Correction to: Docking and *in silico* toxicity assessment of *Arthrospira* compounds as potential antiviral agents against SARS-CoV-2

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Published online: 10 May 2021

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Correction to: J Appl Phycol

<https://doi.org/10.1007/s10811-021-02372-9>

Table 6 in the original version of this article contained an error. The corrected table and table legend are presented below.

The online version of the original article can be found at <https://doi.org/10.1007/s10811-021-02372-9>

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Table 6 Docking results for small molecules vs. Spike RBD of SARS-CoV-2

	Binding energies (kcal.mol ⁻¹)						
Docking softwares	Autodock Vina			Swissdock			
Molecules	Average	Stdev	CV (%)	Average	Stdev	CV (%)	Binding residues
Phycoerythrobilin	-7.45	0.05	0.7%	-10.35	0.0	0.0	ARG403 TYR449 LEU455 SER494** GLY496* ASN501* TYR505*
Phycocyanobilin	-7.25	0.15	2.1	-9.355	0.025	0.3	SER494** GLY496* GLN498*
Dieckol	-8.1	0	0.0	-8.375	0.045	0.5	GLU406 LYS417 TYR453* LEU455 GLY496* THR500* ASN501* TYR505
Phycourobilin	-7.1	0.0	0.0	-9.285	0.425	4.6	ARG403 LYS417 TYR449 TYR453 SER494** GLY496** ASN501* TYR505
Folic acid	-6.95	0.05	0.7	-10.35	0	0.0	ARG403* LEU492** SER494 GLY496** ASN501* TYR505*
Pavetannin C1	-7.3	0.3	4.1	-8.52	0.14	1.6	LEU492* GLN493 SER494* GLY496* TYR505*
Rutin	-7.25	0.05	0.7	-8.085	0.005	0.1	ARG403* GLN493** GLY496* ASN501* TYR505**
β-carotene	-7.15	0.05	0.7	-8.275	0.265	3.2	PHE456 TYR489 PHE490
Astaxanthin	-7.05	0.05	0.7	-8.195	0.375	4.6	PHE456 ALA475 TYR489 PHE490

Underlined residue reflects unfavorable interactions between the molecule studied and the spike RBD; residues in bold are directly involved in the link between ACE2 and spike RBD. Stars were added to amino acids involved in one (*) or two (**) H-bonds

CV: Coefficient of variation; Stdev: Standard deviation

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