# Joseph A. Marsh

List of Publications by Year
in descending order



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|---|---|---|---|
| 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 | 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 |
| 2 | Structure, Dynamics, Assembly, and Evolution of Protein Complexes. Annual Review of Biochemistry, 2015, 84, 551-575. | 5.0 | 351 |
| 3 | Sequence Determinants of Compaction in Intrinsically Disordered Proteins. Biophysical Journal, 2010, 98, 2383-2390. | 0.2 | 342 |
| 4 | Kinetic Analysis of Protein Stability Reveals Age-Dependent Degradation. Cell, 2016, 167, 803-815.e21. | 13.5 | 259 |
| 5 | 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 |
| 6 | Protein Complexes Are under Evolutionary Selection to Assemble via Ordered Pathways. Cell, 2013, 153, 461-470. | 13.5 | 215 |
| 7 | Principles of assembly reveal a periodic table of protein complexes. Science, 2015, 350, aaa2245. | 6.0 | 198 |
| 8 | Relative Solvent Accessible Surface Area Predicts Protein Conformational Changes upon Binding. Structure, 2011, 19, 859-867. | 1.6 | 174 |
| 9 | 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 |
| 10 | Characterization of disordered proteins with ENSEMBLE. Bioinformatics, 2013, 29, 398-399. | 1.8 | 141 |
| 11 | 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 |
| 12 | Mutations in COPA lead to abnormal trafficking of STING to the Golgi and interferon signaling. Journal of Experimental Medicine, 2020, 217, . | 4.2 | 130 |
| 13 | Interrogation of Mammalian Protein Complex Structure, Function, and Membership Using Genome-Scale Fitness Screens. Cell Systems, 2018, 6, 555-568.e7. | 2.9 | 126 |
| 14 | Using deep mutational scanning to benchmark variant effect predictors and identify disease mutations. Molecular Systems Biology, 2020, 16, e9380. | 3.2 | 120 |
| 15 | Structural Diversity in Free and Bound States of Intrinsically Disordered Protein Phosphatase 1 Regulators. Structure, 2010, 18, 1094-1103. | 1.6 | 110 |
| 16 | Gain-of-function DNMT3A mutations cause microcephalic dwarfism and hypermethylation of Polycomb-regulated regions. Nature Genetics, 2019, 51, 96-105. | 9.4 | 110 |
| 17 | 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 |
| 18 | Ensemble modeling of protein disordered states: Experimental restraint contributions and validation. Proteins: Structure, Function and Bioinformatics, 2012, 80, 556-572. | 1.5 | 107 |

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|---|---|---|---|
| 19 | Evolution of condensin and cohesin complexes driven by replacement of Kite by Hawk proteins. Current Biology, 2017, 27, R17-R18. | 1.8 | 98 |
| 20 | Probing the diverse landscape of protein flexibility and binding. Current Opinion in Structural Biology, 2012, 22, 643-650. | 2.6 | 94 |
| 21 | Operon Gene Order Is Optimized for Ordered Protein Complex Assembly. Cell Reports, 2016, 14, 679-685. | 2.9 | 91 |
| 22 | Protein Flexibility Facilitates Quaternary Structure Assembly and Evolution. PLoS Biology, 2014, 12, e1001870. | 2.6 | 89 |
| 23 | Alpha Helices Are More Robust to Mutations than Beta Strands. PLoS Computational Biology, 2016, 12, e1005242. | 1.5 | 85 |
| 24 | Protein aggregation mediates stoichiometry of protein complexes in aneuploid cells. Genes and Development, 2019, 33, 1031-1047. | 2.7 | 83 |
| 25 | 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 |
| 26 | 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 |
| 27 | The emergence of protein complexes: quaternary structure, dynamics and allostery. Biochemical Society Transactions, 2012, 40, 475-491. | 1.6 | 75 |
| 28 | How do proteins gain new domains?. Genome Biology, 2010, 11, 126. | 13.9 | 70 |
| 29 | Parallel dynamics and evolution: Protein conformational fluctuations and assembly reflect evolutionary changes in sequence and structure. BioEssays, 2014, 36, 209-218. | 1.2 | 68 |
| 30 | 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 |
| 31 | Identification of pathogenic missense mutations using protein stability predictors. Scientific Reports, 2020, 10, 15387. | 1.6 | 66 |
| 32 | Buried and Accessible Surface Area Control Intrinsic Protein Flexibility. Journal of Molecular Biology, 2013, 425, 3250-3263. | 2.0 | 62 |
| 33 | Regulation, evolution and consequences of cotranslational protein complex assembly. Current Opinion in Structural Biology, 2017, 42, 90-97. | 2.6 | 62 |
| 34 | Intrinsic lipid binding activity of <scp>ATG</scp> 16L1 supports efficient membrane anchoring and autophagy. EMBO Journal, 2019, 38, . | 3.5 | 59 |
| 35 | The role of protein complexes in human genetic disease. Protein Science, 2019, 28, 1400-1411. | 3.1 | 53 |
| 36 | Synuclein-Î³ Targeting Peptide Inhibitor that Enhances Sensitivity of Breast Cancer Cells to Antimicrotubule Drugs. Cancer Research, 2007, 67, 626-633. | 0.4 | 52 |

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|---|---|---|---|
| 37 | Functional determinants of protein assembly into homomeric complexes. Scientific Reports, 2017, 7, 4932. | 1.6 | 52 |
| 38 | Structural and evolutionary versatility in protein complexes with uneven stoichiometry. Nature Communications, 2015, 6, 6394. | 5.8 | 48 |
| 39 | Structural Signature of the MYPT1â˜PP1 Interaction. Journal of the American Chemical Society, 2011, 133, 73-80. | 6.6 | 44 |
| 40 | Cotranslational protein assembly imposes evolutionary constraints on homomeric proteins. Nature Structural and Molecular Biology, 2018, 25, 279-288. | 3.6 | 43 |
| 41 | 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 |
| 42 | 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 |
| 43 | Longitudinal dynamics of clonal hematopoiesis identifies gene-specific fitness effects. Nature Medicine, 2022, 28, 1439-1446. | 15.2 | 36 |
| 44 | 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 |
| 45 | 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 |
| 46 | Co-translational assembly of protein complexes. Biochemical Society Transactions, 2015, 43, 1221-1226. | 1.6 | 32 |
| 47 | Novel pathogenic mutations in C1QTNF5 support a dominant negative disease mechanism in late-onset retinal degeneration. Scientific Reports, 2017, 7, 12147. | 1.6 | 30 |
| 48 | A WDR35-dependent coat protein complex transports ciliary membrane cargo vesicles to cilia. ELife, 2021, 10, . | 2.8 | 29 |
| 49 | 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 |
| 50 | Interpreting protein variant effects with computational predictors and deep mutational scanning. DMM Disease Models and Mechanisms, 2022, 15, . | 1.2 | 25 |
| 51 | Mouse Idh3a mutations cause retinal degeneration and reduced mitochondrial function. DMM Disease Models and Mechanisms, 2018, 11, . | 1.2 | 23 |
| 52 | PRIM1 deficiency causes a distinctive primordial dwarfism syndrome. Genes and Development, 2020, 34, 1520-1533. | 2.7 | 20 |
| 53 | The properties of human disease mutations at protein interfaces. PLoS Computational Biology, 2022, 18, e1009858. | 1.5 | 19 |
| 54 | Ligand Binding Site Structure Influences the Evolution of Protein Complex Function and Topology. Cell Reports, 2018, 22, 3265-3276. | 2.9 | 18 |

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|---|---|---|---|
| 55 | Biallelic variants in DNA2 cause microcephalic primordial dwarfism. Human Mutation, 2019, 40, 1063-1070. | 1.1 | 16 |
| 56 | The genetic basis and evolution of red blood cell sickling in deer. Nature Ecology and Evolution, 2018, 2, 367-376. | 3.4 | 14 |
| 57 | Signalling assemblies: the odds of symmetry. Biochemical Society Transactions, 2017, 45, 599-611. | 1.6 | 9 |
| 58 | ER stress-induced aggresome trafficking of HtrA1 protects against proteotoxicity. Journal of Molecular Cell Biology, 2017, 9, 516-532. | 1.5 | 9 |
| 59 | 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 |
| 60 | Genetic and functional insights into CDA-I prevalence and pathogenesis. Journal of Medical Genetics, 2021, 58, 185-195. | 1.5 | 9 |
| 61 | Finding Diagnostically Useful Patterns in Quantitative Phenotypic Data. American Journal of Human Genetics, 2019, 105, 933-946. | 2.6 | 8 |
| 62 | Structural Determinants of Sleeping Beauty Transposase Activity. Molecular Therapy, 2016, 24, 1369-1377. | 3.7 | 7 |
| 63 | 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 |
| 64 | Characterization of a novel RP2-OSTF1 interaction and its implication for actin remodeling. Journal of Cell Science, 2018, 131, . | 1.2 | 6 |
| 65 | Rheumatoid factor positive polyarticular juvenile idiopathic arthritis associated with a novel COPA mutation. Rheumatology, 2021, 60, e171-e173. | 0.9 | 6 |
| 66 | Ligand Binding Site Structure Shapes Folding, Assembly and Degradation of Homomeric Protein Complexes. Journal of Molecular Biology, 2019, 431, 3871-3888. | 2.0 | 5 |
| 67 | Experimental Characterization of Protein Complex Structure, Dynamics, and Assembly. Methods in Molecular Biology, 2018, 1764, 3-27. | 0.4 | 4 |
| 68 | Gene-based whole genome sequencing meta-analysis of 250 circulating proteins in three isolated European populations. Molecular Metabolism, 2022, 61, 101509. | 3.0 | 3 |
| 69 | Computational Modelling of Protein Complex Structure and Assembly. Methods in Molecular Biology, 2018, 1764, 347-356. | 0.4 | 2 |
| 70 | 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 |
| 71 | Evolution of protein interfaces in multimers and fibrils. Journal of Chemical Physics, 2019, 150, 225102. | 1.2 | 1 |
| 72 | Editorial overview: Sequences and topology: Dynamic sequences and topologies of proteins. Current Opinion in Structural Biology, 2018, 50, vii-viii. | 2.6 | 0 |

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|---|---|---|---|
| 73 | Novel biallelic USH2A variants in a patient with usher syndrome type IIA- a case report. BMC Ophthalmology, 2022, 22, 140. | 0.6 | 0 |