBX domain in ASPL that disrupts functional p97 hexamers. <i>Nature Communications</i> , 2016, 7, 13047.	5.8	35
50	Self-assembly of Mutant Huntingtin Exon-1 Fragments into Large Complex Fibrillar Structures Involves Nucleated Branching. <i>Journal of Molecular Biology</i> , 2018, 430, 1725-1744.	2.0	35
51	Subcellular Localization And Formation Of Huntingtin Aggregates Correlates With Symptom Onset And Progression In A Huntington's Disease Model. <i>Brain Communications</i> , 2020, 2, fcaa066.	1.5	34
52	Lu <sc>TH</sc> y: a double-readout bioluminescence-based two-hybrid technology for quantitative mapping of protein-protein interactions in mammalian cells. <i>Molecular Systems Biology</i> , 2018, 14, e8071.	3.2	31
53	Identification of Human Proteins That Modify Misfolding and Proteotoxicity of Pathogenic Ataxin-1. <i>PLoS Genetics</i> , 2012, 8, e1002897.	1.5	29
54	DULIP: A Dual Luminescence-Based Co-Immunoprecipitation Assay for Interactome Mapping in Mammalian Cells. <i>Journal of Molecular Biology</i> , 2015, 427, 3375-3388.	2.0	28

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55	Current Approaches Toward Quantitative Mapping of the Interactome. <i>Frontiers in Genetics</i> , 2016, 7, 74.	1.1	28
56	Interleukin-12/23 deficiency differentially affects pathology in male and female Alzheimer's disease-like mice. <i>EMBO Reports</i> , 2020, 21, e48530.	2.0	24
57	The E3 Ubiquitin Ligase MID1 Catalyzes Ubiquitination and Cleavage of Fu. <i>Journal of Biological Chemistry</i> , 2014, 289, 31805-31817.	1.6	23
58	Development and application of a DNA microarray-based yeast two-hybrid system. <i>Nucleic Acids Research</i> , 2013, 41, 1496-1507.	6.5	19
59	Identification of the Mitochondrial MSRB2 as a Binding Partner of LG72. <i>Cellular and Molecular Neurobiology</i> , 2014, 34, 1123-1130.	1.7	18
60	DCAF8, a novel MuRF1 interaction partner, promotes muscle atrophy. <i>Journal of Cell Science</i> , 2019, 132, .	1.2	17
61	Shedding a new light on Huntington's disease: how blood can both propagate and ameliorate disease pathology. <i>Molecular Psychiatry</i> , 2021, 26, 5441-5463.	4.1	16
62	Dynamics of huntingtin protein interactions in the striatum identifies candidate modifiers of Huntington disease. <i>Cell Systems</i> , 2022, 13, 304-320.e5.	2.9	15
63	Pathogenic Polyglutamine Tracts Are Potent Inducers of Spontaneous Sup35 and Rnq1 Amyloidogenesis. <i>PLoS ONE</i> , 2010, 5, e9642.	1.1	14
64	Identification of an RNA Polymerase III Regulator Linked to Disease-Associated Protein Aggregation. <i>Molecular Cell</i> , 2017, 65, 1096-1108.e6.	4.5	14
65	Sclerotiorin Stabilizes the Assembly of Nonfibrillar Abeta42 Oligomers with Low Toxicity, Seeding Activity, and Beta-sheet Content. <i>Journal of Molecular Biology</i> , 2020, 432, 2080-2098.	2.0	12
66	Spontaneous self-assembly of pathogenic huntingtin exon 1 protein into amyloid structures. <i>Essays in Biochemistry</i> , 2014, 56, 167-180.	2.1	12
67	FEZ1 Forms Complexes with CRMP1 and DCC to Regulate Axon and Dendrite Development. <i>ENeuro</i> , 2021, 8, ENEURO.0193-20.2021.	0.9	11
68	A functionally defined high-density NRF2 interactome reveals new conditional regulators of ARE transactivation. <i>Redox Biology</i> , 2020, 37, 101686.	3.9	10
69	The Anti-amyloid Compound DO1 Decreases Plaque Pathology and Neuroinflammation-Related Expression Changes in 5xFAD Transgenic Mice. <i>Cell Chemical Biology</i> , 2019, 26, 109-120.e7.	2.5	8
70	Small, Seeding-Competent Huntingtin Fibrils Are Prominent Aggregate Species in Brains of zQ175 Huntingtin's Disease Knock-in Mice. <i>Frontiers in Neuroscience</i> , 2021, 15, 682172.	1.4	7
71	Assessment of Ethanol-Induced Toxicity on iPSC-Derived Human Neurons Using a Novel High-Throughput Mitochondrial Neuronal Health (MNH) Assay. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 590540.	1.8	6
72	Schizophrenia risk candidate protein ZNF804A interacts with STAT2 and influences interferon-mediated gene transcription in mammalian cells. <i>Journal of Molecular Biology</i> , 2021, 433, 167184.	2.0	6

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73	A Filter Retardation Assay Facilitates the Detection and Quantification of Heat-Stable, Amyloidogenic Mutant Huntingtin Aggregates in Complex Biosamples. <i>Methods in Molecular Biology</i> , 2018, 1780, 31-40.	0.4	5
74	Flexible web-based integration of distributed large-scale human protein interaction maps. <i>Journal of Integrative Bioinformatics</i> , 2007, 4, 40-50.	1.0	3
75	CellFIE: CRISPR- and Cell Fusion-based Two-hybrid Interaction Mapping of Endogenous Proteins. <i>Journal of Molecular Biology</i> , 2021, 433, 167305.	2.0	0
76	<i>Klinische Proteomik.</i> , 2008, , 297-313.		0