

# Kevion K Darmawan

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

8

papers

97

citations

4

h-index

8

g-index

8

ext. papers

150

ext. citations

6.6

avg, IF

2.92

L-index

#	Paper	IF	Citations
8	Molecular modeling of lactoferrin for food and nutraceutical applications: insights from techniques.. <i>Critical Reviews in Food Science and Nutrition</i> , <b>2022</b> , 1-24	11.5	1
7	In silico modelling of apo-lactoferrin under simulated gastric conditions: Structural dynamics, binding with $\beta$ lactoglobulin and $\beta$ lactalbumin, and functional implications. <i>LWT - Food Science and Technology</i> , <b>2021</b> , 148, 111726	5.4	3
6	Computational design of de novo nutraceuticals: Effects of spray drying temperatures on the interaction between apo-lactoferrin whey protein complex and the peptidoglycan layer in lactic acid bacteria. <i>LWT - Food Science and Technology</i> , <b>2021</b> , 151, 112246	5.4	2
5	Effects of low temperatures on the conformation of apo-lactoferrin and its interactions with $\beta$ lactalbumin and $\beta$ lactoglobulin: Application of in silico approaches. <i>Food Hydrocolloids</i> , <b>2021</b> , 121, 107055	10.6	3
4	Interaction of the prototypical $\beta$ ketoamide inhibitor with the SARS-CoV-2 main protease active site in silico: Molecular dynamic simulations highlight the stability of the ligand-protein complex. <i>Computational Biology and Chemistry</i> , <b>2020</b> , 87, 107292	3.6	38
3	High temperature induced structural changes of apo-lactoferrin and interactions with $\beta$ lactoglobulin and $\beta$ lactalbumin for potential encapsulation strategies. <i>Food Hydrocolloids</i> , <b>2020</b> , 105, 105817	10.6	11
2	Site mapping and small molecule blind docking reveal a possible target site on the SARS-CoV-2 main protease dimer interface. <i>Computational Biology and Chemistry</i> , <b>2020</b> , 89, 107372	3.6	16
1	Interaction of small molecules with the SARS-CoV-2 main protease in silico and in vitro validation of potential lead compounds using an enzyme-linked immunosorbent assay. <i>Computational Biology and Chemistry</i> , <b>2020</b> , 89, 107408	3.6	23