Patrick R Griffin

List of Publications by Year
in descending order

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226 papers	21,832 citations	12330 69 h-index	10445 139 g-index
250 all docs	250 docs citations	250 times ranked	27176 citing authors

#	Article	IF	Citations
1	Identification and inhibition of the ICE/CED-3 protease necessary for mammalian apoptosis. Nature, 1995, 376, 37-43.	27.8	3,863
2	Anti-diabetic drugs inhibit obesity-linked phosphorylation of PPARÎ³ by Cdk5. Nature, 2010, 466, 451-456.	27.8	793
3	Crystal structure of rhodopsin bound to arrestin by femtosecond X-ray laser. Nature, 2015, 523, 561-567.	27.8	683
4	Peroxynitrite reductase activity of bacterial peroxiredoxins. Nature, 2000, 407, 211-215.	27.8	629
5	Antidiabetic actions of a non-agonist PPARÎ³ ligand blocking Cdk5-mediated phosphorylation. Nature, 2011, 477, 477-481.	27.8	484
6	Recommendations for performing, interpreting and reporting hydrogen deuterium exchange mass spectrometry (HDX-MS) experiments. Nature Methods, 2019, 16, 595-602.	19.0	452
7	Discovery of a Small Molecule Insulin Mimetic with Antidiabetic Activity in Mice. Science, 1999, 284, 974-977.	12.6	446
8	Suppression of TH17 differentiation and autoimmunity by a synthetic ROR ligand. Nature, 2011, 472, 491-494.	27.8	446
9	Molecular Mimicry Regulates ABA Signaling by SnRK2 Kinases and PP2C Phosphatases. Science, 2012, 335, 85-88.	12.6	439
10	Irisin Mediates Effects on Bone and Fat via Î±V Integrin Receptors. Cell, 2018, 175, 1756-1768.e17.	28.9	372
11	Identification of Phosphorylation Codes for Arrestin Recruitment by G Protein-Coupled Receptors. Cell, 2017, 170, 457-469.e13.	28.9	344
12	Glucocorticoid Receptor Function Regulated by Coordinated Action of the Hsp90 and Hsp70 Chaperone Cycles. Cell, 2014, 157, 1685-1697.	28.9	327
13	Partial Agonists Activate PPARÎ³ Using a Helix 12 Independent Mechanism. Structure, 2007, 15, 1258-1271.	3.3	321
14	TRPV4 Is a Regulator of Adipose Oxidative Metabolism, Inflammation, and Energy Homeostasis. Cell, 2012, 151, 96-110.	28.9	292
15	Probing Protein Ligand Interactions by Automated Hydrogen/Deuterium Exchange Mass Spectrometry. Analytical Chemistry, 2006, 78, 1005-1014.	6.5	289
16	HDX Workbench: Software for the Analysis of H/D Exchange MS Data. Journal of the American Society for Mass Spectrometry, 2012, 23, 1512-1521.	2.8	258
17	Structural basis of JAZ repression of MYC transcription factors in jasmonate signalling. Nature, 2015, 525, 269-273.	27.8	248
18	The Benzenesulfoamide T0901317 [N-(2,2,2-Trifluoroethyl)-N-[4-[2,2,2-trifluoro-1-hydroxy-1-(trifluoromethyl)ethyl]phenyl]-benzenesulfonamide] Is a Novel Retinoic Acid Receptor-Related Orphan Receptor-Î±/Î³ Inverse Agonist. Molecular Pharmacology, 2010, 77, 228-236.	2.3	221

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19	A nuclear-receptor-dependent phosphatidylcholine pathway with antidiabetic effects. Nature, 2011, 474, 506-510.	27.8	213
20	Estrogen receptor alpha somatic mutations Y537S and D538G confer breast cancer endocrine resistance by stabilizing the activating function-2 binding conformation. ELife, 2016, 5, .	6.0	212
21	Differential hydrogen/deuterium exchange mass spectrometry analysis of proteinâ€“ligand interactions. Expert Review of Proteomics, 2011, 8, 43-59.	3.0	208
22	The Role of Dipeptidyl Peptidase IV in the Cleavage of Glucagon Family Peptides. Journal of Biological Chemistry, 2003, 278, 22418-22423.	3.4	205
23	Structural Basis for the RNA-Guided Ribonuclease Activity of CRISPR-Cas13d. Cell, 2018, 175, 212-223.e17.	28.9	195
24	The Secreted Enzyme PM20D1 Regulates Lipidated Amino Acid Uncouplers of Mitochondria. Cell, 2016, 166, 424-435.	28.9	188
25	DNA binding alters coactivator interaction surfaces of the intact VDRâ€“RXR complex. Nature Structural and Molecular Biology, 2011, 18, 556-563.	8.2	185
26	Method To Compare Collision-Induced Dissociation Spectra of Peptides:Â Potential for Library Searching and Subtractive Analysis. Analytical Chemistry, 1998, 70, 3557-3565.	6.5	182
27	Modulation of Retinoic Acid Receptor-related Orphan Receptor Î± and Î³ Activity by 7-Oxygenated Sterol Ligands. Journal of Biological Chemistry, 2010, 285, 5013-5025.	3.4	180
28	Structure of the full-length glucagon class B G-protein-coupled receptor. Nature, 2017, 546, 259-264.	27.8	179
29	Plant systems biology comes of age. Trends in Plant Science, 2008, 13, 165-171.	8.8	165
30	Structural basis for basal activity and autoactivation of abscisic acid (ABA) signaling SnRK2 kinases. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 21259-21264.	7.1	160
31	MLN4924: a novel first-in-class inhibitor of NEDD8-activating enzyme for cancer therapy. Expert Opinion on Investigational Drugs, 2012, 21, 1563-1573.	4.1	154
32	Selective Chemical Inhibition of PGC-1Î± Gluconeogenic Activity Ameliorates Type 2 Diabetes. Cell, 2017, 169, 148-160.e15.	28.9	153
33	Destabilization of strigolactone receptor DWARF14 by binding of ligand and E3-ligase signaling effector DWARF3. Cell Research, 2015, 25, 1219-1236.	12.0	152
34	An alternate binding site for PPARÎ³ ligands. Nature Communications, 2014, 5, 3571.	12.8	148
35	Bufalin Is a Potent Small-Molecule Inhibitor of the Steroid Receptor Coactivators SRC-3 and SRC-1. Cancer Research, 2014, 74, 1506-1517.	0.9	145
36	Identification of SR1078, a Synthetic Agonist for the Orphan Nuclear Receptors RORÎ± and RORÎ³. ACS Chemical Biology, 2010, 5, 1029-1034.	3.4	140

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37	CMT2D neuropathy is linked to the neomorphic binding activity of glycyl-tRNA synthetase. Nature, 2015, 526, 710-714.	27.8	137
38	Advancing Biological Understanding and Therapeutics Discovery with Small-Molecule Probes. Cell, 2015, 161, 1252-1265.	28.9	135
39	A new peptide in the FMRFamide family isolated from the CNS of the hawkmoth, Manduca sexta. Peptides, 1990, 11, 849-856.	2.4	134
40	Ligand and Receptor Dynamics Contribute to the Mechanism of Graded PPARÎ³ Agonism. Structure, 2012, 20, 139-150.	3.3	133
41	Ligand-Dependent Perturbation of the Conformational Ensemble for the GPCR Î²2 Adrenergic Receptor Revealed by HDX. Structure, 2011, 19, 1424-1432.	3.3	129
42	Identification of SR2211: A Potent Synthetic RORÎ³-Selective Modulator. ACS Chemical Biology, 2012, 7, 672-677.	3.4	126
43	Identification and Mechanism of 10-Carbon Fatty Acid as Modulating Ligand of Peroxisome Proliferator-activated Receptors. Journal of Biological Chemistry, 2012, 287, 183-195.	3.4	119
44	Rapid analysis of protein structure and dynamics by hydrogen/deuterium exchange mass spectrometry. Journal of Biomolecular Techniques, 2003, 14, 171-82.	1.5	116
45	Regulation of Adipogenesis by Natural and Synthetic REV-ERB Ligands. Endocrinology, 2010, 151, 3015-3025.	2.8	115
46	Dynamics of the Î²₂-Adrenergic G-Protein Coupled Receptor Revealed by Hydrogenâ^'Deuterium Exchange. Analytical Chemistry, 2010, 82, 1100-1108.	6.5	115
47	Identification of SR3335 (ML-176): A Synthetic RORÎ± Selective Inverse Agonist. ACS Chemical Biology, 2011, 6, 218-222.	3.4	114
48	Structural and mechanistic bases for a potent HIV-1 capsid inhibitor. Science, 2020, 370, 360-364.	12.6	114
49	Resveratrol modulates the inflammatory response via an estrogen receptor-signal integration network. ELife, 2014, 3, e02057.	6.0	113
50	Genomic and Nongenomic Signaling Induced by 1Î±,25(OH)2-Vitamin D3 Promotes the Recovery of Amyloid-Î² Phagocytosis by Alzheimer's Disease Macrophages. Journal of Alzheimer's Disease, 2012, 29, 51-62.	2.6	107
51	Hydrogen/deuterium-exchange (H/D-Ex) of PPARÎ³ LBD in the presence of various modulators. Protein Science, 2006, 15, 1883-1892.	7.6	106
52	The Therapeutic Potential of Nuclear Receptor Modulators for Treatment of Metabolic Disorders: PPARÎ³, RORs, and Rev-erbs. Cell Metabolism, 2014, 19, 193-208.	16.2	106
53	Targeting Orphan Nuclear Receptors for Treatment of Metabolic Diseases and Autoimmunity. Chemistry and Biology, 2012, 19, 51-59.	6.0	101
54	Structural Basis for Ligand Regulation of the Fatty Acid-binding Protein 5, Peroxisome Proliferator-activated Receptor Î²/Î´ (FABP5-PPARÎ²/Î´) Signaling Pathway. Journal of Biological Chemistry, 2014, 289, 14941-14954.	3.4	101

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55	Structural mechanism for signal transduction in RXR nuclear receptor heterodimers. Nature Communications, 2015, 6, 8013.	12.8	101
56	Pharmacological repression of PPARÎ³ promotes osteogenesis. Nature Communications, 2015, 6, 7443.	12.8	99
57	L-764406 Is a Partial Agonist of Human Peroxisome Proliferator-activated Receptor Î³. Journal of Biological Chemistry, 1999, 274, 7913-7922.	3.4	97
58	HD desktop: An integrated platform for the analysis and visualization of H/D exchange data. Journal of the American Society for Mass Spectrometry, 2009, 20, 601-610.	2.8	97
59	Hydrogen/Deuterium Exchange Reveals Distinct Agonist/Partial Agonist Receptor Dynamics within Vitamin D Receptor/Retinoid X Receptor Heterodimer. Structure, 2010, 18, 1332-1341.	3.3	93
60	Direct database searching with MALDI-PSD spectra of peptides. Rapid Communications in Mass Spectrometry, 1995, 9, 1546-1551.	1.5	89
61	Prediction of the tissue-specificity of selective estrogen receptor modulators by using a single biochemical method. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 7171-7176.	7.1	87
62	Structural analysis of proteins by capillary HPLC electrospray tandem mass spectrometry. International Journal of Mass Spectrometry and Ion Processes, 1991, 111, 131-149.	1.8	86
63	SPA70 is a potent antagonist of human pregnane X receptor. Nature Communications, 2017, 8, 741.	12.8	82
64	Pharmacologic Repression of Retinoic Acid Receptorâ€“Related Orphan Nuclear Receptor Î³ Is Therapeutic in the Collagenâ€Induced Arthritis Experimental Model. Arthritis and Rheumatology, 2014, 66, 579-588.	5.6	81
65	Effect of Signal Interference from Dosing Excipients on Pharmacokinetic Screening of Drug Candidates by Liquid Chromatography/Mass Spectrometry. Analytical Chemistry, 2002, 74, 6305-6313.	6.5	80
66	PPARÎ³ Antagonist Gleevec Improves Insulin Sensitivity and Promotes the Browning of White Adipose Tissue. Diabetes, 2016, 65, 829-839.	0.6	80
67	Identification of Specific Hemopexin-like Domain Residues That Facilitate Matrix Metalloproteinase Collagenolytic Activity. Journal of Biological Chemistry, 2009, 284, 24017-24024.	3.4	79
68	Automated Hydrogen/Deuterium Exchange Electron Transfer Dissociation High Resolution Mass Spectrometry Measured at Single-Amide Resolution. Journal of the American Society for Mass Spectrometry, 2012, 23, 301-309.	2.8	79
69	HDX-MS guided drug discovery: small molecules and biopharmaceuticals. Current Opinion in Structural Biology, 2014, 28, 105-111.	5.7	78
70	Antidiabetic phospholipidâ€“nuclear receptor complex reveals the mechanism for phospholipid-driven gene regulation. Nature Structural and Molecular Biology, 2012, 19, 532-537.	8.2	73
71	The SERM/SERD bazedoxifene disrupts ESR1 helix 12 to overcome acquired hormone resistance in breast cancer cells. ELife, 2018, 7, .	6.0	72
72	The AP-1-BATF and -BATF3 module is essential for growth, survival and TH17/ILC3 skewing of anaplastic large cell lymphoma. Leukemia, 2018, 32, 1994-2007.	7.2	70

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73	Nitric Oxide-Induced Conformational Changes in Soluble Guanylate Cyclase. Structure, 2014, 22, 602-611.	3.3	68
74	Identification of a Selective RORÎ³ Ligand That Suppresses T_H17 Cells and Stimulates T Regulatory Cells. ACS Chemical Biology, 2012, 7, 1515-1519.	3.4	67
75	Time Window Expansion for HDX Analysis of an Intrinsically Disordered Protein. Journal of the American Society for Mass Spectrometry, 2013, 24, 1584-1592.	2.8	67
76	Adenosine: A Partial Agonist of the Growth Hormone Secretagogue Receptor. Biochemical and Biophysical Research Communications, 2000, 276, 1306-1313.	2.1	64
77	PPARG Post-translational Modifications Regulate Bone Formation and Bone Resorption. EBioMedicine, 2016, 10, 174-184.	6.1	64
78	Microchemical structural determination of a peptoid covalently bound to a polymeric bead by matrix-assisted laser desorption ionization time-of-flight mass spectrometry. Tetrahedron Letters, 1994, 35, 4283-4286.	1.4	62
79	Biophysical mechanisms for large-effect mutations in the evolution of steroid hormone receptors. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11475-11480.	7.1	61
80	Protein dynamics and conformational changes explored by hydrogen/deuterium exchange mass spectrometry. Current Opinion in Structural Biology, 2019, 58, 305-313.	5.7	58
81	Development of a High Specific Activity Sulfur-35-Labeled Sulfonamide Radioligand That Allowed the Identification of a New Growth Hormone Secretagogue Receptor. Journal of Medicinal Chemistry, 1996, 39, 1767-1770.	6.4	56
82	Potent, Selective and Cell Penetrant Inhibitors of SF-1 by Functional Ultra-High-Throughput Screening. Molecular Pharmacology, 2008, 73, 1776-1784.	2.3	56
83	Disorder-to-order transition underlies the structural basis for the assembly of a transcriptionally active PGC-1Î±/ERRÎ³ complex. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 18678-18683.	7.1	56
84	Ligand regulation of retinoic acid receptor-related orphan receptors: implications for development of novel therapeutics. Current Opinion in Lipidology, 2010, 21, 204-211.	2.7	55
85	Defining a conformational ensemble that directs activation of PPARÎ³. Nature Communications, 2018, 9, 1794.	12.8	53
86	Unique Ligand Binding Patterns between Estrogen Receptor Î± and Î² Revealed by Hydrogenâ^'Deuterium Exchange. Biochemistry, 2009, 48, 9668-9676.	2.5	52
87	A Residue-Resolved Bayesian Approach to Quantitative Interpretation of Hydrogenâ€“Deuterium Exchange from Mass Spectrometry: Application to Characterizing Proteinâ€“Ligand Interactions. Journal of Physical Chemistry B, 2017, 121, 3493-3501.	2.6	52
88	Structural insights into RNA recognition by the Chikungunya virus nsP2 helicase. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 9558-9567.	7.1	50
89	Defining the Communication between Agonist and Coactivator Binding in the Retinoid X Receptor Î± Ligand Binding Domain. Journal of Biological Chemistry, 2014, 289, 814-826.	3.4	49
90	Improving digestion efficiency under H/D exchange conditions with activated pepsinogen coupled columns. International Journal of Mass Spectrometry, 2007, 259, 130-139.	1.5	48

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91	Synthetic RORÎ³t Agonists Enhance Protective Immunity. ACS Chemical Biology, 2016, 11, 1012-1018.	3.4	48
92	Full antagonism of the estrogen receptor without a prototypical ligand side chain. Nature Chemical Biology, 2017, 13, 111-118.	8.0	48
93	Binding of the N-terminal Region of Coactivator TIF2 to the Intrinsically Disordered AF1 Domain of the Glucocorticoid Receptor Is Accompanied by Conformational Reorganizations. Journal of Biological Chemistry, 2012, 287, 44546-44560.	3.4	46
94	Identification of a Small Molecular Insulin Receptor Agonist With Potent Antidiabetes Activity. Diabetes, 2014, 63, 1394-1409.	0.6	45
95	Synergistic Regulation of Coregulator/Nuclear Receptor Interaction by Ligand and DNA. Structure, 2017, 25, 1506-1518.e4.	3.3	45
96	Noncanonical agonist PPARÎ³ ligands modulate the response to DNA damage and sensitize cancer cells to cytotoxic chemotherapy. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 561-566.	7.1	45
97	A molecular switch regulating transcriptional repression and activation of PPARÎ³. Nature Communications, 2020, 11, 956.	12.8	45
98	Methods for the analysis of high precision differential hydrogenâ€“deuterium exchange data. International Journal of Mass Spectrometry, 2011, 302, 59-68.	1.5	44
99	A two-stage differential hydrogen deuterium exchange method for the rapid characterization of protein/ligand interactions. Journal of Biomolecular Techniques, 2007, 18, 194-204.	1.5	44
100	Ablation of PM20D1 reveals N-acyl amino acid control of metabolism and nociception. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E6937-E6945.	7.1	43
101	Regulation of the Structurally Dynamic N-terminal Domain of Progesterone Receptor by Protein-induced Folding. Journal of Biological Chemistry, 2013, 288, 30285-30299.	3.4	42
102	Antiproliferation Activity of a Small Molecule Repressor of Liver Receptor Homolog 1. Molecular Pharmacology, 2015, 87, 296-304.	2.3	42
103	Lipid binding promotes the open conformation and tumor-suppressive activity of neurofibromin 2. Nature Communications, 2018, 9, 1338.	12.8	42
104	Structure of an AMPK complex in an inactive, ATP-bound state. Science, 2021, 373, 413-419.	12.6	42
105	Targeting the Peroxisome Proliferator-Activated Receptor-Î³ to Counter the Inflammatory Milieu in Obesity. Diabetes and Metabolism Journal, 2013, 37, 395.	4.7	40
106	Molecular assembly of rhodopsin with G protein-coupled receptor kinases. Cell Research, 2017, 27, 728-747.	12.0	40
107	PPARÎ³ in Complex with an Antagonist and Inverse Agonist: a Tumble and Trap Mechanism of the Activation Helix. IScience, 2018, 5, 69-79.	4.1	40
108	Structures of the human LONP1 protease reveal regulatory steps involved in protease activation. Nature Communications, 2021, 12, 3239.	12.8	40

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109	Deconvoluting AMP-activated protein kinase (AMPK) adenine nucleotide binding and sensing. Journal of Biological Chemistry, 2017, 292, 12653-12666.	3.4	39
110	HDX reveals the conformational dynamics of DNA sequence specific VDR co-activator interactions. Nature Communications, 2017, 8, 923.	12.8	39
111	Direct interaction of a vancomycin derivative with bacterial enzymes involved in cell wall biosynthesis. Chemistry and Biology, 2001, 8, 1095-1106.	6.0	38
112	Activation of AMP-Activated Protein Kinase Revealed by Hydrogen/Deuterium Exchange Mass Spectrometry. Structure, 2013, 21, 1942-1953.	3.3	38
113	Neddylation requires glycyl-tRNA synthetase to protect activated E2. Nature Structural and Molecular Biology, 2016, 23, 730-737.	8.2	38
114	A structural mechanism for directing corepressor-selective inverse agonism of PPARÎ³. Nature Communications, 2018, 9, 4687.	12.8	38
115	Histone H3 binding to the PHD1 domain of histone demethylase KDM5A enables active site remodeling. Nature Communications, 2019, 10, 94.	12.8	38
116	High-Throughput Screening for Drugs That Inhibit Papain-Like Protease in SARS-CoV-2. SLAS Discovery, 2020, 25, 1152-1161.	2.7	38
117	Identification and function of conformational dynamics in the multidomain <scp>GTP</scp> ase dynamin. EMBO Journal, 2016, 35, 443-457.	7.8	37
118	Defining a Canonical Ligand-Binding Pocket in the Orphan Nuclear Receptor Nurr1. Structure, 2019, 27, 66-77.e5.	3.3	37
119	Multivalent interactions drive nucleosome binding and efficient chromatin deacetylation by SIRT6. Nature Communications, 2020, 11, 5244.	12.8	36
120	Primary structures of two proteins from the venom of the Mexican red knee tarantula (Brachypelma) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.6	35
121	A Steric â€œBall-and-Chainâ€•Mechanism for pH-Mediated Regulation of Gap Junction Channels. Cell Reports, 2020, 31, 107482.	6.4	35
122	Molecular Cloning and Functional Expression of Mannitol-1-phosphatase from the Apicomplexan Parasite Eimeria tenella. Journal of Biological Chemistry, 1998, 273, 4237-4244.	3.4	34
123	SR2067 Reveals a Unique Kinetic and Structural Signature for PPARÎ³ Partial Agonism. ACS Chemical Biology, 2016, 11, 273-283.	3.4	34
124	Development of Novel Pharmacotherapeutics for Tobacco Dependence: Progress and Future Directions. Nicotine and Tobacco Research, 2012, 14, 1300-1318.	2.6	33
125	Antiobesity Effect of a Small Molecule Repressor of RORÎ³. Molecular Pharmacology, 2015, 88, 48-56.	2.3	33
126	Identification of Verrucarin A as a Potent and Selective Steroid Receptor Coactivator-3 Small Molecule Inhibitor. PLoS ONE, 2014, 9, e95243.	2.5	33

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127	The structural basis for recognition of base J containing DNA by a novel DNA binding domain in JBP1. Nucleic Acids Research, 2011, 39, 5715-5728.	14.5	32
128	Protein Conformation Ensembles Monitored by HDX Reveal a Structural Rationale for Abscisic Acid Signaling Protein Affinities and Activities. Structure, 2013, 21, 229-235.	3.3	31
129	The Methionine Transamination Pathway Controls Hepatic Glucose Metabolism through Regulation of the GCN5 Acetyltransferase and the PGC-1Î± Transcriptional Coactivator. Journal of Biological Chemistry, 2016, 291, 10635-10645.	3.4	31
130	Primary structure of Î³-bungarotoxin, a new postsynaptic neurotoxin from venom of Bungarus multicinctus. Toxicon, 1999, 37, 609-625.	1.6	30
131	Affinity Labeling, Molecular Cloning, and Comparative Amino Acid Sequence Analyses of Sex Steroid-Binding Protein of Plasma.. Annals of the New York Academy of Sciences, 1988, 538, 10-24.	3.8	29
132	The Competitive Interplay between Allosteric HIV-1 Integrase Inhibitor BI/D and LEDGF/p75 during the Early Stage of HIV-1 Replication Adversely Affects Inhibitor Potency. ACS Chemical Biology, 2016, 11, 1313-1321.	3.4	29
133	Structures of AMP-activated protein kinase bound to novel pharmacological activators in phosphorylated, non-phosphorylated, and nucleotide-free states. Journal of Biological Chemistry, 2019, 294, 953-967.	3.4	29
134	Small molecule amides as potent ROR-Î³ selective modulators. Bioorganic and Medicinal Chemistry Letters, 2013, 23, 532-536.	2.2	28
135	A Critical Role of the C-terminal Segment for Allosteric Inhibitor-induced Aberrant Multimerization of HIV-1 Integrase. Journal of Biological Chemistry, 2014, 289, 26430-26440.	3.4	28
136	Influence of Domain Interactions on Conformational Mobility of the Progesterone Receptor Detected by Hydrogen/Deuterium Exchange Mass Spectrometry. Structure, 2014, 22, 961-973.	3.3	27
137	Complete enzymatic deglycosylation of native sex steroidâ€binding protein (SBP or SHBG) of human and rabbit plasma: Effect on the steroidâ€binding activity. Protein Science, 1992, 1, 902-909.	7.6	26
138	Mass Spectrometry Screening of Combinatorial Mixtures, Correlation of Measured and Predicted Electrospray Ionization Spectra. Analytical Chemistry, 2001, 73, 2941-2951.	6.5	26
139	Helix 11 Dynamics Is Critical for Constitutive Androstane Receptor Activity. Structure, 2011, 19, 37-44.	3.3	26
140	A Combined Ligandâ€•and Structureâ€Based Virtual Screening Protocol Identifies Submicromolar PPARÎ³ Partial Agonists. ChemMedChem, 2011, 6, 94-103.	3.2	26
141	Synthetic modulators of the retinoic acid receptor-related orphan receptors. MedChemComm, 2013, 4, 764.	3.4	26
142	HDX-MS reveals dysregulated checkpoints that compromise discrimination against self RNA during RIG-I mediated autoimmunity. Nature Communications, 2018, 9, 5366.	12.8	26
143	Structural Basis of Altered Potency and Efficacy Displayed by a Major in Vivo Metabolite of the Antidiabetic PPARÎ³ Drug Pioglitazone. Journal of Medicinal Chemistry, 2019, 62, 2008-2023.	6.4	26
144	An Antibody with a Variableâ€Region Coiledâ€Coil â€œKnobâ€•Domain. Angewandte Chemie - International Edition, 2014, 53, 132-135.	13.8	25

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145	Design, Synthesis, and Biological Evaluation of Indole Biphenylcarboxylic Acids as PPARÎ³ Antagonists. ACS Medicinal Chemistry Letters, 2015, 6, 998-1003.	2.8	25
146	Crystal Structures of the Nuclear Receptor, Liver Receptor Homolog 1, Bound to Synthetic Agonists. Journal of Biological Chemistry, 2016, 291, 25281-25291.	3.4	25
147	Two-Site Evaluation of the Repeatability and Precision of an Automated Dual-Column Hydrogen/Deuterium Exchange Mass Spectrometry Platform. Analytical Chemistry, 2016, 88, 6607-6614.	6.5	25
148	Proteolysis by Granzyme B Enhances Presentation of Autoantigenic Peptidylarginine Deiminase 4 Epitopes in Rheumatoid Arthritis. Journal of Proteome Research, 2017, 16, 355-365.	3.7	25
149	Integration of G Protein Î± (GÎ±) Signaling by the Regulator of G Protein Signaling 14 (RGS14). Journal of Biological Chemistry, 2015, 290, 9037-9049.	3.4	24
150	N-Arylsulfonyl Indolines as Retinoic Acid Receptor-Related Orphan Receptorâ€…Î³ (RORÎ³) Agonists. ChemMedChem, 2016, 11, 2607-2620.	3.2	24
151	Chemical Crosslinking Mass Spectrometry Reveals the Conformational Landscape of the Activation Helix of PPARÎ³; a Model for Ligand-Dependent Antagonism. Structure, 2018, 26, 1431-1439.e6.	3.3	24
152	Cryo-EM structure of human GPR158 receptor coupled to the RGS7-GÎ²5 signaling complex. Science, 2022, 375, 86-91.	12.6	24
153	Inhibiting AMPylation: A Novel Screen To Identify the First Small Molecule Inhibitors of Protein AMPylation. ACS Chemical Biology, 2014, 9, 433-442.	3.4	23
154	PPARG in osteocytes controls sclerostin expression, bone mass, marrow adiposity and mediates TZD-induced bone loss. Bone, 2021, 147, 115913.	2.9	23
155	Ordered assembly of the cytosolic RNA-sensing MDA5-MAVS signaling complex via binding to unanchored K63-linked poly-ubiquitin chains. Immunity, 2021, 54, 2218-2230.e5.	14.3	23
156	Structureâ€“Activity Relationship of 2,4-Dichloro-N-(3,5-dichloro-4-(quinolin-3-yloxy)phenyl)benzenesulfonamide (INT131) Analogs for PPARÎ³-Targeted Antidiabetics. Journal of Medicinal Chemistry, 2017, 60, 4584-4593.	6.4	22
157	Structure and Dynamics of the Liver Receptor Homolog 1â€“PGC1Î± Complex. Molecular Pharmacology, 2017, 92, 1-11.	2.3	22
158	Binding interface and impact on protease cleavage for an RNA aptamer to HIV-1 reverse transcriptase. Nucleic Acids Research, 2020, 48, 2709-2722.	14.5	22
159	One-step construction of circularized nanodiscs using SpyCatcher-SpyTag. Nature Communications, 2021, 12, 5451.	12.8	22
160	Efficient Methodology for the Synthesis of 3-Amino-1,2,4-triazoles. Journal of Organic Chemistry, 2009, 74, 7595-7597.	3.2	21
161	Interactome Analysis Reveals Regulator of G Protein Signaling 14 (RGS14) is a Novel Calcium/Calmodulin (Ca²⁺/CaM) and CaM Kinase II (CaMKII) Binding Partner. Journal of Proteome Research, 2018, 17, 1700-1711.	3.7	21
162	Quantitative structural assessment of graded receptor agonism. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 22179-22188.	7.1	21

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