

Murray Coles

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/821292/publications.pdf>

Version: 2024-02-01

25
papers

1,159
citations

567281

15
h-index

580821

25
g-index

26
all docs

26
docs citations

26
times ranked

1652
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | A topological refactoring design strategy yields highly stable granulopoietic proteins. <i>Nature Communications</i> , 2022, 13, . | 12.8 | 4 |
| 2 | The breakthrough in protein structure prediction. <i>Biochemical Journal</i> , 2021, 478, 1885-1890. | 3.7 | 39 |
| 3 | Design of novel granulopoietic proteins by topological rescaffolding. <i>PLoS Biology</i> , 2020, 18, e3000919. | 5.6 | 8 |
| 4 | Reconstructing the Remote Origins of a Fold Singleton from a Flavodoxin-Like Ancestor. <i>Biochemistry</i> , 2019, 58, 4790-4793. | 2.5 | 9 |
| 5 | Mapping Local Conformational Landscapes of Proteins in Solution. <i>Structure</i> , 2019, 27, 853-865.e5. | 3.3 | 14 |
| 6 | Characterization of MCU-Binding Proteins MCUR1 and CCDC90B – Representatives of a Protein Family Conserved in Prokaryotes and Eukaryotic Organelles. <i>Structure</i> , 2019, 27, 464-475.e6. | 3.3 | 19 |
| 7 | Asymmetric protein design from conserved supersecondary structures. <i>Journal of Structural Biology</i> , 2018, 204, 380-387. | 2.8 | 13 |
| 8 | An Interface-Driven Design Strategy Yields a Novel, Corrugated Protein Architecture. <i>ACS Synthetic Biology</i> , 2018, 7, 2226-2235. | 3.8 | 11 |
| 9 | Distinct mechanisms contribute to immunity in the lantibiotic <i>NAI</i> 107 producer strain <i>Microbispora</i> –... ATCC PTA 5024. <i>Environmental Microbiology</i> , 2016, 18, 118-132. | 3.8 | 24 |
| 10 | Origin of a folded repeat protein from an intrinsically disordered ancestor. <i>ELife</i> , 2016, 5, . | 6.0 | 43 |
| 11 | Structure and Evolution of N-domains in AAA Metalloproteases. <i>Journal of Molecular Biology</i> , 2015, 427, 910-923. | 4.2 | 23 |
| 12 | STAC – A New Domain Associated with Transmembrane Solute Transport and Two-Component Signal Transduction Systems. <i>Journal of Molecular Biology</i> , 2015, 427, 3327-3339. | 4.2 | 17 |
| 13 | Structural Dynamics of the Cereblon Ligand Binding Domain. <i>PLoS ONE</i> , 2015, 10, e0128342. | 2.5 | 22 |
| 14 | Thalidomide mimics uridine binding to an aromatic cage in cereblon. <i>Journal of Structural Biology</i> , 2014, 188, 225-232. | 2.8 | 54 |
| 15 | Crystallographic snapshot of the <i>Escherichia coli</i> EnvZ histidine kinase in an active conformation. <i>Journal of Structural Biology</i> , 2014, 186, 376-379. | 2.8 | 46 |
| 16 | A soluble mutant of the transmembrane receptor Af1503 features strong changes in coiled-coil periodicity. <i>Journal of Structural Biology</i> , 2014, 186, 357-366. | 2.8 | 15 |
| 17 | Your personalized protein structure: Andrei N. Lupas fused to GCN4 adaptors. <i>Journal of Structural Biology</i> , 2014, 186, 380-385. | 2.8 | 15 |
| 18 | A direct interaction between DCP1 and XRN1 couples mRNA decapping to 5' exonucleolytic degradation. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1324-1331. | 8.2 | 144 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 19 | Mechanism of Regulation of Receptor Histidine Kinases. <i>Structure</i> , 2012, 20, 56-66. | 3.3 | 87 |
| 20 | The Mechanisms of HAMP-Mediated Signaling in Transmembrane Receptors. <i>Structure</i> , 2011, 19, 378-385. | 3.3 | 86 |
| 21 | Optimized Measurement Temperature Gives Access to the Solution Structure of a 49 kDa Homohexameric I^2 -Propeller. <i>Journal of the American Chemical Society</i> , 2010, 132, 15692-15698. | 13.7 | 6 |
| 22 | SimShiftDB; local conformational restraints derived from chemical shift similarity searches on a large synthetic database. <i>Journal of Biomolecular NMR</i> , 2009, 43, 179-185. | 2.8 | 14 |
| 23 | CheckShift: automatic correction of inconsistent chemical shift referencing. <i>Journal of Biomolecular NMR</i> , 2007, 39, 223-227. | 2.8 | 22 |
| 24 | The HAMP Domain Structure Implies Helix Rotation in Transmembrane Signaling. <i>Cell</i> , 2006, 126, 929-940. | 28.9 | 351 |
| 25 | An efficient strategy for assignment of cross-peaks in 3D heteronuclear NOESY experiments. <i>Journal of Biomolecular NMR</i> , 1999, 15, 177-180. | 2.8 | 73 |