

Figure S1. <sup>1</sup>H-NMR spectrum (CD<sub>3</sub>OD, 400 MHz) of aureusidin (1)

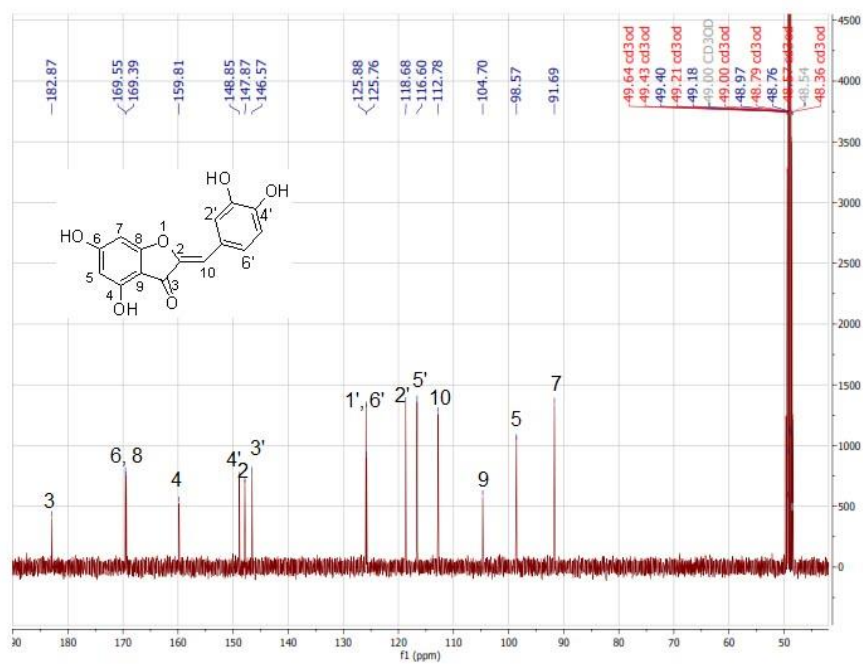


Figure S2. <sup>13</sup>C-NMR spectrum (CD<sub>3</sub>OD, 101 MHz) of aureusidin (1)

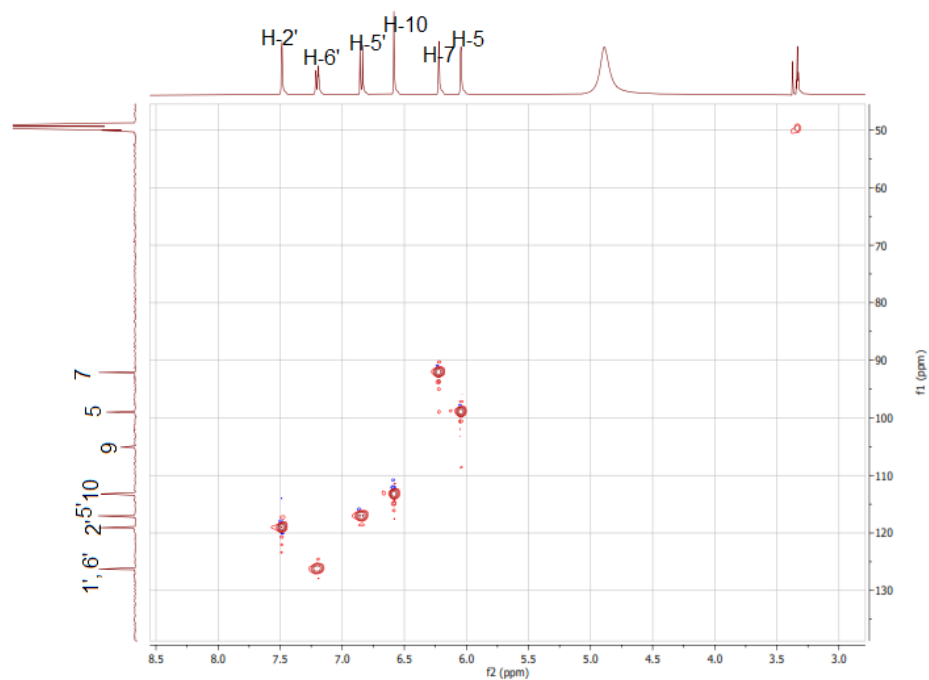


Figure S3. HSQC spectrum of aureusidin (**1**)

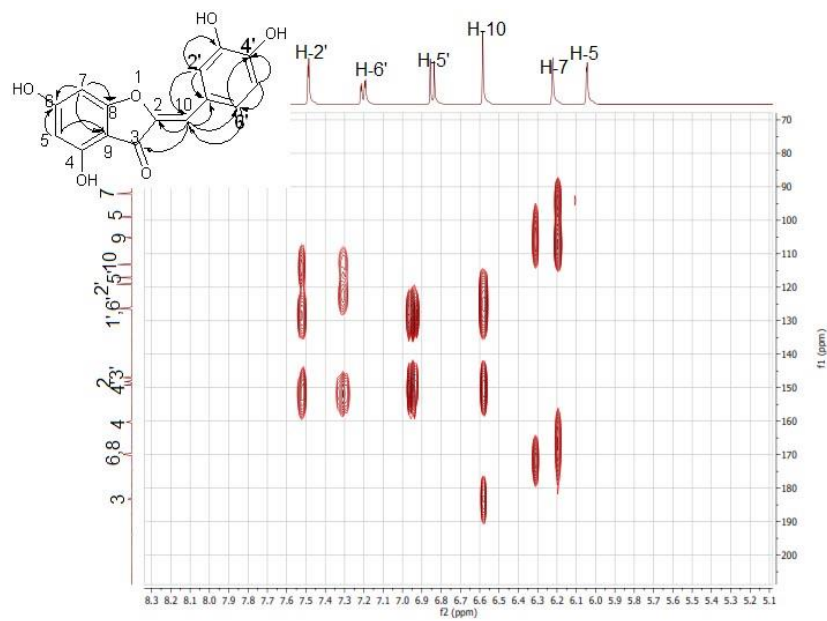


Figure S4. HMBC spectrum of aureusidin (**1**)

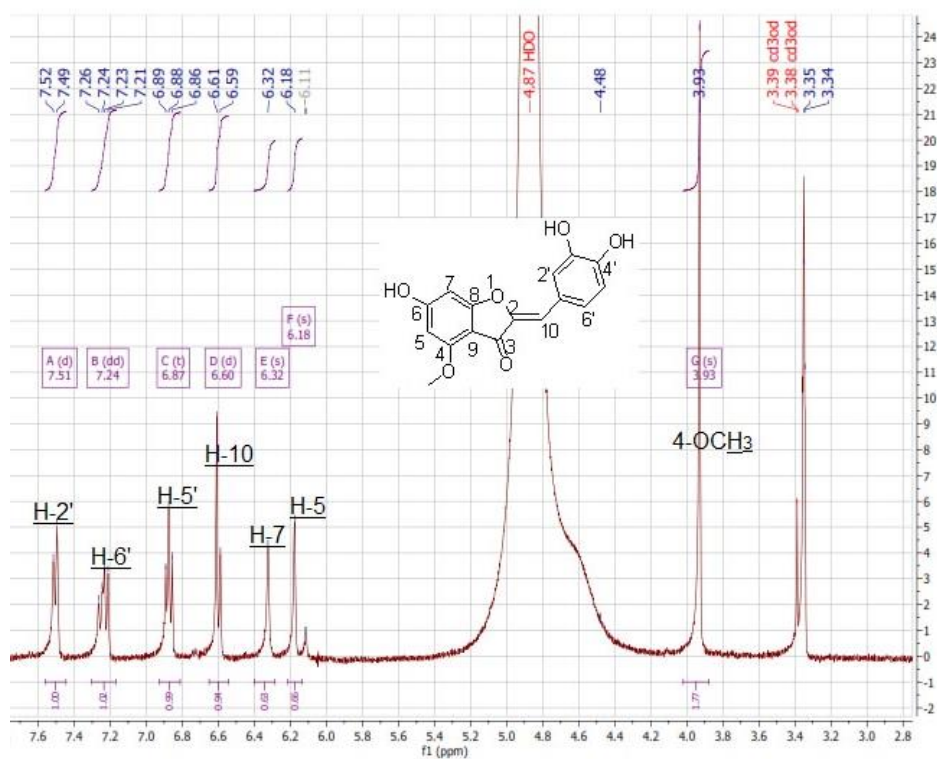


Figure S5. <sup>1</sup>H-NMR spectrum (CD<sub>3</sub>OD, 400 MHz) of aureusidin-4-methyl ether (**2**)

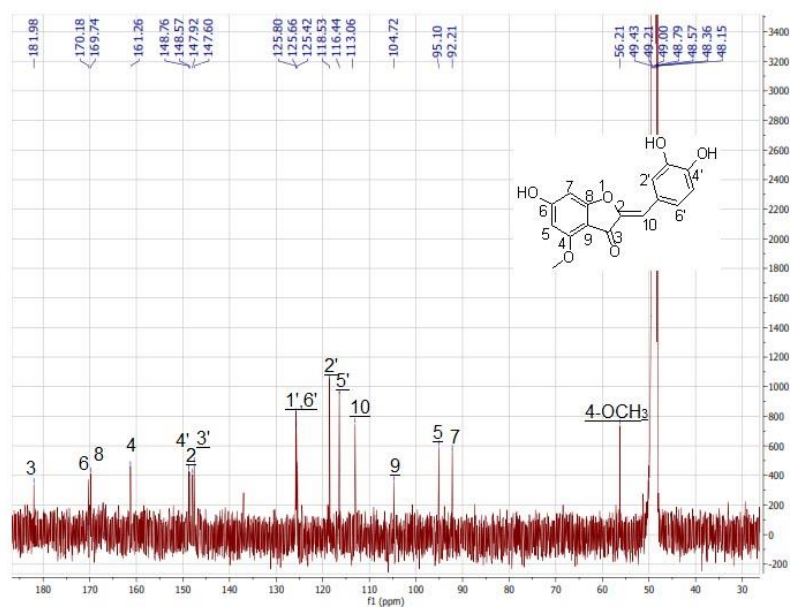


Figure S6. <sup>13</sup>C-NMR spectrum (CD<sub>3</sub>OD, 101 MHz) of aureusidin-4-methyl ether (**2**)

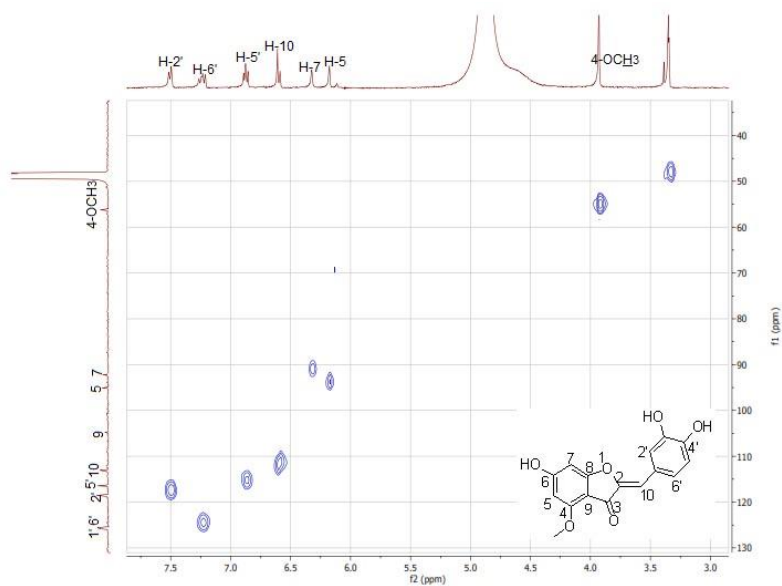


Figure S7. HSQC spectrum of aureusidin-4-methyl ether (2)

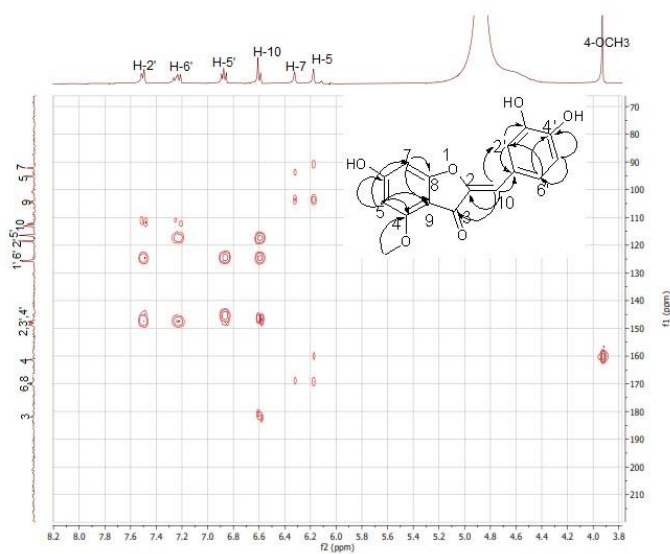


Figure S8. HMBC spectrum of aureusidin-4-methyl ether (2)

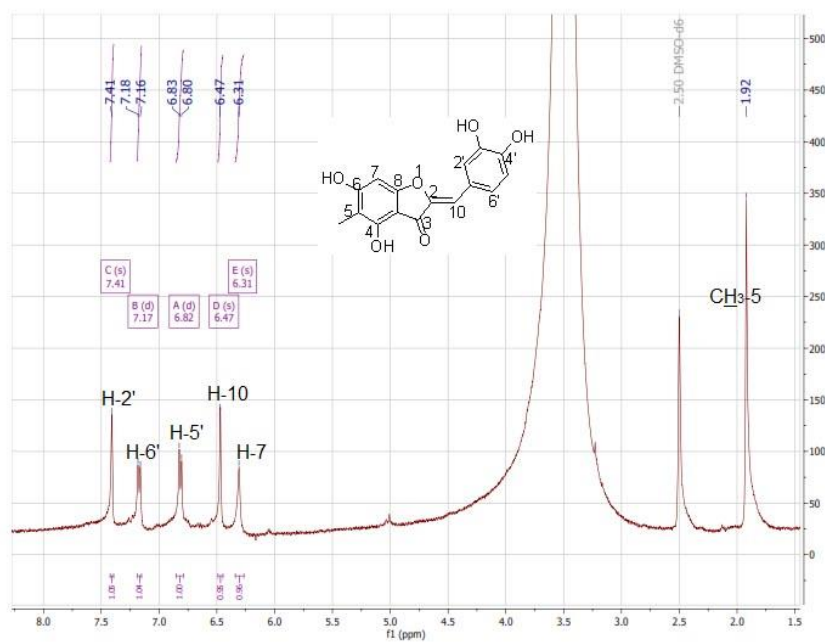


Figure S9. <sup>1</sup>H-NMR spectrum (DMSO-*d*<sub>6</sub>, 400 MHz) of 5-methyl aureusidin (3)

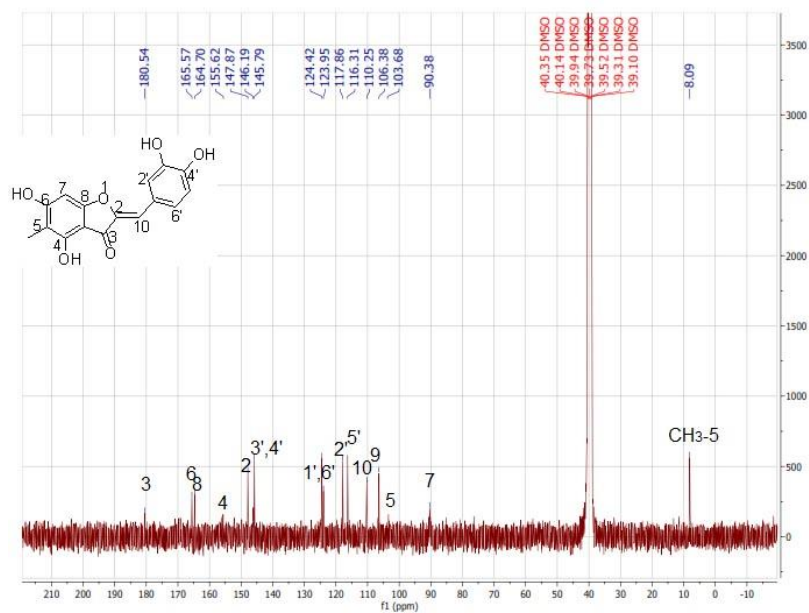


Figure S10. <sup>13</sup>C-NMR spectrum (DMSO-*d*<sub>6</sub>, 101 MHz) of 5-methyl aureusidin (3)

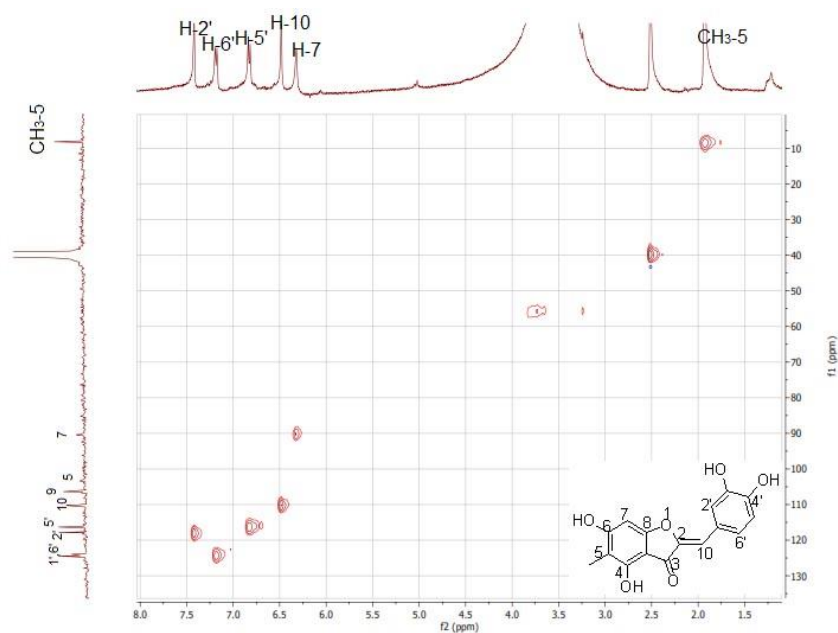


Figure S11. HSQC spectrum of 5-methyl aureusidin (**3**)

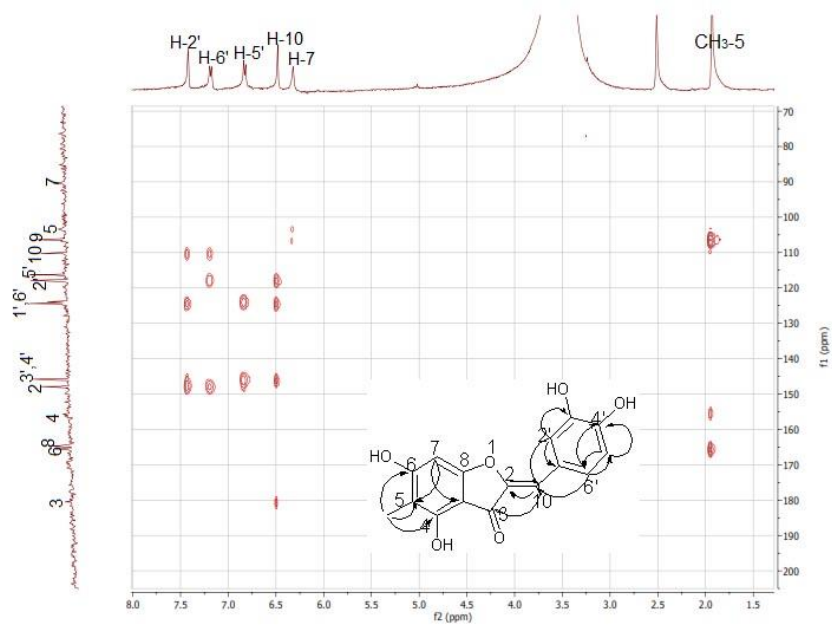


Figure S12. HMBC spectrum of 5-methyl aureusidin (**3**)

**Table S1:** Receptor interactions and binding energies of the tested compounds, and acarbose inside the binding pocket of  $\alpha$ -amylase.

Tested compound	S Score Kcal/mole	RMSD_Refine	Amino acid bond	Distance Å
<b>Acarbose</b>	-22.09	1.82	Lys200/H-donor	2.17
			Lys200/H-donor	2.24
			His201/H-acceptor	3.44
			Gly306/H-acceptor	1.85
			Asp197/H-acceptor	2.4
			Asp300/H-acceptor	2.27
<b>1</b>	-17.55	2.00	Asp197/H-acceptor	2.04
<b>3</b>	-16.42	1.84	Asp197/H-acceptor	2.15
<b>2</b>	-15.21	1.46	Asp300/H-acceptor	2.74

**Table S2:** Receptor interactions and binding energies of the tested compounds, and acarbose inside the binding pocket of  $\alpha$ -glucosidase.

Tested compound	S Score Kcal/mole	RMSD_Refine	Amino acid bond	Distance Å
<b>Acarbose</b>	-30.42	1.05	Asn258/H-acceptor	1.85
			Asp326/H-acceptor	1.87
			Asp326/H-acceptor	2.43
			Asp326/H-acceptor	1.83
			Arg411/H-donor	2.02
			Arg411/H-donor	2.33
			Ser 384/ H-acceptor	2.14
			His325/ H-acceptor	3.2
<b>3</b>	-21.61	2.10	Tyr63/ arene-arene	3.93
			Arg411/H-donor	2.19
			Asp382/H-acceptor	2.08
<b>1</b>	-20.64	2.54	Tyr63/ arene-arene	3.85
			Arg411/H-donor	2.24
			Asp382/H-acceptor	1.93
<b>2</b>	-20.47	1.36	Tyr63/ arene-arene	1.39



**Table S3:** Receptor interactions and binding energies of the tested compounds, and CP-91149 inside the binding pocket of glycogen phosphorylase.

Tested compound	S Score Kcal/mole	RMSD_Refine	Amino acid bond	Distance Å
<b>CP-91149</b>	-17.77	1.74	Lys191/ arene-cation	3.92
			Lys191/ arene-cation	3.74
			Arg193/ arene-cation	4.69
			Arg60/ H-donor	2.11
<b>2</b>	-13.42	1.41	Arg193/ arene-cation	2.09
			Arg60/arene-cation	3.11
			Lys191/ H-donor	3.55
<b>1</b>	-13.20	0.80	Arg60/ arene-cation	3.27
<b>3</b>	-12.84	1.72	Arg60/arene-cation	3.92
			Arg193/ arene-cation	3.96