

# Ewan R G Main

## List of Publications by Year in descending order

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Version: 2024-02-01

24  
papers

1,455  
citations

623188

14  
h-index

642321

23  
g-index

26  
all docs

26  
docs citations

26  
times ranked

1367  
citing authors

#	ARTICLE	IF	CITATIONS
1	Decoupling a tandem-repeat protein: Impact of multiple loop insertions on a modular scaffold. <i>Scientific Reports</i> , 2019, 9, 15439.	1.6	3
2	Scalable Geometrically Designed Protein Cages Assembled via Genetically Encoded Split Inteins. <i>Structure</i> , 2019, 27, 776-784.e4.	1.6	9
3	Programmed Protein Self-Assembly Driven by Genetically Encoded Intein-Mediated Native Chemical Ligation. <i>ACS Synthetic Biology</i> , 2018, 7, 1067-1074.	1.9	7
4	PyFolding: Open-Source Graphing, Simulation, and Analysis of the Biophysical Properties of Proteins. <i>Biophysical Journal</i> , 2018, 114, 516-521.	0.2	7
5	Context-Dependent Energetics of Loop Extensions in a Family of Tandem-Repeat Proteins. <i>Biophysical Journal</i> , 2018, 114, 2552-2562.	0.2	10
6	Dissecting and reprogramming the folding and assembly of tandem-repeat proteins. <i>Biochemical Society Transactions</i> , 2015, 43, 881-888.	1.6	11
7	Repeat protein engineering: creating functional nanostructures/biomaterials from modular building blocks. <i>Biochemical Society Transactions</i> , 2013, 41, 1152-1158.	1.6	19
8	LcrH, a Class II Chaperone from the Type Three Secretion System, Has a Highly Flexible Native Structure. <i>Journal of Biological Chemistry</i> , 2013, 288, 4048-4055.	1.6	12
9	Fibrous Nanostructures from the Self-Assembly of Designed Repeat Protein Modules. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 13132-13135.	7.2	33
10	A high-throughput fluorescence chemical denaturation assay as a general screen for protein-ligand binding. <i>Analytical Biochemistry</i> , 2011, 411, 155-157.	1.1	29
11	Protein denaturation and protein:drugs interactions from intrinsic protein fluorescence measurements at the nanolitre scale. <i>Protein Science</i> , 2010, 19, 1544-1554.	3.1	22
12	Characterisation of the SUMO-Like Domains of <i>Schizosaccharomyces pombe</i> Rad60. <i>PLoS ONE</i> , 2010, 5, e13009.	1.1	3
13	Exploring the folding energy landscape of a series of designed consensus tetratricopeptide repeat proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 17383-17388.	3.3	45
14	A recurring theme in protein engineering: the design, stability and folding of repeat proteins. <i>Current Opinion in Structural Biology</i> , 2005, 15, 464-471.	2.6	119
15	Local and long-range stability in tandemly arrayed tetratricopeptide repeats. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 5721-5726.	3.3	90
16	A New Folding Paradigm for Repeat Proteins. <i>Journal of the American Chemical Society</i> , 2005, 127, 10188-10190.	6.6	132
17	Protein folding: Defining a "standard" set of experimental conditions and a preliminary kinetic data set of two-state proteins. <i>Protein Science</i> , 2005, 14, 602-616.	3.1	207
18	The folding and design of repeat proteins: reaching a consensus. <i>Current Opinion in Structural Biology</i> , 2003, 13, 482-489.	2.6	118

#	ARTICLE	IF	CITATIONS
19	Design of Stable $\alpha$ -Helical Arrays from an Idealized TPR Motif. <i>Structure</i> , 2003, 11, 497-508.	1.6	256
20	Does trifluoroethanol affect folding pathways and can it be used as a probe of structure in transition states?. , 1999, 6, 831-835.		47
21	Folding Pathway of FKBP12 and Characterisation of the Transition State. <i>Journal of Molecular Biology</i> , 1999, 291, 429-444.	2.0	101
22	Mapping the Interactions Present in the Transition State for Unfolding/Folding of FKBP12. <i>Journal of Molecular Biology</i> , 1999, 291, 445-461.	2.0	124
23	Context-Dependent Nature of Destabilizing Mutations on the Stability of FKBP12. <i>Biochemistry</i> , 1998, 37, 6145-6153.	1.2	49
24	Scalable Geometrically Designed Protein Cages Assembled via Genetically Encoded Split Inteins. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0