

R Leo Brady

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

1,643
citations

430874

18
h-index

677142

22
g-index

26
all docs

26
docs citations

26
times ranked

2087
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural resolution of switchable states of a de novo peptide assembly. <i>Nature Communications</i> , 2021, 12, 1530.	12.8	16
2	How Coiled-Coil Assemblies Accommodate Multiple Aromatic Residues. <i>Biomacromolecules</i> , 2021, 22, 2010-2019.	5.4	5
3	Constructing ion channels from water-soluble α -helical barrels. <i>Nature Chemistry</i> , 2021, 13, 643-650.	13.6	59
4	Coiled coils 9-to-5: rational de novo design of α -helical barrels with tunable oligomeric states. <i>Chemical Science</i> , 2021, 12, 6923-6928.	7.4	31
5	Structural effects of the highly protective V127 polymorphism on human prion protein. <i>Communications Biology</i> , 2020, 3, 402.	4.4	5
6	Navigating the Structural Landscape of De Novo α -Helical Bundles. <i>Journal of the American Chemical Society</i> , 2019, 141, 8787-8797.	13.7	42
7	<i>Fusobacterium</i> spp. target human CEACAM1 via the trimeric autotransporter adhesin CbpF. <i>Journal of Oral Microbiology</i> , 2019, 11, 1565043.	2.7	38
8	Maintaining and breaking symmetry in homomeric coiled-coil assemblies. <i>Nature Communications</i> , 2018, 9, 4132.	12.8	45
9	Downsizing Proto-oncogene cFos to Short Helix-Constrained Peptides That Bind Jun. <i>ACS Chemical Biology</i> , 2017, 12, 2051-2061.	3.4	43
10	ISAMBARD: an open-source computational environment for biomolecular analysis, modelling and design. <i>Bioinformatics</i> , 2017, 33, 3043-3050.	4.1	48
11	Installing hydrolytic activity into a completely de novo protein framework. <i>Nature Chemistry</i> , 2016, 8, 837-844.	13.6	172
12	Modular Design of Self-Assembling Peptide-Based Nanotubes. <i>Journal of the American Chemical Society</i> , 2015, 137, 10554-10562.	13.7	137
13	Computational design of water-soluble α -helical barrels. <i>Science</i> , 2014, 346, 485-488.	12.6	306
14	CCBuilder: an interactive web-based tool for building, designing and assessing coiled-coil protein assemblies. <i>Bioinformatics</i> , 2014, 30, 3029-3035.	4.1	103
15	Accessibility, Reactivity, and Selectivity of Side Chains within a Channel of de Novo Peptide Assembly. <i>Journal of the American Chemical Society</i> , 2013, 135, 12524-12527.	13.7	30
16	A Basis Set of de Novo Coiled-Coil Peptide Oligomers for Rational Protein Design and Synthetic Biology. <i>ACS Synthetic Biology</i> , 2012, 1, 240-250.	3.8	226
17	A de novo peptide hexamer with a mutable channel. <i>Nature Chemical Biology</i> , 2011, 7, 935-941.	8.0	172
18	A Novel EKLK Mutation in a Patient with Dyserythropoietic Anemia: The First Association of EKLK with Disease in Man.. <i>Blood</i> , 2009, 114, 162-162.	1.4	22

#	ARTICLE	IF	CITATIONS
19	The Moraxella adhesin UspA1 binds to its human CEACAM1 receptor by a deformable trimeric coiled-coil. EMBO Journal, 2008, 27, 1779-1789.	7.8	79
20	Characterisation of the Laminin 10/11 Binding Site on the Lutheran Glycoprotein Suggests a Novel Type of Protein-Protein Interaction.. Blood, 2006, 108, 1566-1566.	1.4	1
21	Structure-Based Approaches to the Development of Novel Anti-Malarials. Current Drug Targets, 2004, 5, 137-149.	2.1	42
22	Reflections on a peptide. Nature, 1994, 368, 692-693.	27.8	20