Erich E Wanker

List of Publications by Year
in descending order

76 papers	14,802 citations	66336 42 h-index	71682 76 g-index
80 all docs	80 docs citations	80 times ranked	17759 citing authors

#	Article	IF	Citations
1	Dynamics of huntingtin protein interactions in the striatum identifies candidate modifiers of Huntington disease. Cell Systems, 2022, 13, 304-320.e5.	6.2	15
2	Shedding a new light on Huntingtonâ€™s disease: how blood can both propagate and ameliorate disease pathology. Molecular Psychiatry, 2021, 26, 5441-5463.	7.9	16
3	FEZ1 Forms Complexes with CRMP1 and DCC to Regulate Axon and Dendrite Development. ENeuro, 2021, 8, ENEURO.0193-20.2021.	1.9	11
4	Defective metabolic programming impairs early neuronal morphogenesis in neural cultures and an organoid model of Leigh syndrome. Nature Communications, 2021, 12, 1929.	12.8	55
5	Small, Seeding-Competent Huntingtin Fibrils Are Prominent Aggregate Species in Brains of zQ175 Huntingtonâ€™s Disease Knock-in Mice. Frontiers in Neuroscience, 2021, 15, 682172.	2.8	7
6	Schizophrenia risk candidate protein ZNF804A interacts with STAT2 and influences interferon-mediated gene transcription in mammalian cells. Journal of Molecular Biology, 2021, 433, 167184.	4.2	6
7	CellFIE: CRISPR- and Cell Fusion-based Two-hybrid Interaction Mapping of Endogenous Proteins. Journal of Molecular Biology, 2021, 433, 167305.	4.2	0
8	Assessment of Ethanol-Induced Toxicity on iPSC-Derived Human Neurons Using a Novel High-Throughput Mitochondrial Neuronal Health (MNH) Assay. Frontiers in Cell and Developmental Biology, 2020, 8, 590540.	3.7	6
9	Interactome Mapping Provides a Network of Neurodegenerative Disease Proteins and Uncovers Widespread Protein Aggregation in Affected Brains. Cell Reports, 2020, 32, 108050.	6.4	64
10	A functionally defined high-density NRF2 interactome reveals new conditional regulators of ARE transactivation. Redox Biology, 2020, 37, 101686.	9.0	10
11	Interleukinâ€12/23 deficiency differentially affects pathology in male and female Alzheimer's diseaseâ€like mice. EMBO Reports, 2020, 21, e48530.	4.5	24
12	Subcellular Localization And Formation Of Huntingtin Aggregates Correlates With Symptom Onset And Progression In A Huntingtonâ€™S Disease Model. Brain Communications, 2020, 2, fcaa066.	3.3	34
13	Mixing AÎ²(1â€“40) and AÎ²(1â€“42) peptides generates unique amyloid fibrils. Chemical Communications, 2020, 56, 8830-8833.	4.1	39
14	Sclerotiorin Stabilizes the Assembly of Nonfibrillar Abeta42 Oligomers with Low Toxicity, Seeding Activity, and Beta-sheet Content. Journal of Molecular Biology, 2020, 432, 2080-2098.	4.2	12
15	The pathobiology of perturbed mutant huntingtin proteinâ€“protein interactions in Huntington's disease. Journal of Neurochemistry, 2019, 151, 507-519.	3.9	70
16	DCAF8, a novel MuRF1 interaction partner, promotes muscle atrophy. Journal of Cell Science, 2019, 132, .	2.0	17
17	Maximizing binary interactome mapping with a minimal number of assays. Nature Communications, 2019, 10, 3907.	12.8	57
18	The Anti-amyloid Compound DO1 Decreases Plaque Pathology and Neuroinflammation-Related Expression Changes in 5xFAD Transgenic Mice. Cell Chemical Biology, 2019, 26, 109-120.e7.	5.2	8

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19	Self-assembly of Mutant Huntingtin Exon-1 Fragments into Large Complex Fibrillar Structures Involves Nucleated Branching. Journal of Molecular Biology, 2018, 430, 1725-1744.	4.2	35
20	mHTT Seeding Activity: A Marker of Disease Progression and Neurotoxicity in Models of Huntingtonâ€™s Disease. Molecular Cell, 2018, 71, 675-688.e6.	9.7	50
21	A Filter Retardation Assay Facilitates the Detection and Quantification of Heat-Stable, Amyloidogenic Mutant Huntingtin Aggregates in Complex Biosamples. Methods in Molecular Biology, 2018, 1780, 31-40.	0.9	5
22	Lu <scp>TH</scp> y: a doubleâ€readout bioluminescenceâ€based twoâ€hybrid technology for quantitative mapping of proteinâ€“protein interactions in mammalian cells. Molecular Systems Biology, 2018, 14, e8071.	7.2	31
23	Metformin reverses early cortical network dysfunction and behavior changes in Huntingtonâ€™s disease. ELife, 2018, 7, .	6.0	64
24	Human iPSC-Derived Neural Progenitors Are an Effective Drug Discovery Model for Neurological mtDNA Disorders. Cell Stem Cell, 2017, 20, 659-674.e9.	11.1	126
25	Inhibition of Huntingtin Exon-1 Aggregation by the Molecular Tweezer CLR01. Journal of the American Chemical Society, 2017, 139, 5640-5643.	13.7	49
26	Identification of an RNA Polymerase III Regulator Linked to Disease-Associated Protein Aggregation. Molecular Cell, 2017, 65, 1096-1108.e6.	9.7	14
27	Aggregation of Full-length Immunoglobulin Light Chains from Systemic Light Chain Amyloidosis (AL) Patients Is Remodeled by Epigallocatechin-3-gallate. Journal of Biological Chemistry, 2017, 292, 2328-2344.	3.4	37
28	Current Approaches Toward Quantitative Mapping of the Interactome. Frontiers in Genetics, 2016, 7, 74.	2.3	28
29	Amyloid-Î²(1â€“42) Aggregation Initiates Its Cellular Uptake and Cytotoxicity. Journal of Biological Chemistry, 2016, 291, 19590-19606.	3.4	91
30	Quantitative interaction mapping reveals an extended UBX domain in ASPL that disrupts functional p97 hexamers. Nature Communications, 2016, 7, 13047.	12.8	35
31	An integer programming framework for inferring disease complexes from network data. Bioinformatics, 2016, 32, i271-i277.	4.1	44
32	Modulation of human IAPP fibrillation: cosolutes, crowders and chaperones. Physical Chemistry Chemical Physics, 2015, 17, 8338-8348.	2.8	59
33	Quantitative Interaction Proteomics of Neurodegenerative Disease Proteins. Cell Reports, 2015, 11, 1134-1146.	6.4	88
34	DULIP: A Dual Luminescence-Based Co-Immunoprecipitation Assay for Interactome Mapping in Mammalian Cells. Journal of Molecular Biology, 2015, 427, 3375-3388.	4.2	28
35	The green tea polyphenol (â^')â€epigallocatechin gallate prevents the aggregation of tau protein into toxic oligomers at substoichiometric ratios. FEBS Letters, 2015, 589, 77-83.	2.8	172
36	Identification of the Mitochondrial MSRB2 as a Binding Partner of LG72. Cellular and Molecular Neurobiology, 2014, 34, 1123-1130.	3.3	18

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37	The palmitoyl acyltransferase HIP14 shares a high proportion of interactors with huntingtin: implications for a role in the pathogenesis of Huntington's disease. Human Molecular Genetics, 2014, 23, 4142-4160.	2.9	58
38	The E3 Ubiquitin Ligase MID1 Catalyzes Ubiquitination and Cleavage of Fu. Journal of Biological Chemistry, 2014, 289, 31805-31817.	3.4	23
39	Prion-like proteins sequester and suppress the toxicity of huntingtin exon 1. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 12085-12090.	7.1	47
40	Spontaneous self-assembly of pathogenic huntingtin exon 1 protein into amyloid structures. Essays in Biochemistry, 2014, 56, 167-180.	4.7	12
41	Epigallocatechin-3-gallate: a useful, effective and safe clinical approach for targeted prevention and individualised treatment of neurological diseases?. EPMA Journal, 2013, 4, 5.	6.1	80
42	Aggregation of polyQâ€extended proteins is promoted by interaction with their natural coiledâ€coil partners. BioEssays, 2013, 35, 503-507.	2.5	39
43	Translation of HTT mRNA with expanded CAG repeats is regulated by the MID1â€“PP2A protein complex. Nature Communications, 2013, 4, 1511.	12.8	84
44	A Y2H-seq approach defines the human protein methyltransferase interactome. Nature Methods, 2013, 10, 339-342.	19.0	99
45	Development and application of a DNA microarray-based yeast two-hybrid system. Nucleic Acids Research, 2013, 41, 1496-1507.	14.5	19
46	Identification of Human Proteins That Modify Misfolding and Proteotoxicity of Pathogenic Ataxin-1. PLoS Genetics, 2012, 8, e1002897.	3.5	29
47	Phosphorylation-regulated axonal dependent transport of syntaxin 1 is mediated by a Kinesin-1 adapter. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 5862-5867.	7.1	44
48	Evolution and function of CAG/polyglutamine repeats in proteinâ€protein interaction networks. Nucleic Acids Research, 2012, 40, 4273-4287.	14.5	166
49	Small-molecule conversion of toxic oligomers to nontoxic Î²-sheetâ€rich amyloid fibrils. Nature Chemical Biology, 2012, 8, 93-101.	8.0	400
50	HIPPIE: Integrating Protein Interaction Networks with Experiment Based Quality Scores. PLoS ONE, 2012, 7, e31826.	2.5	297
51	A Directed Protein Interaction Network for Investigating Intracellular Signal Transduction. Science Signaling, 2011, 4, rs8.	3.6	313
52	Pathogenic Polyglutamine Tracts Are Potent Inducers of Spontaneous Sup35 and Rnq1 Amyloidogenesis. PLoS ONE, 2010, 5, e9642.	2.5	14
53	EGCG remodels mature Î±-synuclein and amyloid-Î² fibrils and reduces cellular toxicity. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 7710-7715.	7.1	888
54	UniHI 4: new tools for query, analysis and visualization of the human proteinâ€protein interactome. Nucleic Acids Research, 2009, 37, D657-D660.	14.5	58

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55	Detection of Alpha-Rod Protein Repeats Using a Neural Network and Application to Huntingtin. PLoS Computational Biology, 2009, 5, e1000304.	3.2	59
56	An empirical framework for binary interactome mapping. Nature Methods, 2009, 6, 83-90.	19.0	800
57	EGCG redirects amyloidogenic polypeptides into unstructured, off-pathway oligomers. Nature Structural and Molecular Biology, 2008, 15, 558-566.	8.2	1,249
58	Klinische Proteomik. , 2008, , 297-313.		0
59	Flexible web-based integration of distributed large-scale human protein interaction maps. Journal of Integrative Bioinformatics, 2007, 4, 40-50.	1.5	3
60	An arginine/lysine-rich motif is crucial for VCP/p97-mediated modulation of ataxin-3 fibrillogenesis. EMBO Journal, 2006, 25, 1547-1558.	7.8	142
61	The value of high quality proteinâ€“protein interaction networks for systems biology. Current Opinion in Chemical Biology, 2006, 10, 551-558.	6.1	100
62	Identification of VCP/p97, Carboxyl Terminus of Hsp70-interacting Protein (CHIP), and Amphiphysin II Interaction Partners Using Membrane-based Human Proteome Arrays. Molecular and Cellular Proteomics, 2006, 5, 234-244.	3.8	48
63	Green tea (â^)-epigallocatechin-gallate modulates early events in huntingtin misfolding and reduces toxicity in Huntington's disease models. Human Molecular Genetics, 2006, 15, 2743-2751.	2.9	357
64	Multiplex approaches in protein microarray technology. Expert Review of Proteomics, 2005, 2, 499-510.	3.0	39
65	A Human Protein-Protein Interaction Network: A Resource for Annotating the Proteome. Cell, 2005, 122, 957-968.	28.9	2,169
66	A Protein Interaction Network Links GIT1, an Enhancer of Huntingtin Aggregation, to Huntington's Disease. Molecular Cell, 2004, 15, 853-865.	9.7	398
67	The hunt for huntingtin function: interaction partners tell many different stories. Trends in Biochemical Sciences, 2003, 28, 425-433.	7.5	456
68	Mutant Huntingtin Promotes the Fibrillogenesis of Wild-type Huntingtin. Journal of Biological Chemistry, 2003, 278, 41452-41461.	3.4	107
69	Identification of benzothiazoles as potential polyglutamine aggregation inhibitors of Huntington's disease by using an automated filter retardation assay. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16400-16406.	7.1	199
70	Accumulation of Mutant Huntingtin Fragments in Aggresome-like Inclusion Bodies as a Result of Insufficient Protein Degradation. Molecular Biology of the Cell, 2001, 12, 1393-1407.	2.1	583
71	Protein Aggregation and Pathogenesis of Huntingtons Disease: Mechanisms and Correlations. Biological Chemistry, 2000, 381, 937-942.	2.5	134
72	[24] Membrane filter assay for detection of amyloid-like polyglutamine-containing protein aggregates. Methods in Enzymology, 1999, 309, 375-386.	1.0	217

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73	SH3GL3 Associates with the Huntingtin Exon 1 Protein and Promotes the Formation of Polygln-Containing Protein Aggregates. Molecular Cell, 1998, 2, 427-436.	9.7	208
74	Ataxin-3 is transported into the nucleus and associates with the nuclear matrix. Human Molecular Genetics, 1998, 7, 991-997.	2.9	104
75	Formation of Neuronal Intranuclear Inclusions Underlies the Neurological Dysfunction in Mice Transgenic for the HD Mutation. Cell, 1997, 90, 537-548.	28.9	2,105
76	Huntingtin-Encoded Polyglutamine Expansions Form Amyloid-like Protein Aggregates In Vitro and In Vivo. Cell, 1997, 90, 549-558.	28.9	1,224