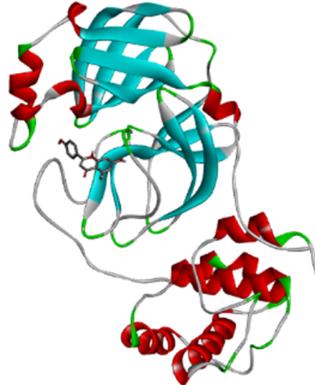
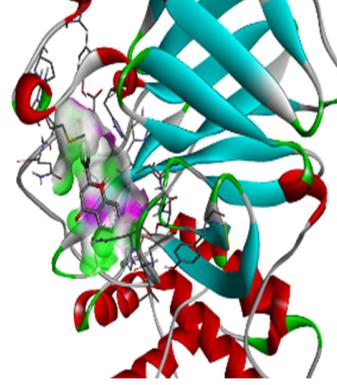
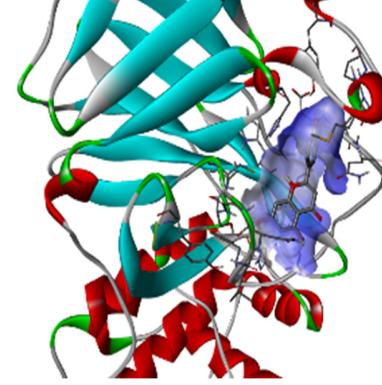
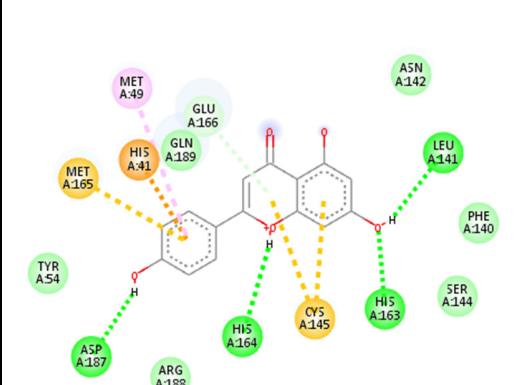
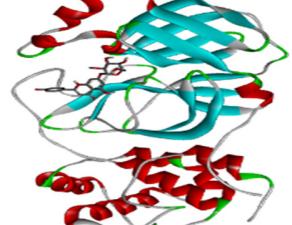
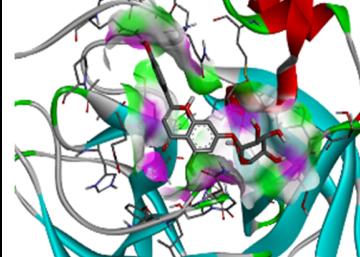
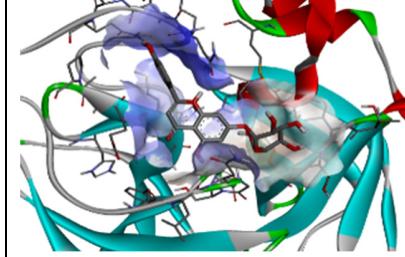
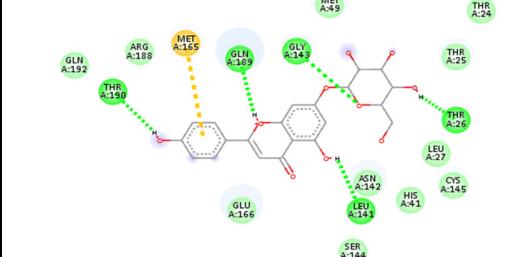
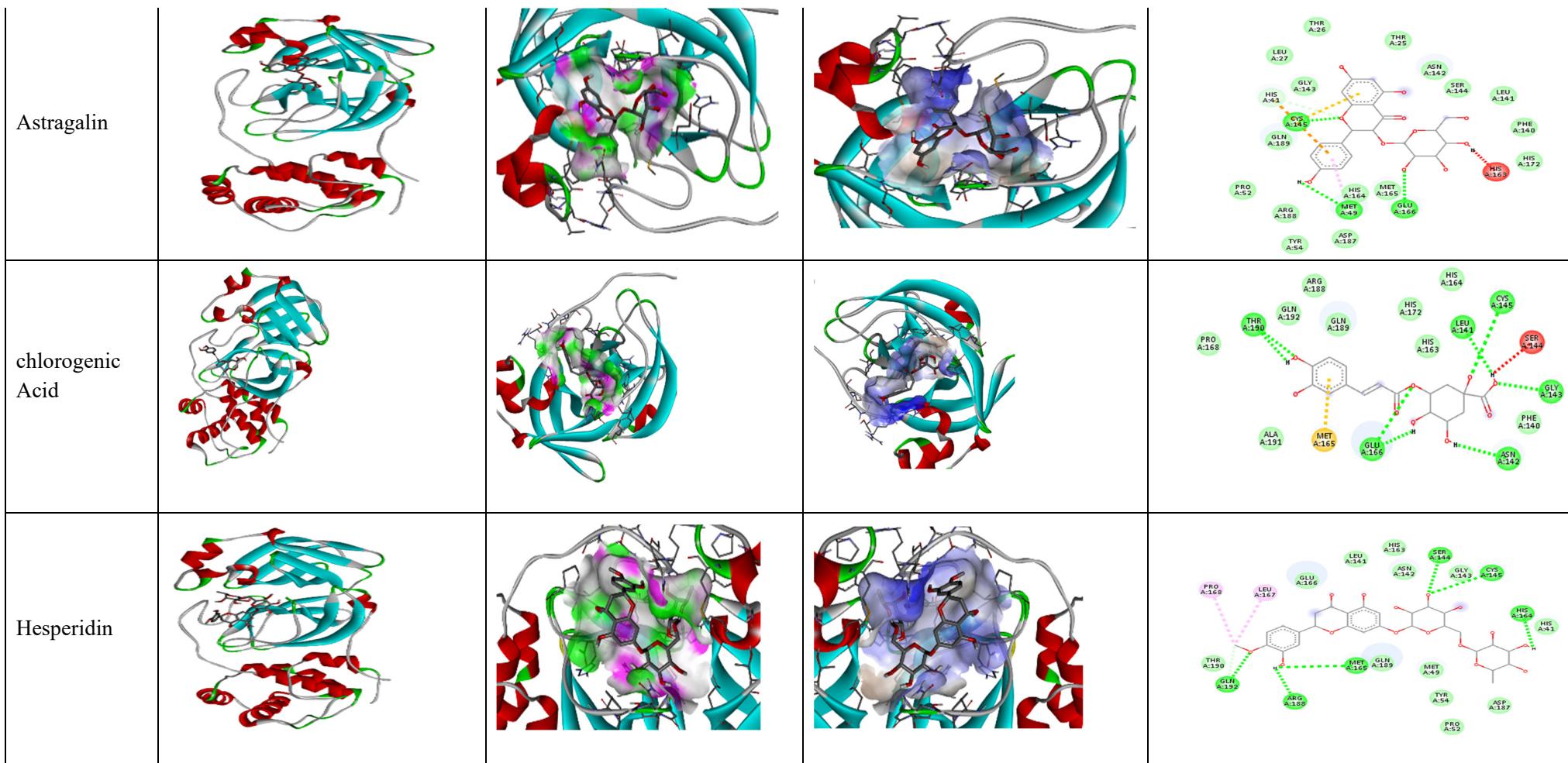
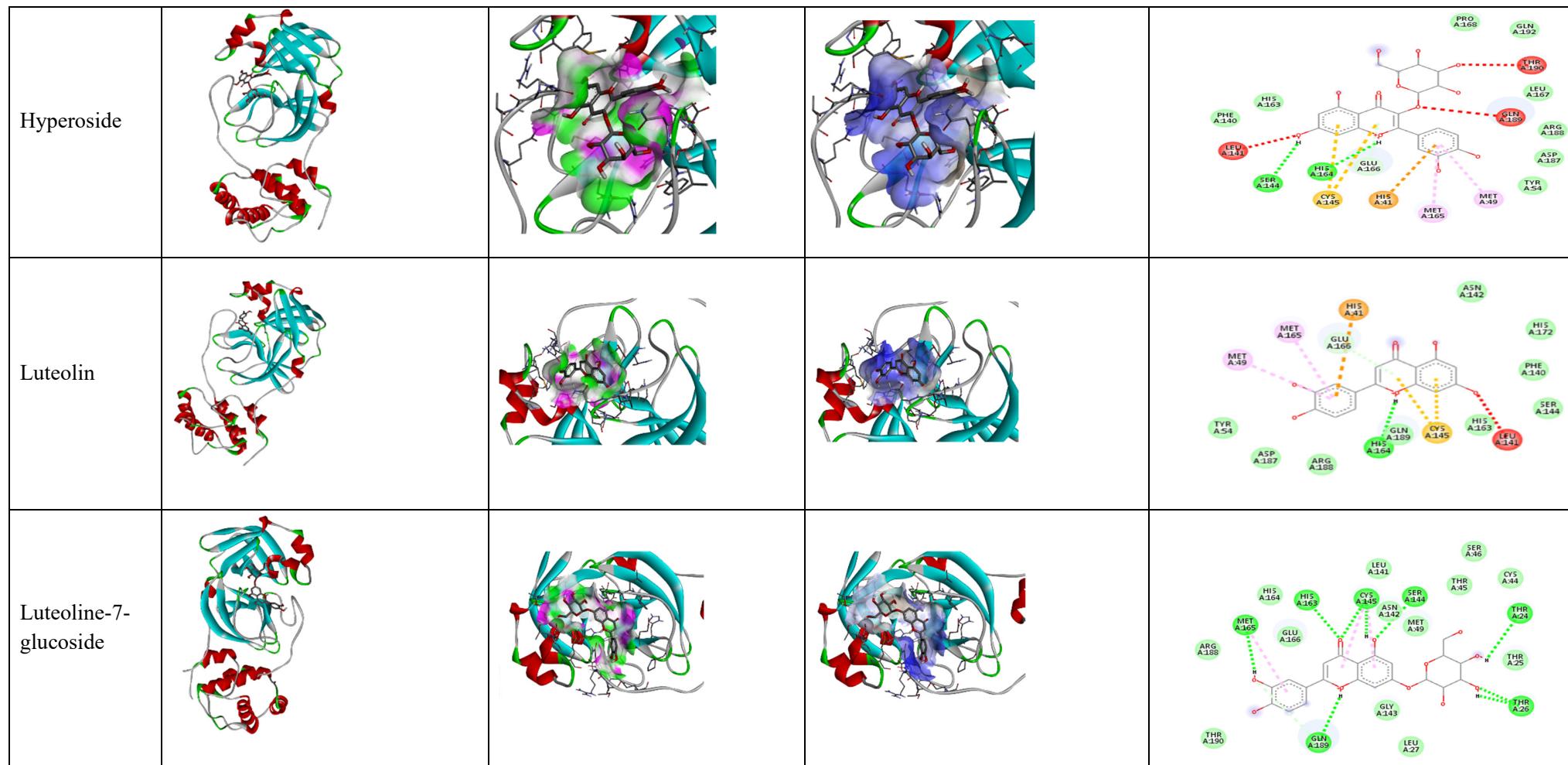
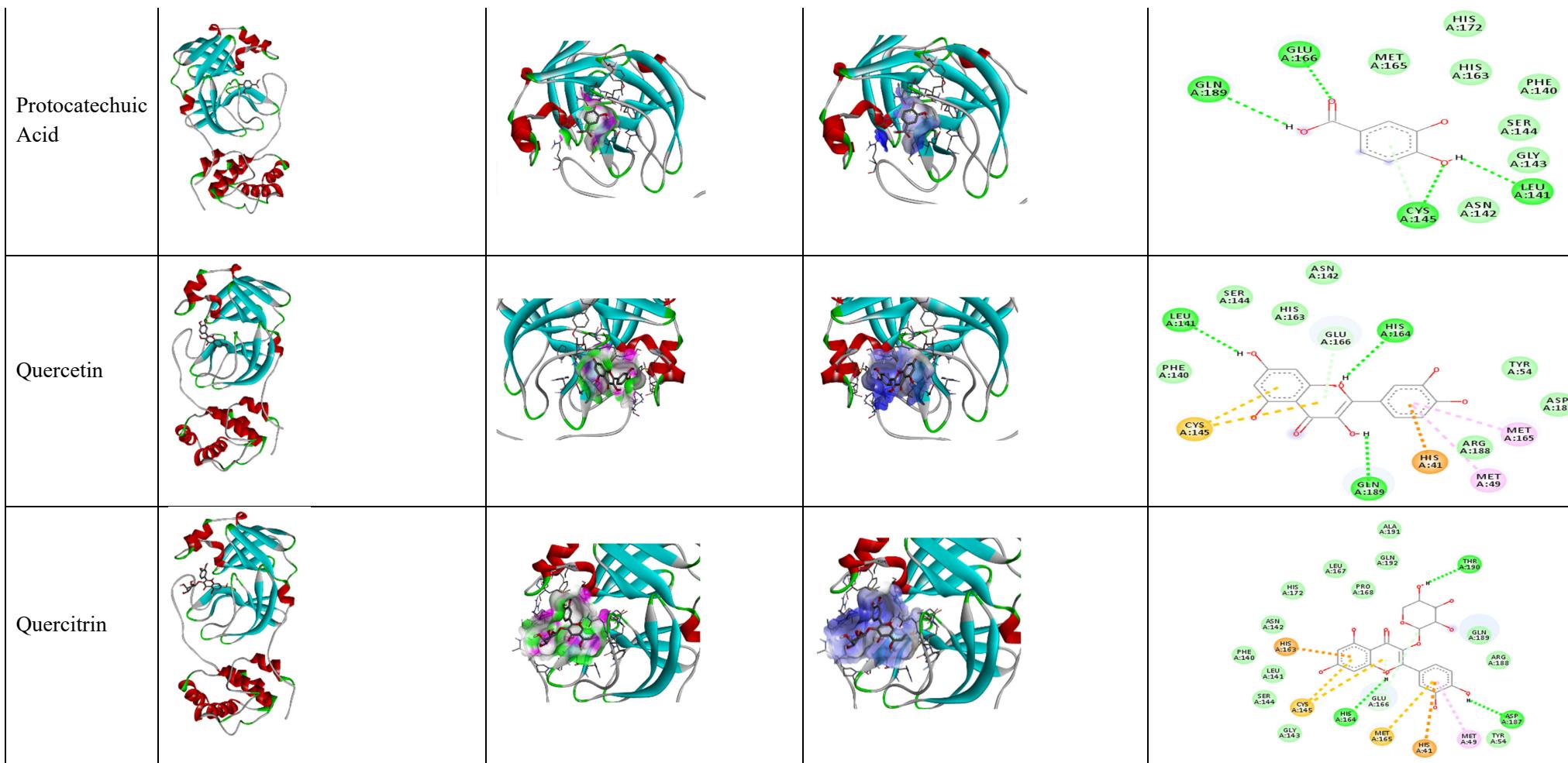


Table S1. Superposition and intermolecular interactions between the different ligand determined in Algerian fir and the main protease of Sars-cov 2 virus using PM7 Method (Covid19)

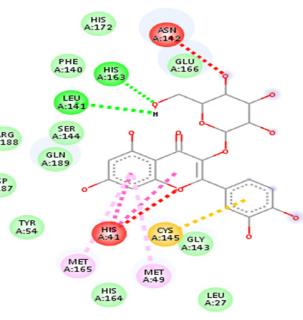
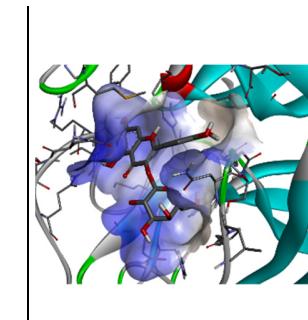
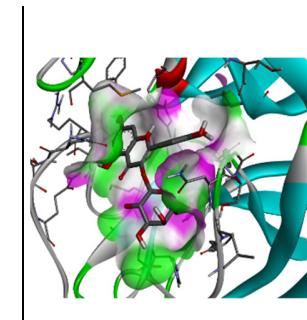
| Compounds | Molecular Docking | H-Bond | Hydrophobic | Interactions |
|-----------|--|---|--|--|
| Apigenin |  |  |  |  |
| Apigetrin |  |  |  |  |



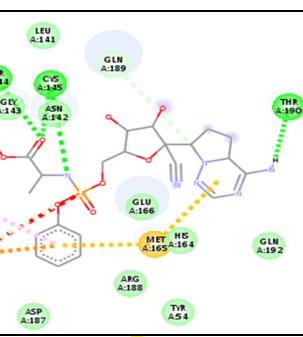
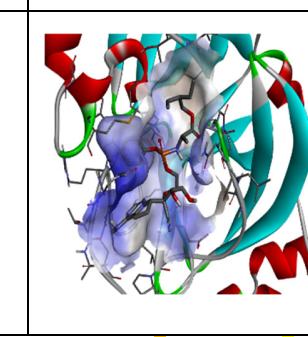
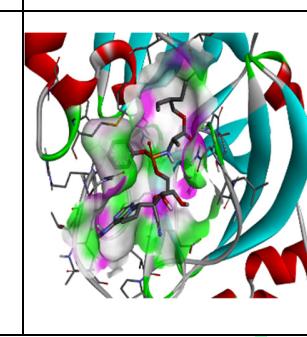
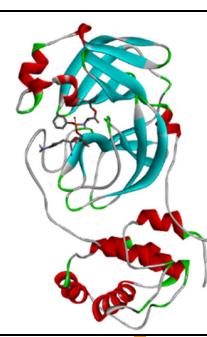




Rutin



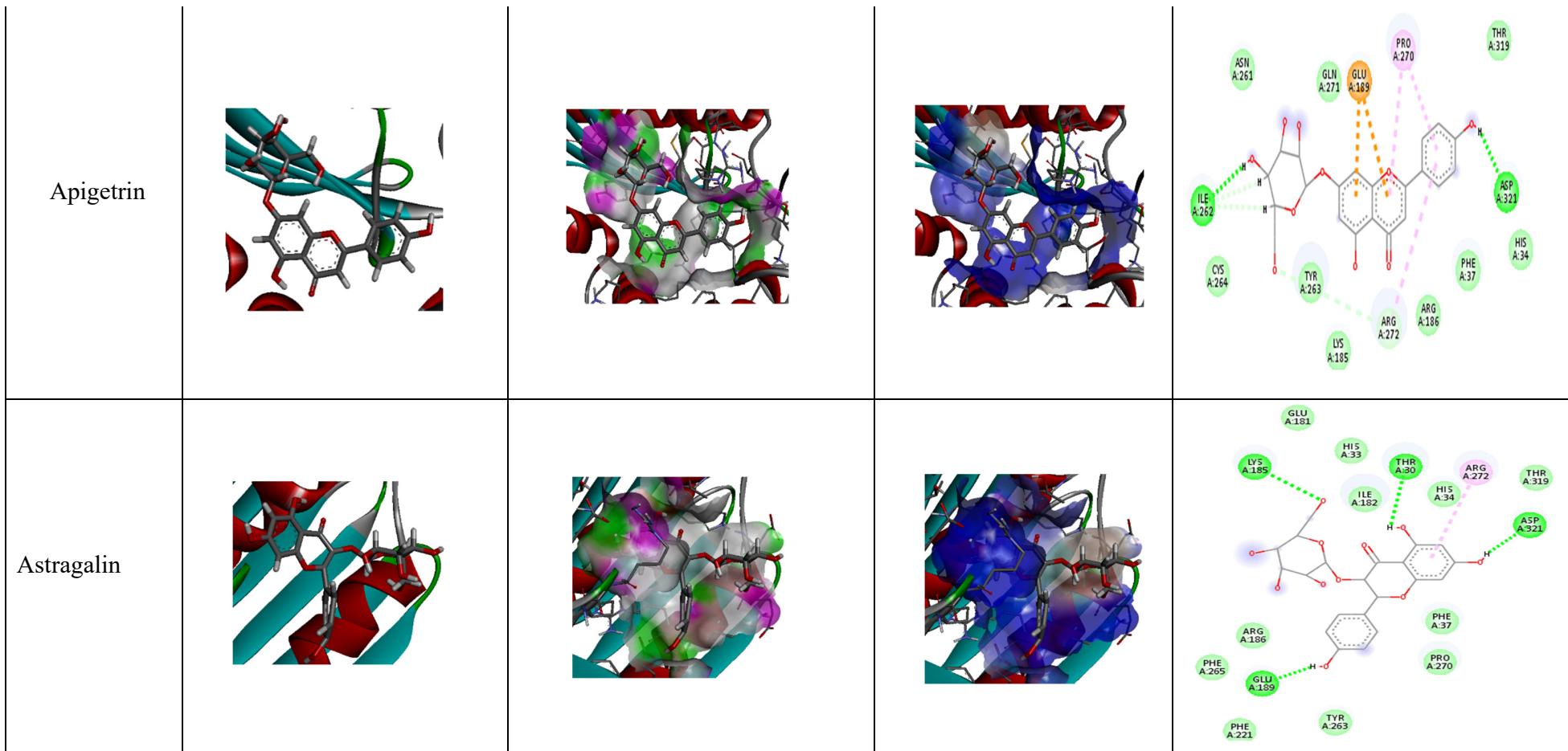
Redmisivir

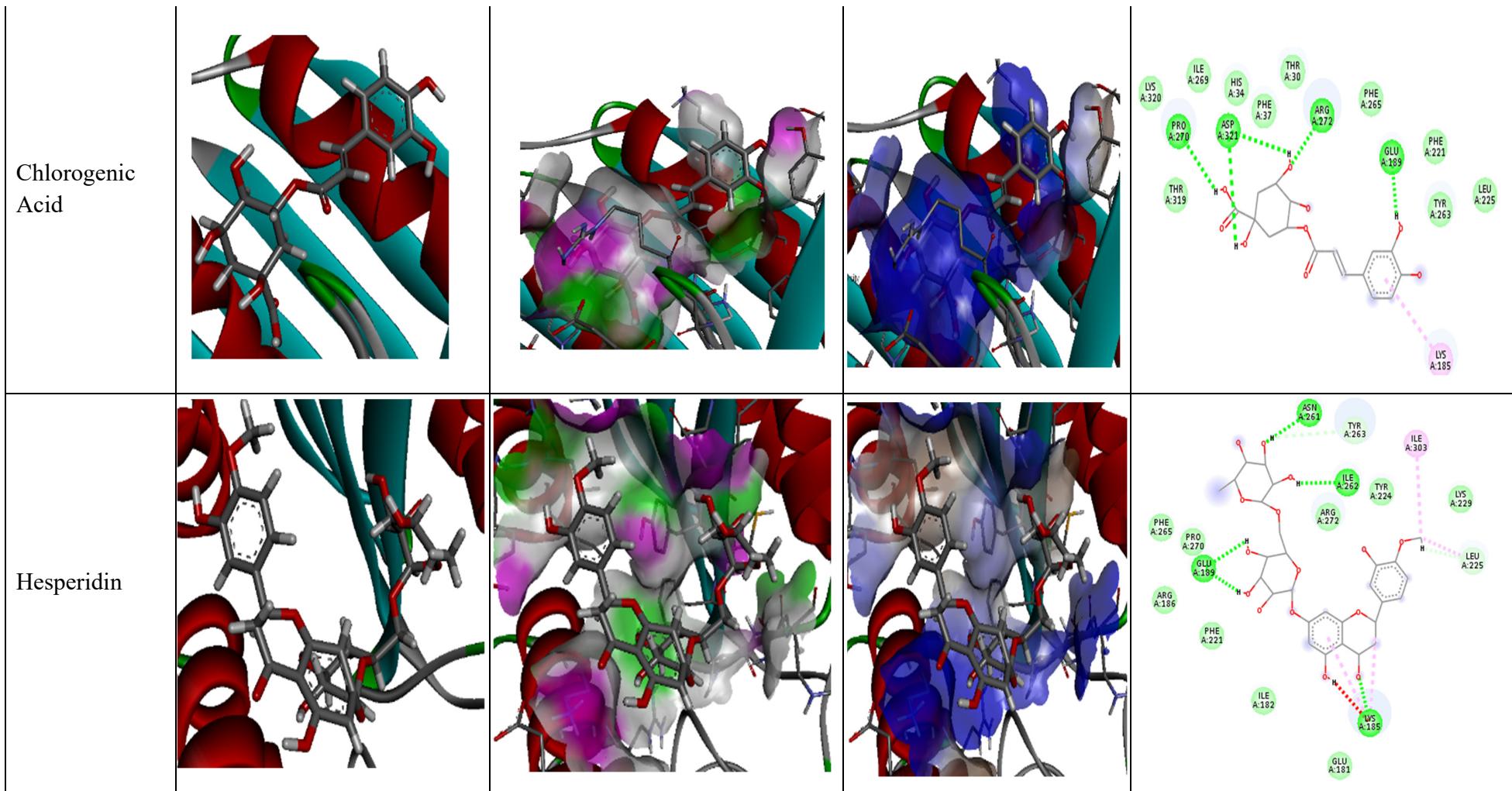


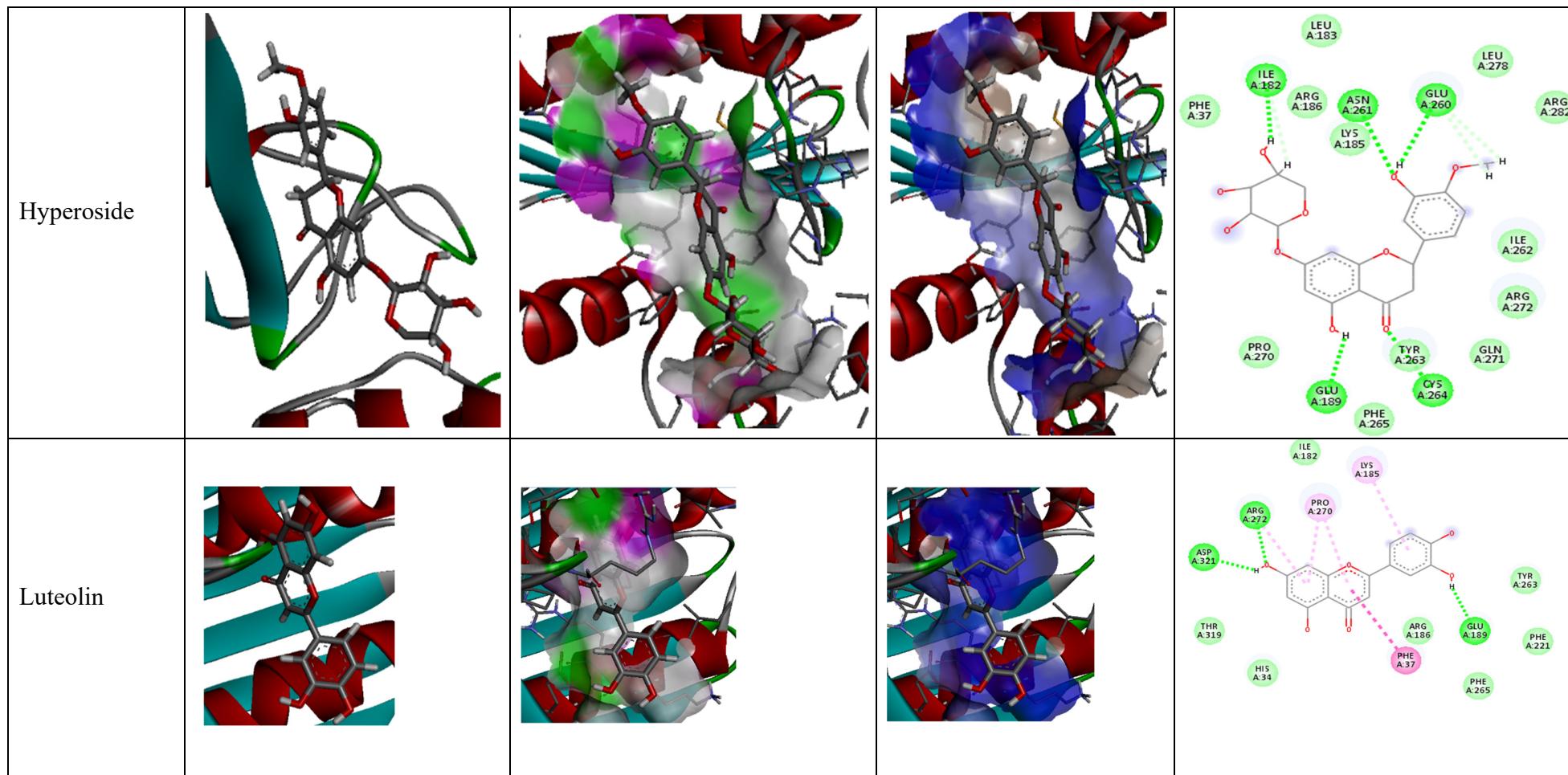
+: Van der Waals; +: Pi-Cation; +: Unfavorable Acceptor -Acceptor; +: Pi-Donor Hydrogen Bond; +: Pi-Sulfur; +: Pi-Sigma; +: Conventional Hydrogen Bond; +: Sulfur-X; +: Pi-Alkyl.

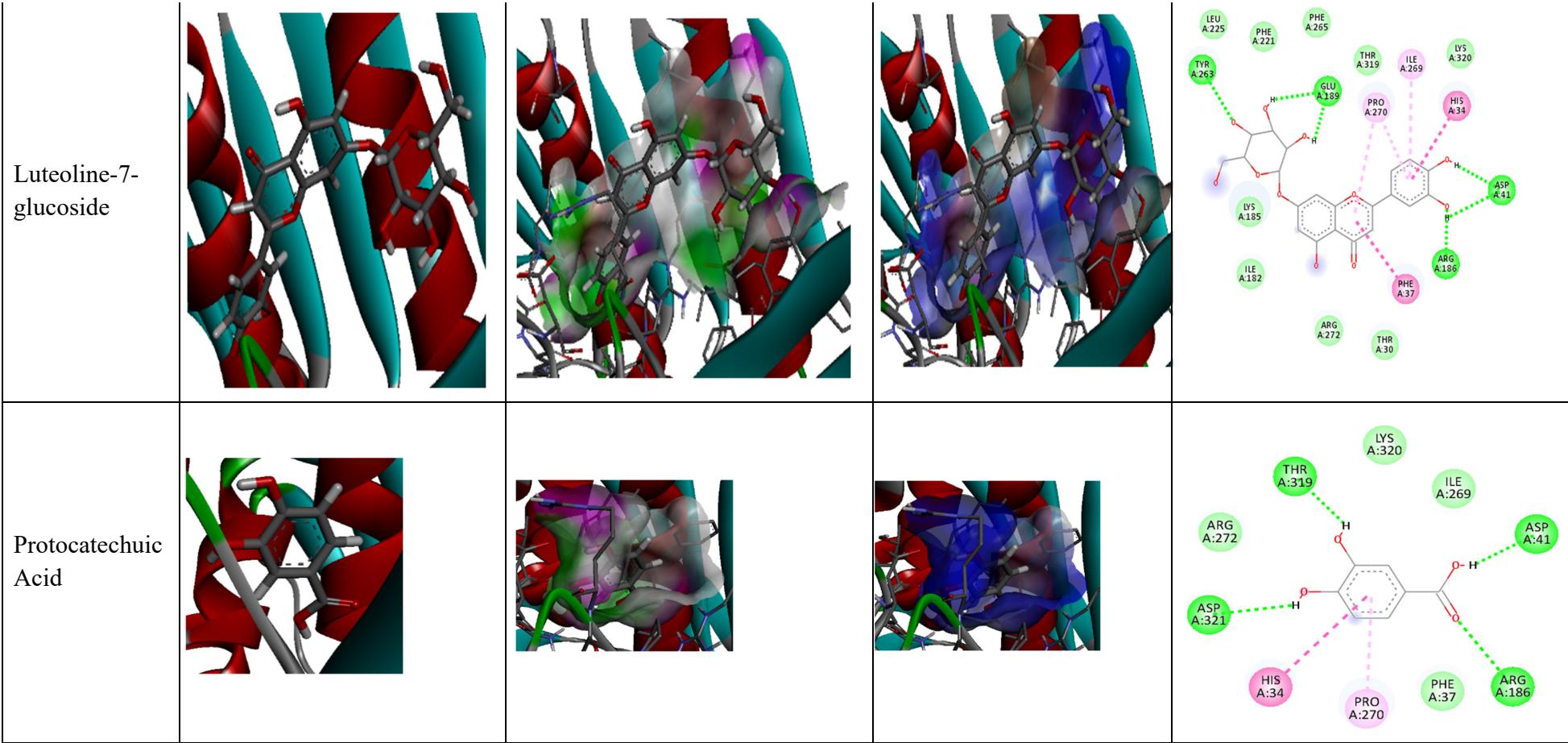
Table S2. Superposition and intermolecular interactions between the different ligand determined in Algerian fir and 4PRV presents in *E. coli* using PM7 Method

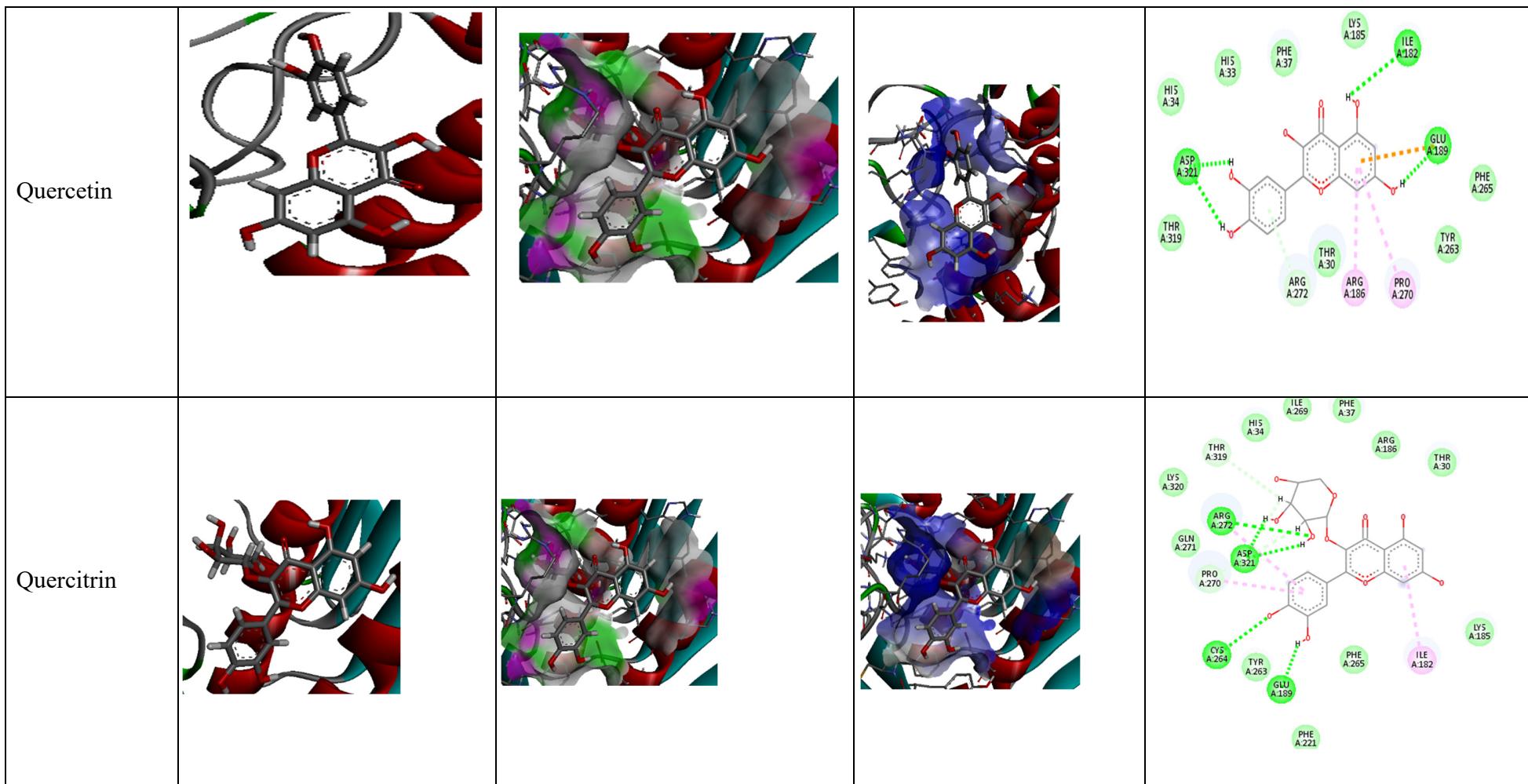
| Molecule | Molecular Docking | H-Bond | Hydrophobic | Interactions |
|----------|-------------------|--------|-------------|--------------|
| Apigenin | | | | |











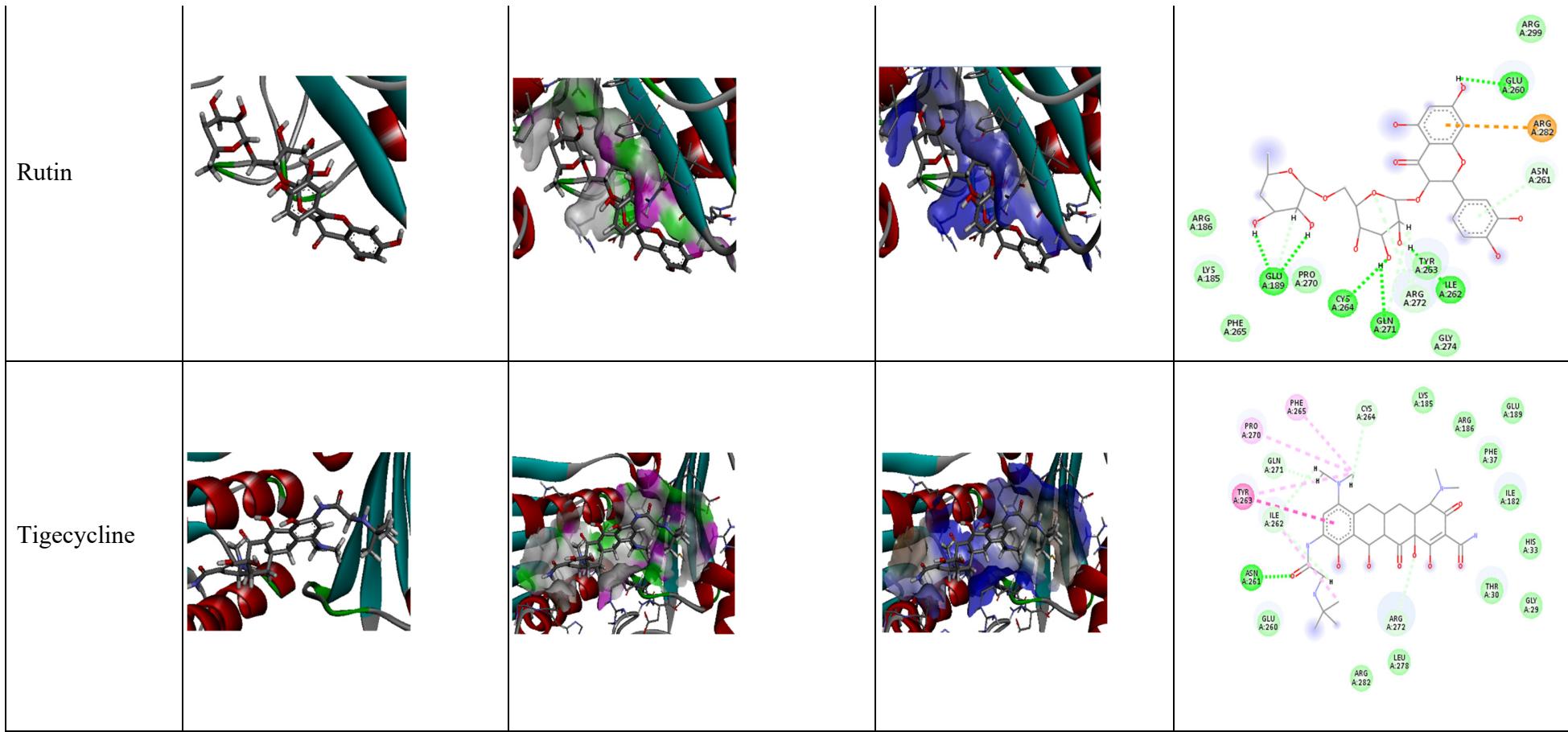
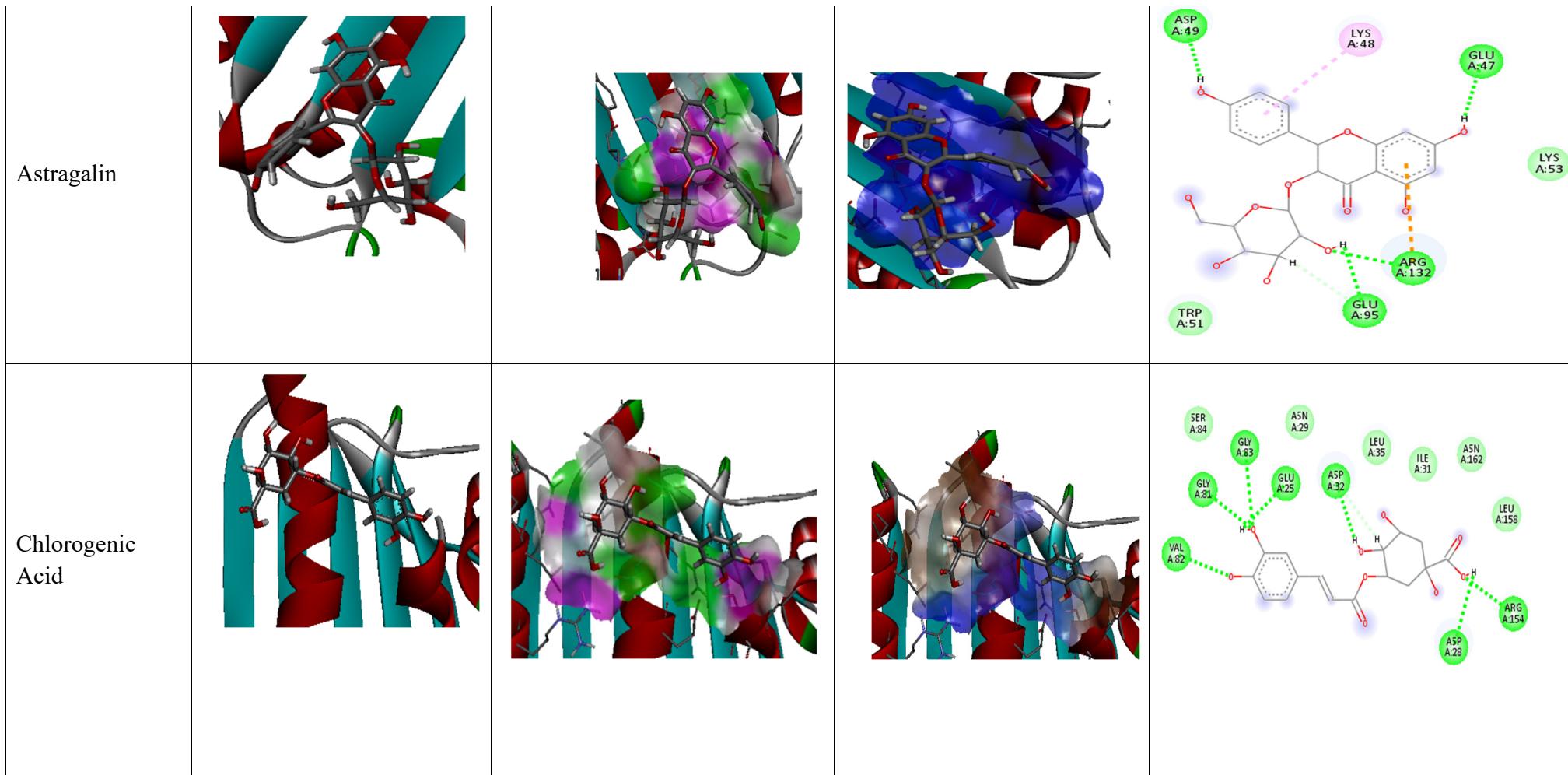
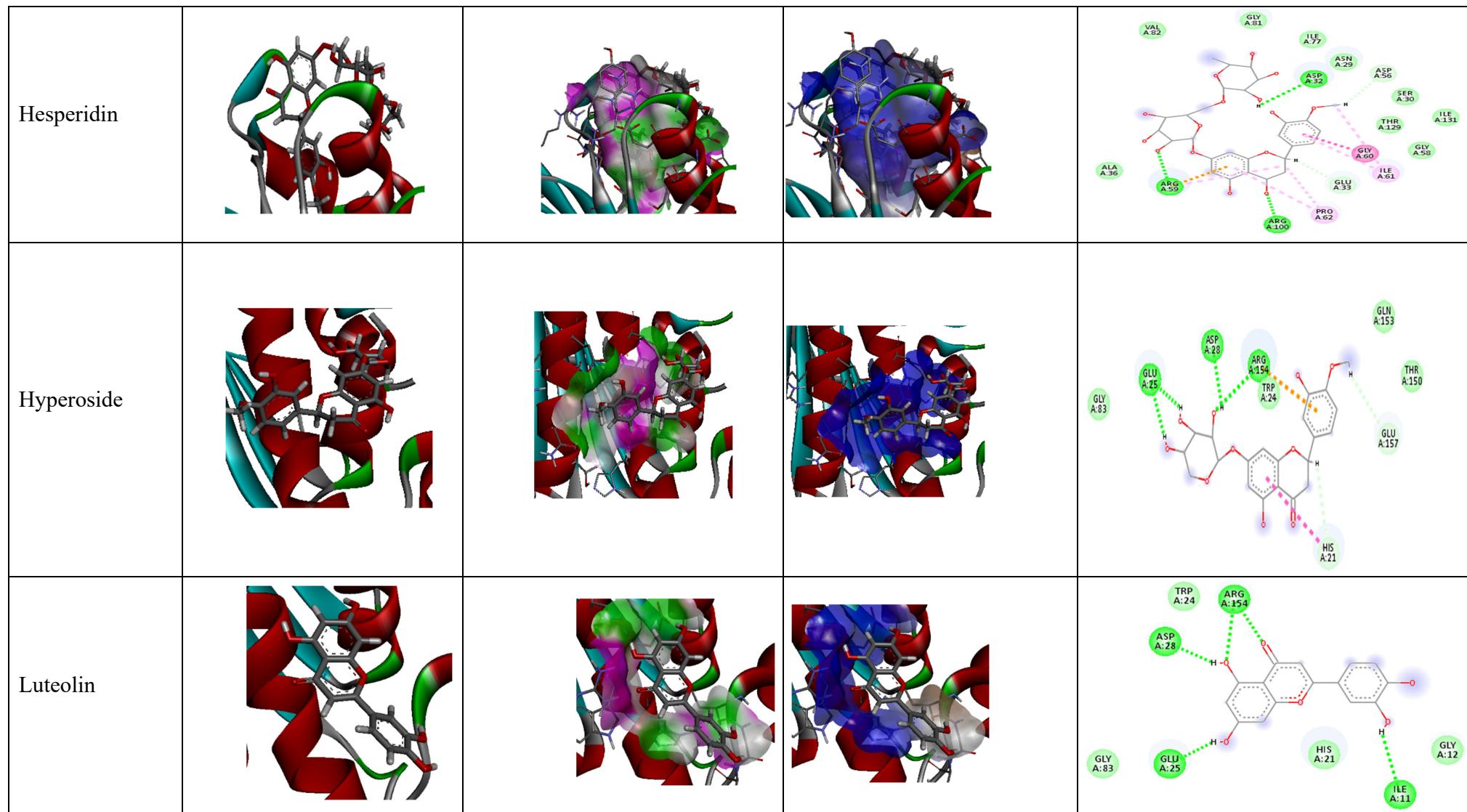
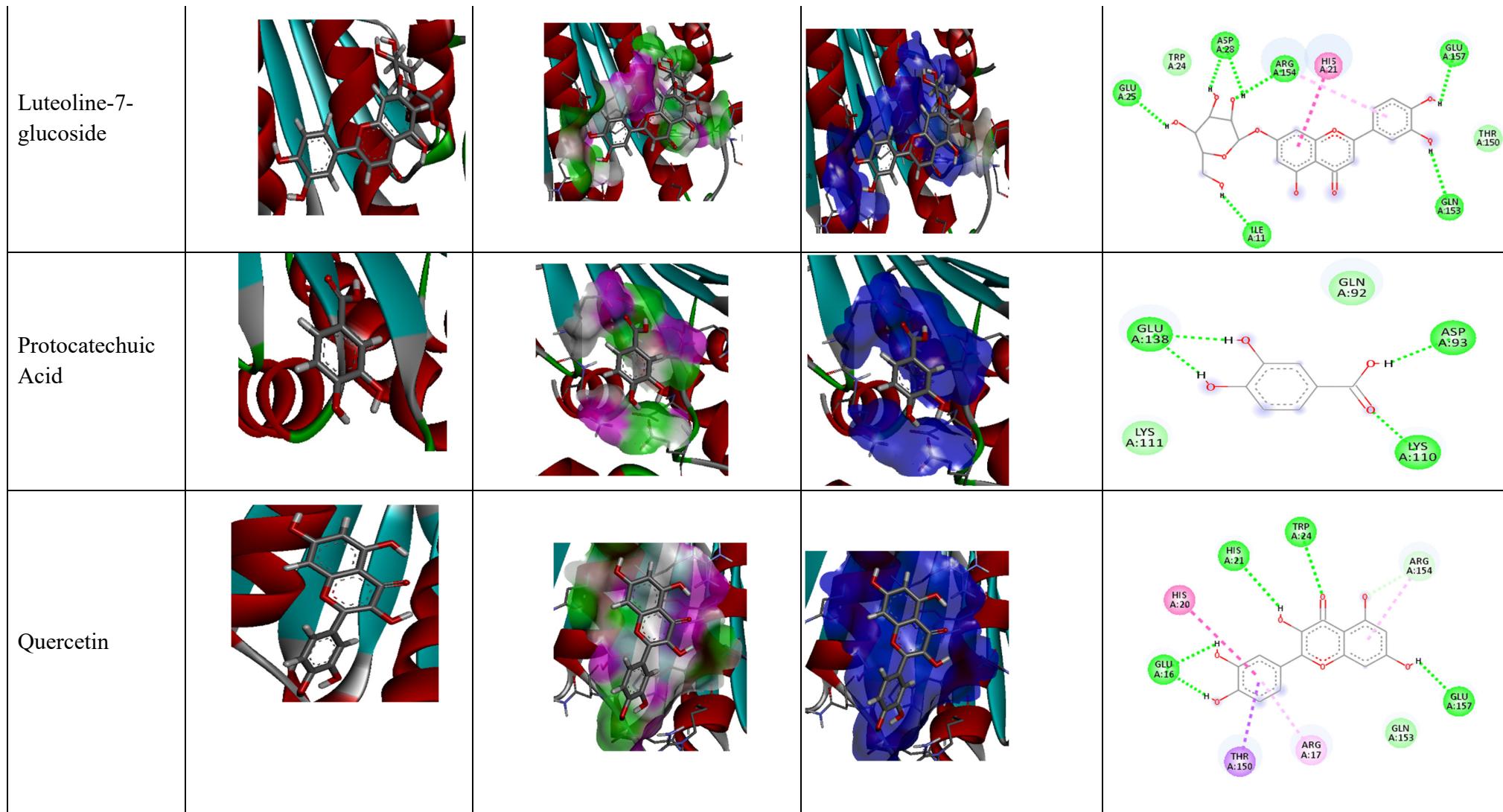


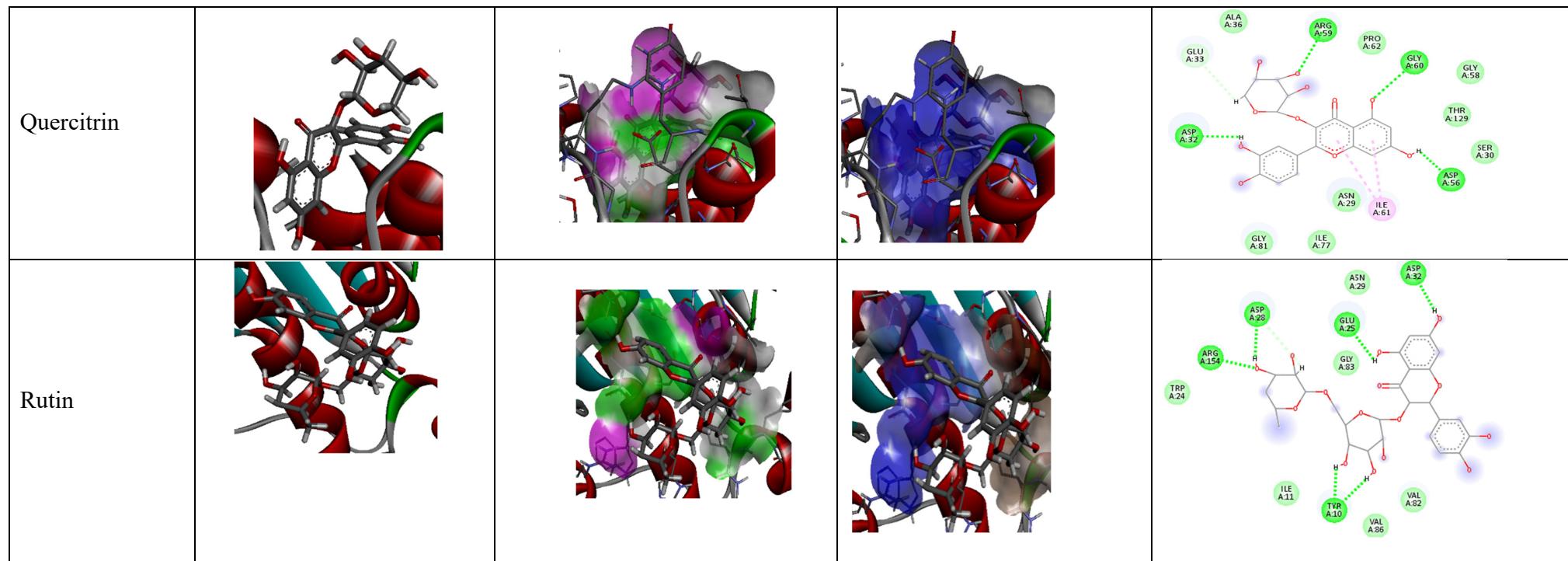
Table S3. Superposition and intermolecular interactions between the different ligand determined in Algerian fir and *S. aureus* 4URO protein receptor using PM7 Method

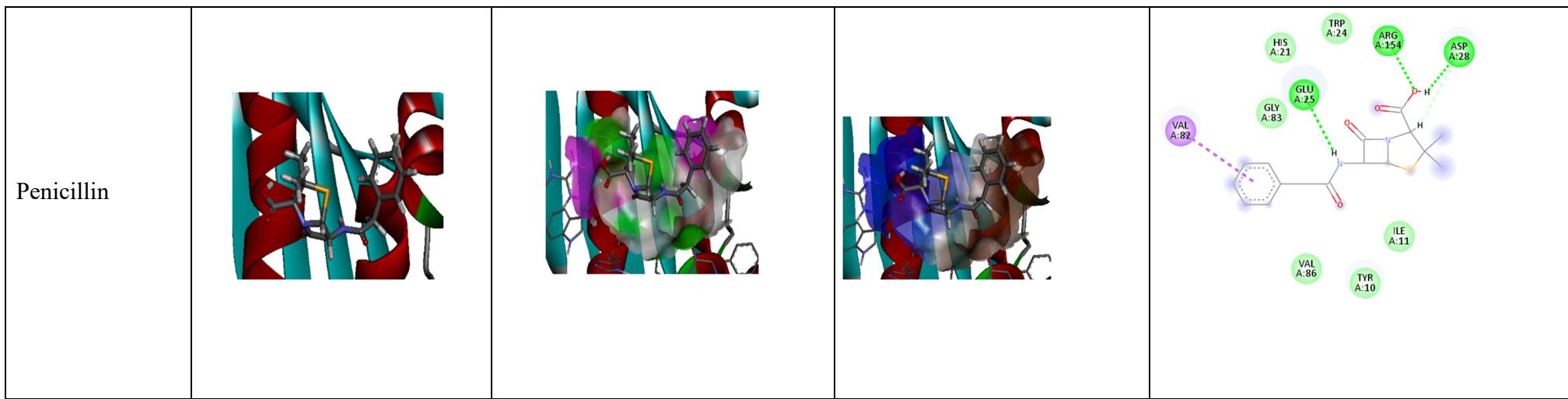
| Molecule | Molecular Docking | H-Bond | Hydrophobic | Interactions |
|----------|-------------------|--------|-------------|--------------|
| Apigenin | | | | |
| Apigetin | | | | |











+: Van der Waals; +: Pi-Cation; +: Unfavorable Acceptor -Acceptor; +: Pi-Donor Hydrogen Bond; +: Pi-Sulfur; +: Pi-Sigma; +: Conventional Hydrogen Bond; +: Sulfur-X; +: Pi-Alkyl.