

Morten Kallberg

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11702092/publications.pdf>

Version: 2024-02-01

10
papers

3,502
citations

1307594

7
h-index

1474206

9
g-index

12
all docs

12
docs citations

12
times ranked

10073
citing authors

#	ARTICLE	IF	CITATIONS
1	Strelka2: fast and accurate calling of germline and somatic variants. <i>Nature Methods</i> , 2018, 15, 591-594.	19.0	939
2	A reference data set of 5.4 million phased human variants validated by genetic inheritance from sequencing a three-generation 17-member pedigree. <i>Genome Research</i> , 2017, 27, 157-164.	5.5	338
3	RaptorX server: A Resource for Template-Based Protein Structure Modeling. <i>Methods in Molecular Biology</i> , 2014, 1137, 17-27.	0.9	232
4	Isaac: ultra-fast whole-genome secondary analysis on Illumina sequencing platforms. <i>Bioinformatics</i> , 2013, 29, 2041-2043.	4.1	292
5	A structure-based protocol for learning the family-specific mechanisms of membrane-binding domains. <i>Bioinformatics</i> , 2012, 28, i431-i437.	4.1	4
6	Cholesterol modulates cell signaling and protein networking by specifically interacting with PDZ domain-containing scaffold proteins. <i>Nature Communications</i> , 2012, 3, 1249.	12.8	129
7	Genome-wide Functional Annotation of Dual-Specificity Protein- and Lipid-Binding Modules that Regulate Protein Interactions. <i>Molecular Cell</i> , 2012, 46, 226-237.	9.7	62
8	Template-based protein structure modeling using the RaptorX web server. <i>Nature Protocols</i> , 2012, 7, 1511-1522.	12.0	1,474
9	An improved machine learning protocol for the identification of correct Sequest search results. <i>BMC Bioinformatics</i> , 2010, 11, 591.	2.6	4
10	Structural feature extraction protocol for classifying reversible membrane binding protein domains. , 2009, 2009, 6735-8.		1