

Joseph A Marsh

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

5,126
citations

109137

35
h-index

128067

60
g-index

70
all docs

70
docs citations

70
times ranked

7349
citing authors

#	ARTICLE	IF	CITATIONS
1	The properties of human disease mutations at protein interfaces. <i>PLoS Computational Biology</i> , 2022, 18, e1009858.	1.5	19
2	Novel biallelic USH2A variants in a patient with usher syndrome type IIA- a case report. <i>BMC Ophthalmology</i> , 2022, 22, 140.	0.6	0
3	Interpreting protein variant effects with computational predictors and deep mutational scanning. <i>DMM Disease Models and Mechanisms</i> , 2022, 15, .	1.2	25
4	Longitudinal dynamics of clonal hematopoiesis identifies gene-specific fitness effects. <i>Nature Medicine</i> , 2022, 28, 1439-1446.	15.2	36
5	Genetic and functional insights into CDA-I prevalence and pathogenesis. <i>Journal of Medical Genetics</i> , 2021, 58, 185-195.	1.5	9
6	Heterozygous lamin B1 and lamin B2 variants cause primary microcephaly and define a novel laminopathy. <i>Genetics in Medicine</i> , 2021, 23, 408-414.	1.1	35
7	A WDR35-dependent coat protein complex transports ciliary membrane cargo vesicles to cilia. <i>ELife</i> , 2021, 10, .	2.8	29
8	Recurrent heterozygous PAX6 missense variants cause severe bilateral microphthalmia via predictable effects on DNA-protein interaction. <i>Genetics in Medicine</i> , 2020, 22, 598-609.	1.1	43
9	Identification of pathogenic missense mutations using protein stability predictors. <i>Scientific Reports</i> , 2020, 10, 15387.	1.6	66
10	PRIM1 deficiency causes a distinctive primordial dwarfism syndrome. <i>Genes and Development</i> , 2020, 34, 1520-1533.	2.7	20
11	Using deep mutational scanning to benchmark variant effect predictors and identify disease mutations. <i>Molecular Systems Biology</i> , 2020, 16, e9380.	3.2	120
12	Ligand Binding Site Structure Shapes Folding, Assembly and Degradation of Homomeric Protein Complexes. <i>Journal of Molecular Biology</i> , 2019, 431, 3871-3888.	2.0	5
13	Evolution of protein interfaces in multimers and fibrils. <i>Journal of Chemical Physics</i> , 2019, 150, 225102.	1.2	1
14	The role of protein complexes in human genetic disease. <i>Protein Science</i> , 2019, 28, 1400-1411.	3.1	53
15	Ligands and Receptors with Broad Binding Capabilities Have Common Structural Characteristics: An Antibiotic Design Perspective. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 9357-9374.	2.9	9
16	Protein aggregation mediates stoichiometry of protein complexes in aneuploid cells. <i>Genes and Development</i> , 2019, 33, 1031-1047.	2.7	83
17	Biallelic variants in <i>DNA2</i> cause microcephalic primordial dwarfism. <i>Human Mutation</i> , 2019, 40, 1063-1070.	1.1	16
18	Ligand-Binding-Site Structure Shapes Allosteric Signal Transduction and the Evolution of Allostery in Protein Complexes. <i>Molecular Biology and Evolution</i> , 2019, 36, 1711-1727.	3.5	33

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19	Gain-of-function DNMT3A mutations cause microcephalic dwarfism and hypermethylation of Polycomb-regulated regions. <i>Nature Genetics</i> , 2019, 51, 96-105.	9.4	110
20	A Graph-Based Approach for Detecting Sequence Homology in Highly Diverged Repeat Protein Families. <i>Methods in Molecular Biology</i> , 2019, 1851, 251-261.	0.4	2
21	Cotranslational protein assembly imposes evolutionary constraints on homomeric proteins. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 279-288.	3.6	43
22	Experimental Characterization of Protein Complex Structure, Dynamics, and Assembly. <i>Methods in Molecular Biology</i> , 2018, 1764, 3-27.	0.4	4
23	Computational Modelling of Protein Complex Structure and Assembly. <i>Methods in Molecular Biology</i> , 2018, 1764, 347-356.	0.4	2
24	Ligand Binding Site Structure Influences the Evolution of Protein Complex Function and Topology. <i>Cell Reports</i> , 2018, 22, 3265-3276.	2.9	18
25	Interrogation of Mammalian Protein Complex Structure, Function, and Membership Using Genome-Scale Fitness Screens. <i>Cell Systems</i> , 2018, 6, 555-568.e7.	2.9	126
26	SMCHD1 mutations associated with a rare muscular dystrophy can also cause isolated arhinia and Bosma arhinia microphthalmia syndrome. <i>Nature Genetics</i> , 2017, 49, 238-248.	9.4	131
27	Evolution of condensin and cohesin complexes driven by replacement of Kite by Hawk proteins. <i>Current Biology</i> , 2017, 27, R17-R18.	1.8	98
28	Signalling assemblies: the odds of symmetry. <i>Biochemical Society Transactions</i> , 2017, 45, 599-611.	1.6	9
29	Regulation, evolution and consequences of cotranslational protein complex assembly. <i>Current Opinion in Structural Biology</i> , 2017, 42, 90-97.	2.6	62
30	Novel pathogenic mutations in C1QTNF5 support a dominant negative disease mechanism in late-onset retinal degeneration. <i>Scientific Reports</i> , 2017, 7, 12147.	1.6	30
31	ER stress-induced aggresome trafficking of HtrA1 protects against proteotoxicity. <i>Journal of Molecular Cell Biology</i> , 2017, 9, 516-532.	1.5	9
32	Functional determinants of protein assembly into homomeric complexes. <i>Scientific Reports</i> , 2017, 7, 4932.	1.6	52
33	Alpha Helices Are More Robust to Mutations than Beta Strands. <i>PLoS Computational Biology</i> , 2016, 12, e1005242.	1.5	85
34	A Restricted Repertoire of De Novo Mutations in ITPR1 Cause Gillespie Syndrome with Evidence for Dominant-Negative Effect. <i>American Journal of Human Genetics</i> , 2016, 98, 981-992.	2.6	81
35	Operon Gene Order Is Optimized for Ordered Protein Complex Assembly. <i>Cell Reports</i> , 2016, 14, 679-685.	2.9	91
36	Kinetic Analysis of Protein Stability Reveals Age-Dependent Degradation. <i>Cell</i> , 2016, 167, 803-815.e21.	13.5	259

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37	Co-translational assembly of protein complexes. <i>Biochemical Society Transactions</i> , 2015, 43, 1221-1226.	1.6	32
38	Principles of assembly reveal a periodic table of protein complexes. <i>Science</i> , 2015, 350, aaa2245.	6.0	198
39	Fast and Accurate Resonance Assignment of Small-to-Large Proteins by Combining Automated and Manual Approaches. <i>PLoS Computational Biology</i> , 2015, 11, e1004022.	1.5	6
40	Structural and evolutionary versatility in protein complexes with uneven stoichiometry. <i>Nature Communications</i> , 2015, 6, 6394.	5.8	48
41	Structure, Dynamics, Assembly, and Evolution of Protein Complexes. <i>Annual Review of Biochemistry</i> , 2015, 84, 551-575.	5.0	351
42	Protein Flexibility Facilitates Quaternary Structure Assembly and Evolution. <i>PLoS Biology</i> , 2014, 12, e1001870.	2.6	89
43	Parallel dynamics and evolution: Protein conformational fluctuations and assembly reflect evolutionary changes in sequence and structure. <i>BioEssays</i> , 2014, 36, 209-218.	1.2	68
44	The Role of Salt Bridges, Charge Density, and Subunit Flexibility in Determining Disassembly Routes of Protein Complexes. <i>Structure</i> , 2013, 21, 1325-1337.	1.6	82
45	Buried and Accessible Surface Area Control Intrinsic Protein Flexibility. <i>Journal of Molecular Biology</i> , 2013, 425, 3250-3263.	2.0	62
46	Characterization of disordered proteins with ENSEMBLE. <i>Bioinformatics</i> , 2013, 29, 398-399.	1.8	141
47	Protein Complexes Are under Evolutionary Selection to Assemble via Ordered Pathways. <i>Cell</i> , 2013, 153, 461-470.	13.5	215
48	The emergence of protein complexes: quaternary structure, dynamics and allostery. <i>Biochemical Society Transactions</i> , 2012, 40, 475-491.	1.6	75
49	Probing the diverse landscape of protein flexibility and binding. <i>Current Opinion in Structural Biology</i> , 2012, 22, 643-650.	2.6	94
50	Ensemble modeling of protein disordered states: Experimental restraint contributions and validation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 556-572.	1.5	107
51	Structural Signature of the MYPT1~PP1 Interaction. <i>Journal of the American Chemical Society</i> , 2011, 133, 73-80.	6.6	44
52	Relative Solvent Accessible Surface Area Predicts Protein Conformational Changes upon Binding. <i>Structure</i> , 2011, 19, 859-867.	1.6	174
53	Structural Diversity in Free and Bound States of Intrinsically Disordered Protein Phosphatase 1 Regulators. <i>Structure</i> , 2010, 18, 1094-1103.	1.6	110
54	Sequence Determinants of Compaction in Intrinsically Disordered Proteins. <i>Biophysical Journal</i> , 2010, 98, 2383-2390.	0.2	342

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55	Structure and Disorder in an Unfolded State under Nondenaturing Conditions from Ensemble Models Consistent with a Large Number of Experimental Restraints. <i>Journal of Molecular Biology</i> , 2009, 391, 359-374.	2.0	144
56	Calculation of Residual Dipolar Couplings from Disordered State Ensembles Using Local Alignment. <i>Journal of the American Chemical Society</i> , 2008, 130, 7804-7805.	6.6	67
57	Synuclein- β Targeting Peptide Inhibitor that Enhances Sensitivity of Breast Cancer Cells to Antimicrotubule Drugs. <i>Cancer Research</i> , 2007, 67, 626-633.	0.4	52
58	Improved Structural Characterizations of the drkN SH3 Domain Unfolded State Suggest a Compact Ensemble with Native-like and Non-native Structure. <i>Journal of Molecular Biology</i> , 2007, 367, 1494-1510.	2.0	109
59	Oxygen as a Paramagnetic Probe of Clustering and Solvent Exposure in Folded and Unfolded States of an SH3 Domain. <i>Journal of the American Chemical Society</i> , 2007, 129, 1826-1835.	6.6	28
60	Sensitivity of secondary structure propensities to sequence differences between β - and β -synuclein: Implications for fibrillation. <i>Protein Science</i> , 2006, 15, 2795-2804.	3.1	648