Joseph A. Marsh

List of Publications by Year
in descending order

73 papers	5,739 citations	94269 37 h-index	88477 70 g-index
87 all docs	87 docs citations	87 times ranked	8097 citing authors

#	Article	IF	Citations
1	The properties of human disease mutations at protein interfaces. PLoS Computational Biology, 2022, 18, e1009858.	1.5	19
2	Novel biallelic USH2A variants in a patient with usher syndrome type IIA- a case report. BMC Ophthalmology, 2022, 22, 140.	0.6	0
3	Diverse Molecular Mechanisms Underlying Pathogenic Protein Mutations: Beyond the Loss-of-Function Paradigm. Annual Review of Genomics and Human Genetics, 2022, 23, 475-498.	2.5	41
4	Gene-based whole genome sequencing meta-analysis of 250 circulating proteins in three isolated European populations. Molecular Metabolism, 2022, 61, 101509.	3.0	3
5	Interpreting protein variant effects with computational predictors and deep mutational scanning. DMM Disease Models and Mechanisms, 2022, 15, .	1.2	25
6	Longitudinal dynamics of clonal hematopoiesis identifies gene-specific fitness effects. Nature Medicine, 2022, 28, 1439-1446.	15.2	36
7	Genetic and functional insights into CDA-I prevalence and pathogenesis. Journal of Medical Genetics, 2021, 58, 185-195.	1.5	9
8	Heterozygous lamin B1 and lamin B2 variants cause primary microcephaly and define a novel laminopathy. Genetics in Medicine, 2021, 23, 408-414.	1.1	35
9	Rheumatoid factor positive polyarticular juvenile idiopathic arthritis associated with a novel COPA mutation. Rheumatology, 2021, 60, e171-e173.	0.9	6
10	A WDR35-dependent coat protein complex transports ciliary membrane cargo vesicles to cilia. ELife, 2021, 10, .	2.8	29
11	Recurrent heterozygous PAX6 missense variants cause severe bilateral microphthalmia via predictable effects on DNAâ€“protein interaction. Genetics in Medicine, 2020, 22, 598-609.	1.1	43
12	Identification of pathogenic missense mutations using protein stability predictors. Scientific Reports, 2020, 10, 15387.	1.6	66
13	Mutations in COPA lead to abnormal trafficking of STING to the Golgi and interferon signaling. Journal of Experimental Medicine, 2020, 217, .	4.2	130
14	PRIM1 deficiency causes a distinctive primordial dwarfism syndrome. Genes and Development, 2020, 34, 1520-1533.	2.7	20
15	Using deep mutational scanning to benchmark variant effect predictors and identify disease mutations. Molecular Systems Biology, 2020, 16, e9380.	3.2	120
16	Ligand Binding Site Structure Shapes Folding, Assembly and Degradation of Homomeric Protein Complexes. Journal of Molecular Biology, 2019, 431, 3871-3888.	2.0	5
17	Evolution of protein interfaces in multimers and fibrils. Journal of Chemical Physics, 2019, 150, 225102.	1.2	1
18	The role of protein complexes in human genetic disease. Protein Science, 2019, 28, 1400-1411.	3.1	53

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19	Finding Diagnostically Useful Patterns in Quantitative Phenotypic Data. American Journal of Human Genetics, 2019, 105, 933-946.	2.6	8
20	Ligands and Receptors with Broad Binding Capabilities Have Common Structural Characteristics: An Antibiotic Design Perspective. Journal of Medicinal Chemistry, 2019, 62, 9357-9374.	2.9	9
21	Protein aggregation mediates stoichiometry of protein complexes in aneuploid cells. Genes and Development, 2019, 33, 1031-1047.	2.7	83
22	Biallelic variants in DNA2 cause microcephalic primordial dwarfism. Human Mutation, 2019, 40, 1063-1070.	1.1	16
23	Ligand-Binding-Site Structure Shapes Allosteric Signal Transduction and the Evolution of Allostery in Protein Complexes. Molecular Biology and Evolution, 2019, 36, 1711-1727.	3.5	33
24	Intrinsic lipid binding activity of <scp>ATG</scp> 16L1 supports efficient membrane anchoring and autophagy. EMBO Journal, 2019, 38, .	3.5	59
25	Gain-of-function DNMT3A mutations cause microcephalic dwarfism and hypermethylation of Polycomb-regulated regions. Nature Genetics, 2019, 51, 96-105.	9.4	110
26	A Graph-Based Approach for Detecting Sequence Homology in Highly Diverged Repeat Protein Families. Methods in Molecular Biology, 2019, 1851, 251-261.	0.4	2
27	Characterization of a novel RP2-OSTF1 interaction and its implication for actin remodeling. Journal of Cell Science, 2018, 131, .	1.2	6
28	Cotranslational protein assembly imposes evolutionary constraints on homomeric proteins. Nature Structural and Molecular Biology, 2018, 25, 279-288.	3.6	43
29	The genetic basis and evolution of red blood cell sickling in deer. Nature Ecology and Evolution, 2018, 2, 367-376.	3.4	14
30	Experimental Characterization of Protein Complex Structure, Dynamics, and Assembly. Methods in Molecular Biology, 2018, 1764, 3-27.	0.4	4
31	Computational Modelling of Protein Complex Structure and Assembly. Methods in Molecular Biology, 2018, 1764, 347-356.	0.4	2
32	Ligand Binding Site Structure Influences the Evolution of Protein Complex Function and Topology. Cell Reports, 2018, 22, 3265-3276.	2.9	18
33	Mouse Idh3a mutations cause retinal degeneration and reduced mitochondrial function. DMM Disease Models and Mechanisms, 2018, 11, .	1.2	23
34	Interrogation of Mammalian Protein Complex Structure, Function, and Membership Using Genome-Scale Fitness Screens. Cell Systems, 2018, 6, 555-568.e7.	2.9	126
35	Editorial overview: Sequences and topology: Dynamic sequences and topologies of proteins. Current Opinion in Structural Biology, 2018, 50, vii-viii.	2.6	0
36	SMCHD1 mutations associated with a rare muscular dystrophy can also cause isolated arhinia and Bosma arhinia microphthalmia syndrome. Nature Genetics, 2017, 49, 238-248.	9.4	131

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37	Evolution of condensin and cohesin complexes driven by replacement of Kite by Hawk proteins. Current Biology, 2017, 27, R17-R18.	1.8	98
38	Signalling assemblies: the odds of symmetry. Biochemical Society Transactions, 2017, 45, 599-611.	1.6	9
39	Regulation, evolution and consequences of cotranslational protein complex assembly. Current Opinion in Structural Biology, 2017, 42, 90-97.	2.6	62
40	Novel pathogenic mutations in C1QTNF5 support a dominant negative disease mechanism in late-onset retinal degeneration. Scientific Reports, 2017, 7, 12147.	1.6	30
41	ER stress-induced aggresome trafficking of HtrA1 protects against proteotoxicity. Journal of Molecular Cell Biology, 2017, 9, 516-532.	1.5	9
42	Functional determinants of protein assembly into homomeric complexes. Scientific Reports, 2017, 7, 4932.	1.6	52
43	Alpha Helices Are More Robust to Mutations than Beta Strands. PLoS Computational Biology, 2016, 12, e1005242.	1.5	85
44	A Restricted Repertoire of De Novo Mutations in ITPR1 Cause Gillespie Syndrome with Evidence for Dominant-Negative Effect. American Journal of Human Genetics, 2016, 98, 981-992.	2.6	81
45	Operon Gene Order Is Optimized for Ordered Protein Complex Assembly. Cell Reports, 2016, 14, 679-685.	2.9	91
46	Kinetic Analysis of Protein Stability Reveals Age-Dependent Degradation. Cell, 2016, 167, 803-815.e21.	13.5	259
47	Structural Determinants of Sleeping Beauty Transposase Activity. Molecular Therapy, 2016, 24, 1369-1377.	3.7	7
48	Co-translational assembly of protein complexes. Biochemical Society Transactions, 2015, 43, 1221-1226.	1.6	32
49	Principles of assembly reveal a periodic table of protein complexes. Science, 2015, 350, aaa2245.	6.0	198
50	Fast and Accurate Resonance Assignment of Small-to-Large Proteins by Combining Automated and Manual Approaches. PLoS Computational Biology, 2015, 11, e1004022.	1.5	6
51	Structural and evolutionary versatility in protein complexes with uneven stoichiometry. Nature Communications, 2015, 6, 6394.	5.8	48
52	Structure, Dynamics, Assembly, and Evolution of Protein Complexes. Annual Review of Biochemistry, 2015, 84, 551-575.	5.0	351
53	Protein Flexibility Facilitates Quaternary Structure Assembly and Evolution. PLoS Biology, 2014, 12, e1001870.	2.6	89
54	Parallel dynamics and evolution: Protein conformational fluctuations and assembly reflect evolutionary changes in sequence and structure. BioEssays, 2014, 36, 209-218.	1.2	68

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55	The Role of Salt Bridges, Charge Density, and Subunit Flexibility in Determining Disassembly Routes of Protein Complexes. Structure, 2013, 21, 1325-1337.	1.6	82
56	Buried and Accessible Surface Area Control Intrinsic Protein Flexibility. Journal of Molecular Biology, 2013, 425, 3250-3263.	2.0	62
57	Characterization of disordered proteins with ENSEMBLE. Bioinformatics, 2013, 29, 398-399.	1.8	141
58	Protein Complexes Are under Evolutionary Selection to Assemble via Ordered Pathways. Cell, 2013, 153, 461-470.	13.5	215
59	The emergence of protein complexes: quaternary structure, dynamics and allostery. Biochemical Society Transactions, 2012, 40, 475-491.	1.6	75
60	Probing the diverse landscape of protein flexibility and binding. Current Opinion in Structural Biology, 2012, 22, 643-650.	2.6	94
61	Ensemble modeling of protein disordered states: Experimental restraint contributions and validation. Proteins: Structure, Function and Bioinformatics, 2012, 80, 556-572.	1.5	107
62	Structural Signature of the MYPT1â^'PP1 Interaction. Journal of the American Chemical Society, 2011, 133, 73-80.	6.6	44
63	Relative Solvent Accessible Surface Area Predicts Protein Conformational Changes upon Binding. Structure, 2011, 19, 859-867.	1.6	174
64	Structure/Function Implications in a Dynamic Complex of the Intrinsically Disordered Sic1 with the Cdc4 Subunit of an SCF Ubiquitin Ligase. Structure, 2010, 18, 494-506.	1.6	239
65	Structural Diversity in Free and Bound States of Intrinsically Disordered Protein Phosphatase 1 Regulators. Structure, 2010, 18, 1094-1103.	1.6	110
66	Sequence Determinants of Compaction in Intrinsically Disordered Proteins. Biophysical Journal, 2010, 98, 2383-2390.	0.2	342
67	How do proteins gain new domains?. Genome Biology, 2010, 11, 126.	13.9	70
68	Structure and Disorder in an Unfolded State under Nondenaturing Conditions from Ensemble Models Consistent with a Large Number of Experimental Restraints. Journal of Molecular Biology, 2009, 391, 359-374.	2.0	144
69	Calculation of Residual Dipolar Couplings from Disordered State Ensembles Using Local Alignment. Journal of the American Chemical Society, 2008, 130, 7804-7805.	6.6	67
70	Synuclein-Î³ Targeting Peptide Inhibitor that Enhances Sensitivity of Breast Cancer Cells to Antimicrotubule Drugs. Cancer Research, 2007, 67, 626-633.	0.4	52
71	Improved Structural Characterizations of the drkN SH3 Domain Unfolded State Suggest a Compact Ensemble with Native-like and Non-native Structure. Journal of Molecular Biology, 2007, 367, 1494-1510.	2.0	109
72	Oxygen as a Paramagnetic Probe of Clustering and Solvent Exposure in Folded and Unfolded States of an SH3 Domain. Journal of the American Chemical Society, 2007, 129, 1826-1835.	6.6	28

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73	Sensitivity of secondary structure propensities to sequence differences between Î±- and Î³-synuclein: Implications for fibrillation. Protein Science, 2006, 15, 2795-2804.	3.1	648