

David Haselbach

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

1,429
citations

567281

15
h-index

713466

21
g-index

27
all docs

27
docs citations

27
times ranked

2150
citing authors

#	ARTICLE	IF	CITATIONS
1	Cryo-EM Structure of a Pre-catalytic Human Spliceosome Primed for Activation. <i>Cell</i> , 2017, 170, 701-713.e11.	28.9	217
2	Structure and Conformational Dynamics of the Human Spliceosomal Bact Complex. <i>Cell</i> , 2018, 172, 454-464.e11.	28.9	175
3	Quantifying the heterogeneity of macromolecular machines by mass photometry. <i>Nature Communications</i> , 2020, 11, 1772.	12.8	146
4	Dual RING E3 Architectures Regulate Multiubiquitination and Ubiquitin Chain Elongation by APC/C. <i>Cell</i> , 2016, 165, 1440-1453.	28.9	126
5	Cryo-EM of Mitotic Checkpoint Complex-Bound APC/C Reveals Reciprocal and Conformational Regulation of Ubiquitin Ligation. <i>Molecular Cell</i> , 2016, 63, 593-607.	9.7	123
6	Mechanism of APC/C ^{CDC20} activation by mitotic phosphorylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E2570-8.	7.1	112
7	ProteoPlex: stability optimization of macromolecular complexes by sparse-matrix screening of chemical space. <i>Nature Methods</i> , 2015, 12, 859-865.	19.0	87
8	Moyamoya disease factor RNF213 is a giant E3 ligase with a dynein-like core and a distinct ubiquitin-transfer mechanism. <i>ELife</i> , 2020, 9, .	6.0	74
9	Structural basis for cooperativity of CRM1 export complex formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 960-965.	7.1	64
10	Long-range allosteric regulation of the human 26S proteasome by 20S proteasome-targeting cancer drugs. <i>Nature Communications</i> , 2017, 8, 15578.	12.8	63
11	AKIRIN2 controls the nuclear import of proteasomes in vertebrates. <i>Nature</i> , 2021, 599, 491-496.	27.8	55
12	The linear ubiquitin chain assembly complex (LUBAC) generates heterotypic ubiquitin chains. <i>ELife</i> , 2021, 10, .	6.0	38
13	HUWE1 employs a giant substrate-binding ring to feed and regulate its HECT E3 domain. <i>Nature Chemical Biology</i> , 2021, 17, 1084-1092.	8.0	24
14	Structural and Functional Analyses of the Human PDH Complex Suggest a "Division-of-Labor" Mechanism by Local E1 and E3 Clusters. <i>Structure</i> , 2019, 27, 1124-1136.e4.	3.3	23
15	Protein engineering of a ubiquitin-variant inhibitor of APC/C identifies a cryptic K48 ubiquitin chain binding site. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17280-17289.	7.1	22
16	Structural Determinants and Mechanism of Mammalian CRM1 Allostery. <i>Structure</i> , 2013, 21, 1350-1360.	3.3	17
17	Structure of the peripheral arm of a minimalistic respiratory complex I. <i>Structure</i> , 2022, 30, 80-94.e4.	3.3	13
18	A DNAzyme based label-free detection system for miniaturized assays. <i>Molecular BioSystems</i> , 2011, 7, 2882.	2.9	12

#	ARTICLE	IF	CITATIONS
19	miR-1 sustains muscle physiology by controlling V-ATPase complex assembly. <i>Science Advances</i> , 2021, 7, eabh1434.	10.3	12
20	Structural basis for inhibition of the AAA-ATPase Drg1 by diazaborine. <i>Nature Communications</i> , 2021, 12, 3483.	12.8	10
21	Cryo-EM structure of the plant 26S proteasome. <i>Plant Communications</i> , 2022, 3, 100310.	7.7	7