John W R Schwabe

List of Publications by Citations

107 papers	10,529 citations	49 h-index	102 g-index
118 ext. papers	11,789 ext. citations	12.6 avg, IF	5.88 L-index

#	Paper	IF	Citations
107	Dominant negative mutations in human PPARgamma associated with severe insulin resistance, diabetes mellitus and hypertension. *Nature*, **1999**, 402, 880-3	50.4	1129
106	The crystal structure of the estrogen receptor DNA-binding domain bound to DNA: how receptors discriminate between their response elements. *Cell*, **1993**, 75, 567-78	56.2	635
105	Zinc fingers. *FASEB Journal*, **1995**, 9, 597-604	0.9	504
104	Solution structure of the DNA-binding domain of the oestrogen receptor. *Nature*, **1990**, 348, 458-61	50.4	416
103	The crystal structure of a two zinc-finger peptide reveals an extension to the rules for zinc-finger/DNA recognition. *Nature*, **1993**, 366, 483-7	50.4	326
102	Mechanism of corepressor binding and release from nuclear hormone receptors. *Genes and Development*, **1999**, 13, 3209-16	12.6	323
101	Structural basis for the activation of PPARgamma by oxidized fatty acids. *Nature Structural and Molecular Biology*, **2008**, 15, 924-31	17.6	321
100	Structure of HDAC3 bound to co-repressor and inositol tetraphosphate. *Nature*, **2012**, 481, 335-40	50.4	319
99	Mechanism of the nuclear receptor molecular switch. *Trends in Biochemical Sciences*, **2004**, 29, 317-24	10.3	318
98	A mutation in the thyroid hormone receptor alpha gene. *New England Journal of Medicine*, **2012**, 366, 243-9	59.2	288
97	STAT6 transcription factor is a facilitator of the nuclear receptor PPAR□regulated gene expression in macrophages and dendritic cells. *Immunity*, **2010**, 33, 699-712	32.3	284
96	Class I HDACs share a common mechanism of regulation by inositol phosphates. *Molecular Cell*, **2013**, 51, 57-67	17.6	247
95	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	17.6	237
94	Mutations in the selenocysteine insertion sequence-binding protein 2 gene lead to a multisystem selenoprotein deficiency disorder in humans. *Journal of Clinical Investigation*, **2010**, 120, 4220-35	15.9	229
93	A dominant-negative peroxisome proliferator-activated receptor gamma (PPARgamma) mutant is a constitutive repressor and inhibits PPARgamma-mediated adipogenesis. *Journal of Biological Chemistry*, **2000**, 275, 5754-9	5.4	222
92	St John□s wort, a herbal antidepressant, activates the steroid X receptor. *Journal of Endocrinology*, **2000**, 166, R11-6	4.7	200
91	Radical fringe positions the apical ectodermal ridge at the dorsoventral boundary of the vertebrate limb. *Nature*, **1997**, 386, 360-6	50.4	186

90	International Union of Pharmacology. LXVI. Orphan nuclear receptors. *Pharmacological Reviews*, **2006**, 58, 798-836	22.5	175
89	The role of water in protein-DNA interactions. *Current Opinion in Structural Biology*, **1997**, 7, 126-34	8.1	161
88	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, 834-49	17.6	143
87	Non-DNA binding, dominant-negative, human PPARgamma mutations cause lipodystrophic insulin resistance. *Cell Metabolism*, **2006**, 4, 303-11	24.6	143
86	Beyond zinc fingers: steroid hormone receptors have a novel structural motif for DNA recognition. *Trends in Biochemical Sciences*, **1991**, 16, 291-6	10.3	141
85	A dynamic mechanism of nuclear receptor activation and its perturbation in a human disease. *Nature Structural Biology*, **2003**, 10, 136-40		134
84	Targeting the CoREST complex with dual histone deacetylase and demethylase inhibitors. *Nature Communications*, **2018**, 9, 53	17.4	116
83	Aster Proteins Facilitate Nonvesicular Plasma Membrane to ER Cholesterol Transport in Mammalian Cells. *Cell*, **2018**, 175, 514-529.e20	56.2	116
82	Structural basis for the assembly of the SMRT/NCoR core transcriptional repression machinery. *Nature Structural and Molecular Biology*, **2011**, 18, 177-84	17.6	114
81	Insights into the activation mechanism of class I HDAC complexes by inositol phosphates. *Nature Communications*, **2016**, 7, 11262	17.4	113
80	Nuclear hormone receptor co-repressors: structure and function. *Molecular and Cellular Endocrinology*, **2012**, 348, 440-9	4.4	112
79	The phantom ligand effect: allosteric control of transcription by the retinoid X receptor. *Genes and Development*, **1997**, 11, 299-308	12.6	112
78	A conserved structural motif reveals the essential transcriptional repression function of Spen proteins and their role in developmental signaling. *Genes and Development*, **2003**, 17, 1909-20	12.6	111
77	DNA recognition by the oestrogen receptor: from solution to the crystal. *Structure*, **1993**, 1, 187-204	5.2	96
76	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, 9840-5	11.5	93
75	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, 2278-83	11.5	88
74	The oestrogen receptor recognizes an imperfectly palindromic response element through an alternative side-chain conformation. *Structure*, **1995**, 3, 201-13	5.2	87
73	Targeting Class I Histone Deacetylases in a "Complex" Environment. *Trends in Pharmacological Sciences*, **2017**, 38, 363-377	13.2	85

72	Solution structures of two zinc-finger domains from SWI5 obtained using two-dimensional 1H nuclear magnetic resonance spectroscopy. A zinc-finger structure with a third strand of beta-sheet. *Journal of Molecular Biology*, **1992**, 228, 637-51	6.5	78
71	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, 6009-14	11.5	76
70	Negative regulation by nuclear receptors: a plethora of mechanisms. *Trends in Endocrinology and Metabolism*, **2011**, 22, 87-93	8.8	72
69	Residual activity of mutant androgen receptors explains wolffian duct development in the complete androgen insensitivity syndrome. *Journal of Clinical Endocrinology and Metabolism*, **2004**, 89, 5815-22	5.6	69
68	The structure of the core NuRD repression complex provides insights into its interaction with chromatin. *ELife*, **2016**, 5, e13941	8.9	68
67	An evolving understanding of nuclear receptor coregulator proteins. *Journal of Molecular Endocrinology*, **2013**, 51, T23-36	4.5	63
66	The IDOL-UBE2D complex mediates sterol-dependent degradation of the LDL receptor. *Genes and Development*, **2011**, 25, 1262-74	12.6	62
65	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, 11385-91	5.4	59
64	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	11.5	59
63	Limbs are moving: where are they going?. *Trends in Genetics*, **1998**, 14, 229-35	8.5	55
62	Mutations in TBL1X Are Associated With Central Hypothyroidism. *Journal of Clinical Endocrinology and Metabolism*, **2016**, 101, 4564-4573	5.6	54
61	Towards an understanding of protein-DNA recognition. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **1996**, 351, 501-9	5.8	54
60	Tyrosine agonists reverse the molecular defects associated with dominant-negative mutations in human peroxisome proliferator-activated receptor gamma. *Endocrinology*, **2004**, 145, 1527-38	4.8	51
59	Disruption of the Class IIa HDAC Corepressor Complex Increases Energy Expenditure and Lipid Oxidation. *Cell Reports*, **2016**, 16, 2802-2810	10.6	48
58	Identification of a novel co-regulator interaction surface on the ligand binding domain of Nurr1 using NMR footprinting. *Journal of Biological Chemistry*, **2004**, 279, 53338-45	5.4	48
57	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, 361-8	4.5	44
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, 1424-34	12.7	43
55	Histone deacetylase (HDAC) 1 and 2 complexes regulate both histone acetylation and crotonylation in vivo. *Scientific Reports*, **2018**, 8, 14690	4.9	41

54	A specific mutation in TBL1XR1 causes Pierpont syndrome. *Journal of Medical Genetics*, **2016**, 53, 330-7	5.8	40
53	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, 6733-41	3.2	39
52	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, 20107-12	11.5	38
51	A dominant negative human peroxisome proliferator-activated receptor (PPAR){alpha} is a constitutive transcriptional corepressor and inhibits signaling through all PPAR isoforms. *Endocrinology*, **2005**, 146, 1871-82	4.8	38
50	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, 2033-44	20.1	36
49	PROTAC-mediated degradation of class I histone deacetylase enzymes in corepressor complexes. *Chemical Communications*, **2020**, 56, 4476-4479	5.8	36
48	Mzt1/Tam4, a fission yeast MOZART1 homologue, is an essential component of the γ-tubulin complex and directly interacts with GCP3(Alp6). *Molecular Biology of the Cell*, **2013**, 24, 3337-49	3.5	36
47	Recombinant protein expression for structural biology in HEK 293F suspension cells: a novel and accessible approach. *Journal of Visualized Experiments*, **2014**, e51897	1.6	33
46	Mechanism of Crosstalk between the LSD1 Demethylase and HDAC1 Deacetylase in the CoREST Complex. *Cell Reports*, **2020**, 30, 2699-2711.e8	10.6	31
45	BIM-mediated membrane insertion of the BAK pore domain is an essential requirement for apoptosis. *Cell Reports*, **2013**, 5, 409-20	10.6	31
44	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	5.4	30
43	Lysine-14 acetylation of histone H3 in chromatin confers resistance to the deacetylase and demethylase activities of an epigenetic silencing complex. *ELife*, **2018**, 7,	8.9	29
42	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, 209-22	1.4	28
41	Towards an understanding of the structure and function of MTA1. *Cancer and Metastasis Reviews*, **2014**, 33, 857-67	9.6	28
40	A novel albumin gene mutation (R222I) in familial dysalbuminemic hyperthyroxinemia. *Journal of Clinical Endocrinology and Metabolism*, **2014**, 99, E1381-6	5.6	26
39	Contrasting Phenotypes in Resistance to Thyroid Hormone Alpha Correlate with Divergent Properties of Thyroid Hormone Receptor α Mutant Proteins. *Thyroid*, **2017**, 27, 973-982	6.2	25
38	The steroid/nuclear receptors: from three-dimensional structure to complex function. *Vitamins and Hormones*, **1994**, 49, 1-47	2.5	25
37	Molecular determinants of the balance between co-repressor and co-activator recruitment to the retinoic acid receptor. *Journal of Biological Chemistry*, **2003**, 278, 43797-806	5.4	24

36	Maternal isodisomy for chromosome 9 causing homozygosity for a novel FOXE1 mutation in syndromic congenital hypothyroidism. *Journal of Clinical Endocrinology and Metabolism*, **2010**, 95, 4031-6	5.6	22
35	A variant NuRD complex containing PWWP2A/B excludes MBD2/3 to regulate transcription at active genes. *Nature Communications*, **2018**, 9, 3798	17.4	22
34	A Pharmacogenetic Approach to the Treatment of Patients With Mutations. *Diabetes*, **2018**, 67, 1086-1092	22.9	21
33	Nuclear receptors: the evolution of diversity. *Science Signaling*, **2004**, 2004, pe4	8.8	20
32	Transcriptional control: how nuclear receptors get turned on. *Current Biology*, **1996**, 6, 372-4	6.3	20
31	Two de novo mutations in the AR gene cause the complete androgen insensitivity syndrome in a pair of monozygotic twins. *Journal of Clinical Endocrinology and Metabolism*, **2002**, 87, 1057-61	5.6	19
30	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	11.5	16
29	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, 253-60	3.4	15
28	What is evolution playing at?. *Current Biology*, **1993**, 3, 628-30	6.3	15
27	Diverse nucleosome Site-Selectivity among histone deacetylase complexes. *ELife*, **2020**, 9,	8.9	15
26	Histone deacetylase 3 indirectly modulates tubulin acetylation. *Biochemical Journal*, **2015**, 472, 367-77	3.8	14
25	Genetic disorders of nuclear receptors. *Journal of Clinical Investigation*, **2017**, 127, 1181-1192	15.9	14
24	The MiDAC histone deacetylase complex is essential for embryonic development and has a unique multivalent structure. *Nature Communications*, **2020**, 11, 3252	17.4	13
23	The ansamycin antibiotic, rifamycin SV, inhibits BCL6 transcriptional repression and forms a complex with the BCL6-BTB/POZ domain. *PLoS ONE*, **2014**, 9, e90889	3.7	13
22	A novel CYP11B2 gene mutation in an Asian family with aldosterone synthase deficiency. *Journal of Clinical Endocrinology and Metabolism*, **2009**, 94, 914-9	5.6	13
21	Spurring on transcription?. *Current Biology*, **1993**, 3, 898-900	6.3	10
20	A de novo substitution in BCL11B leads to loss of interaction with transcriptional complexes and craniosynostosis. *Human Molecular Genetics*, **2019**, 28, 2501-2513	5.6	9
19	Synthesis of HDAC Substrate Peptidomimetic Inhibitors Using Fmoc Amino Acids Incorporating Zinc-Binding Groups. *Organic Letters*, **2019**, 21, 3178-3182	6.2	8

18	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, 141-7	3.9	8
17	HDAC3 deacetylates the DNA mismatch repair factor MutSβ to stimulate triplet repeat expansions. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 23597-23605	11.5	8
16	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	17.4	8
15	Transcriptional repression by nuclear receptors: mechanisms and role in disease. *Biochemical Society Transactions*, **2000**, 28, 390	5.1	7
14	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,	11.5	6
13	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	3.1	5
12	The topology of chromatin-binding domains in the NuRD deacetylase complex. *Nucleic Acids Research*, **2020**, 48, 12972-12982	20.1	4
11	Backbone resonance assignment of the BCL6-BTB/POZ domain. *Biomolecular NMR Assignments*, **2018**, 12, 47-50	0.7	3
10	Radical fringe positions the apical ectodermal ridge at the dorsoventral boundary of the vertebrate limb. *Nature*, **1997**, 388, 906-906	50.4	3
9	Signal transduction: fast lane to transcriptional activation. *Current Biology*, **1998**, 8, R765-7	6.3	3
8	Histone H2B Deacylation Selectivity: Exploring Chromatin's Dark Matter with an Engineered Sortase.. *Journal of the American Chemical Society*, **2022**,	16.4	3
7	Distinctly different...or really much the same?. *Current Biology*, **1992**, 2, 237-9	6.3	2
6	Hyperthyroxinemia and Hypercortisolemia due to Familial Dysalbuminemia. *Thyroid*, **2020**, 30, 1681-1684	6.2	1
5	Structure-guided approach to relieving transcriptional repression inResistance to Thyroid Hormone β. *Molecular and Cellular Biology*, **2021**, MCB0036321	4.8	0
4	Nuclear receptor: co-repressor interactions. *Biochemical Society Transactions*, **2000**, 28, A63-A63	5.1	
3	DNA between the sheets. *Current Biology*, **1992**, 2, 661-3	6.3	
2	Analysis of CoREST Complex-Chromatin Interactions with Chemical Tools. *FASEB Journal*, **2018**, 32, 524.7	0.9	
1	Assembly and Regulation of Nuclear Receptor Corepressor Complexes **2015**, 155-175		