Carlos A Castaneda

List of Publications by Year
in descending order

44 papers	2,487 citations	318942 23 h-index	286692 43 g-index
49 all docs	49 docs citations	49 times ranked	3665 citing authors

#	Article	IF	Citations
1	Polyubiquitin effects on phase transitions of shuttle protein UBQLN2. FASEB Journal, 2022, 36, .	0.2	0
2	Effects of Modulating Multivalent Ligand Binding Accessibility & Affinity on Liquidâ€Liquid Phase Separation. FASEB Journal, 2022, 36, .	0.2	0
3	Mechanistic insights into enhancement or inhibition of phase separation by different polyubiquitin chains. EMBO Reports, 2022, 23, .	2.0	26
4	Structure analysis suggests Ess1 isomerizes the carboxy-terminal domain of RNA polymerase II via a bivalent anchoring mechanism. Communications Biology, 2021, 4, 398.	2.0	7
5	Previously uncharacterized interactions between the folded and intrinsically disordered domains impart asymmetric effects on UBQLN2 phase separation. Protein Science, 2021, 30, 1467-1481.	3.1	24
6	ALSâ€linked mutations impair UBQLN2 stressâ€induced biomolecular condensate assembly in cells. Journal of Neurochemistry, 2021, 159, 145-155.	2.1	12
7	Ubiquitinâ€Modulated Phase Separation of Shuttle Proteins: Does Condensate Formation Promote Protein Degradation?. BioEssays, 2020, 42, e2000036.	1.2	33
8	Structure, dynamics and functions of UBQLNs: at the crossroads of protein quality control machinery. Biochemical Journal, 2020, 477, 3471-3497.	1.7	33
9	Phase separation in biology and diseaseâ€”a symposium report. Annals of the New York Academy of Sciences, 2019, 1452, 3-11.	1.8	14
10	ALS-Linked Mutations Affect UBQLN2 Oligomerization and Phase Separation in a Position- and Amino Acid-Dependent Manner. Structure, 2019, 27, 937-951.e5.	1.6	75
11	Single Amino Acid Substitutions in Stickers, but Not Spacers, Substantially Alter UBQLN2 Phase Transitions and Dense Phase Material Properties. Journal of Physical Chemistry B, 2019, 123, 3618-3629.	1.2	60
12	Kemp Eliminases of the AlleyCat Family Possess High Substrate Promiscuity. ChemCatChem, 2019, 11, 1425-1430.	1.8	3
13	Hydrophobic Mutations Promote UBQLN2 Oligomerization And Phase Separation. FASEB Journal, 2019, 33, 464.2.	0.2	0
14	Ubiquitin Modulates Liquid-Liquid Phase Separation of UBQLN2 via Disruption of Multivalent Interactions. Molecular Cell, 2018, 69, 965-978.e6.	4.5	257
15	Cancer Mutations in SPOP Put a Stop to Its Inter-compartmental Hops. Molecular Cell, 2018, 72, 1-3.	4.5	21
16	Functional tuning of the catalytic residue p <i>K</i> _a in a <i>de novo</i> designed esterase. Proteins: Structure, Function and Bioinformatics, 2017, 85, 1656-1665.	1.5	8
17	Structural Basis for the Inhibitory Effects of Ubistatins in the Ubiquitin-Proteasome Pathway. Structure, 2017, 25, 1839-1855.e11.	1.6	15
18	Linkage via K27 Bestows Ubiquitin Chains with Unique Properties among Polyubiquitins. Structure, 2016, 24, 423-436.	1.6	56

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19	Linkage-specific conformational ensembles of non-canonical polyubiquitin chains. Physical Chemistry Chemical Physics, 2016, 18, 5771-5788.	1.3	58
20	Base-CP proteasome can serve as a platform for stepwise lid formation. Bioscience Reports, 2015, 35, .	1.1	18
21	DNA-Damage-Inducible 1 Protein (Ddi1) Contains an Uncharacteristic Ubiquitin-like Domain that Binds Ubiquitin. Structure, 2015, 23, 542-557.	1.6	71
22	Engineered Domain Swapping as an On/Off Switch for Protein Function. Chemistry and Biology, 2015, 22, 1384-1393.	6.2	28
23	Unexpected Trypsin Cleavage at Ubiquitinated Lysines. Analytical Chemistry, 2015, 87, 8144-8148.	3.2	16
24	Preparing to read the ubiquitin code: a middleâ€out strategy for characterization of all lysineâ€linked diubiquitins. Journal of Mass Spectrometry, 2014, 49, 1272-1278.	0.7	7
25	Structural and thermodynamic consequences of burial of an artificial ion pair in the hydrophobic interior of a protein. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11685-11690.	3.3	37
26	Alanine Scan of Core Positions in Ubiquitin Reveals Links between Dynamics, Stability, and Function. Journal of Molecular Biology, 2014, 426, 1377-1389.	2.0	21
27	Modifying the Vicinity of the Isopeptide Bond To Reveal Differential Behavior of Ubiquitin Chains with Interacting Proteins: Organic Chemistry Applied to Synthetic Proteins. Angewandte Chemie - International Edition, 2013, 52, 11149-11153.	7.2	26
28	Nonenzymatic assembly of branched polyubiquitin chains for structural and biochemical studies. Bioorganic and Medicinal Chemistry, 2013, 21, 3421-3429.	1.4	35
29	Unique Structural, Dynamical, and Functional Properties of K11-Linked Polyubiquitin Chains. Structure, 2013, 21, 1168-1181.	1.6	56
30	Recovering a Representative Conformational Ensemble from Underdetermined Macromolecular Structural Data. Journal of the American Chemical Society, 2013, 135, 16595-16609.	6.6	106
31	Evidence for Cooperative and Domain-specific Binding of the Signal Transducing Adaptor Molecule 2 (STAM2) to Lys63-linked Diubiquitin. Journal of Biological Chemistry, 2012, 287, 18687-18699.	1.6	21
32	Controlled enzymatic synthesis of natural-linkage, defined-length polyubiquitin chains using lysines with removable protecting groups. Chemical Communications, 2011, 47, 2026.	2.2	36
33	Nonenzymatic Assembly of Natural Polyubiquitin Chains of Any Linkage Composition and Isotopic Labeling Scheme. Journal of the American Chemical Society, 2011, 133, 17855-17868.	6.6	85
34	Structural Origins of High Apparent Dielectric Constants Experienced by Ionizable Groups in the Hydrophobic Core of a Protein. Journal of Molecular Biology, 2011, 405, 361-377.	2.0	36
35	Segmental Isotopic Labeling of Ubiquitin Chains To Unravel Monomerâ€Specific Molecular Behavior. Angewandte Chemie - International Edition, 2011, 50, 11210-11214.	7.2	30
36	Large shifts in pK _a values of lysine residues buried inside a protein. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5260-5265.	3.3	379

#	ARTICLE	IF	CITATIONS
37	Condensed E. coli cultures for highly efficient production of proteins containing unnatural amino acids. Bioorganic and Medicinal Chemistry Letters, 2010, 20, 5613-5616.	1.0	11
38	Charges in the hydrophobic interior of proteins. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 16096-16100.	3.3	195
39	Molecular determinants of the p<i>K</i>_a values of Asp and Glu residues in staphylococcal nuclease. Proteins: Structure, Function and Bioinformatics, 2009, 77, 570-588.	1.5	150
40	The pKa Values of Acidic and Basic Residues Buried at the Same Internal Location in a Protein Are Governed by Different Factors. Journal of Molecular Biology, 2009, 389, 34-47.	2.0	120
41	Direct Evidence for Deprotonation of a Lysine Side Chain Buried in the Hydrophobic Core of a Protein. Journal of the American Chemical Society, 2008, 130, 6714-6715.	6.6	52
42	High tolerance for ionizable residues in the hydrophobic interior of proteins. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 17784-17788.	3.3	120
43	Mapping and Initial Analysis of Human Subtelomeric Sequence Assemblies. Genome Research, 2003, 14, 18-28.	2.4	107
44	Human Subtelomeric DNA. Cold Spring Harbor Symposia on Quantitative Biology, 2003, 68, 39-48.	2.0	4