Table 1. LC–HR–ESIMS dereplication results of the alcoholic extract of *Livistona decipens* leaves and fruits

No.	Metabolite name	*L. decipiens*		RT (min.)	MF	*m/z*	Calculated *m/z*
		Leaves	Fruits				
1	ρ-Hydroxybenzoic acid	×	√	2.0135	$C_7H_6O_3$	137.0238	138.0317
2	Syringol	×	√	2.0486	$C_8H_{10}O_3$	153.0557	154.0629
3	Neochlorogenic acid	√	√	2.2486	$C_{16}H_{18}O_9$	353.0881	354.0951
4	Isoorientin	√	√	2.3678	$C_{21}H_{20}O_{11}$	447.0932	448.1006
5	Caffeic acid	√	√	2.3739	$C_9H_8O_4$	179.0346	180.0422
6	(+)-Catechin	√	√	2.4451	$C_{15}H_{14}O_6$	289.0713	290.0790
7	Vitexin	√	×	2.6408	$C_{21}H_{20}O_{10}$	431.0974	432.1056
8	Isoquercetin	√	√	2.7137	$C_{21}H_{20}O_{12}$	463.0876	464.0955
9	Quercetin	×	√	2.7605	$C_{15}H_{10}O_7$	301.0351	302.0427
10	(-)-Epiafzelechin	×	√	2.9733	$C_{15}H_{14}O_5$	273.0766	274.0841
11	Tricin	×	√	3.8475	$C_{17}H_{14}O_7$	329.0658	330. 0739
12	Luteolin	√	√	4.2993	$C_{15}H_{10}O_6$	285.0763	286.0477

MF: molecular formula, RT: retention time, min: minute.

Table 2: Predicted binding free energy (ΔG) in kcal/mol for dereplicated compounds with the active site of COVID-19 virus M^{pro} (PDB 7BQY; co-crystallized with N3) compared to two structurally similar COVID-19 virus M^{pro} inhibitors, namely cinanserin and shikonin.

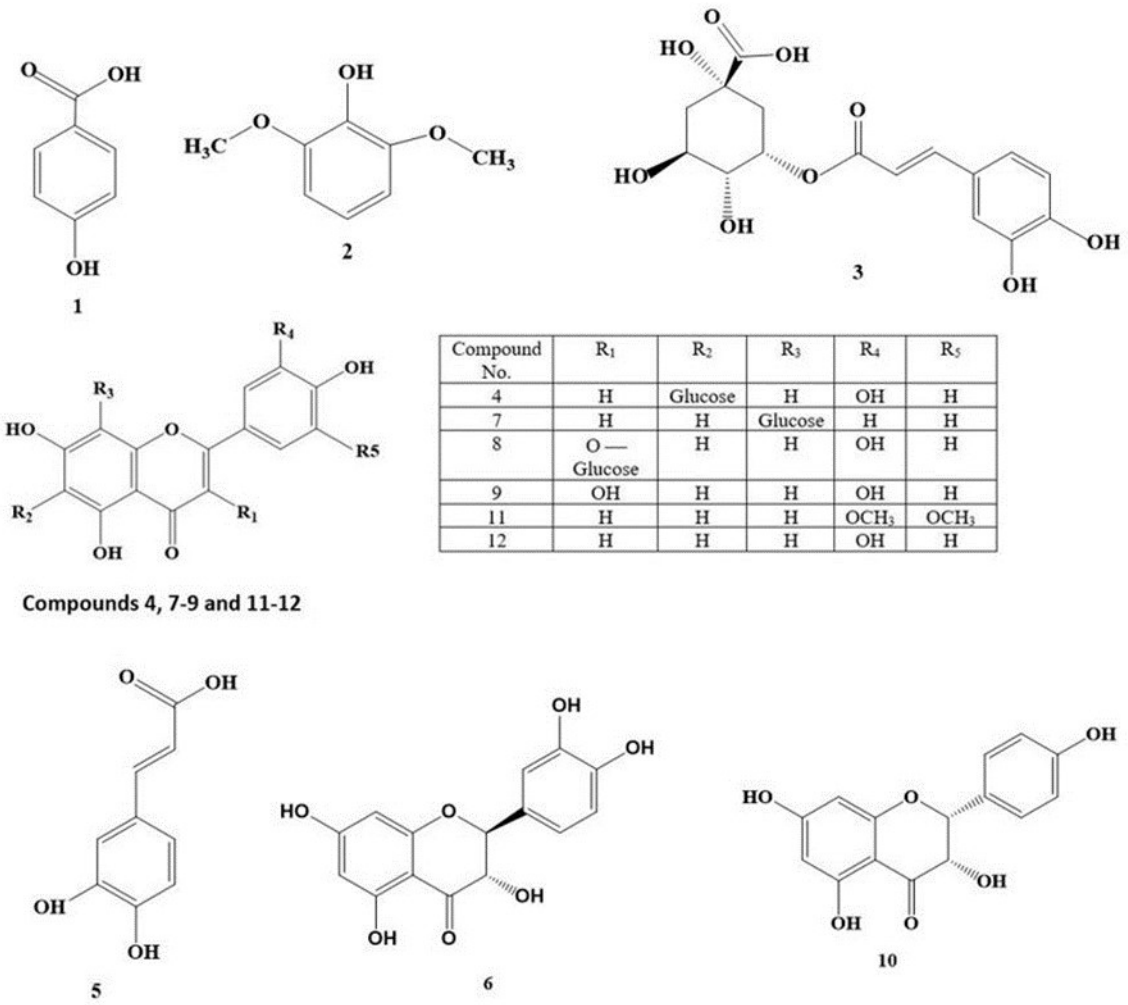
Ligand	Predicted ΔG (kcal/mol) COVID-19 virus M^{pro}	*In vitro* COVID-19 virus M^{pro} IC_{50} (μM)[a]	Antiviral activity determined by qRT-PCR (μM) [a]
Isoquercetin (8)	-8.2	ND[b]	ND[b]
Vitexin (7)	-7.6	ND[b]	ND[b]
Isoorientin (4)	-7.6	ND[b]	ND[b]
Cinanserin	-6.9	124.93 ± 7.89	20.61 ± 0.97
Neochlorogenic acid (3)	-6.8	ND[b]	ND[b]
Tricin (11)	-6.7	ND[b]	ND[b]
Shikonin	-6.5	15.75 ± 8.22	ND[b]
Quercetin (9)	-6.4	ND[b]	ND[b]
Luteolin (12)	-6.2	ND[b]	ND[b]
Epiafzelechin (10)	-6.2	ND[b]	ND[b]
Catechin (6)	-5.8	ND[b]	ND[b]
Caffeic acid (5)	-4.8	ND[b]	ND[b]
Syringol (2)	-4.8	ND[b]	ND[b]
Aesculetin	-4.7	ND[b]	ND[b]
ρ-Hydroxybenzoic acid (1)	-4.4	ND[b]	ND[b]

[a] *In vitro* COVID-19 virus M^{pro} IC_{50} and antiviral activity shown as reported (Jin et al. 2020).

[b] ND, not determined.

Table 3. Drug-likeness based on Lipinski's rule of five, ADME properties and medicinal chemistry parameters.

Ligand	# of violations	Pgp substrate	GI Absorption	Bioavailability score	PAINS alerts
Isoquercetin (8)	2	No	Low	0.17	1
Vitexin (7)	1	No	Low	0.55	0
Isoorientin (4)	2	No	Low	0.17	1
Cinanserin	0	No	High	0.55	0
Neochlorogenic acid (3)	1	No	Low	0.11	1
Tricin (11)	0	No	High	0.55	0
Shikonin	0	No	High	0.55	2
Quercetin (9)	0	No	High	0.55	1
Luteolin (12)	0	No	High	0.55	1
Epiafzelechin (10)	0	Yes	High	0.55	0
Catechin (6)	0	Yes	High	0.55	1
Caffeic acid (5)	0	No	High	0.56	1
Syringol (2)	0	No	High	0.55	0
Aesculetin	0	No	High	0.55	1
ρ-Hydroxybenzoic acid (1)	0	No	High	0.56	0



Compound No.	R_1	R_2	R_3	R_4	R_5
4	H	Glucose	H	OH	H
7	H	H	Glucose	H	H
8	O—Glucose	H	H	OH	H
9	OH	H	H	OH	H
11	H	H	H	OCH_3	OCH_3
12	H	H	H	OH	H

Figure 1. Structures of the dereplicated metabolites from the alcoholic extract of *Livistona decipens* leaves and fruits

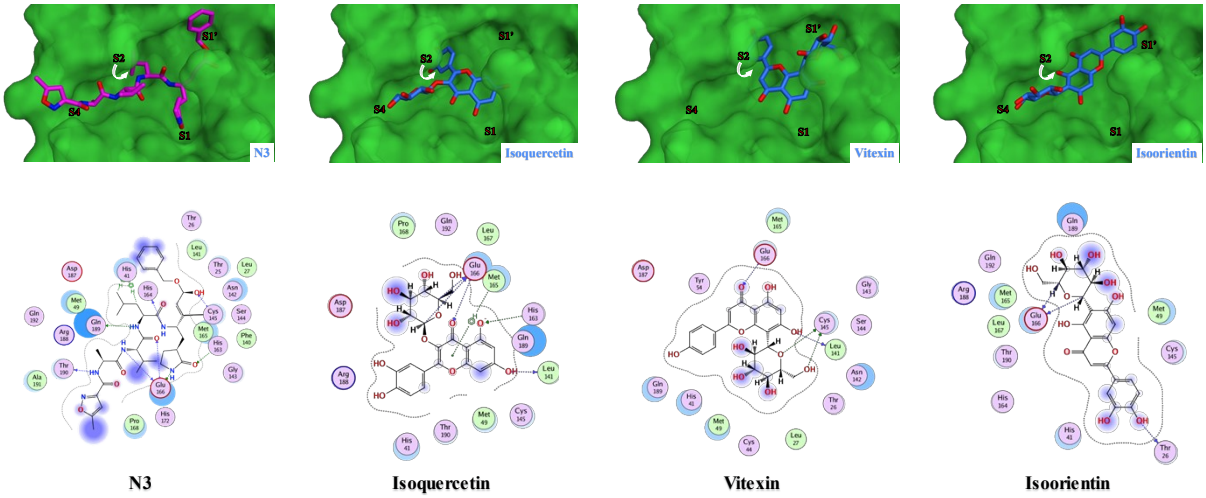


Figure 2. Predicted 2D/3D docking poses of three flavonoid glucosides (isoquercetin, vitexin, and isoorientin) occupying the same pocket as the co-crystallized ligand (N3) showing their binding interactions with the key amino acids in the active site of COVID-19 virus M^{pro}. M^{pro} is shown as green background, N3 is in magenta and flavonoids are in blue.

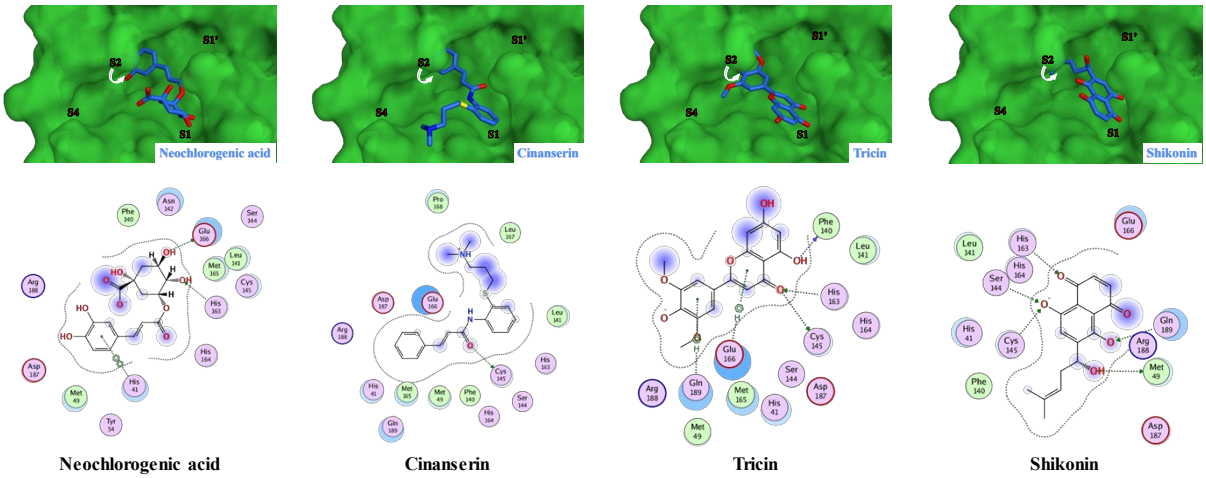


Figure 3. Predicted 2D/3D docking poses of neochlorogenic acid and tricin compared to their corresponding structurally similar COVID-19 virus M^{pro} inhibitors, namely cinanserin and shikonin showing their binding interactions with the key amino acids in the active site of COVID-19 virus M^{pro}. M^{pro} is shown as green background and ligands are in blue.

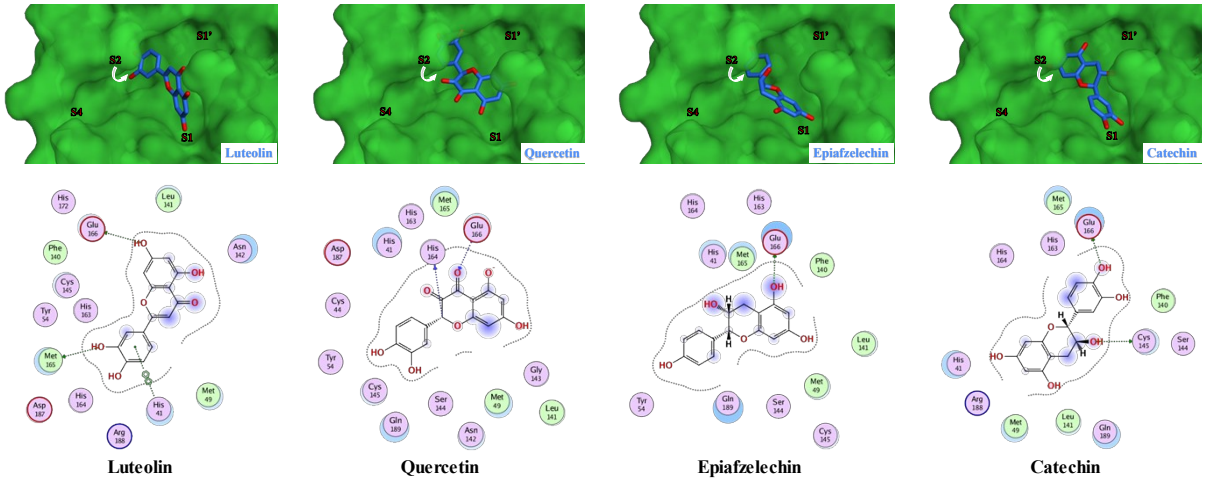


Figure 4. Predicted 2D/3D docking poses of four flavonoids (luteolin, quercetin, epiafzelechin and catechin) showing their binding interactions with the key amino acids in the active site of COVID-19 virus M^{pro}. M^{pro} is shown as green background and ligands are in blue.

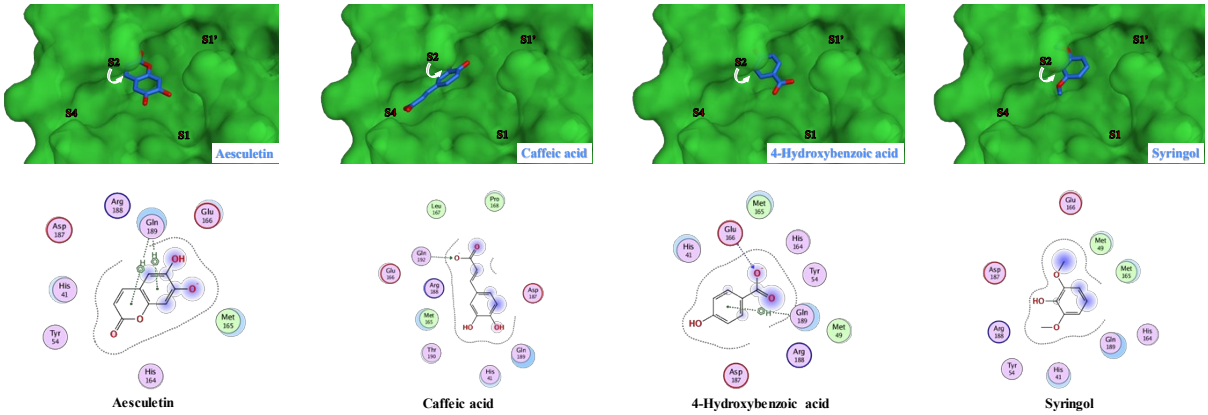


Figure 5. Predicted 2D/3D docking poses of four dereplicated compounds (aesculetin, caffeic acid, 4-hydroxybenzoic acid and syringol) showing their binding interactions with the key amino acids in the active site of COVID-19 virus M^{pro}. M^{pro} is shown as green background and ligands are in blue.