## Joseph S Harrison

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3409894/publications.pdf

Version: 2024-02-01

28 1,038 16 28 papers citations h-index g-index

33 33 33 1891

times ranked

citing authors

docs citations

all docs

#	Article	IF	CITATIONS
1	Glutamine Triggers Acetylation-Dependent Degradation of Glutamine Synthetase via the Thalidomide Receptor Cereblon. Molecular Cell, 2016, 61, 809-820.	9.7	132
2	Dual RING E3 Architectures Regulate Multiubiquitination and Ubiquitin Chain Elongation by APC/C. Cell, 2016, 165, 1440-1453.	28.9	126
3	Hemi-methylated DNA regulates DNA methylation inheritance through allosteric activation of H3 ubiquitylation by UHRF1. ELife, 2016, 5, .	6.0	111
4	An Allosteric Interaction Links USP7 to Deubiquitination and Chromatin Targeting of UHRF1. Cell Reports, 2015, 12, 1400-1406.	6.4	78
5	Identification and Characterization of MCM3 as a Kelch-like ECH-associated Protein 1 (KEAP1) Substrate. Journal of Biological Chemistry, 2016, 291, 23719-23733.	3.4	68
6	Inhibition of Ebola Virus Entry by a C-peptide Targeted to Endosomes. Journal of Biological Chemistry, 2011, 286, 15854-15861.	3.4	59
7	A Bifunctional Role for the UHRF1ÂUBL Domain in the Control of Hemi-methylated DNA-Dependent Histone Ubiquitylation. Molecular Cell, 2018, 72, 753-765.e6.	9.7	58
8	Role of Electrostatic Repulsion in Controlling pH-Dependent Conformational Changes of Viral Fusion Proteins. Structure, 2013, 21, 1085-1096.	3.3	53
9	Designed protein mimics of the Ebola virus glycoprotein GP2 αâ€helical bundle: Stability and pH effects. Protein Science, 2011, 20, 1587-1596.	7.6	41
10	Crystal Structure of the Marburg Virus GP2 Core Domain in Its Postfusion Conformation. Biochemistry, 2012, 51, 7665-7675.	2.5	37
11	Marburg Virus Glycoprotein GP2: pH-Dependent Stability of the Ectodomain α-Helical Bundle. Biochemistry, 2012, 51, 2515-2525.	2.5	35
12	Sulfite Reduction in Mycobacteria. Journal of Bacteriology, 2007, 189, 6714-6722.	2.2	34
13	Linkage-specific ubiquitin chain formation depends on a lysine hydrocarbon ruler. Nature Chemical Biology, 2021, 17, 272-279.	8.0	26
14	Structural Characterization of the Glycoprotein GP2 Core Domain from the CAS Virus, a Novel Arenavirus-Like Species. Journal of Molecular Biology, 2014, 426, 1452-1468.	4.2	25
15	Comparative biochemical analysis of UHRF proteins reveals molecular mechanisms that uncouple UHRF2 from DNA methylation maintenance. Nucleic Acids Research, 2018, 46, 4405-4416.	14.5	25
16	Designed, highly expressing, thermostable dengue virus 2 envelope protein dimers elicit quaternary epitope antibodies. Science Advances, 2021, 7, eabg4084.	10.3	22
17	UbSRD: The Ubiquitin Structural Relational Database. Journal of Molecular Biology, 2016, 428, 679-687.	4.2	18
18	Contribution of Light Chain Residues to High Affinity Binding in an HIV-1 Antibody Explored by Combinatorial Scanning Mutagenesis. Biochemistry, 2010, 49, 5464-5472.	2.5	15

#	Article	IF	CITATIONS
19	Mechanism of Lysine 48 Selectivity during Polyubiquitin Chain Formation by the Ube2R1/2 Ubiquitin-Conjugating Enzyme. Molecular and Cellular Biology, 2016, 36, 1720-1732.	2.3	14
20	KRAS Ubiquitination at Lysine 104 Retains Exchange Factor Regulation by Dynamically Modulating the Conformation of the Interface. IScience, 2020, 23, 101448.	4.1	14
21	Identification of disease-linked hyperactivating mutations in UBE3A through large-scale functional variant analysis. Nature Communications, 2021, 12, 6809.	12.8	10
22	Functional conservation and divergence of the helixâ€turnâ€helix motif of E2 ubiquitinâ€conjugating enzymes. EMBO Journal, 2022, 41, e108823.	7.8	8
23	In silico APC/C substrate discovery reveals cell cycle-dependent degradation of UHRF1 and other chromatin regulators. PLoS Biology, 2020, 18, e3000975.	5.6	7
24	Coevolutionary Analysis Implicates Toll-Like Receptor 9 in Papillomavirus Restriction. MBio, 2022, 13, e0005422.	4.1	5
25	Side chain requirements for affinity and specificity in D5, an HIV-1 antibody derived from the VH1-69 germline segment. BMC Biochemistry, 2013, 14, 9.	4.4	3
26	Data in support of UbSRD: The Ubiquitin Structural Relational Database. Data in Brief, 2015, 5, 605-615.	1.0	3
27	Mechanically transduced immunosorbent assay to measure protein-protein interactions. ELife, 2021, $10$ ,	6.0	3
28	From Protein Design to the Energy Landscape of a Cold Unfolding Protein. Journal of Physical Chemistry B, 2022, 126, 1212-1231.	2.6	3