

# Natalia Sanchez de Groot

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2630253/publications.pdf>

Version: 2024-02-01

52  
papers

4,369  
citations

126708

33  
h-index

214527

47  
g-index

58  
all docs

58  
docs citations

58  
times ranked

5977  
citing authors

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 1  | The Interplay Between Disordered Regions in RNAs and Proteins Modulates Interactions Within Stress Granules and Processing Bodies. <i>Journal of Molecular Biology</i> , 2022, 434, 167159.     | 2.0 | 15        |
| 2  | RNA-protein interactions: Central players in coordination of regulatory networks. <i>BioEssays</i> , 2021, 43, e2000118.  | 1.2 | 17        |
| 3  | RNA-binding and prion domains: the Yin and Yang of phase separation. <i>Nucleic Acids Research</i> , 2020, 48, 9491-9504.   | 6.5 | 57        |
| 4  | Bacteria use structural imperfect mimicry to hijack the host interactome. <i>PLoS Computational Biology</i> , 2020, 16, e1008395.   | 1.5 | 9         |
| 5  | RNA structure drives interaction with proteins. <i>Nature Communications</i> , 2019, 10, 3246.  | 5.8 | 123       |
| 6  | A Coordinated Response at The Transcriptome and Interactome Level is Required to Ensure Uropathogenic <i>Escherichia coli</i> Survival during Bacteremia. <i>Microorganisms</i> , 2019, 7, 292. | 1.6 | 5         |
| 7  | The fitness cost and benefit of phase-separated protein deposits. <i>Molecular Systems Biology</i> , 2019, 15, e8075.   | 3.2 | 10        |
| 8  | RNA as a key factor in driving or preventing self-assembly of the TAR DNA-binding protein 43. <i>Journal of Molecular Biology</i> , 2019, 431, 1671-1688.                                       | 2.0 | 65        |
| 9  | Cells alter their tRNA abundance to selectively regulate protein synthesis during stress conditions. <i>Science Signaling</i> , 2018, 11, .   | 1.6 | 201       |
| 10 | Discovering Putative Prion-Like Proteins in <i>Plasmodium falciparum</i> : A Computational and Experimental Analysis. <i>Frontiers in Microbiology</i> , 2018, 9, 1737.                         | 1.5 | 42        |
| 11 | Centrality in the host-pathogen interactome is associated with pathogen fitness during infection. <i>Nature Communications</i> , 2017, 8, 14092.  | 5.8 | 62        |
| 12 | Protein aggregation into insoluble deposits protects from oxidative stress. <i>Redox Biology</i> , 2017, 12, 699-711.   | 3.9 | 32        |
| 13 | Characterization of Soft Amyloid Cores in Human Prion-Like Proteins. <i>Scientific Reports</i> , 2017, 7, 12134.  | 1.6 | 38        |
| 14 | Constraints and consequences of the emergence of amino acid repeats in eukaryotic proteins. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 765-777.                                 | 3.6 | 53        |
| 15 | Benzbromarone, Quercetin, and Folic Acid Inhibit Amylin Aggregation. <i>International Journal of Molecular Sciences</i> , 2016, 17, 964.  | 1.8 | 38        |
| 16 | Advances in the characterization of RNA-binding proteins. <i>Wiley Interdisciplinary Reviews RNA</i> , 2016, 7, 793-810.  | 3.2 | 89        |
| 17 | Characterization of Amyloid Cores in Prion Domains. <i>Scientific Reports</i> , 2016, 6, 34274.   | 1.6 | 56        |
| 18 | Affinity and competition for TBP are molecular determinants of gene expression noise. <i>Nature Communications</i> , 2016, 7, 10417.  | 5.8 | 55        |

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|----|---|-----|-----------|
| 19 | Computational analysis of candidate prion-like proteins in bacteria and their role. <i>Frontiers in Microbiology</i> , 2015, 6, 1123.                                     | 1.5 | 37        |
| 20 | Proteome response at the edge of protein aggregation. <i>Open Biology</i> , 2015, 5, 140221.  | 1.5 | 9         |
| 21 | Is membrane homeostasis the missing link between inflammation and neurodegenerative diseases?. <i>Cellular and Molecular Life Sciences</i> , 2015, 72, 4795-4805.         | 2.4 | 33        |
| 22 | <i>Frontiers in Medicinal Chemistry</i> . , 2015, , .   |     | 0         |
| 23 | Structural and Computational Insights into Conformational Diseases: A Review. , 2015, , 134-182.  |     | 0         |
| 24 | Intrinsically Disordered Segments Affect Protein Half-Life in the Cell and during Evolution. <i>Cell Reports</i> , 2014, 8, 1832-1844.                                    | 2.9 | 192       |
| 25 | INTRINSICALLY DISORDERED PROTEINS: REGULATION AND DISEASE. , 2013, , 346-361.   |     | 0         |
| 26 | Contribution of Disulfide Bonds to Stability, Folding, and Amyloid Fibril Formation: The PI3-SH3 Domain Case. <i>Antioxidants and Redox Signaling</i> , 2012, 16, 1-15.   | 2.5 | 32        |
| 27 | AGGRESCAN: Method, Application, and Perspectives for Drug Design. <i>Methods in Molecular Biology</i> , 2012, 819, 199-220.   | 0.4 | 64        |
| 28 | The Effect of Amyloidogenic Peptides on Bacterial Aging Correlates with Their Intrinsic Aggregation Propensity. <i>Journal of Molecular Biology</i> , 2012, 421, 270-281. | 2.0 | 27        |
| 29 | Using bacterial inclusion bodies to screen for amyloid aggregation inhibitors. <i>Microbial Cell Factories</i> , 2012, 11, 55.  | 1.9 | 33        |
| 30 | Evolutionary selection for protein aggregation. <i>Biochemical Society Transactions</i> , 2012, 40, 1032-1037.  | 1.6 | 32        |
| 31 | Linking amyloid protein aggregation and yeast survival. <i>Molecular BioSystems</i> , 2011, 7, 1121.  | 2.9 | 26        |
| 32 | Biological role of bacterial inclusion bodies: a model for amyloid aggregation. <i>FEBS Journal</i> , 2011, 278, 2419-2427.   | 2.2 | 68        |
| 33 | Intrinsically disordered proteins: regulation and disease. <i>Current Opinion in Structural Biology</i> , 2011, 21, 432-440.  | 2.6 | 518       |
| 34 | Protein folding and aggregation in bacteria. <i>Cellular and Molecular Life Sciences</i> , 2010, 67, 2695-2715.   | 2.4 | 76        |
| 35 | Protein Aggregation Profile of the Bacterial Cytosol. <i>PLoS ONE</i> , 2010, 5, e9383.   | 1.1 | 53        |
| 36 | Modulation of A $\beta$ aggregation by glycosaminoglycan structure. <i>FASEB Journal</i> , 2010, 24, 4250-4261.   | 0.2 | 66        |

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|----|---|-----|-----------|
| 37 | The Role of Protein Sequence and Amino Acid Composition in Amyloid Formation: Scrambling and Backward Reading of IAPP Amyloid Fibrils. <i>Journal of Molecular Biology</i> , 2010, 404, 337-352.                                    | 2.0 | 38        |
| 38 | Amyloids in bacterial inclusion bodies. <i>Trends in Biochemical Sciences</i> , 2009, 34, 408-416.  | 3.7 | 137       |
| 39 | Design, Selection, and Characterization of Thioflavin-Based Intercalation Compounds with Metal Chelating Properties for Application in Alzheimer's Disease. <i>Journal of the American Chemical Society</i> , 2009, 131, 1436-1451. | 6.6 | 196       |
| 40 | Studies on bacterial inclusion bodies. <i>Future Microbiology</i> , 2008, 3, 423-435.   | 1.0 | 34        |
| 41 | The in Vivo and in Vitro Aggregation Properties of Globular Proteins Correlate With Their Conformational Stability: The SH3 Case. <i>Journal of Molecular Biology</i> , 2008, 378, 1116-1131.                                       | 2.0 | 56        |
| 42 | Recent Structural and Computational Insights into Conformational Diseases. <i>Current Medicinal Chemistry</i> , 2008, 15, 1336-1349.  | 1.2 | 62        |
| 43 | Prion and Non-prion Amyloids of the HET-s Prion forming Domain. <i>Journal of Molecular Biology</i> , 2007, 370, 768-783.   | 2.0 | 68        |
| 44 | Ile-Phe Dipeptide Self-Assembly: Clues to Amyloid Formation. <i>Biophysical Journal</i> , 2007, 92, 1732-1741.  | 0.2 | 129       |
| 45 | AGGRESKAN: a server for the prediction and evaluation of "hot spots" of aggregation in polypeptides. <i>BMC Bioinformatics</i> , 2007, 8, 65.   | 1.2 | 845       |
| 46 | Protein aggregation into bacterial inclusion bodies is a specific kinetically driven process. <i>Microbial Cell Factories</i> , 2006, 5, S9.  | 1.9 | 0         |
| 47 | Protein activity in bacterial inclusion bodies correlates with predicted aggregation rates. <i>Journal of Biotechnology</i> , 2006, 125, 110-113.   | 1.9 | 64        |
| 48 | Effect of temperature on protein quality in bacterial inclusion bodies. <i>FEBS Letters</i> , 2006, 580, 6471-6476.   | 1.3 | 133       |
| 49 | Mutagenesis of the central hydrophobic cluster in Aβ <sub>42</sub> Alzheimer's peptide. Side-chain properties correlate with aggregation propensities. <i>FEBS Journal</i> , 2006, 273, 658-668.                                    | 2.2 | 164       |
| 50 | Prediction of "hot spots" of aggregation in disease-linked polypeptides. <i>BMC Structural Biology</i> , 2005, 5, 18.   | 2.3 | 173       |
| 51 | Amyloid fibril formation by bovine cytochrome c. <i>Spectroscopy</i> , 2005, 19, 199-205.   | 0.8 | 28        |
| 52 | Microbiome Impact on Amyloidogenesis. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .   | 1.6 | 3         |