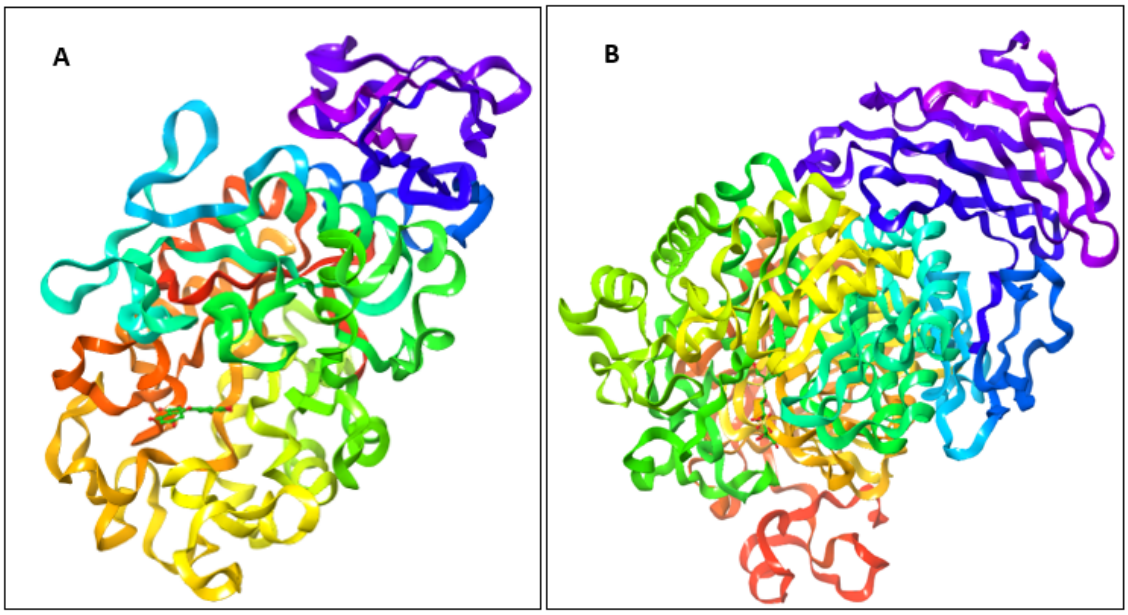

Figure S1. Three-dimensional structures of α-amylase (A) with PDB ID 4GQR and α-glucosidase (B) with PDB ID 3L4Y. The structures were compiled using Maestro 12.9 from Schrödinger and accessed from RCSB protein data bank.

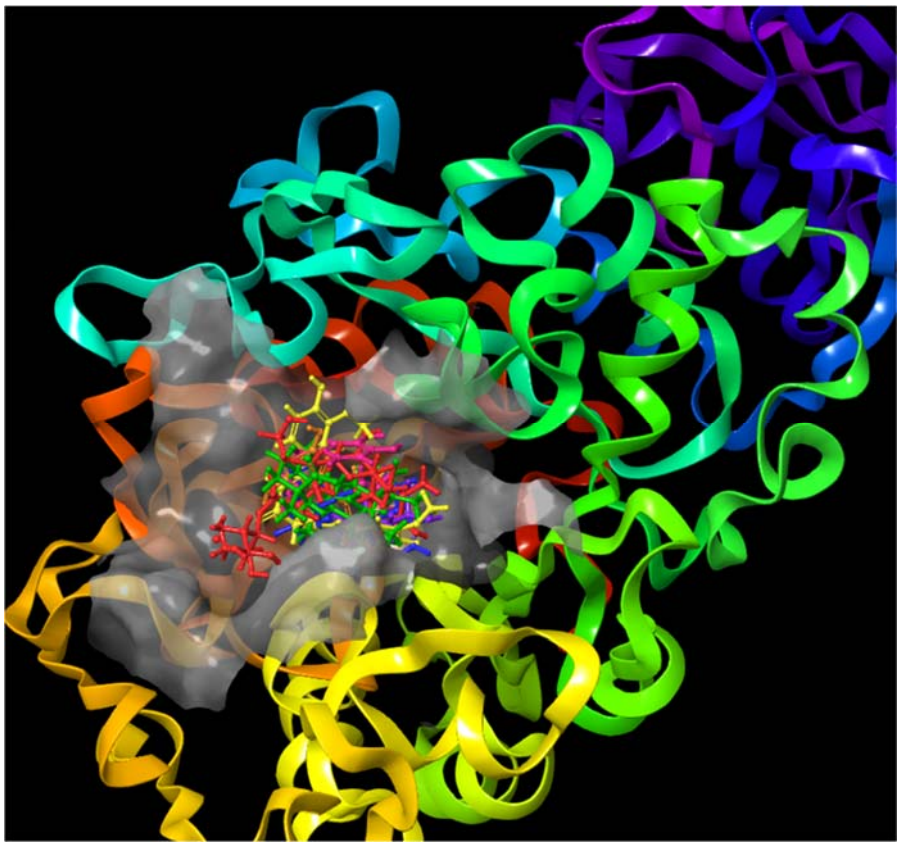

Figure S2. Representation of the compounds on the active side of α-amylase. This shows that all the compounds were docked in the same binding site in the enzyme pocket. The following

colours represent the compounds: red (acarbose), yellow (curcumin), green (18α-GA), blue (nerolidol), orange (quercetin), purple (quinic acid) and pink (rosmarinic acid).

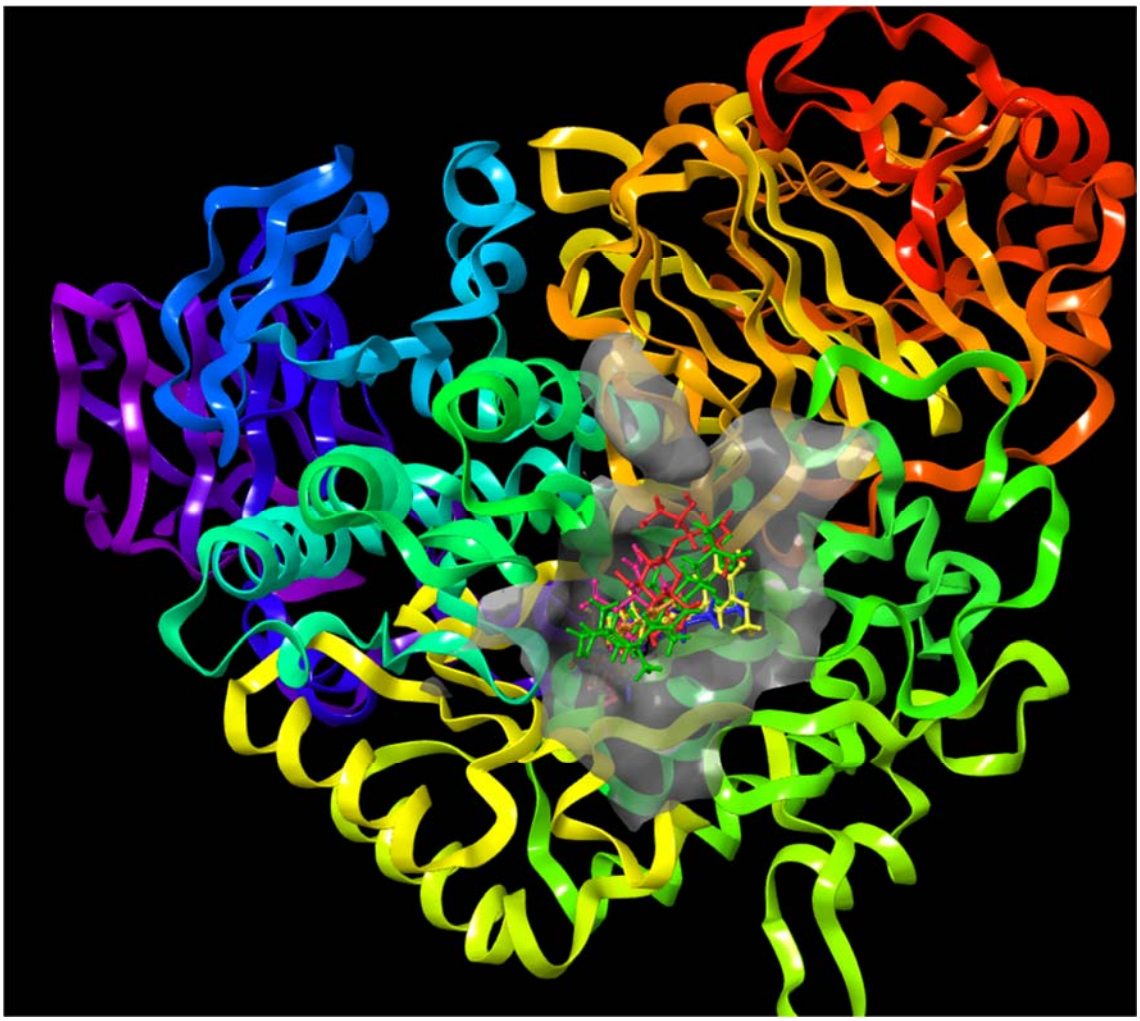

Figure S3. Representation of the compounds on the active side of α-glucosidase. This shows that all the compounds were docked in the same binding site in the enzyme pocket. The following colours represent the compounds: red (acarbose), yellow (curcumin), green (18α-GA), blue (nerolidol), orange (quercetin), purple (quinic acid) and pink (rosmarinic acid).

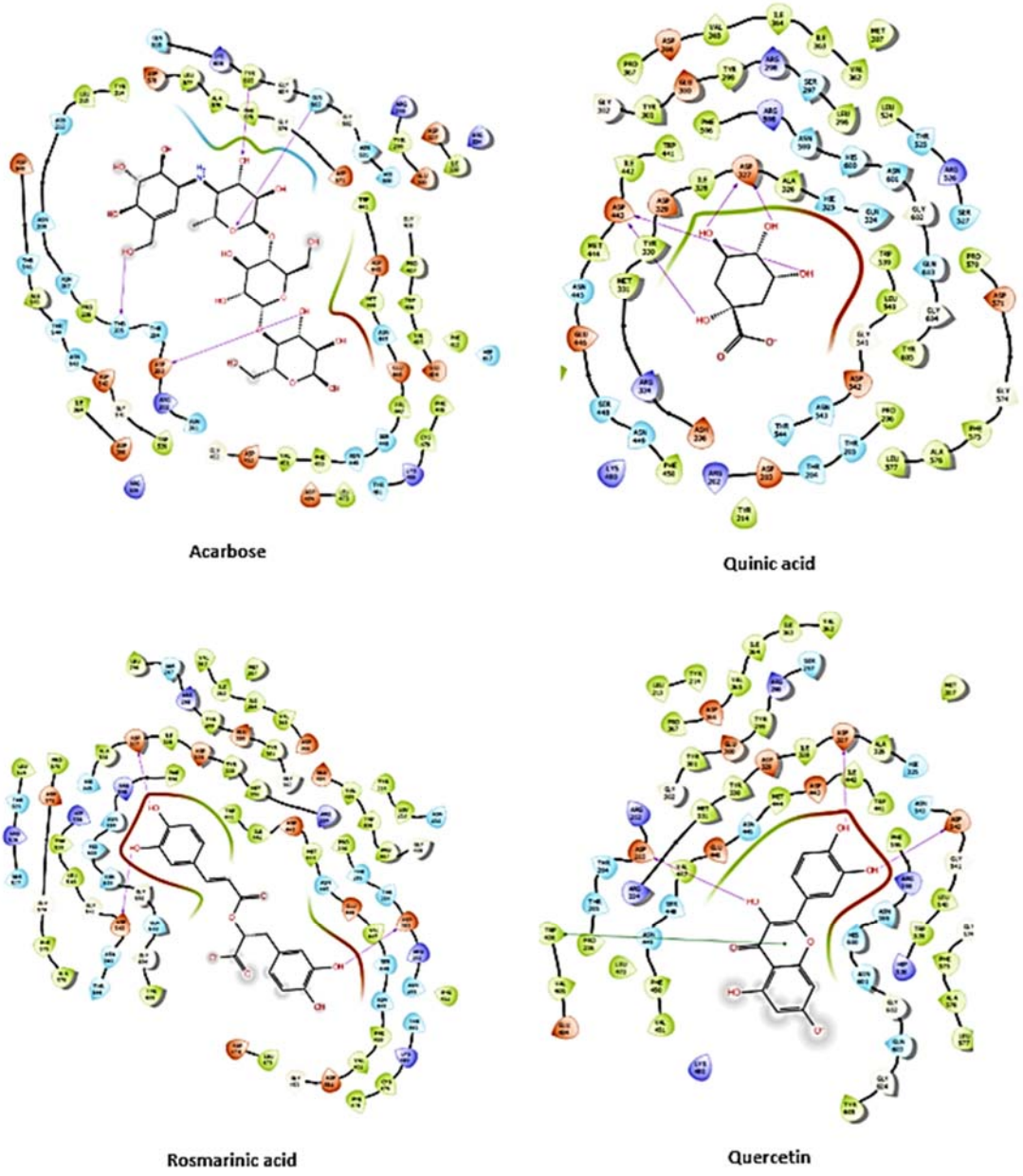

Figure S4. The interactions of acarbose, quinic acid, rosmarinic acid and quercetin in the binding pocket of α-glucosidase. Showing the composition of the binding pocket; hydrogen bonds (purple arrow) and pi-pi stacking (green arrow) interactions between the enzyme and the compounds.

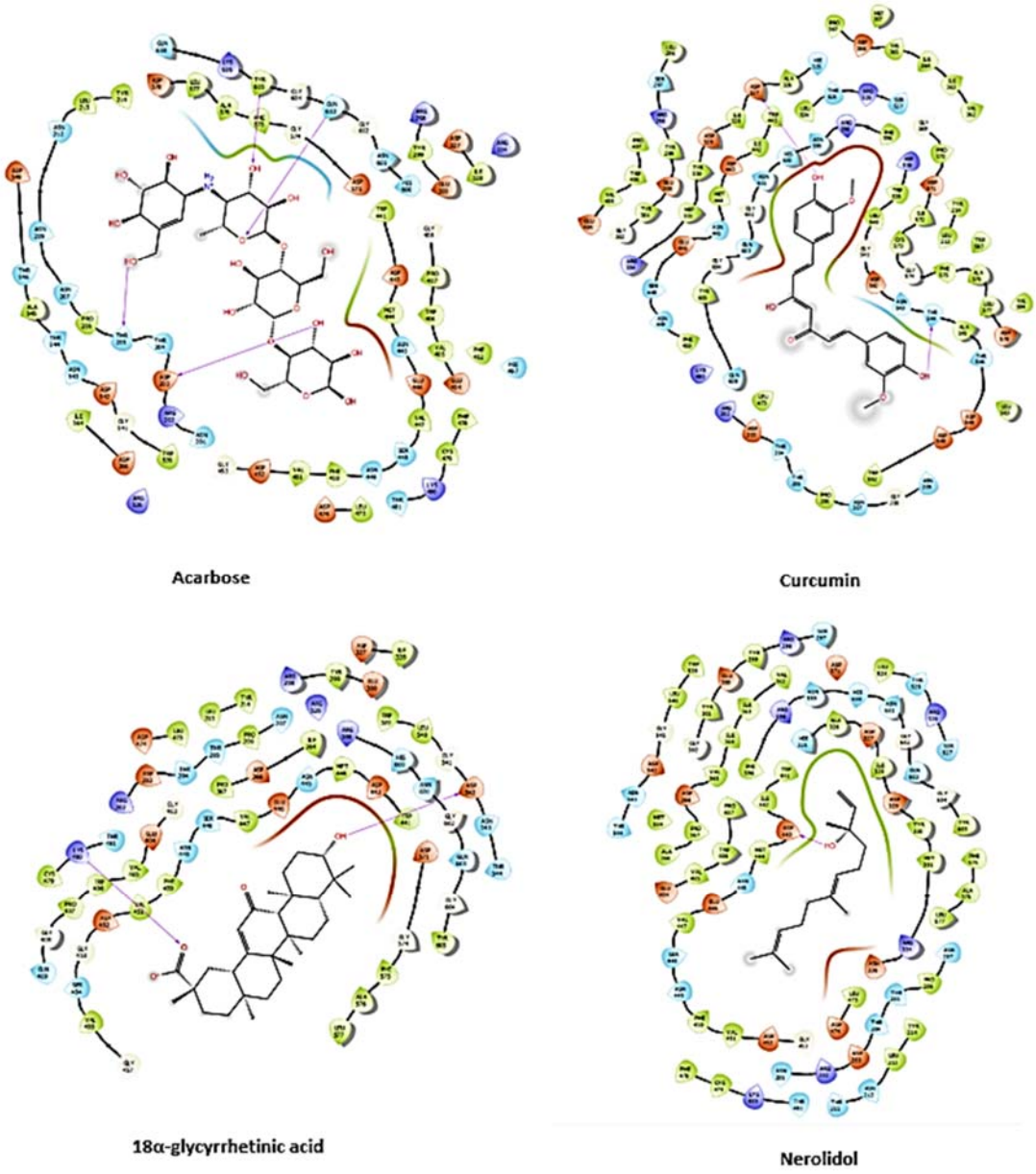

Figure S5. The interactions of acarbose, curcumin, 18α-GA and nerolidol in the binding pocket of α-glucosidase. Showing the composition of the binding pocket; hydrogen bonds (purple arrow) between the enzyme and the compounds.

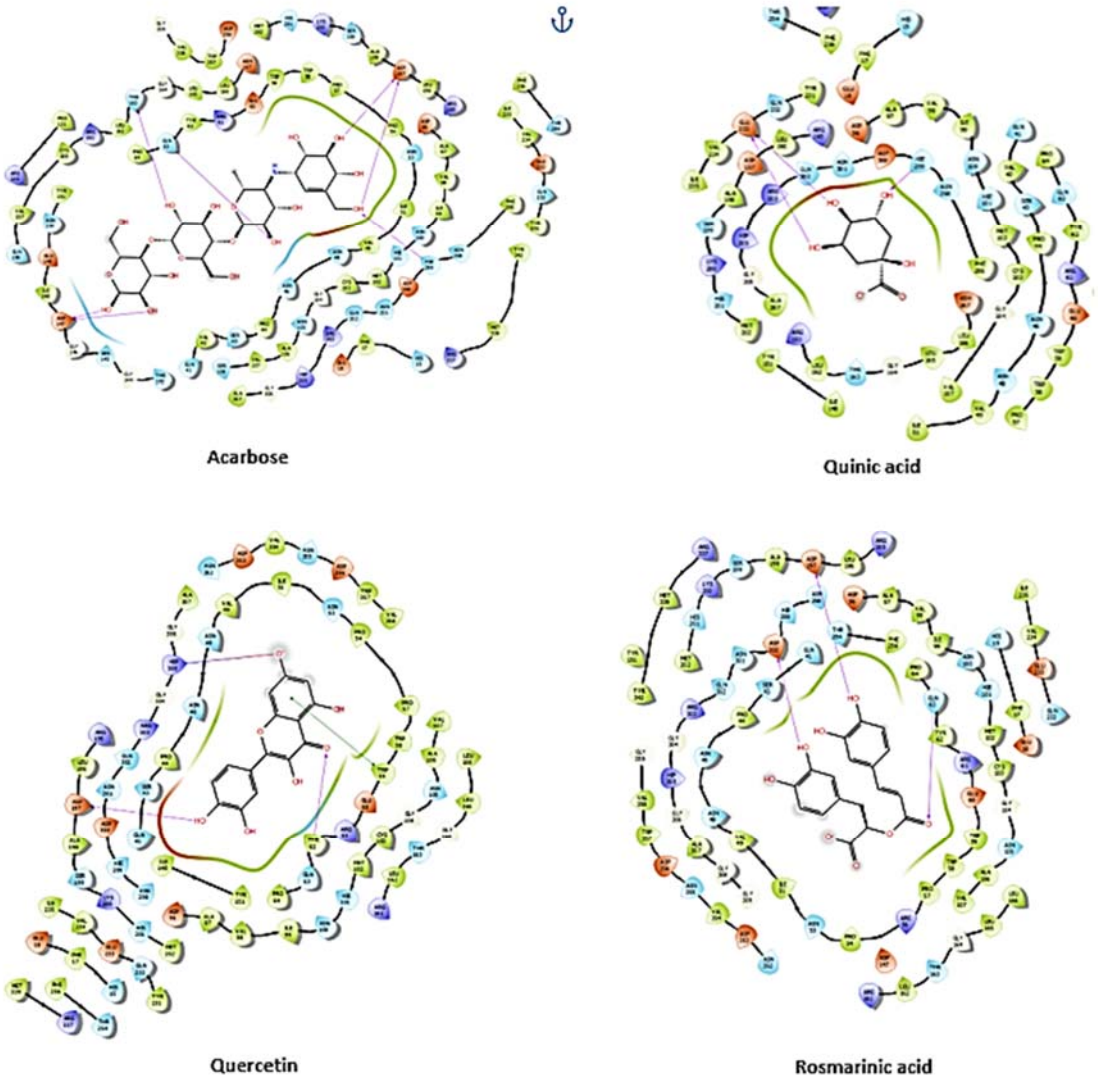

Figure S6. The interactions of acarbose, quinic acid, quercetin and rosmarinic acid in the binding pocket of α-amylase. Showing the composition of the binding pocket; hydrogen bonds (purple arrow) and pi-pi stacking (green arrow) interactions between the enzyme and the compounds.

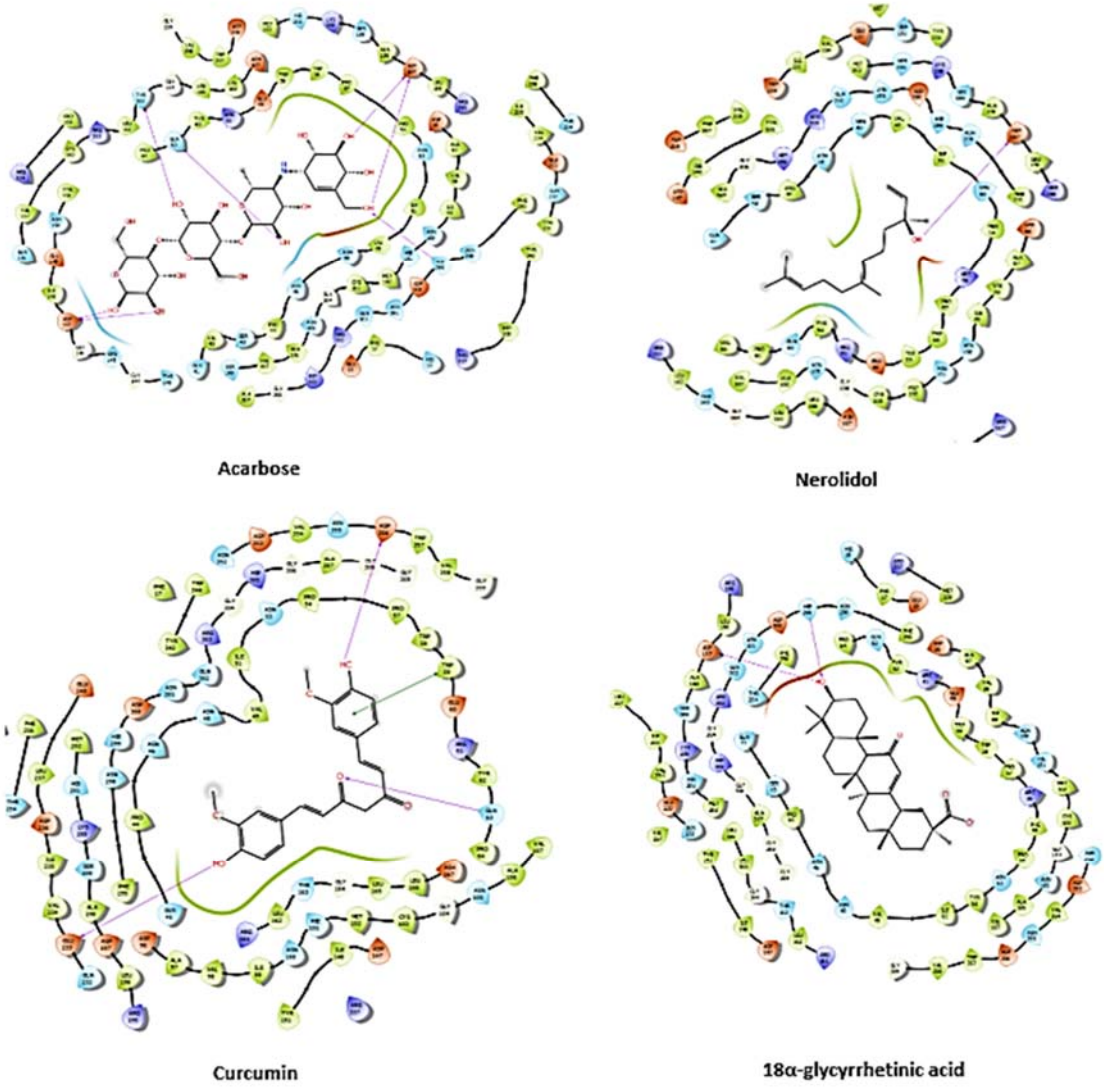

Figure S7. The interactions of acarbose, nerolidol, curcumin and 18α-GA in the binding pocket of α-amylase. Showing the composition of the binding pocket; hydrogen bonds (purple arrow) and pi-pi stacking (green arrow) between the enzyme and the compounds.

1.1. Annexure B: Lineweaver burk plots

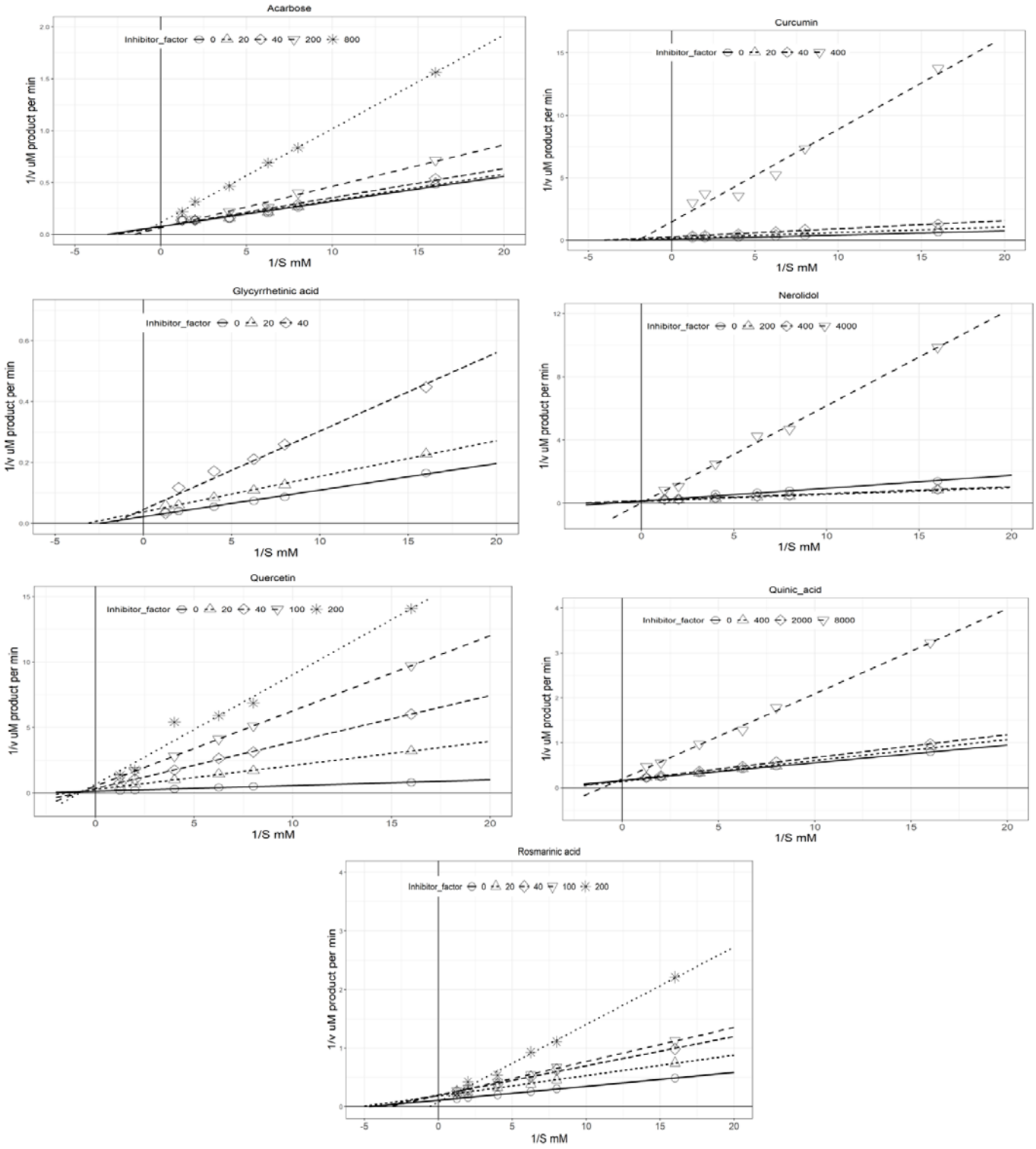

Figure S8. Lineweaver-Burk graphs of the inhibition of α-glucoside by compounds with [I] in µM.

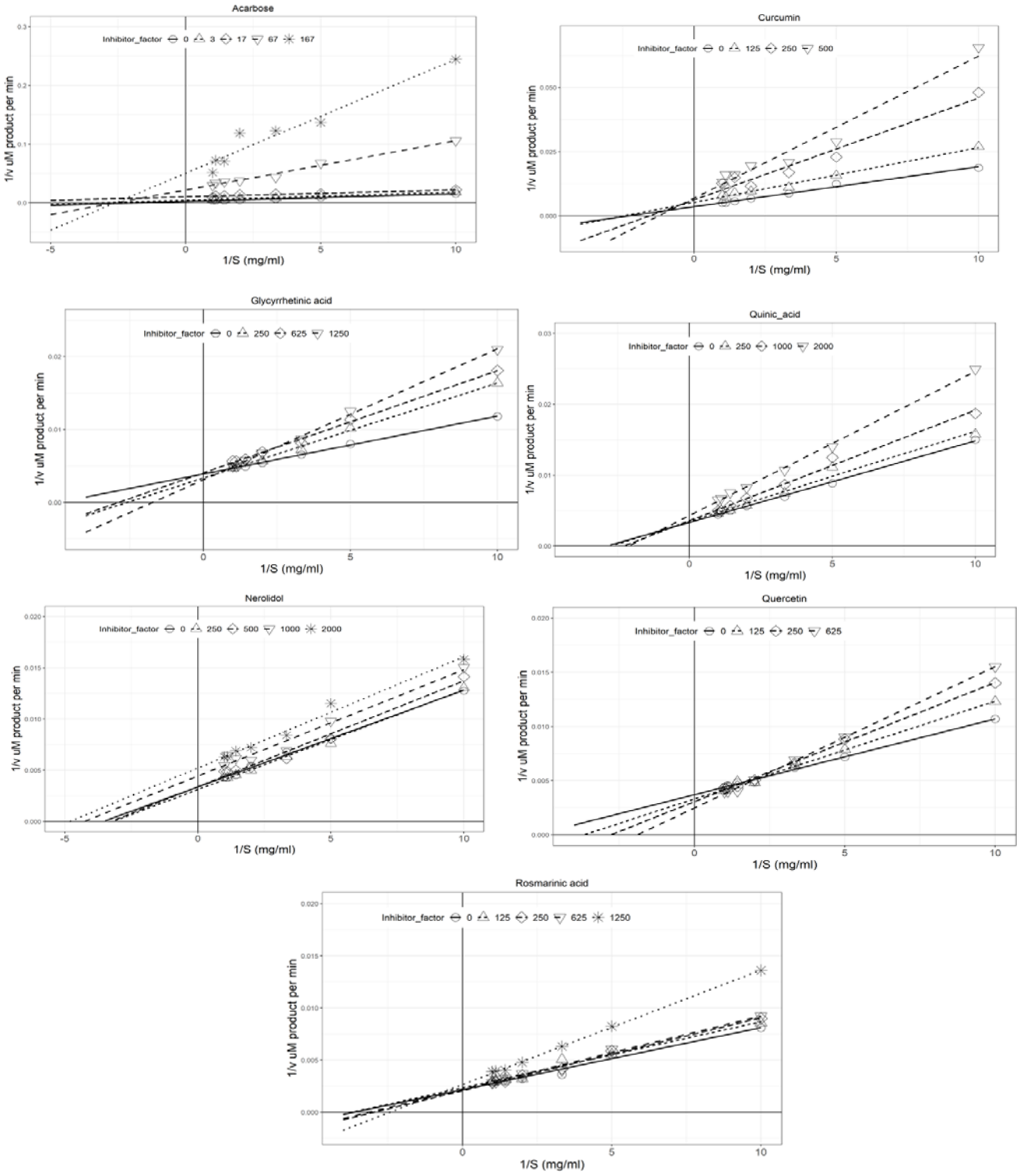

Figure S9. Lineweaver-Burk graphs of the inhibition of α-amylase by compounds with [I] in μM