

Erich E Wanker

List of Publications by Year in Descending Order

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

76
papers

12,436
citations

37
h-index

80
g-index

80
ext. papers

13,810
ext. citations

11
avg, IF

5.62
L-index

#	Paper	IF	Citations
76	Dynamics of huntingtin protein interactions in the striatum identifies candidate modifiers of Huntington disease.. <i>Cell Systems</i> , 2022 ,	10.6	1
75	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	15.1	8
74	CellFIE: CRISPR- and Cell Fusion-based Two-hybrid Interaction Mapping of Endogenous Proteins. <i>Journal of Molecular Biology</i> , 2021 , 433, 167305	6.5	
73	Defective metabolic programming impairs early neuronal morphogenesis in neural cultures and an organoid model of Leigh syndrome. <i>Nature Communications</i> , 2021 , 12, 1929	17.4	17
72	Small, Seeding-Competent Huntingtin Fibrils Are Prominent Aggregate Species in Brains of zQ175 Huntington's Disease Knock-in Mice. <i>Frontiers in Neuroscience</i> , 2021 , 15, 682172	5.1	2
71	FEZ1 Forms Complexes with CRMP1 and DCC to Regulate Axon and Dendrite Development. <i>ENeuro</i> , 2021 , 8,	3.9	3
70	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	6.5	0
69	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	4.5	16
68	Mixing A β (1-40) and A β (1-42) peptides generates unique amyloid fibrils. <i>Chemical Communications</i> , 2020 , 56, 8830-8833	5.8	13
67	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	6.5	4
66	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	5.7	2
65	Interactome Mapping Provides a Network of Neurodegenerative Disease Proteins and Uncovers Widespread Protein Aggregation in Affected Brains. <i>Cell Reports</i> , 2020 , 32, 108050	10.6	20
64	A functionally defined high-density NRF2 interactome reveals new conditional regulators of ARE transactivation. <i>Redox Biology</i> , 2020 , 37, 101686	11.3	4
63	Interleukin-12/23 deficiency differentially affects pathology in male and female Alzheimer's disease-like mice. <i>EMBO Reports</i> , 2020 , 21, e48530	6.5	11
62	DCAF8, a novel MuRF1 interaction partner, promotes muscle atrophy. <i>Journal of Cell Science</i> , 2019 , 132,	5.3	12
61	Maximizing binary interactome mapping with a minimal number of assays. <i>Nature Communications</i> , 2019 , 10, 3907	17.4	21
60	The pathobiology of perturbed mutant huntingtin protein-protein interactions in Huntington's disease. <i>Journal of Neurochemistry</i> , 2019 , 151, 507-519	6	31

59	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	8.2	6
58	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	6.5	22
57	LuTHY: 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	12.2	15
56	Metformin reverses early cortical network dysfunction and behavior changes in Huntington's disease. <i>ELife</i> , 2018 , 7,	8.9	37
55	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	17.6	33
54	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	1.4	4
53	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	18	84
52	Inhibition of Huntingtin Exon-1 Aggregation by the Molecular Tweezer CLR01. <i>Journal of the American Chemical Society</i> , 2017 , 139, 5640-5643	16.4	34
51	Identification of an RNA Polymerase III Regulator Linked to Disease-Associated Protein Aggregation. <i>Molecular Cell</i> , 2017 , 65, 1096-1108.e6	17.6	7
50	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 ²⁶	5.4	26
49	Quantitative interaction mapping reveals an extended UBX domain in ASPL that disrupts functional p97 hexamers. <i>Nature Communications</i> , 2016 , 7, 13047	17.4	15
48	An integer programming framework for inferring disease complexes from network data. <i>Bioinformatics</i> , 2016 , 32, i271-i277	7.2	37
47	Current Approaches Toward Quantitative Mapping of the Interactome. <i>Frontiers in Genetics</i> , 2016 , 7, 74	4.5	18
46	Amyloid- β (1-42) Aggregation Initiates Its Cellular Uptake and Cytotoxicity. <i>Journal of Biological Chemistry</i> , 2016 , 291, 19590-606	5.4	61
45	Quantitative interaction proteomics of neurodegenerative disease proteins. <i>Cell Reports</i> , 2015 , 11, 1134-1146	11.6	62
44	DULIP: A Dual Luminescence-Based Co-Immunoprecipitation Assay for Interactome Mapping in Mammalian Cells. <i>Journal of Molecular Biology</i> , 2015 , 427, 3375-88	6.5	21
43	The green tea polyphenol (-)-epigallocatechin gallate prevents the aggregation of tau protein into toxic oligomers at substoichiometric ratios. <i>FEBS Letters</i> , 2015 , 589, 77-83	3.8	134
42	Modulation of human IAPP fibrillation: cosolutes, crowders and chaperones. <i>Physical Chemistry Chemical Physics</i> , 2015 , 17, 8338-48	3.6	48

41	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, 12085-90	11.5	44
40	Identification of the mitochondrial MSRB2 as a binding partner of LG72. <i>Cellular and Molecular Neurobiology</i> , 2014 , 34, 1123-30	4.6	16
39	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, 4142-60	5.6	44
38	The E3 ubiquitin ligase MID1 catalyzes ubiquitination and cleavage of Fu. <i>Journal of Biological Chemistry</i> , 2014 , 289, 31805-31817	5.4	17
37	Spontaneous self-assembly of pathogenic huntingtin exon 1 protein into amyloid structures. <i>Essays in Biochemistry</i> , 2014 , 56, 167-80	7.6	12
36	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	8.8	60
35	Aggregation of polyQ-extended proteins is promoted by interaction with their natural coiled-coil partners. <i>BioEssays</i> , 2013 , 35, 503-7	4.1	28
34	Translation of HTT mRNA with expanded CAG repeats is regulated by the MID1-PP2A protein complex. <i>Nature Communications</i> , 2013 , 4, 1511	17.4	66
33	A Y2H-seq approach defines the human protein methyltransferase interactome. <i>Nature Methods</i> , 2013 , 10, 339-42	21.6	73
32	Development and application of a DNA microarray-based yeast two-hybrid system. <i>Nucleic Acids Research</i> , 2013 , 41, 1496-507	20.1	15
31	Evolution and function of CAG/polyglutamine repeats in protein-protein interaction networks. <i>Nucleic Acids Research</i> , 2012 , 40, 4273-87	20.1	132
30	Identification of human proteins that modify misfolding and proteotoxicity of pathogenic ataxin-1. <i>PLoS Genetics</i> , 2012 , 8, e1002897	6	23
29	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, 5862-7	11.5	33
28	HIPPIE: Integrating protein interaction networks with experiment based quality scores. <i>PLoS ONE</i> , 2012 , 7, e31826	3.7	235
27	Small-molecule conversion of toxic oligomers to nontoxic β -sheet-rich amyloid fibrils. <i>Nature Chemical Biology</i> , 2011 , 8, 93-101	11.7	337
26	A directed protein interaction network for investigating intracellular signal transduction. <i>Science Signaling</i> , 2011 , 4, rs8	8.8	248
25	Pathogenic polyglutamine tracts are potent inducers of spontaneous Sup35 and Rnq1 amyloidogenesis. <i>PLoS ONE</i> , 2010 , 5, e9642	3.7	13
24	EGCG remodels mature alpha-synuclein and amyloid-beta fibrils and reduces cellular toxicity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 7710-5	11.5	726

23	UniHI 4: new tools for query, analysis and visualization of the human protein-protein interactome. <i>Nucleic Acids Research</i> , 2009 , 37, D657-60	20.1	56
22	Detection of alpha-rod protein repeats using a neural network and application to huntingtin. <i>PLoS Computational Biology</i> , 2009 , 5, e1000304	5	50
21	An empirical framework for binary interactome mapping. <i>Nature Methods</i> , 2009 , 6, 83-90	21.6	674
20	EGCG redirects amyloidogenic polypeptides into unstructured, off-pathway oligomers. <i>Nature Structural and Molecular Biology</i> , 2008 , 15, 558-66	17.6	1065
19	Klinische Proteomik 2008 , 297-313		
18	Flexible web-based integration of distributed large-scale human protein interaction maps. <i>Journal of Integrative Bioinformatics</i> , 2007 , 4, 40-50	3.8	2
17	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, 234-44	7.6	41
16	Green tea (-)-epigallocatechin-gallate modulates early events in huntingtin misfolding and reduces toxicity in Huntington's disease models. <i>Human Molecular Genetics</i> , 2006 , 15, 2743-51	5.6	318
15	An arginine/lysine-rich motif is crucial for VCP/p97-mediated modulation of ataxin-3 fibrillogenesis. <i>EMBO Journal</i> , 2006 , 25, 1547-58	13	131
14	The value of high quality protein-protein interaction networks for systems biology. <i>Current Opinion in Chemical Biology</i> , 2006 , 10, 551-8	9.7	80
13	Multiplex approaches in protein microarray technology. <i>Expert Review of Proteomics</i> , 2005 , 2, 499-510	4.2	33
12	A human protein-protein interaction network: a resource for annotating the proteome. <i>Cell</i> , 2005 , 122, 957-68	56.2	1848
11	A protein interaction network links GIT1, an enhancer of huntingtin aggregation, to Huntington's disease. <i>Molecular Cell</i> , 2004 , 15, 853-65	17.6	345
10	Mutant huntingtin promotes the fibrillogenesis of wild-type huntingtin: a potential mechanism for loss of huntingtin function in Huntington's disease. <i>Journal of Biological Chemistry</i> , 2003 , 278, 41452-61	5.4	95
9	The hunt for huntingtin function: interaction partners tell many different stories. <i>Trends in Biochemical Sciences</i> , 2003 , 28, 425-33	10.3	401
8	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 Suppl 4, 16400-6	11.5	182
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, 1393-407	3.5	544
6	Protein aggregation and pathogenesis of Huntington's disease: mechanisms and correlations. <i>Biological Chemistry</i> , 2000 , 381, 937-42	4.5	118

5	Membrane filter assay for detection of amyloid-like polyglutamine-containing protein aggregates. <i>Methods in Enzymology</i> , 1999 , 309, 375-86	1.7	193
4	SH3GL3 associates with the Huntingtin exon 1 protein and promotes the formation of polyglu-containing protein aggregates. <i>Molecular Cell</i> , 1998 , 2, 427-36	17.6	189
3	Ataxin-3 is transported into the nucleus and associates with the nuclear matrix. <i>Human Molecular Genetics</i> , 1998 , 7, 991-7	5.6	86
2	Formation of neuronal intranuclear inclusions underlies the neurological dysfunction in mice transgenic for the HD mutation. <i>Cell</i> , 1997 , 90, 537-48	56.2	1918
1	Huntingtin-encoded polyglutamine expansions form amyloid-like protein aggregates in vitro and in vivo. <i>Cell</i> , 1997 , 90, 549-58	56.2	1114