

Jens Erik Nielsen

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3751335/publications.pdf>

Version: 2024-02-01

35
papers

3,126
citations

394421

19
h-index

377865

34
g-index

35
all docs

35
docs citations

35
times ranked

4779
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Structure of a GH51 β -D-arabinofuranosidase from <i>Meripilus giganteus</i> : conserved substrate recognition from bacteria to fungi. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 1124-1133. | 2.3 | 8 |
| 2 | Structure and Dynamics of a Promiscuous Xanthan Lyase from <i>Paenibacillus nanensis</i> and the Design of Variants with Increased Stability and Activity. <i>Cell Chemical Biology</i> , 2019, 26, 191-202.e6. | 5.2 | 13 |
| 3 | Investigation of Ionization Pattern of the Adjacent Acidic Residues in the DXDXE Motif of GH-18 Chitinases Using Theoretical pK _a Calculations. <i>Journal of Chemical Information and Modeling</i> , 2017, 57, 572-583. | 5.4 | 7 |
| 4 | Coupled effect of salt and pH on proteins probed with NMR spectroscopy. <i>Chemical Physics Letters</i> , 2013, 579, 114-121. | 2.6 | 13 |
| 5 | Protein Dielectric Constants Determined from NMR Chemical Shift Perturbations. <i>Journal of the American Chemical Society</i> , 2013, 135, 16968-16976. | 13.7 | 82 |
| 6 | Highly Perturbed pKa Values in the Unfolded State of Hen Egg White Lysozyme. <i>Biophysical Journal</i> , 2012, 102, 1636-1645. | 0.5 | 9 |
| 7 | DataPipeline: Automated importing and fitting of large amounts of biophysical data. <i>Journal of Computational Chemistry</i> , 2012, 33, 2357-2362. | 3.3 | 2 |
| 8 | Toward Fast Determination of Protein Stability Maps: Experimental and Theoretical Analysis of Mutants of a <i>Nocardiopsis prasina</i> Serine Protease. <i>Biochemistry</i> , 2012, 51, 5339-5347. | 2.5 | 6 |
| 9 | A collaborative environment for developing and validating predictive tools for protein biophysical characteristics. <i>Journal of Computer-Aided Molecular Design</i> , 2012, 26, 387-396. | 2.9 | 1 |
| 10 | Predicting the open conformations of protein kinases using molecular dynamics simulations. <i>Biopolymers</i> , 2012, 97, 65-72. | 2.4 | 7 |
| 11 | Constructing and Evaluating Predictive Models for Protein Biophysical Characteristics. <i>Annual Reports in Computational Chemistry</i> , 2011, , 101-124. | 1.7 | 2 |
| 12 | Integrated prediction of the effect of mutations on multiple protein characteristics. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 165-178. | 2.6 | 19 |
| 13 | Remeasuring HEWL pK _a values by NMR spectroscopy: Methods, analysis, accuracy, and implications for theoretical pK _a calculations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 685-702. | 2.6 | 89 |
| 14 | On the development of protein pK _a calculation algorithms. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 3287-3298. | 2.6 | 19 |
| 15 | Progress in the prediction of pK _a values in proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 3260-3275. | 2.6 | 229 |
| 16 | Calculating pK _a values in the cAMP-dependent protein kinase: The effect of conformational change and ligand binding. <i>Protein Science</i> , 2010, 19, 2485-2497. | 7.6 | 4 |
| 17 | Titration_DB: Storage and analysis of NMR-monitored protein pH titration curves. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 843-857. | 2.6 | 37 |
| 18 | Improving the analysis of NMR spectra tracking pH-induced conformational changes: Removing artefacts of the electric field on the NMR chemical shift. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 971-984. | 2.6 | 20 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 19 | Capturing, sharing and analysing biophysical data from protein engineering and protein characterization studies. <i>Nucleic Acids Research</i> , 2010, 38, e186-e186. | 14.5 | 5 |
| 20 | Electrostatics in proteins and protein-ligand complexes. <i>Future Medicinal Chemistry</i> , 2010, 2, 647-666. | 2.3 | 75 |
| 21 | Designed Human Serum Hyaluronidase 1 Variant, HYAL1 ^H L, Exhibits Activity up to pH 5.9. <i>Journal of Biological Chemistry</i> , 2009, 284, 19173-19177. | 3.4 | 8 |
| 22 | Structural Artifacts in Protein-Ligand X-ray Structures: Implications for the Development of Docking Scoring Functions. <i>Journal of Medicinal Chemistry</i> , 2009, 52, 5673-5684. | 6.4 | 49 |
| 23 | Chapter 9 Analyzing Enzymatic pH Activity Profiles and Protein Titration Curves Using Structure-Based pKa Calculations and Titration Curve Fitting. <i>Methods in Enzymology</i> , 2009, 454, 233-258. | 1.0 | 20 |
| 24 | Analyzing Protein NMR pH-Titration Curves. <i>Annual Reports in Computational Chemistry</i> , 2008, 4, 89-106. | 1.7 | 4 |
| 25 | Determination of Electrostatic Interaction Energies and Protonation State Populations in Enzyme Active Sites. <i>Journal of Molecular Biology</i> , 2008, 376, 269-287. | 4.2 | 28 |
| 26 | Analysing the pH-dependent properties of proteins using pKa calculations. <i>Journal of Molecular Graphics and Modelling</i> , 2007, 25, 691-699. | 2.4 | 38 |
| 27 | Redesigning protein pKa values. <i>Protein Science</i> , 2006, 16, 239-249. | 7.6 | 59 |
| 28 | pKD: re-designing protein pKa values. <i>Nucleic Acids Research</i> , 2006, 34, W48-W51. | 14.5 | 33 |
| 29 | Calculating pKa values in enzyme active sites. <i>Protein Science</i> , 2003, 12, 1894-1901. | 7.6 | 147 |
| 30 | On the evaluation and optimization of protein X-ray structures for pKa calculations. <i>Protein Science</i> , 2003, 12, 313-326. | 7.6 | 108 |
| 31 | Rational Redesign of Enzymes. , 2003, , . | | 0 |
| 32 | Predicting Changes in the Stability of Proteins and Protein Complexes: A Study of More Than 1000 Mutations. <i>Journal of Molecular Biology</i> , 2002, 320, 369-387. | 4.2 | 1,609 |
| 33 | The determinants of α -amylase pH-activity profiles. <i>Protein Engineering, Design and Selection</i> , 2001, 14, 505-512. | 2.1 | 92 |
| 34 | The ionization of a buried glutamic acid is thermodynamically linked to the stability of <i>Leishmania mexicana</i> triose phosphate isomerase. <i>FEBS Journal</i> , 2000, 267, 2516-2524. | 0.2 | 49 |
| 35 | Protein engineering of bacterial α -amylases. <i>BBA - Proteins and Proteomics</i> , 2000, 1543, 253-274. | 2.1 | 235 |