## Yannick G Spill

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6213740/publications.pdf

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|          |                | 1162367      | 1281420        |  |
|----------|----------------|--------------|----------------|--|
| 11       | 583            | 8            | 11             |  |
| papers   | citations      | h-index      | g-index        |  |
|          |                |              |                |  |
|          |                |              |                |  |
|          |                |              |                |  |
| 13       | 13             | 13           | 1439           |  |
| all docs | docs citations | times ranked | citing authors |  |
|          |                |              |                |  |

| #  | Article  | IF  | CITATIONS |
|----|--|-----|-----------|
| 1  | Automatic Bayesian Weighting for SAXS Data. Frontiers in Molecular Biosciences, 2021, 8, 671011.   | 1.6 | 4         |
| 2  | Binless normalization of Hi-C data provides significant interaction and difference detection independent of resolution. Nature Communications, 2019, 10, 1938.   | 5.8 | 12        |
| 3  | Promoter bivalency favors an open chromatin architecture in embryonic stem cells. Nature Genetics, 2018, 50, 1452-1462.  | 9.4 | 113       |
| 4  | SAS profile correlations reveal SAS hierarchical nature and information content. PLoS ONE, 2017, 12, e0177309.   | 1.1 | 6         |
| 5  | On the demultiplexing of chromosome capture conformation data. FEBS Letters, 2015, 589, 3005-3013.   | 1.3 | 23        |
| 6  | Restraintâ€based threeâ€dimensional modeling of genomes and genomic domains. FEBS Letters, 2015, 589, 2987-2995.   | 1.3 | 93        |
| 7  | ModBase, a database of annotated comparative protein structure models and associated resources.<br>Nucleic Acids Research, 2014, 42, D336-D346.  | 6.5 | 275       |
| 8  | Convective Replica-Exchange in Ergodic Regimes. Journal of Chemical Theory and Computation, 2014, 10, 953-958.   | 2.3 | 3         |
| 9  | <i>SAXS Merge</i> : an automated statistical method to merge SAXS profiles using Gaussian processes. Journal of Synchrotron Radiation, 2014, 21, 203-208.  | 1.0 | 15        |
| 10 | A convective replicaâ€exchange method for sampling new energy basins. Journal of Computational Chemistry, 2013, 34, 132-140.   | 1.5 | 18        |
| 11 | Impact of Thermostats on Folding and Aggregation Properties of Peptides Using the Optimized Potential for Efficient Structure Prediction Coarse-Grained Model. Journal of Chemical Theory and Computation, 2011, 7, 1502-1510. | 2.3 | 20        |