

Erich E Wanker

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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	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
75	A human protein-protein interaction network: a resource for annotating the proteome. <i>Cell</i> , 2005 , 122, 957-68	56.2	1848
74	Huntingtin-encoded polyglutamine expansions form amyloid-like protein aggregates in vitro and in vivo. <i>Cell</i> , 1997 , 90, 549-58	56.2	1114
73	EGCG redirects amyloidogenic polypeptides into unstructured, off-pathway oligomers. <i>Nature Structural and Molecular Biology</i> , 2008 , 15, 558-66	17.6	1065
72	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
71	An empirical framework for binary interactome mapping. <i>Nature Methods</i> , 2009 , 6, 83-90	21.6	674
70	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
69	The hunt for huntingtin function: interaction partners tell many different stories. <i>Trends in Biochemical Sciences</i> , 2003 , 28, 425-33	10.3	401
68	A protein interaction network links GIT1, an enhancer of huntingtin aggregation, to Huntington ^Δ disease. <i>Molecular Cell</i> , 2004 , 15, 853-65	17.6	345
67	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
66	Green tea (-)-epigallocatechin-gallate modulates early events in huntingtin misfolding and reduces toxicity in Huntington ^Δ disease models. <i>Human Molecular Genetics</i> , 2006 , 15, 2743-51	5.6	318
65	A directed protein interaction network for investigating intracellular signal transduction. <i>Science Signaling</i> , 2011 , 4, rs8	8.8	248
64	HIPPIE: Integrating protein interaction networks with experiment based quality scores. <i>PLoS ONE</i> , 2012 , 7, e31826	3.7	235
63	Membrane filter assay for detection of amyloid-like polyglutamine-containing protein aggregates. <i>Methods in Enzymology</i> , 1999 , 309, 375-86	1.7	193
62	SH3GL3 associates with the Huntingtin exon 1 protein and promotes the formation of polygluN-containing protein aggregates. <i>Molecular Cell</i> , 1998 , 2, 427-36	17.6	189
61	Identification of benzothiazoles as potential polyglutamine aggregation inhibitors of Huntington ^Δ 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
60	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

59	Evolution and function of CAG/polyglutamine repeats in protein-protein interaction networks. <i>Nucleic Acids Research</i> , 2012 , 40, 4273-87	20.1	132
58	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
57	Protein aggregation and pathogenesis of Huntington's disease: mechanisms and correlations. <i>Biological Chemistry</i> , 2000 , 381, 937-42	4.5	118
56	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
55	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
54	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
53	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
52	A Y2H-seq approach defines the human protein methyltransferase interactome. <i>Nature Methods</i> , 2013 , 10, 339-42	21.6	73
51	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
50	Quantitative interaction proteomics of neurodegenerative disease proteins. <i>Cell Reports</i> , 2015 , 11, 1134-1146	14.6	62
49	Amyloid- β (1-42) Aggregation Initiates Its Cellular Uptake and Cytotoxicity. <i>Journal of Biological Chemistry</i> , 2016 , 291, 19590-606	5.4	61
48	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
47	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
46	Detection of alpha-rod protein repeats using a neural network and application to huntingtin. <i>PLoS Computational Biology</i> , 2009 , 5, e1000304	5	50
45	Modulation of human IAPP fibrillation: cosolutes, crowders and chaperones. <i>Physical Chemistry Chemical Physics</i> , 2015 , 17, 8338-48	3.6	48
44	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
43	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
42	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

41	An integer programming framework for inferring disease complexes from network data. <i>Bioinformatics</i> , 2016 , 32, i271-i277	7.2	37
40	Metformin reverses early cortical network dysfunction and behavior changes in Huntington's disease. <i>ELife</i> , 2018 , 7,	8.9	37
39	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
38	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	11.5	33
37	Multiplex approaches in protein microarray technology. <i>Expert Review of Proteomics</i> , 2005 , 2, 499-510	4.2	33
36	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
35	The pathobiology of perturbed mutant huntingtin protein-protein interactions in Huntington's disease. <i>Journal of Neurochemistry</i> , 2019 , 151, 507-519	6	31
34	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
33	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	5.4	26
32	Identification of human proteins that modify misfolding and proteotoxicity of pathogenic ataxin-1. <i>PLoS Genetics</i> , 2012 , 8, e1002897	6	23
31	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
30	Maximizing binary interactome mapping with a minimal number of assays. <i>Nature Communications</i> , 2019 , 10, 3907	17.4	21
29	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
28	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
27	Current Approaches Toward Quantitative Mapping of the Interactome. <i>Frontiers in Genetics</i> , 2016 , 7, 74	4.5	18
26	The E3 ubiquitin ligase MID1 catalyzes ubiquitination and cleavage of Fu. <i>Journal of Biological Chemistry</i> , 2014 , 289, 31805-31817	5.4	17
25	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
24	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

23	Identification of the mitochondrial MSRB2 as a binding partner of LG72. <i>Cellular and Molecular Neurobiology</i> , 2014 , 34, 1123-30	4.6	16
22	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
21	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
20	Development and application of a DNA microarray-based yeast two-hybrid system. <i>Nucleic Acids Research</i> , 2013 , 41, 1496-507	20.1	15
19	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
18	Pathogenic polyglutamine tracts are potent inducers of spontaneous Sup35 and Rnq1 amyloidogenesis. <i>PLoS ONE</i> , 2010 , 5, e9642	3.7	13
17	DCAF8, a novel MuRF1 interaction partner, promotes muscle atrophy. <i>Journal of Cell Science</i> , 2019 , 132,	5.3	12
16	Spontaneous self-assembly of pathogenic huntingtin exon 1 protein into amyloid structures. <i>Essays in Biochemistry</i> , 2014 , 56, 167-80	7.6	12
15	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
14	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
13	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
12	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
11	Sclerotiorin Stabilizes the Assembly of Nonfibrillar A β 42 Oligomers with Low Toxicity, Seeding Activity, and Beta-sheet Content. <i>Journal of Molecular Biology</i> , 2020 , 432, 2080-2098	6.5	4
10	A functionally defined high-density NRF2 interactome reveals new conditional regulators of ARE transactivation. <i>Redox Biology</i> , 2020 , 37, 101686	11.3	4
9	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
8	FEZ1 Forms Complexes with CRMP1 and DCC to Regulate Axon and Dendrite Development. <i>ENeuro</i> , 2021 , 8,	3.9	3
7	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
6	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

- 5 Small, Seeding-Competent Huntingtin Fibrils Are Prominent Aggregate Species in Brains of zQ175 Huntington's Disease Knock-in Mice. *Frontiers in Neuroscience*, **2021**, 15, 682172 5.1 2
- 4 Dynamics of huntingtin protein interactions in the striatum identifies candidate modifiers of Huntington disease.. *Cell Systems*, **2022**, 10.6 1
- 3 Schizophrenia risk candidate protein ZNF804A interacts with STAT2 and influences interferon-mediated gene transcription in mammalian cells. *Journal of Molecular Biology*, **2021**, 433, 167184 6.5 0
- 2 Klinische Proteomik **2008**, 297-313
- 1 CellFIE: CRISPR- and Cell Fusion-based Two-hybrid Interaction Mapping of Endogenous Proteins. *Journal of Molecular Biology*, **2021**, 433, 167305 6.5