Bruce D Pascal

List of Publications by Year in descending order

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43

all docs

279701 302012 3,708 39 23 39 citations h-index g-index papers

43

43 5872 docs citations times ranked citing authors

#	Article	IF	CITATIONS
1	Crystal structure of rhodopsin bound to arrestin by femtosecond X-ray laser. Nature, 2015, 523, 561-567.	13.7	683
2	Recommendations for performing, interpreting and reporting hydrogen deuterium exchange mass spectrometry (HDX-MS) experiments. Nature Methods, 2019, 16, 595-602.	9.0	452
3	Irisin Mediates Effects on Bone and Fat via αV Integrin Receptors. Cell, 2018, 175, 1756-1768.e17.	13.5	372
4	Probing Protein Ligand Interactions by Automated Hydrogen/Deuterium Exchange Mass Spectrometry. Analytical Chemistry, 2006, 78, 1005-1014.	3.2	289
5	HDX Workbench: Software for the Analysis of H/D Exchange MS Data. Journal of the American Society for Mass Spectrometry, 2012, 23, 1512-1521.	1.2	258
6	Differential hydrogen/deuterium exchange mass spectrometry analysis of protein–ligand interactions. Expert Review of Proteomics, 2011, 8, 43-59.	1.3	208
7	DNA binding alters coactivator interaction surfaces of the intact VDR–RXR complex. Nature Structural and Molecular Biology, 2011, 18, 556-563.	3.6	185
8	Dynamics of the \hat{l}^2 (sub>2-Adrenergic G-Protein Coupled Receptor Revealed by Hydrogenâ' Deuterium Exchange. Analytical Chemistry, 2010, 82, 1100-1108.	3.2	115
9	Conformational states of the full-length glucagon receptor. Nature Communications, 2015, 6, 7859.	5.8	110
10	The Therapeutic Potential of Nuclear Receptor Modulators for Treatment of Metabolic Disorders: $PPAR\hat{I}^3$, RORs, and Rev-erbs. Cell Metabolism, 2014, 19, 193-208.	7.2	106
11	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.	1.2	97
12	Hydrogen/Deuterium Exchange Reveals Distinct Agonist/Partial Agonist Receptor Dynamics within Vitamin D Receptor/Retinoid X Receptor Heterodimer. Structure, 2010, 18, 1332-1341.	1.6	93
13	Nitric Oxide-Induced Conformational Changes in Soluble Guanylate Cyclase. Structure, 2014, 22, 602-611.	1.6	68
14	Time Window Expansion for HDX Analysis of an Intrinsically Disordered Protein. Journal of the American Society for Mass Spectrometry, 2013, 24, 1584-1592.	1.2	67
15	Protein dynamics and conformational changes explored by hydrogen/deuterium exchange mass spectrometry. Current Opinion in Structural Biology, 2019, 58, 305-313.	2.6	58
16	Unique Ligand Binding Patterns between Estrogen Receptor \hat{l}_{\pm} and \hat{l}_{\pm}^2 Revealed by Hydrogenâ-'Deuterium Exchange. Biochemistry, 2009, 48, 9668-9676.	1.2	52
17	A Residue-Resolved Bayesian Approach to Quantitative Interpretation of Hydrogen–Deuterium Exchange from Mass Spectrometry: Application to Characterizing Protein–Ligand Interactions. Journal of Physical Chemistry B, 2017, 121, 3493-3501.	1.2	52
18	Methods for the analysis of high precision differential hydrogen–deuterium exchange data. International Journal of Mass Spectrometry, 2011, 302, 59-68.	0.7	44

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19	A two-stage differential hydrogen deuterium exchange method for the rapid characterization of protein/ligand interactions. Journal of Biomolecular Techniques, 2007, 18, 194-204.	0.8	44
20	HDX reveals the conformational dynamics of DNA sequence specific VDR co-activator interactions. Nature Communications, 2017, 8, 923.	5.8	39
21	Activation of AMP-Activated Protein Kinase Revealed by Hydrogen/Deuterium Exchange Mass Spectrometry. Structure, 2013, 21, 1942-1953.	1.6	38
22	Protein Conformation Ensembles Monitored by HDX Reveal a Structural Rationale for Abscisic Acid Signaling Protein Affinities and Activities. Structure, 2013, 21, 229-235.	1.6	31
23	Influence of Domain Interactions on Conformational Mobility of the Progesterone Receptor Detected by Hydrogen/Deuterium Exchange Mass Spectrometry. Structure, 2014, 22, 961-973.	1.6	27
24	HDX-MS reveals dysregulated checkpoints that compromise discrimination against self RNA during RIG-I mediated autoimmunity. Nature Communications, 2018, 9, 5366.	5 . 8	26
25	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.	3.2	25
26	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.	6.6	23
27	Nucleotide Binding to ARL2 in the TBCD â^™ ARL2 â^™ β-Tubulin Complex Drives Conformational Changes in β-Tubulin. Journal of Molecular Biology, 2017, 429, 3696-3716.	2.0	18
28	Structural organization of a major neuronal G protein regulator, the RGS7-GÎ 2 5-R7BP complex. ELife, 2018, 7, .	2.8	18
29	Identification of Bexarotene as a PPAR <mml:math id="M1" xmlns:mml="http://www.w3.org/1998/Math/MathML"><mml:mrow><mml:mi mathvariant="bold-italic">γ</mml:mi></mml:mrow></mml:math> Antagonist with HDX. PPAR Research, 2015, 2015, 1-6.	1.1	17
30	Dual-mechanism estrogen receptor inhibitors. Proceedings of the National Academy of Sciences of the United States of America, $2021,118,118$	3.3	16
31	A Decoupled Automation Platform for Hydrogen/Deuterium Exchange Mass Spectrometry Experiments. Journal of the American Society for Mass Spectrometry, 2019, 30, 2580-2583.	1.2	14
32	Glucagon-Like Peptide-1 Receptor Ligand Interactions: Structural Cross Talk between Ligands and the Extracellular Domain. PLoS ONE, 2014, 9, e105683.	1.1	13
33	Comparative Analysis of Cleavage Specificities of Immobilized Porcine Pepsin and Nepenthesin II under Hydrogen/Deuterium Exchange Conditions. Analytical Chemistry, 2020, 92, 11018-11028.	3.2	12
34	SERBP1 Is a Component of the Liver Receptor Homologue-1 Transcriptional Complex. Journal of Proteome Research, 2015, 14, 4571-4580.	1.8	9
35	The intrinsically disordered CARDsâ€Helicase linker in RIGâ€I is a molecular gate for RNA proofreading. EMBO Journal, 2022, 41, e109782.	3.5	9
36	Integrative structural biology studies of HIV-1 reverse transcriptase binding to a high-affinity DNA aptamer. Current Research in Structural Biology, 2020, 2, 116-129.	1.1	8

BRUCE D PASCAL

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37	Structural and Dynamic Elucidation of a Non-acid PPAR \hat{I}^3 Partial Agonist: SR1988. Nuclear Receptor Research, 2018, 5, .	2.5	5
38	Differential Isotopic Enrichment To Facilitate Characterization of Asymmetric Multimeric Proteins Using Hydrogen/Deuterium Exchange Mass Spectrometry. Analytical Chemistry, 2015, 87, 4015-4022.	3.2	4
39	Software Analysis of Uncorrelated MS1 Peaks for Discovery of Post-Translational Modifications. Journal of the American Society for Mass Spectrometry, 2015, 26, 2133-2140.	1.2	2