

Bruce D Pascal

List of Publications by Year in descending order

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papers

3,708
citations

279798

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302126

39
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43
docs citations

43
times ranked

5872
citing authors

#	ARTICLE	IF	CITATIONS
1	The intrinsically disordered CARDsâ€Helicase linker in RIGâ€ is a molecular gate for RNA proofreading. EMBO Journal, 2022, 41, e109782.	7.8	9
2	Dual-mechanism estrogen receptor inhibitors. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	16
3	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
4	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.	2.2	8
5	Comparative Analysis of Cleavage Specificities of Immobilized Porcine Pepsin and Nepenthesin II under Hydrogen/Deuterium Exchange Conditions. Analytical Chemistry, 2020, 92, 11018-11028.	6.5	12
6	Protein dynamics and conformational changes explored by hydrogen/deuterium exchange mass spectrometry. Current Opinion in Structural Biology, 2019, 58, 305-313.	5.7	58
7	Recommendations for performing, interpreting and reporting hydrogen deuterium exchange mass spectrometry (HDX-MS) experiments. Nature Methods, 2019, 16, 595-602.	19.0	452
8	A Decoupled Automation Platform for Hydrogen/Deuterium Exchange Mass Spectrometry Experiments. Journal of the American Society for Mass Spectrometry, 2019, 30, 2580-2583.	2.8	14
9	Structural organization of a major neuronal G protein regulator, the RGS7-GÎ²5-R7BP complex. ELife, 2018, 7, .	6.0	18
10	HDX-MS reveals dysregulated checkpoints that compromise discrimination against self RNA during RIG-I mediated autoimmunity. Nature Communications, 2018, 9, 5366.	12.8	26
11	Irisin Mediates Effects on Bone and Fat via Î±V Integrin Receptors. Cell, 2018, 175, 1756-1768.e17.	28.9	372
12	Structural and Dynamic Elucidation of a Non-acid PPARÎ³ Partial Agonist: SR1988. Nuclear Receptor Research, 2018, 5, .	2.5	5
13	Nucleotide Binding to ARL2 in the TBCD â™ ARL2 â™ Î²-Tubulin Complex Drives Conformational Changes in Î²-Tubulin. Journal of Molecular Biology, 2017, 429, 3696-3716.	4.2	18
14	HDX reveals the conformational dynamics of DNA sequence specific VDR co-activator interactions. Nature Communications, 2017, 8, 923.	12.8	39
15	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
16	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
17	Identification of Bexarotene as a PPAR<math xmlns:mml="http://www.w3.org/1998/Math/MathML" id="M1"><mml:mrow><mml:mi mathvariant="bold-italic">Î³</mml:mi></mml:mrow></mml:math> Antagonist with HDX. PPAR Research, 2015. 2015, 1-6.	2.4	17
18	Conformational states of the full-length glucagon receptor. Nature Communications, 2015, 6, 7859.	12.8	110

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19	Crystal structure of rhodopsin bound to arrestin by femtosecond X-ray laser. <i>Nature</i> , 2015, 523, 561-567.	27.8	683
20	Differential Isotopic Enrichment To Facilitate Characterization of Asymmetric Multimeric Proteins Using Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Analytical Chemistry</i> , 2015, 87, 4015-4022.	6.5	4
21	SERBP1 Is a Component of the Liver Receptor Homologue-1 Transcriptional Complex. <i>Journal of Proteome Research</i> , 2015, 14, 4571-4580.	3.7	9
22	Software Analysis of Uncorrelated MS1 Peaks for Discovery of Post-Translational Modifications. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 2133-2140.	2.8	2
23	Glucagon-Like Peptide-1 Receptor Ligand Interactions: Structural Cross Talk between Ligands and the Extracellular Domain. <i>PLoS ONE</i> , 2014, 9, e105683.	2.5	13
24	The Therapeutic Potential of Nuclear Receptor Modulators for Treatment of Metabolic Disorders: PPAR β , RORs, and Rev-erbs. <i>Cell Metabolism</i> , 2014, 19, 193-208.	16.2	106
25	Nitric Oxide-Induced Conformational Changes in Soluble Guanylate Cyclase. <i>Structure</i> , 2014, 22, 602-611.	3.3	68
26	Influence of Domain Interactions on Conformational Mobility of the Progesterone Receptor Detected by Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Structure</i> , 2014, 22, 961-973.	3.3	27
27	Time Window Expansion for HDX Analysis of an Intrinsically Disordered Protein. <i>Journal of the American Society for Mass Spectrometry</i> , 2013, 24, 1584-1592.	2.8	67
28	Activation of AMP-Activated Protein Kinase Revealed by Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Structure</i> , 2013, 21, 1942-1953.	3.3	38
29	Protein Conformation Ensembles Monitored by HDX Reveal a Structural Rationale for Abscisic Acid Signaling Protein Affinities and Activities. <i>Structure</i> , 2013, 21, 229-235.	3.3	31
30	HDX Workbench: Software for the Analysis of H/D Exchange MS Data. <i>Journal of the American Society for Mass Spectrometry</i> , 2012, 23, 1512-1521.	2.8	258
31	Differential hydrogen/deuterium exchange mass spectrometry analysis of protein-ligand interactions. <i>Expert Review of Proteomics</i> , 2011, 8, 43-59.	3.0	208
32	DNA binding alters coactivator interaction surfaces of the intact VDR-RXR complex. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 556-563.	8.2	185
33	Methods for the analysis of high precision differential hydrogen-deuterium exchange data. <i>International Journal of Mass Spectrometry</i> , 2011, 302, 59-68.	1.5	44
34	Hydrogen/Deuterium Exchange Reveals Distinct Agonist/Partial Agonist Receptor Dynamics within Vitamin D Receptor/Retinoid X Receptor Heterodimer. <i>Structure</i> , 2010, 18, 1332-1341.	3.3	93
35	Dynamics of the β_2 -Adrenergic G-Protein Coupled Receptor Revealed by Hydrogen-Deuterium Exchange. <i>Analytical Chemistry</i> , 2010, 82, 1100-1108.	6.5	115
36	HD desktop: An integrated platform for the analysis and visualization of H/D exchange data. <i>Journal of the American Society for Mass Spectrometry</i> , 2009, 20, 601-610.	2.8	97

#	ARTICLE	IF	CITATIONS
37	Unique Ligand Binding Patterns between Estrogen Receptor α and β Revealed by Hydrogen-Deuterium Exchange. <i>Biochemistry</i> , 2009, 48, 9668-9676.	2.5	52
38	A two-stage differential hydrogen deuterium exchange method for the rapid characterization of protein/ligand interactions. <i>Journal of Biomolecular Techniques</i> , 2007, 18, 194-204.	1.5	44
39	Probing Protein Ligand Interactions by Automated Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Analytical Chemistry</i> , 2006, 78, 1005-1014.	6.5	289