# Lynne Regan

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/9440620/publications.pdf

Version: 2024-02-01

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|---|---|---|---|
| 40 papers | 2,924 citations | 361045<br>20 h-index | 288905<br>40 g-index |
| 42 all docs | 42 docs citations | 42 times ranked | 4475 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | TPR proteins: the versatile helix. Trends in Biochemical Sciences, 2003, 28, 655-662. | 3.7 | 994 |
| 2 | A Thermodynamic Scale for the .beta.-Sheet Forming Tendencies of the Amino Acids. Biochemistry, 1994, 33, 5510-5517. | 1.2 | 412 |
| 3 | Proteinâ€“protein interactions: General trends in the relationship between binding affinity and interfacial buried surface area. Protein Science, 2013, 22, 510-515. | 3.1 | 231 |
| 4 | What makes a protein a protein? Hydrophobic core designs that specify stability and structural properties. Protein Science, 1996, 5, 1584-1593. | 3.1 | 189 |
| 5 | Protein alchemy: Changing Î²-sheet into Î±-helix. Nature Structural Biology, 1997, 4, 548-552. | 9.7 | 164 |
| 6 | Stimuli-Responsive Smart Gels Realized via Modular Protein Design. Journal of the American Chemical Society, 2010, 132, 14024-14026. | 6.6 | 105 |
| 7 | The role of backbone conformational heat capacity in protein stability: Temperature dependent dynamics of the B1 domain of <i>Streptococcal</i> protein G. Protein Science, 2000, 9, 1177-1193. | 3.1 | 88 |
| 8 | A uniform survey of allele-specific binding and expression over 1000-Genomes-Project individuals. Nature Communications, 2016, 7, 11101. | 5.8 | 78 |
| 9 | The past, present and future of protein-based materials. Open Biology, 2018, 8, . | 1.5 | 73 |
| 10 | The de novo design of a rubredoxinâ€like fe site. Protein Science, 1998, 7, 1939-1946. | 3.1 | 59 |
| 11 | Understanding the sequence determinants of conformational switching using protein design. Protein Science, 2000, 9, 1651-1659. | 3.1 | 47 |
| 12 | Surface point mutations that significantly alter the structure and stability of a protein's denatured state. Protein Science, 1996, 5, 2009-2019. | 3.1 | 46 |
| 13 | Screening Libraries To Identify Proteins with Desired Binding Activities Using a Split-GFP Reassembly Assay. ACS Chemical Biology, 2010, 5, 553-562. | 1.6 | 45 |
| 14 | A modular approach to the design of proteinâ€based smart gels. Biopolymers, 2012, 97, 508-517. | 1.2 | 40 |
| 15 | LIVE-PAINT allows super-resolution microscopy inside living cells using reversible peptide-protein interactions. Communications Biology, 2020, 3, 458. | 2.0 | 39 |
| 16 | Protein design: Past, present, and future. Biopolymers, 2015, 104, 334-350. | 1.2 | 38 |
| 17 | All Repeats Are Not Equal: A Module-Based Approach to Guide Repeat Protein Design. Journal of Molecular Biology, 2013, 425, 1826-1838. | 2.0 | 32 |
| 18 | Design of Proteinâ€“Peptide Interaction Modules for Assembling Supramolecular Structures <i>in Vivo</i> and <i>in Vitro</i>. ACS Chemical Biology, 2015, 10, 2108-2115. | 1.6 | 29 |

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|---|---|---|---|
| 19 | The Power of Hard-Sphere Models: Explaining Side-Chain Dihedral Angle Distributions of Thr and Val. Biophysical Journal, 2012, 102, 2345-2352. | 0.2 | 27 |
| 20 | Fabrication of Modularly Functionalizable Microcapsules Using Protein-Based Technologies. ACS Biomaterials Science and Engineering, 2016, 2, 1856-1861. | 2.6 | 23 |
| 21 | Random close packing in protein cores. Physical Review E, 2016, 93, 032415. | 0.8 | 21 |
| 22 | NextGen protein design. Biochemical Society Transactions, 2013, 41, 1131-1136. | 1.6 | 18 |
| 23 | PAINT using proteins: A new brush for superâ€resolution artists. Protein Science, 2020, 29, 2142-2149. | 3.1 | 17 |
| 24 | Analyses of protein cores reveal fundamental differences between solution and crystal structures. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1154-1161. | 1.5 | 13 |
| 25 | Facile Protein Immobilization Using Engineered Surface-Active Biofilm Proteins. ACS Applied Nano Materials, 2018, 1, 2483-2488. | 2.4 | 12 |
| 26 | Routes to DNA Accessibility: Alternative Pathways for Nucleosome Unwinding. Biophysical Journal, 2014, 107, 384-392. | 0.2 | 10 |
| 27 | Understanding the physical basis for the sideâ€chain conformational preferences of methionine. Proteins: Structure, Function and Bioinformatics, 2016, 84, 900-911. | 1.5 | 10 |
| 28 | Flat Drops, Elastic Sheets, and Microcapsules by Interfacial Assembly of a Bacterial Biofilm Protein, BslA. Langmuir, 2017, 33, 13590-13597. | 1.6 | 10 |
| 29 | Void distributions reveal structural link between jammed packings and protein cores. Physical Review E, 2019, 99, 022416. | 0.8 | 9 |
| 30 | Reads meet rotamers: structural biology in the age of deep sequencing. Current Opinion in Structural Biology, 2015, 35, 125-134. | 2.6 | 6 |
| 31 | A designed repeat protein as an affinity capture reagent. Biochemical Society Transactions, 2015, 43, 874-880. | 1.6 | 5 |
| 32 | Equilibrium transitions between side-chain conformations in leucine and isoleucine. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1488-1499. | 1.5 | 5 |
| 33 | Designed Proteins as Novel Imaging Reagents in Living <i>Escherichia coli</i>. ChemBioChem, 2016, 17, 1652-1657. | 1.3 | 5 |
| 34 | A threonine zipper that mediates proteinâ€"protein interactions: Structure and prediction. Protein Science, 2018, 27, 1969-1977. | 3.1 | 5 |
| 35 | Using physical features of protein core packing to distinguish real proteins from decoys. Protein Science, 2020, 29, 1931-1944. | 3.1 | 4 |
| 36 | Protein engineering strategies with potential applications for altering clinically relevant cellular pathways at the protein level. Expert Review of Proteomics, 2016, 13, 481-493. | 1.3 | 3 |

| # | Article | IF | Citations |
|---|---|---|---|
| 37 | Rational Design and Self-Assembly of Coiled-Coil Linked SasG Protein Fibrils. ACS Synthetic Biology, 2020, 9, 1599-1607. | 1.9 | 3 |
| 38 | Intensification: A Resource for Amplifying Population-Genetic Signals with Protein Repeats. Journal of Molecular Biology, 2017, 429, 435-445. | 2.0 | 2 |
| 39 | Reply to: Comment on â€œRevisiting the Ramachandran plot from a new angleâ€• Protein Science, 2011, 20, 1774-1774. | 3.1 | 1 |
| 40 | Core packing of wellâ€defined Xâ€ray and <scp>NMR</scp> structures is the same. Protein Science, 2022, 31, . | 3.1 | 1 |