

# 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	The HAMP Domain Structure Implies Helix Rotation in Transmembrane Signaling. <i>Cell</i> , 2006, 126, 929-940.	28.9	351
2	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
3	Mechanism of Regulation of Receptor Histidine Kinases. <i>Structure</i> , 2012, 20, 56-66.	3.3	87
4	The Mechanisms of HAMP-Mediated Signaling in Transmembrane Receptors. <i>Structure</i> , 2011, 19, 378-385.	3.3	86
5	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
6	Thalidomide mimics uridine binding to an aromatic cage in cereblon. <i>Journal of Structural Biology</i> , 2014, 188, 225-232.	2.8	54
7	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
8	Origin of a folded repeat protein from an intrinsically disordered ancestor. <i>ELife</i> , 2016, 5, .	6.0	43
9	The breakthrough in protein structure prediction. <i>Biochemical Journal</i> , 2021, 478, 1885-1890.	3.7	39
10	Distinct mechanisms contribute to immunity in the lantibiotic <i>NAI</i> producer strain <i>Microbispora</i> ATCC PTA 5024. <i>Environmental Microbiology</i> , 2016, 18, 118-132.	3.8	24
11	Structure and Evolution of N-domains in AAA Metalloproteases. <i>Journal of Molecular Biology</i> , 2015, 427, 910-923.	4.2	23
12	CheckShift: automatic correction of inconsistent chemical shift referencing. <i>Journal of Biomolecular NMR</i> , 2007, 39, 223-227.	2.8	22
13	Structural Dynamics of the Cereblon Ligand Binding Domain. <i>PLoS ONE</i> , 2015, 10, e0128342.	2.5	22
14	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
15	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
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	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

#	ARTICLE	IF	CITATIONS
19	Mapping Local Conformational Landscapes of Proteins in Solution. <i>Structure</i> , 2019, 27, 853-865.e5.	3.3	14
20	Asymmetric protein design from conserved supersecondary structures. <i>Journal of Structural Biology</i> , 2018, 204, 380-387.	2.8	13
21	An Interface-Driven Design Strategy Yields a Novel, Corrugated Protein Architecture. <i>ACS Synthetic Biology</i> , 2018, 7, 2226-2235.	3.8	11
22	Reconstructing the Remote Origins of a Fold Singleton from a Flavodoxin-Like Ancestor. <i>Biochemistry</i> , 2019, 58, 4790-4793.	2.5	9
23	Design of novel granulopoietic proteins by topological rescaffolding. <i>PLoS Biology</i> , 2020, 18, e3000919.	5.6	8
24	Optimized Measurement Temperature Gives Access to the Solution Structure of a 49 kDa Homohexameric I <sup>2</sup> -Propeller. <i>Journal of the American Chemical Society</i> , 2010, 132, 15692-15698.	13.7	6
25	A topological refactoring design strategy yields highly stable granulopoietic proteins. <i>Nature Communications</i> , 2022, 13, .	12.8	4