John W R Schwabe

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/8553088/publications.pdf

Version: 2024-02-01

113 papers	12,858 citations	31902 53 h-index	25716 108 g-index
120 all docs	120 docs citations	120 times ranked	14760 citing authors

#	Article	IF	Citations
1	Dominant negative mutations in human PPARÎ³ associated with severe insulin resistance, diabetes mellitus and hypertension. Nature, 1999, 402, 880-883.	13.7	1,286
2	The crystal structure of the estrogen receptor DNA-binding domain bound to DNA: How receptors discriminate between their response elements. Cell, 1993, 75, 567-578.	13.5	703
3	Zinc fingers. FASEB Journal, 1995, 9, 597-604.	0.2	565
4	Solution structure of the DMA-binding domain of the oestrogen receptor. Nature, 1990, 348, 458-461.	13.7	478
5	Structure of HDAC3 bound to co-repressor and inositol tetraphosphate. Nature, 2012, 481, 335-340.	13.7	398
6	Structural basis for the activation of PPARÎ³ by oxidized fatty acids. Nature Structural and Molecular Biology, 2008, 15, 924-931.	3.6	380
7	Mechanism of corepressor binding and release from nuclear hormone receptors. Genes and Development, 1999, 13, 3209-3216.	2.7	367
8	The crystal structure of a two zinc-finger peptide reveals an extension to the rules for zinc-finger/DNA recognition. Nature, 1993, 366, 483-487.	13.7	361
9	STAT6 Transcription Factor Is a Facilitator of the Nuclear Receptor PPARÎ³-Regulated Gene Expression in Macrophages and Dendritic Cells. Immunity, 2010, 33, 699-712.	6.6	352
10	Mechanism of the nuclear receptor molecular switch. Trends in Biochemical Sciences, 2004, 29, 317-324.	3.7	349
11	A Mutation in the Thyroid Hormone Receptor Alpha Gene. New England Journal of Medicine, 2012, 366, 243-249.	13.9	340
12	Class I HDACs Share a Common Mechanism of Regulation by Inositol Phosphates. Molecular Cell, 2013, 51, 57-67.	4.5	314
13	A Death Effector Domain Chain DISC Model Reveals a Crucial Role for Caspase-8 Chain Assembly in Mediating Apoptotic Cell Death. Molecular Cell, 2012, 47, 291-305.	4.5	279
14	Mutations in the selenocysteine insertion sequenceâ€“binding protein 2 gene lead to a multisystem selenoprotein deficiency disorder in humans. Journal of Clinical Investigation, 2010, 120, 4220-4235.	3.9	268
15	A Dominant-negative Peroxisome Proliferator-activated Receptor Î³ (PPARÎ³) Mutant Is a Constitutive Repressor and Inhibits PPARÎ³-mediated Adipogenesis. Journal of Biological Chemistry, 2000, 275, 5754-5759.	1.6	249
16	Zinc mining for protein domains. Nature Structural and Molecular Biology, 1994, 1, 345-349.	3.6	239
17	St John's wort, a herbal antidepressant, activates the steroid X receptor. Journal of Endocrinology, 2000, 166, R11-R16.	1.2	230
18	Co-operative and Hierarchical Binding of c-FLIP and Caspase-8: A Unified Model Defines How c-FLIP Isoforms Differentially Control Cell Fate. Molecular Cell, 2016, 61, 834-849.	4.5	202

#	Article	IF	Citations
19	Radical fringe positions the apical ectodermal ridge at the dorsoventral boundary of the vertebrate limb. Nature, 1997, 386, 360-366.	13.7	201
20	International Union of Pharmacology. LXVI. Orphan Nuclear Receptors. Pharmacological Reviews, 2006, 58, 798-836.	7.1	195
21	Aster Proteins Facilitate Nonvesicular Plasma Membrane to ER Cholesterol Transport in Mammalian Cells. Cell, 2018, 175, 514-529.e20.	13.5	177
22	The role of water in proteinâ€"DNA interactions. Current Opinion in Structural Biology, 1997, 7, 126-134.	2.6	176
23	Targeting the CoREST complex with dual histone deacetylase and demethylase inhibitors. Nature Communications, 2018, 9, 53.	5.8	175
24	Insights into the activation mechanism of class I HDAC complexes by inositol phosphates. Nature Communications, 2016, 7, 11262.	5.8	172
25	Beyond zinc fingers: steroid hormone receptors have a novel structural motif for DNA recognition. Trends in Biochemical Sciences, 1991, 16, 291-296.	3.7	166
26	Non-DNA binding, dominant-negative, human PPARÎ³ mutations cause lipodystrophic insulin resistance. Cell Metabolism, 2006, 4, 303-311.	7.2	164
27	Structural basis for the assembly of the SMRT/NCoR core transcriptional repression machinery. Nature Structural and Molecular Biology, 2011, 18, 177-184.	3.6	156
28	A dynamic mechanism of nuclear receptor activation and its perturbation in a human disease. Nature Structural Biology, 2003, 10, 136-140.	9.7	150
29	Nuclear hormone receptor co-repressors: Structure and function. Molecular and Cellular Endocrinology, 2012, 348, 440-449.	1.6	148
30	A conserved structural motif reveals the essential transcriptional repression function of Spen proteins and their role in developmental signaling. Genes and Development, 2003, 17, 1909-1920.	2.7	144
31	Targeting Class I Histone Deacetylases in a â€œComplexâ€•Environment. Trends in Pharmacological Sciences, 2017, 38, 363-377.	4.0	143
32	Histone deacetylase (HDAC) 1 and 2 are essential for accurate cell division and the pluripotency of embryonic stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 9840-9845.	3.3	130
33	The phantom ligand effect: allosteric control of transcription by the retinoid X receptor.. Genes and Development, 1997, 11, 299-308.	2.7	122
34	DNA recognition by the oestrogen receptor: from solution to the crystal. Structure, 1993, 1, 187-204.	1.6	112
35	The structure of the core NuRD repression complex provides insights into its interaction with chromatin. ELife, 2016, 5, e13941.	2.8	108
36	The oestrogen receptor recognizes an imperfectly palindromic response element through an alternative side-chain conformation. Structure, 1995, 3, 201-213.	1.6	95

#	Article	IF	Citations
37	Coexpression of nuclear receptor partners increases their solubility and biological activities. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 2278-2283.	3.3	91
38	Structural insights into the interaction and activation of histone deacetylase 3 by nuclear receptor corepressors. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 6009-6014.	3.3	88
39	Solution structures of two zinc-finger domains from SWI5 obtained using two-dimensional 1H nuclear magnetic resonance spectroscopy. Journal of Molecular Biology, 1992, 228, 637-651.	2.0	87
40	Histone deacetylase (HDAC) 1 and 2 complexes regulate both histone acetylation and crotonylation in vivo. Scientific Reports, 2018, 8, 14690.	1.6	84
41	An evolving understanding of nuclear receptor coregulator proteins. Journal of Molecular Endocrinology, 2013, 51, T23-T36.	1.1	80
42	Negative regulation by nuclear receptors: a plethora of mechanisms. Trends in Endocrinology and Metabolism, 2011, 22, 87-93.	3.1	79
43	Residual Activity of Mutant Androgen Receptors Explains Wolffian Duct Development in the Complete Androgen Insensitivity Syndrome. Journal of Clinical Endocrinology and Metabolism, 2004, 89, 5815-5822.	1.8	77
44	The IDOLâ€“UBE2D complex mediates sterol-dependent degradation of the LDL receptor. Genes and Development, 2011, 25, 1262-1274.	2.7	75
45	PROTAC-mediated degradation of class I histone deacetylase enzymes in corepressor complexes. Chemical Communications, 2020, 56, 4476-4479.	2.2	75
46	Mechanism of Crosstalk between the LSD1 Demethylase and HDAC1 Deacetylase in the CoREST Complex. Cell Reports, 2020, 30, 2699-2711.e8.	2.9	74
47	Mutations in TBL1X Are Associated With Central Hypothyroidism. Journal of Clinical Endocrinology and Metabolism, 2016, 101, 4564-4573.	1.8	73
48	The structure of the ultraspiracle ligand-binding domain reveals a nuclear receptor locked in an inactive conformation. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 1549-54.	3.3	71
49	Disruption of the Class IIa HDAC Corepressor Complex Increases Energy Expenditure and Lipid Oxidation. Cell Reports, 2016, 16, 2802-2810.	2.9	68
50	The Structural Basis for the Specificity of Retinoid-X Receptor-selective Agonists: New Insights Into the Role of Helix H12. Journal of Biological Chemistry, 2002, 277, 11385-11391.	1.6	65
51	Limbs are moving: where are they going?. Trends in Genetics, 1998, 14, 229-235.	2.9	61
52	Towards an understanding of protein-DNA recognition. Philosophical Transactions of the Royal Society B: Biological Sciences, 1996, 351, 501-509.	1.8	59
53	Identification of a Novel Co-regulator Interaction Surface on the Ligand Binding Domain of Nurr1 Using NMR Footprinting. Journal of Biological Chemistry, 2004, 279, 53338-53345.	1.6	55
54	Tyrosine Agonists Reverse the Molecular Defects Associated with Dominant-Negative Mutations in Human Peroxisome Proliferator-Activated Receptor Î³. Endocrinology, 2004, 145, 1527-1538.	1.4	55

#	Article	IF	Citations
55	FERM-dependent E3 ligase recognition is a conserved mechanism for targeted degradation of lipoprotein receptors. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 20107-20112.	3.3	53
56	NOXA, a sensor of proteasome integrity, is degraded by 26S proteasomes by an ubiquitin-independent pathway that is blocked by MCL-1. Cell Death and Differentiation, 2012, 19, 1424-1434.	5.0	52
57	Structural and functional characterization of a cell cycle associated HDAC1/2 complex reveals the structural basis for complex assembly and nucleosome targeting. Nucleic Acids Research, 2015, 43, 2033-2044.	6.5	51
58	A specific mutation inTBL1XR1causes Pierpont syndrome. Journal of Medical Genetics, 2016, 53, 330-337.	1.5	51
59	The MiDAC histone deacetylase complex is essential for embryonic development and has a unique multivalent structure. Nature Communications, 2020, 11, 3252.	5.8	51
60	Human androgen receptor gene ligand-binding-domain mutations leading to disrupted interaction between the N- and C-terminal domains. Journal of Molecular Endocrinology, 2006, 36, 361-368.	1.1	48
61	Recombinant Protein Expression for Structural Biology in HEK 293F Suspension Cells: A Novel and Accessible Approach. Journal of Visualized Experiments, 2014, , e51897.	0.2	45
62	Mzt1/Tam4, a fission yeast MOZART1 homologue, is an essential component of the Î³-tubulin complex and directly interacts with GCP3^{Alp6}. Molecular Biology of the Cell, 2013, 24, 3337-3349.	0.9	44
63	Insights into the Recruitment of Class IIa Histone Deacetylases (HDACs) to the SMRT/NCoR Transcriptional Repression Complex. Journal of Biological Chemistry, 2015, 290, 18237-18244.	1.6	44
64	Lysine-14 acetylation of histone H3 in chromatin confers resistance to the deacetylase and demethylase activities of an epigenetic silencing complex. ELife, 2018, 7, .	2.8	43
65	Channels at the catalytic site of glycogen phosphorylase b: binding and kinetic studies with the .beta.-glycosidase inhibitor D-gluconohydroximo-1,5-lactone N-phenylurethane. Biochemistry, 1988, 27, 6733-6741.	1.2	42
66	A variant NuRD complex containing PWWP2A/B excludes MBD2/3 to regulate transcription at active genes. Nature Communications, 2018, 9, 3798.	5.8	40
67	A Dominant Negative Human Peroxisome Proliferator-Activated Receptor (PPAR)Î± Is a Constitutive Transcriptional Corepressor and Inhibits Signaling through All PPAR Isoforms. Endocrinology, 2005, 146, 1871-1882.	1.4	39
68	Towards an understanding of the structure and function of MTA1. Cancer and Metastasis Reviews, 2014, 33, 857-867.	2.7	39
69	Contrasting Phenotypes in Resistance to Thyroid Hormone Alpha Correlate with Divergent Properties of Thyroid Hormone Receptor Î±1 Mutant Proteins. Thyroid, 2017, 27, 973-982.	2.4	39
70	Cryo-EM structural analysis of FADD:Caspase-8 complexes defines the catalytic dimer architecture for co-ordinated control of cell fate. Nature Communications, 2021, 12, 819.	5.8	38
71	Diverse nucleosome Site-Selectivity among histone deacetylase complexes. ELife, 2020, 9, .	2.8	37
72	BIM-Mediated Membrane Insertion of the BAK Pore Domain Is an Essential Requirement for Apoptosis. Cell Reports, 2013, 5, 409-420.	2.9	36

#	Article	IF	Citations
73	Heme binding to human CLOCK affects interactions with the E-box. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 19911-19916.	3.3	35
74	Transient Expression in HEK 293 Cells: An Alternative to E. coli for the Production of Secreted and Intracellular Mammalian Proteins. Methods in Molecular Biology, 2015, 1258, 209-222.	0.4	34
75	Optimization of Class I Histone Deacetylase PROTACs Reveals that HDAC1/2 Degradation is Critical to Induce Apoptosis and Cell Arrest in Cancer Cells. Journal of Medicinal Chemistry, 2022, 65, 5642-5659.	2.9	32
76	A Pharmacogenetic Approach to the Treatment of Patients With PPARG Mutations. Diabetes, 2018, 67, 1086-1092.	0.3	30
77	The Steroid/Nuclear Receptors: From Three-Dimensional Structure to Complex Function. Vitamins and Hormones, 1994, 49, 1-47.	0.7	28
78	Molecular Determinants of the Balance between Co-repressor and Co-activator Recruitment to the Retinoic Acid Receptor. Journal of Biological Chemistry, 2003, 278, 43797-43806.	1.6	28
79	Maternal Isodisomy for Chromosome 9 Causing Homozygosity for a NovelFOXE1Mutation in Syndromic Congenital Hypothyroidism. Journal of Clinical Endocrinology and Metabolism, 2010, 95, 4031-4036.	1.8	28
80	A Novel Albumin Gene Mutation (R222I) in Familial Dysalbuminemic Hyperthyroxinemia. Journal of Clinical Endocrinology and Metabolism, 2014, 99, E1381-E1386.	1.8	28
81	The topology of chromatin-binding domains in the NuRD deacetylase complex. Nucleic Acids Research, 2020, 48, 12972-12982.	6.5	28
82	Genetic disorders of nuclear receptors. Journal of Clinical Investigation, 2017, 127, 1181-1192.	3.9	28
83	Nuclear Receptors: The Evolution of Diversity. Science Signaling, 2004, 2004, pe4-pe4.	1.6	26
84	Histone H2B Deacylation Selectivity: Exploring Chromatinâ€™s Dark Matter with an Engineered Sortase. Journal of the American Chemical Society, 2022, 144, 3360-3364.	6.6	24
85	A de novo substitution in BCL11B leads to loss of interaction with transcriptional complexes and craniosynostosis. Human Molecular Genetics, 2019, 28, 2501-2513.	1.4	23
86	Histone deacetylase 3 indirectly modulates tubulin acetylation. Biochemical Journal, 2015, 472, 367-377.	1.7	22
87	Twode NovoMutations in the AR Gene Cause the Complete Androgen Insensitivity Syndrome in a Pair of Monozygotic Twins. Journal of Clinical Endocrinology and Metabolism, 2002, 87, 1057-1061.	1.8	21
88	Selective Aster inhibitors distinguish vesicular and nonvesicular sterol transport mechanisms. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	21
89	Transcriptional control: How nuclear receptors get turned on. Current Biology, 1996, 6, 372-374.	1.8	20
90	What is evolution playing at?. Current Biology, 1993, 3, 628-630.	1.8	19

#	Article	IF	Citations
91	Comparison of the molecular consequences of different mutations at residue 754 and 690 of the androgen receptor (AR) and androgen insensitivity syndrome (AIS) phenotype. Clinical Endocrinology, 2009, 71, 253-260.	1.2	19
92	HDAC3 deacetylates the DNA mismatch repair factor MutSÎ² to stimulate triplet repeat expansions. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 23597-23605.	3.3	19
93	The Ansamycin Antibiotic, Rifamycin SV, Inhibits BCL6 Transcriptional Repression and Forms a Complex with the BCL6-BTB/POZ Domain. PLoS ONE, 2014, 9, e90889.	1.1	17
94	A NovelCYP11B2Gene Mutation in an Asian Family with Aldosterone Synthase Deficiency. Journal of Clinical Endocrinology and Metabolism, 2009, 94, 914-919.	1.8	15
95	Linkers made to measure. Nature Structural Biology, 1997, 4, 680-683.	9.7	13
96	Spurring on transcription?. Current Biology, 1993, 3, 898-900.	1.8	12
97	Synthesis of HDAC Substrate Peptidomimetic Inhibitors Using Fmoc Amino Acids Incorporating Zinc-Binding Groups. Organic Letters, 2019, 21, 3178-3182.	2.4	11
98	All wrapped up. Nature Structural Biology, 1998, 5, 253-255.	9.7	10
99	Expression and Purification of Protein Complexes Suitable for Structural Studies Using Mammalian HEK 293F Cells. Current Protocols in Protein Science, 2017, 90, 5.28.1-5.28.16.	2.8	9
100	The Cocrystal Structures of Two Zinc-stabilized DNA-binding Domains Illustrate Different Ways of Achieving Sequence-specific DNA Recognition. Cold Spring Harbor Symposia on Quantitative Biology, 1993, 58, 141-147.	2.0	9
101	Transcriptional repression by nuclear receptors: mechanisms and role in disease. Biochemical Society Transactions, 2000, 28, 390.	1.6	7
102	Complex behaviour. Nature, 1991, 352, 478-479.	13.7	6
103	Backbone resonance assignment of the BCL6-BTB/POZ domain. Biomolecular NMR Assignments, 2018, 12, 47-50.	0.4	6
104	Radical fringe positions the apical ectodermal ridge at the dorsoventral boundary of the vertebrate limb. Nature, 1997, 388, 906-906.	13.7	5
105	Signal transduction: Fast lane to transcriptional activation. Current Biology, 1998, 8, R765-R767.	1.8	3
106	Hyperthyroxinemia and Hypercortisolemia due to Familial Dysalbuminemia. Thyroid, 2020, 30, 1681-1684.	2.4	3
107	Structure-Guided Approach to Relieving Transcriptional Repression in Resistance to Thyroid Hormone Î±. Molecular and Cellular Biology, 2022, 42, MCB0036321.	1.1	3
108	Distinctly differentâ€¦ or really much the same?. Current Biology, 1992, 2, 237-238.	1.8	2

#	Article	IF	Citations
109	DNA between the sheets. Current Biology, 1992, 2, 661-663.	1.8	0
110	Nuclear receptor: co-repressor interactions. Biochemical Society Transactions, 2000, 28, A63-A63.	1.6	0
111	P057 Cytokine mediated regulation of PPARg activity in human macrophages. Cytokine, 2012, 59, 536.	1.4	0
112	Assembly and Regulation of Nuclear Receptor Corepressor Complexes. , 2015, , 155-175.		0
113	Analysis of CoREST Complexâ€Chromatin Interactions with Chemical Tools. FASEB Journal, 2018, 32, 524.7.	0.2	0