

Rodrigo U Gallardo

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7939612/publications.pdf>

Version: 2024-02-01

34
papers

2,372
citations

293460

24
h-index

406436

35
g-index

38
all docs

38
docs citations

38
times ranked

4339
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteostasis of Islet Amyloid Polypeptide: A Molecular Perspective of Risk Factors and Protective Strategies for Type II Diabetes. <i>Chemical Reviews</i> , 2021, 121, 1845-1893.	23.0	129
2	Synthetic Pept-Ins as a Generic Amyloid-Like Aggregation-Based Platform for In Vivo PET Imaging of Intracellular Targets. <i>Bioconjugate Chemistry</i> , 2021, 32, 2052-2064.	1.8	4
3	Targeting S100B with Peptides Encoding Intrinsic Aggregation-Prone Sequence Segments. <i>Molecules</i> , 2021, 26, 440.	1.7	6
4	The cellular modifier MOAG ϵ /SERF drives amyloid formation through charge complementation. <i>EMBO Journal</i> , 2021, 40, e107568.	3.5	15
5	Amyloid structures: much more than just a cross- β fold. <i>Current Opinion in Structural Biology</i> , 2020, 60, 7-16.	2.6	150
6	Fibril structures of diabetes-related amylin variants reveal a basis for surface-templated assembly. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 1048-1056.	3.6	71
7	Thermodynamic and Evolutionary Coupling between the Native and Amyloid State of Globular Proteins. <i>Cell Reports</i> , 2020, 31, 107512.	2.9	34
8	Reverse engineering synthetic antiviral amyloids. <i>Nature Communications</i> , 2020, 11, 2832.	5.8	25
9	Processing Induced Changes in Food Proteins: Amyloid Formation during Boiling of Hen Egg White. <i>Biomacromolecules</i> , 2020, 21, 2218-2228.	2.6	34
10	Entropic Bristles Tune the Seeding Efficiency of Prion-Nucleating Fragments. <i>Cell Reports</i> , 2020, 30, 2834-2845.e3.	2.9	12
11	The structural basis for an "off switch" controlling G β -mediated inhibition of TRPM3 channels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 29090-29100.	3.3	17
12	Autonomous aggregation suppression by acidic residues explains why chaperones favour basic residues. <i>EMBO Journal</i> , 2020, 39, e102864.	3.5	33
13	Structure and nucleotide-induced conformational dynamics of the <i>Chlorobium tepidum</i> Roco protein. <i>Biochemical Journal</i> , 2019, 476, 51-66.	1.7	21
14	Aggregating sequences that occur in many proteins constitute weak spots of bacterial proteostasis. <i>Nature Communications</i> , 2018, 9, 866.	5.8	53
15	Hsp90 Mediates Membrane Deformation and Exosome Release. <i>Molecular Cell</i> , 2018, 71, 689-702.e9.	4.5	103
16	Prediction and Reduction of the Aggregation of Monoclonal Antibodies. <i>Journal of Molecular Biology</i> , 2017, 429, 1244-1261.	2.0	112
17	A homologue of the Parkinson's disease-associated protein LRRK2 undergoes a monomer-dimer transition during GTP turnover. <i>Nature Communications</i> , 2017, 8, 1008.	5.8	53
18	Alzheimer's-Causing Mutations Shift A β Length by Destabilizing β -Secretase-A β n Interactions. <i>Cell</i> , 2017, 170, 443-456.e14.	13.5	199

#	ARTICLE	IF	CITATIONS
19	Protein aggregation as an antibiotic design strategy. <i>Molecular Microbiology</i> , 2016, 99, 849-865.	1.2	44
20	Structural hot spots for the solubility of globular proteins. <i>Nature Communications</i> , 2016, 7, 10816.	5.8	57
21	De novo design of a biologically active amyloid. <i>Science</i> , 2016, 354, .	6.0	63
22	Frizzled 7 and PIP2 binding by syntenin PDZ2 domain supports Frizzled 7 trafficking and signalling. <i>Nature Communications</i> , 2016, 7, 12101.	5.8	35
23	Sequence-specific protein aggregation generates defined protein knockdowns in plants. <i>Plant Physiology</i> , 2016, 171, pp.00335.2016.	2.3	24
24	Solubis: a webserver to reduce protein aggregation through mutation. <i>Protein Engineering, Design and Selection</i> , 2016, 29, 285-289.	1.0	51
25	Structure of the Extracellular Domain of Matrix Protein 2 of Influenza A Virus in Complex with a Protective Monoclonal Antibody. <i>Journal of Virology</i> , 2015, 89, 3700-3711.	1.5	57
26	Sequence-dependent Internalization of Aggregating Peptides. <i>Journal of Biological Chemistry</i> , 2015, 290, 242-258.	1.6	22
27	WALTZ-DB: a benchmark database of amyloidogenic hexapeptides. <i>Bioinformatics</i> , 2015, 31, 1698-1700.	1.8	61
28	The Alzheimer Disease Protective Mutation A2T Modulates Kinetic and Thermodynamic Properties of Amyloid- β^2 (A β^2) Aggregation. <i>Journal of Biological Chemistry</i> , 2014, 289, 30977-30989.	1.6	132
29	β -Galactosidase Aggregation Is a Determinant of Pharmacological Chaperone Efficacy on Fabry Disease Mutants. <i>Journal of Biological Chemistry</i> , 2012, 287, 28386-28397.	1.6	31
30	Peptides based on the presenilin-1 APP binding domain inhibit APP processing and A β^2 production through interfering with the APP transmembrane domain. <i>FASEB Journal</i> , 2012, 26, 3765-3778.	0.2	11
31	Gain of function of mutant p53 by coaggregation with multiple tumor suppressors. <i>Nature Chemical Biology</i> , 2011, 7, 285-295.	3.9	450
32	Structural Diversity of PDZ-Lipid Interactions. <i>ChemBioChem</i> , 2010, 11, 456-467.	1.3	41
33	Increased Monomerization of Mutant HSPB1 Leads to Protein Hyperactivity in Charcot-Marie-Tooth Neuropathy. <i>Journal of Biological Chemistry</i> , 2010, 285, 12778-12786.	1.6	95
34	Accurate Prediction of DnaK-Peptide Binding via Homology Modelling and Experimental Data. <i>PLoS Computational Biology</i> , 2009, 5, e1000475.	1.5	118