

Thomas Alfred Edwards

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

62

papers

2,292

citations

27

h-index

47

g-index

74

ext. papers

2,637

ext. citations

7.4

avg, IF

4.73

L-index

#	Paper	IF	Citations
62	Transcription corepressor CtBP is an NAD(+)-regulated dehydrogenase. <i>Molecular Cell</i> , 2002 , 10, 857-69	17.6	221
61	Structure of Pumilio reveals similarity between RNA and peptide binding motifs. <i>Cell</i> , 2001 , 105, 281-9	56.2	204
60	ABC-F Proteins Mediate Antibiotic Resistance through Ribosomal Protection. <i>MBio</i> , 2016 , 7, e01975	7.8	129
59	Oligobenzamide proteomimetic inhibitors of the p53-hDM2 protein-protein interaction. <i>Chemical Communications</i> , 2009 , 5091-3	5.8	113
58	Crystal structure of the catalytic core of human DNA polymerase kappa. <i>Structure</i> , 2004 , 12, 1395-404	5.2	94
57	Model of the brain tumor-Pumilio translation repressor complex. <i>Genes and Development</i> , 2003 , 17, 2508-13	8.1	86
56	Crystal structure of the SF3 helicase from adeno-associated virus type 2. <i>Structure</i> , 2003 , 11, 1025-35	5.2	81
55	Structure, function, and evolution of the Crimean-Congo hemorrhagic fever virus nucleocapsid protein. <i>Journal of Virology</i> , 2012 , 86, 10914-23	6.6	80
54	N-alkylated oligoamide alpha-helical proteomimetics. <i>Organic and Biomolecular Chemistry</i> , 2010 , 8, 2344-51	3.9	74
53	Genetic Analysis of <i>Physcomitrella patens</i> Identifies ABSCISIC ACID NON-RESPONSIVE, a Regulator of ABA Responses Unique to Basal Land Plants and Required for Desiccation Tolerance. <i>Plant Cell</i> , 2016 , 28, 1310-27	11.6	73
52	Selective and potent proteomimetic inhibitors of intracellular protein-protein interactions. <i>Angewandte Chemie - International Edition</i> , 2015 , 54, 2960-5	16.4	70
51	ATP-driven remodeling of the linker domain in the dynein motor. <i>Structure</i> , 2012 , 20, 1670-80	5.2	68
50	Helix-mediated protein-protein interactions as targets for intervention using foldamers. <i>Amino Acids</i> , 2011 , 41, 743-54	3.5	62
49	Hydrocarbon constrained peptides - understanding preorganisation and binding affinity. <i>Chemical Science</i> , 2016 , 7, 3694-3702	9.4	53
48	Crystal structure of the essential transcription antiterminator M2-1 protein of human respiratory syncytial virus and implications of its phosphorylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 1580-5	11.5	53
47	Stereocontrolled protein surface recognition using chiral oligoamide proteomimetic foldamers. <i>Chemical Science</i> , 2015 , 6, 2434-2443	9.4	52
46	Small-molecule proteomimetic inhibitors of the HIF-1 β -p300 protein-protein interaction. <i>ChemBioChem</i> , 2014 , 15, 1083-7	3.8	52

45	Nucleocapsid protein structures from orthobunyaviruses reveal insight into ribonucleoprotein architecture and RNA polymerization. <i>Nucleic Acids Research</i> , 2013 , 41, 5912-26	20.1	46
44	Kinked β -strands mediate high-affinity recognition of mRNA targets by the germ-cell regulator DAZL. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 18266-71	11.5	46
43	2-O-alkylated para-benzamide β -helix mimetics: the role of scaffold curvature. <i>Organic and Biomolecular Chemistry</i> , 2012 , 10, 6469-72	3.9	42
42	Microwave assisted solid phase synthesis of highly functionalized N-alkylated oligobenzamide β -helix mimetics. <i>Bioorganic and Medicinal Chemistry</i> , 2013 , 21, 4034-40	3.4	37
41	Predicting and Experimentally Validating Hot-Spot Residues at Protein-Protein Interfaces. <i>ACS Chemical Biology</i> , 2019 , 14, 2252-2263	4.9	33
40	Ribosome clearance by FusB-type proteins mediates resistance to the antibiotic fusidic acid. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 2102-7	11.5	31
39	Generation of specific inhibitors of SUMO-1- and SUMO-2/3-mediated protein-protein interactions using Affimer (Adhiron) technology. <i>Science Signaling</i> , 2017 , 10,	8.8	30
38	Exploration of the HIF-1 α /p300 interface using peptide and Adhiron phage display technologies. <i>Molecular BioSystems</i> , 2015 , 11, 2738-49		27
37	A beta-sheet interaction interface directs the tetramerisation of the Miz-1 POZ domain. <i>Journal of Molecular Biology</i> , 2007 , 373, 820-6	6.5	27
36	Heat Shock Protein 70 Family Members Interact with Crimean-Congo Hemorrhagic Fever Virus and Hazara Virus Nucleocapsid Proteins and Perform a Functional Role in the Nairovirus Replication Cycle. <i>Journal of Virology</i> , 2016 , 90, 9305-16	6.6	27
35	Hypertrophic cardiomyopathy mutations in the calponin-homology domain of ACTN2 affect actin binding and cardiomyocyte Z-disc incorporation. <i>Biochemical Journal</i> , 2016 , 473, 2485-93	3.8	25
34	Selective and Potent Proteomimetic Inhibitors of Intracellular Protein-Protein Interactions. <i>Angewandte Chemie</i> , 2015 , 127, 3003-3008	3.6	23
33	Aromatic Oligoamide Foldamers with a Wet Edge as Inhibitors of the β -Helix-Mediated p53 β DM2 Protein-Protein Interaction. <i>European Journal of Organic Chemistry</i> , 2013 , 2013, 3504-3512	3.2	23
32	Co-occupancy of two Pumilio molecules on a single hunchback NRE. <i>Rna</i> , 2009 , 15, 1029-35	5.8	23
31	Orthogonal functionalisation of β -helix mimetics. <i>Organic and Biomolecular Chemistry</i> , 2014 , 12, 6794-9	3.9	22
30	Structure and RNA binding of the mouse Pumilio-2 Puf domain. <i>Journal of Structural Biology</i> , 2009 , 167, 271-6	3.4	22
29	The crystal structure of the Hazara virus nucleocapsid protein. <i>BMC Structural Biology</i> , 2015 , 15, 24	2.7	21
28	Conformational properties of O-alkylated benzamides. <i>Tetrahedron</i> , 2012 , 68, 4485-4491	2.4	20

27	The Structure of the Human Respiratory Syncytial Virus M2-1 Protein Bound to the Interaction Domain of the Phosphoprotein P Defines the Orientation of the Complex. <i>MBio</i> , 2018 , 9,	7.8	20
26	Hypoxia inducible factor (HIF) as a model for studying inhibition of protein-protein interactions. <i>Chemical Science</i> , 2017 , 8, 4188-4202	9.4	18
25	Towards "bionic" proteins: replacement of continuous sequences from HIF-1 α with proteomimetics to create functional p300 binding HIF-1 α mimics. <i>Chemical Communications</i> , 2016 , 52, 5421-4	5.8	16
24	Crystallization and characterization of Pumilo: a novel RNA binding protein. <i>Journal of Structural Biology</i> , 2000 , 132, 251-4	3.4	15
23	Crystal structure of BstYI at 1.85Å resolution: a thermophilic restriction endonuclease with overlapping specificities to BamHI and BglIII. <i>Journal of Molecular Biology</i> , 2004 , 338, 725-33	6.5	14
22	Modeling of arylamide helix mimetics in the p53 peptide binding site of hDM2 suggests parallel and anti-parallel conformations are both stable. <i>PLoS ONE</i> , 2012 , 7, e43253	3.7	13
21	Synthesis of highly functionalized oligobenzamide proteomimetic foldamers by late stage introduction of sensitive groups. <i>Organic and Biomolecular Chemistry</i> , 2016 , 14, 3782-6	3.9	13
20	Solution structure of the Vts1 SAM domain in the presence of RNA. <i>Journal of Molecular Biology</i> , 2006 , 356, 1065-72	6.5	12
19	Identification of a small molecule inhibitor of Ebola virus genome replication and transcription using in silico screening. <i>Antiviral Research</i> , 2018 , 156, 46-54	10.8	10
18	A missense variant in specificity protein 6 (SP6) is associated with amelogenesis imperfecta. <i>Human Molecular Genetics</i> , 2020 , 29, 1417-1425	5.6	9
17	Crystallization and characterization of Smaug: a novel RNA-binding motif. <i>Biochemical and Biophysical Research Communications</i> , 2002 , 297, 1085-8	3.4	7
16	Bespoke RNA recognition by Pumilios. <i>Biochemical Society Transactions</i> , 2015 , 43, 801-6	5.1	6
15	Stapled Peptides as HIF-1 α /p300 Inhibitors: Helicity Enhancement in the Bound State Increases Inhibitory Potency. <i>Chemistry - A European Journal</i> , 2020 , 26, 7638-7646	4.8	6
14	Structure and Function of the Human Respiratory Syncytial Virus M2-1 Protein. <i>Sub-Cellular Biochemistry</i> , 2018 , 88, 245-260	5.5	4
13	Probing bunyavirus N protein oligomerisation using mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2014 , 28, 793-800	2.2	4
12	Mutagenesis mapping of the protein-protein interaction underlying FusB-type fusidic acid resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2013 , 57, 4640-4	5.9	4
11	Structure of the 70S Ribosome from the Human Pathogen <i>Acinetobacter baumannii</i> in Complex with Clinically Relevant Antibiotics. <i>Structure</i> , 2020 , 28, 1087-1100.e3	5.2	4
10	Development of a multiplex assay for antibody detection in serum against pathogens affecting ruminants. <i>Transboundary and Emerging Diseases</i> , 2021 , 68, 1229-1239	4.2	4

9	Selective Affimers Recognise the BCL-2 Family Proteins BCL-x and MCL-1 through Noncanonical Structural Motifs*. <i>ChemBioChem</i> , 2021 , 22, 232-240	3.8	4
8	Tula orthohantavirus nucleocapsid protein is cleaved in infected cells and may sequester activated caspase-3 during persistent infection to suppress apoptosis. <i>Journal of General Virology</i> , 2019 , 100, 1208-1221	4.9	3
7	RAS-inhibiting biologics identify and probe druggable pockets including an SII- β allosteric site. <i>Nature Communications</i> , 2021 , 12, 4045	17.4	3
6	Probing Protein Surfaces: QSAR Analysis with Helix Mimetics. <i>ChemBioChem</i> , 2016 , 17, 768-73	3.8	3
5	Identification of β -strand mediated protein-protein interaction inhibitors using ligand-directed fragment ligation. <i>Chemical Science</i> , 2021 , 12, 2286-2293	9.4	2
4	Characterization and applications of a Crimean-Congo hemorrhagic fever virus nucleoprotein-specific Affimer: Inhibitory effects in viral replication and development of colorimetric diagnostic tests. <i>PLoS Neglected Tropical Diseases</i> , 2020 , 14, e0008364	4.8	1
3	Disruption of six <i>Saccharomyces cerevisiae</i> ORFs on chromosome XII results in three lethal disruptants. <i>Yeast</i> , 2002 , 19, 79-86	3.4	1
2	Query-guided protein-protein interaction inhibitor discovery. <i>Chemical Science</i> , 2021 , 12, 4753-4762	9.4	1
1	Towards optimizing peptide-based inhibitors of protein-protein interactions: predictive saturation variation scanning (PreSaVS). <i>RSC Chemical Biology</i> , 2021 , 2, 1474-1478	3	1