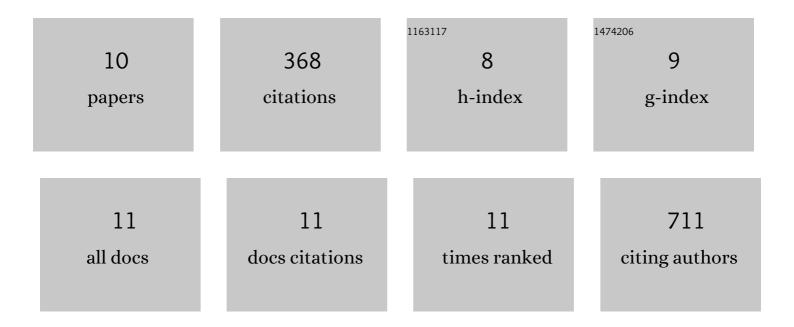
## **Adrian Guthals**

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/11278641/publications.pdf Version: 2024-02-01



| #  | Article  | IF  | CITATIONS |
|----|--|-----|-----------|
| 1  | Direct Determination of Antibody Chain Pairing by Top-down and Middle-down Mass Spectrometry<br>Using Electron Capture Dissociation and Ultraviolet Photodissociation. Analytical Chemistry, 2020,<br>92, 766-773. | 6.5 | 50        |
| 2  | A multi-protease, multi-dissociation, bottom-up-to-top-down proteomic view of the Loxosceles intermedia venom. Scientific Data, 2017, 4, 170090.   | 5.3 | 21        |
| 3  | De Novo MS/MS Sequencing of Native Human Antibodies. Journal of Proteome Research, 2017, 16, 45-54.  | 3.7 | 41        |
| 4  | The Generating Function Approach for Peptide Identification in Spectral Networks. Journal of Computational Biology, 2015, 22, 353-366.   | 1.6 | 5         |
| 5  | The Generating Function Approach for Peptide Identification in Spectral Networks. Lecture Notes in Computer Science, 2014, , 85-99.  | 1.3 | 1         |
| 6  | Sequencing-Grade <i>De novo</i> Analysis of MS/MS Triplets (CID/HCD/ETD) From Overlapping Peptides.<br>Journal of Proteome Research, 2013, 12, 2846-2857.  | 3.7 | 63        |
| 7  | Neutron-encoded Signatures Enable Product Ion Annotation From Tandem Mass Spectra. Molecular and Cellular Proteomics, 2013, 12, 3812-3823.   | 3.8 | 20        |
| 8  | Shotgun Protein Sequencing with Meta-contig Assembly. Molecular and Cellular Proteomics, 2012, 11, 1084-1096.  | 3.8 | 25        |
| 9  | The spectral networks paradigm in high throughput mass spectrometry. Molecular BioSystems, 2012, 8, 2535.  | 2.9 | 79        |
| 10 | Peptide Identification by Tandem Mass Spectrometry with Alternate Fragmentation Modes. Molecular and Cellular Proteomics, 2012, 11, 550-557.   | 3.8 | 63        |