SUPPLEMENTARY MATERIALS

Selective Antimicrobial Profiling of Crocatin A from *Piper crocatum*: A Potential Therapeutic Modulator for Caries-Driven Oral Dysbiosis

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General
NMR spectra were recorded on Bruker Avance Neo 700MHz NMR spectrometers (1H: 700 MHz, 13C: 175 MHz). ESI-TQD-MS were calculated on Acquity TQD, Waters Corporation, MA, USA. IR spectra were recorded on Shimidzu 4800.

1. Structural Characterization of Compound 1

a. IR Spectrum

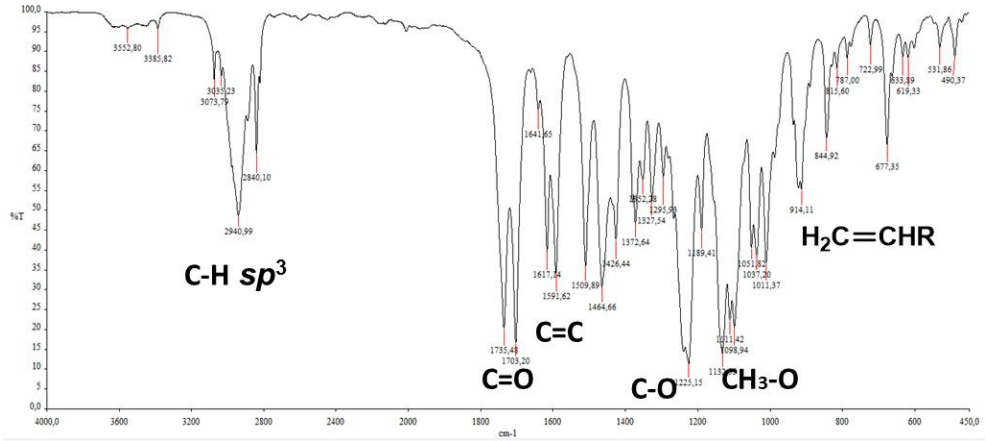

Figure S1. IR Spectrum of Compound **1** (KBr)

Table S1. FTIR wavenumbers of Compound **1**

vmax (cm−1)	Band Shape	Intensity	Assignment
2940	Sharp	Medium	C-H sp^3
1735	Sharp	Strong	C=O unsaturated
1703	Sharp	Strong	C=O
1591	Sharp	Strong	C=C
1509	Sharp	Strong	
1225	Sharp	Strong	C-O-CH_3 stretch
1132	Broad	Strong	O-CH_3 stretch
914	Sharp	Weak	Vinyl
677	Sharp	Weak	Aromatic

b. **^{13}C-NMR and DEPT Spectra of Crocatin A (1)**

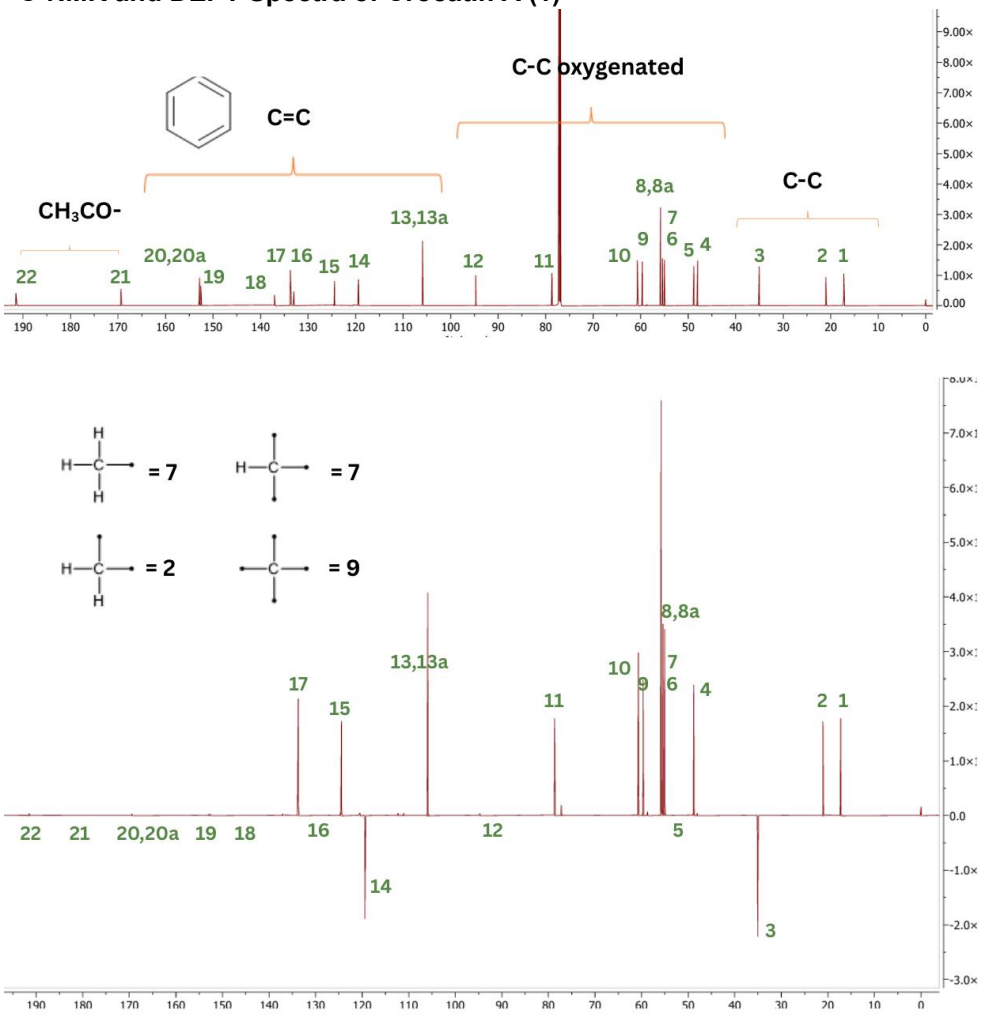

Figure S2. ^{13}C-NMR (175 MHz, $CDCl_3$) and DEPT 135° spectrum of **1** in $CDCl_3$

Table S2. ^{13}C-NMR and DEPT 135° chemical shifts of Compound **1** (175 MHz, $CDCl_3$)

No	δC	CH^3 / CH	CH^2	Cq
1	17.2	1		
2	21.0	1		
3	35.0		1	
4	48.0	1		
5	48.8			1
6	54.0	1		
7	55.0	1		
8	55.4	1		
8a	55.4	1		
9	59.6	1		
10	60.6	1		
11	78.6	1		
12	94.7			1
13	105.9	1		
13a	105.9	1		
14	119.3		1	
15	124.4	1		
16	133.0			1
17	133.7	1		
18	137.0			1
19	152.0			1
20	152.5			1
20a	152.5			1
21	169.39			1
22	191.47			1

c. ^{1}H-NMR Spectrum of Crocatin A (1)

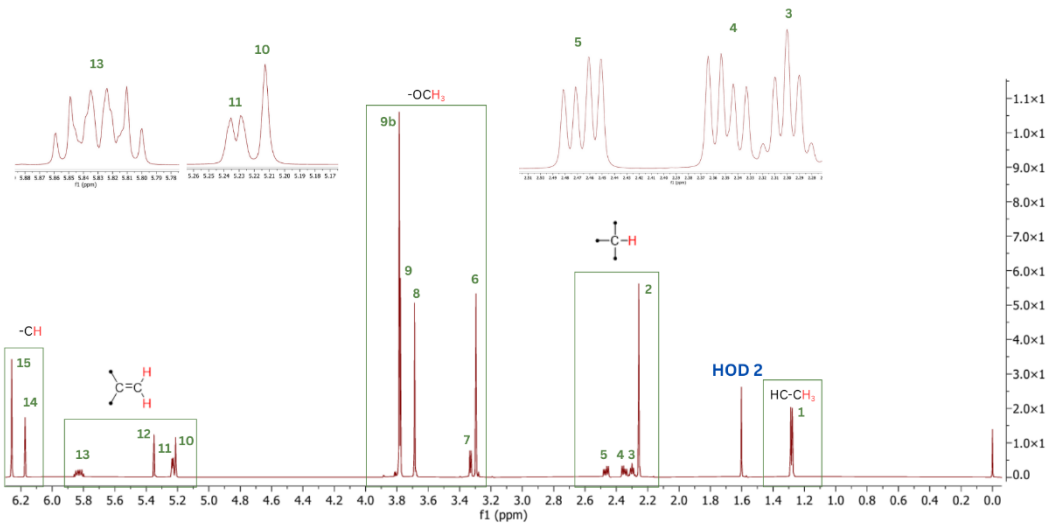

Figure S3. ^{1}H-NMR (700 MHz, $CDCl_3$) spectrum of **1** in $CDCl_3$.

Table S3. ^{1}H-NMR chemical shifts of Compound **1** (700 MHz, $CDCl_3$)

No	δH	Mult. / J (Hz)	ΣH
1	1.27	*d, J=8.4*	3
2	2.25	*s*	3
3	2.27–2.31	*m*	1
4	2.33–2.36	*m*	1
5	2.45–2.48	*m*	1
6	3.29	*s*	3
7	3.32	*d, J=6.3*	1
8	3.68	*s*	3
9	3.77	*s*	3
9b	3.78	*s*	6
10	5.21	*s*	1
11	5.22	*d, J=7.0*	1
12	5.35	*s*	1
13	5.80–5.85	*m*	1
14	6.17	*s*	1
15	6.25	*s*	2

Table S4. Comparison of ^{1}H-NMR and ^{13}C-NMR data of Compound **1** with literature values for Crocatin A

Position	Compound 1		Crocatin A (Arbain et al. 2018):	
	δH (ppm)	**δC (ppm)**	**δH (ppm)**	**δC (ppm)**
1	-	133.0	-	133.0
2	6.25 (s, 2H)	105.9	6.26 (s, 3H)	105.9
3	-	152.8	-	152.8
4	-	137.0	-	137.1
5	-	152.8	-	152.8
6	6.25 (s, 2H)	105.9	6.26 (s, 3H)	105.9
7	3.32 (d, 1H)	59.6	3.33 (d, 1H)	59.6
8	2.27 (m, 1H)	48.8	2.30 (m, 1H)	48.8
9	1.27 (d, 3H)	17.2	1.28 (d, 3H)	17.2
1'	-	48.0	-	48.0
2'	5.35 (s, 1H)	78.6	5.35 (s, 1H)	78.7
3'	-	94.7	-	94.7
4'	-	191.4	-	191.5
5'	-	152.5	-	152.6
6'	6.17 (s, 1H)	124.4	6.17 (s, 1H)	124.5
	2.45 (m, 1H)		2.46 (m, 1H)	
7'		35.0		35.1
	2.33 (m, 1H)		2.34 (m, 1H)	
8'	5.80 (m, 1H)	133.7	5.83 (m, 1H)	133.7
9'	5.22 (d, 1H) / 5.21 (s, 1H)	119.3	5.23 (d, 1H) / 5.20 (s, 1H)	119.4
COO	-	169.3	-	169.4
OCH$_3$	3.29 (m, 15H)	55.0 – 60.7	3.29 (15H)	55.0
COOCH$_3$	2.26 (s, 3H)	21.0	2.25 (s, 3H)	

d. Mass Spectrum of Compound 1

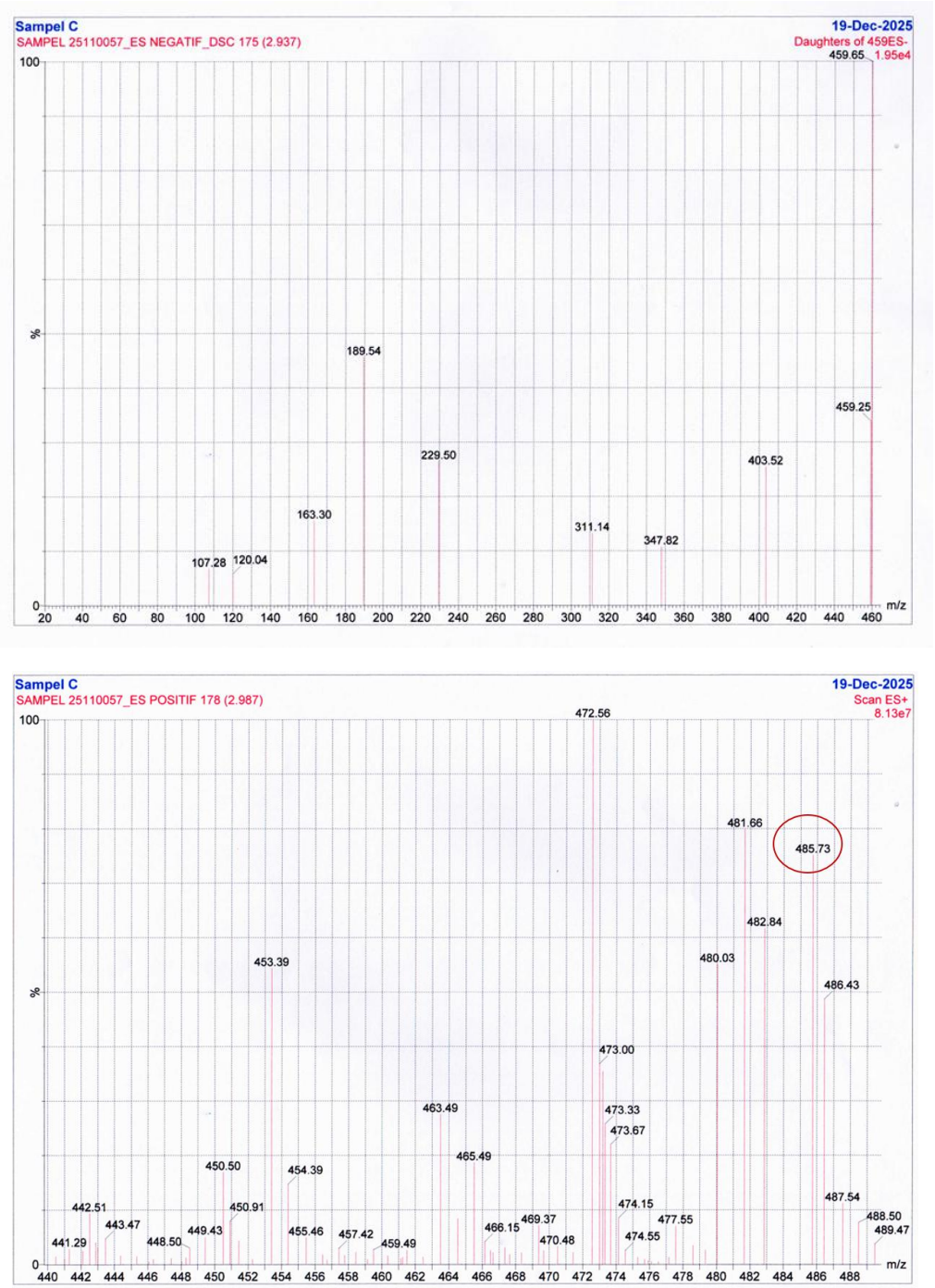

Figure S4. Daughter-MS (MS/MS or Tandem MS) of compound **1**

2. In silico Molecular Docking Simulation

a. GftB (PDB ID: 8FKL)

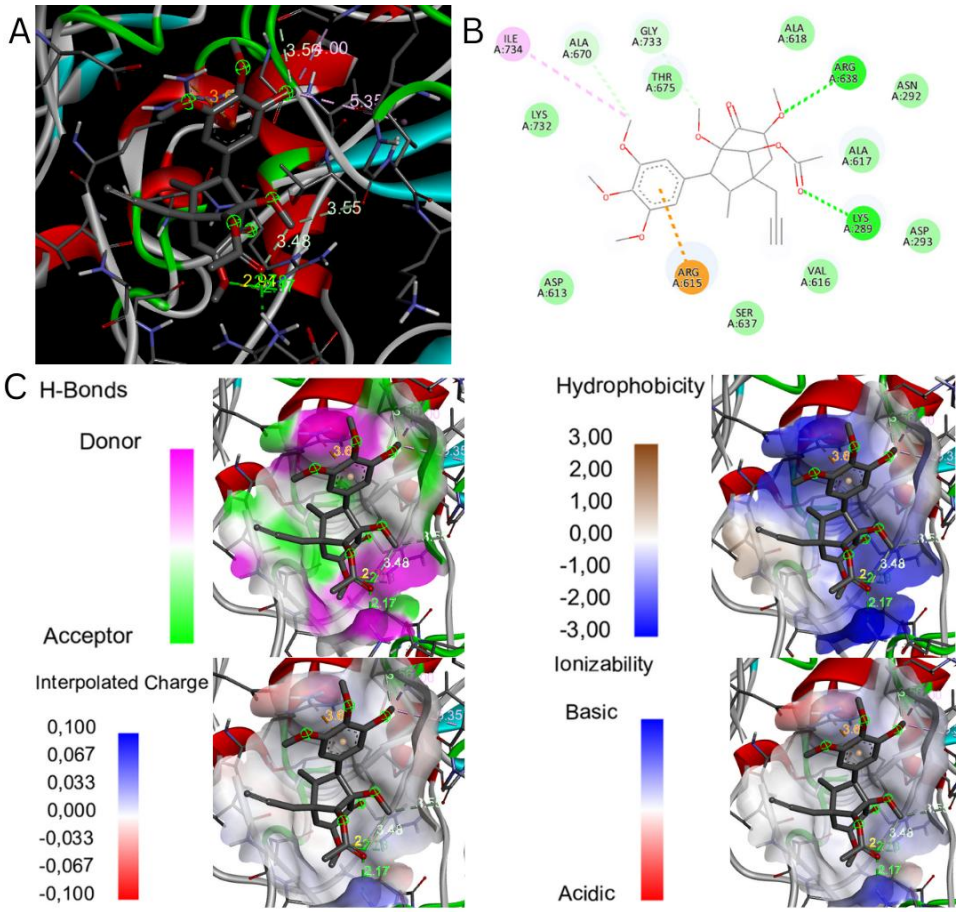

Figure S5. Visualization of the binding mode and binding site surface analysis of Crocatin A on the GtfB receptor. (A) 3D visualization of ligand-receptor interactions within the binding pocket; (B) 2D interaction diagram depicting key amino acid residues and specific interaction types; (C) Receptor surface maps illustrating the physicochemical properties of the binding site, including Hydrogen Bonds (Donor/Acceptor), Hydrophobicity, Interpolated Charge, and Ionizability.

b. SpaP (PDB ID: 3QE5)

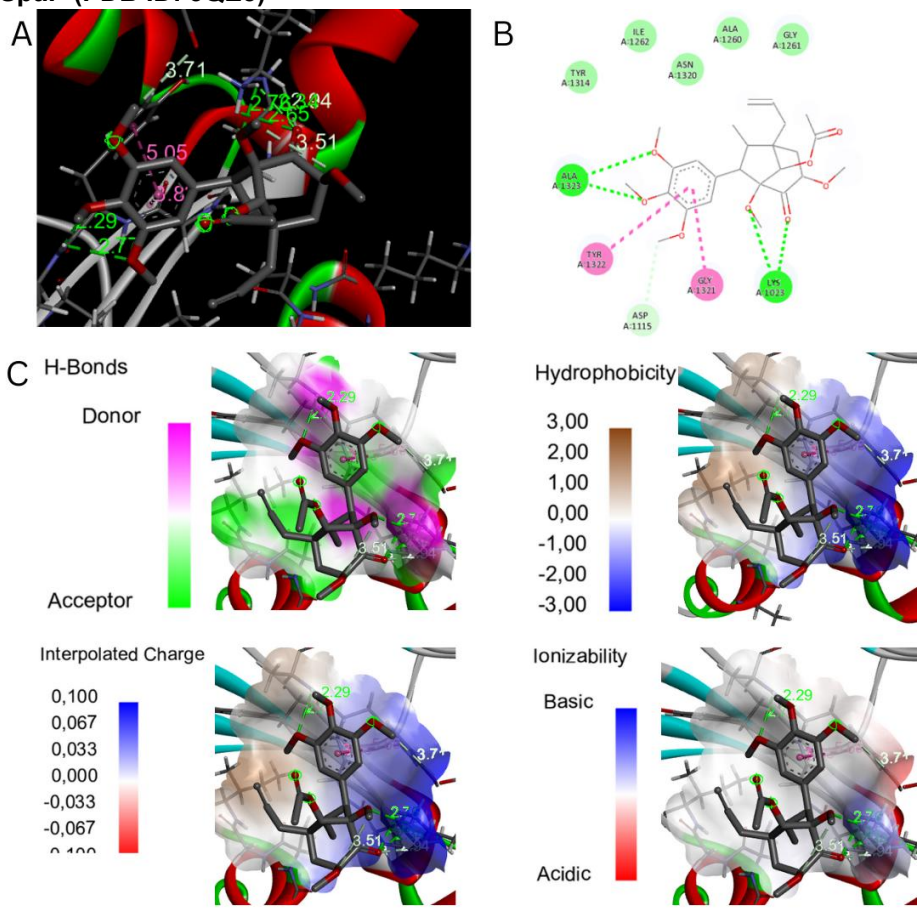

Figure S6. Visualization of the binding mode and binding site surface analysis of Crocatin A on the SpaP. (A) 3D visualization of ligand-receptor interactions within the binding pocket; (B) 2D interaction diagram depicting key amino acid residues and specific interaction types; (C) Receptor surface maps illustrating the physicochemical properties of the binding site, including Hydrogen Bonds (Donor/Acceptor), Hydrophobicity, Interpolated Charge, and Ionizability.

c. GspB (PDB ID: 3QC5)

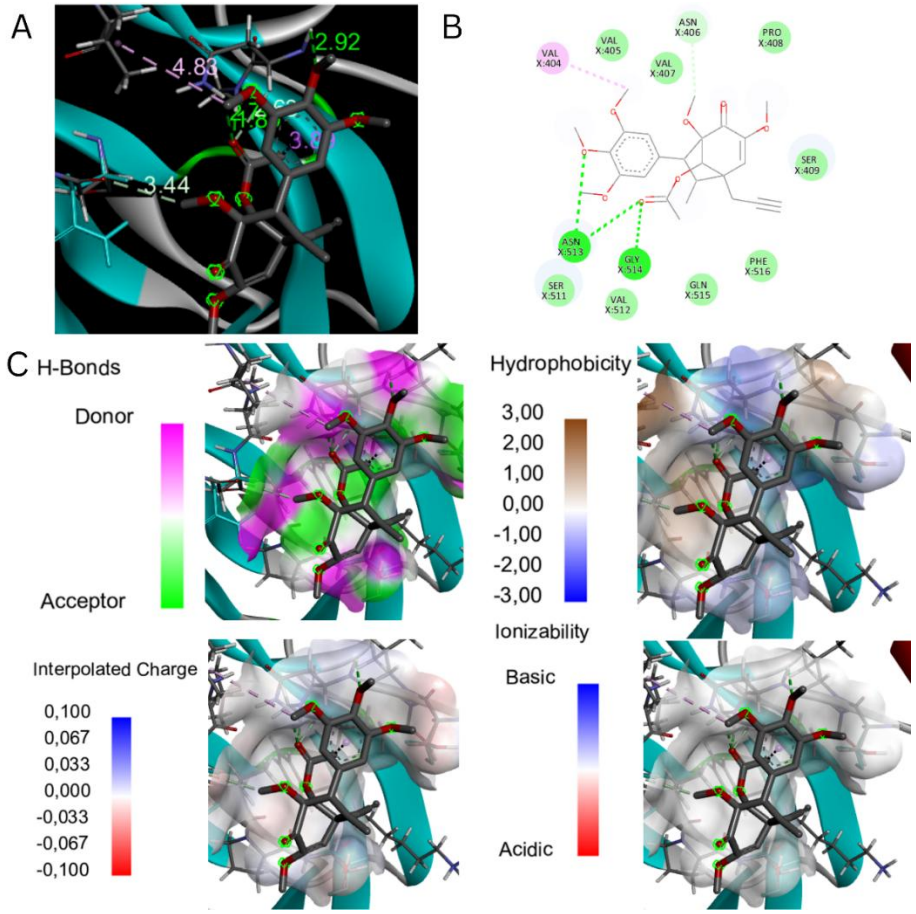

Figure S7. Visualization of the binding mode and binding site surface analysis of Crocatin A on the GspB. (A) 3D visualization of ligand-receptor interactions within the binding pocket; (B) 2D interaction diagram depicting key amino acid residues and specific interaction types; (C) Receptor surface maps illustrating the physicochemical properties of the binding site, including Hydrogen Bonds (Donor/Acceptor), Hydrophobicity, Interpolated Charge, and Ionizability.

d. SrpA (PDB ID: 5EQ3)

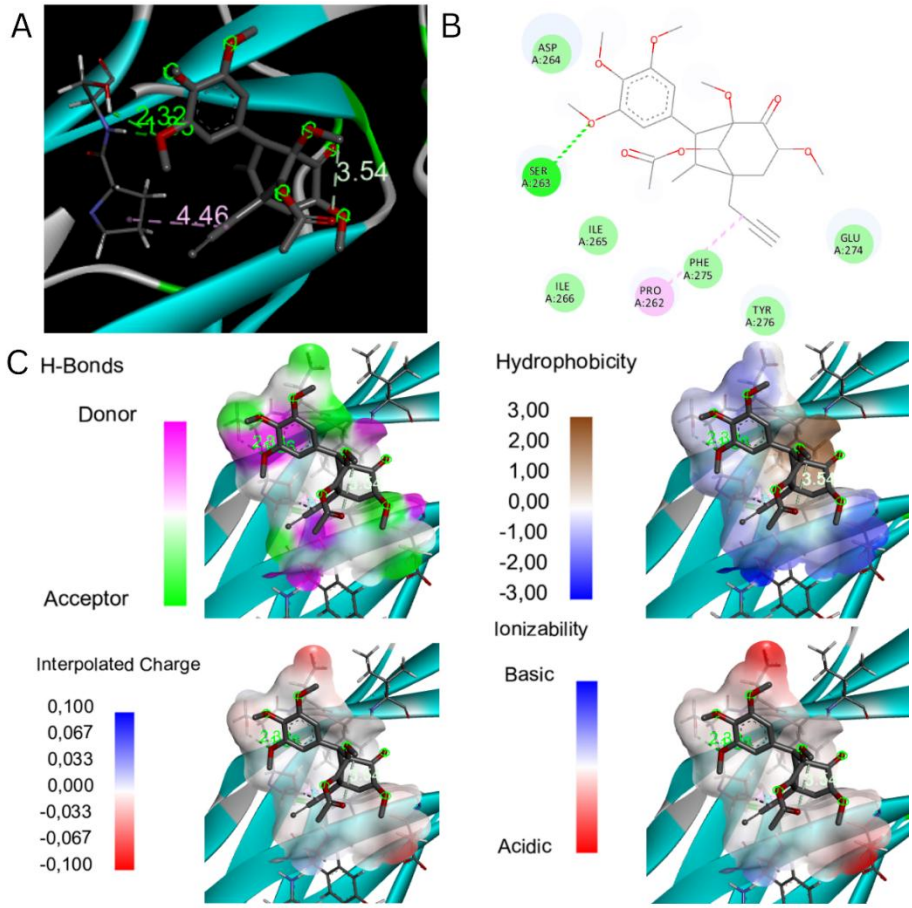

Figure S8. Visualization of the binding mode and binding site surface analysis of Crocatin A on the SrpA. (A) 3D visualization of ligand-receptor interactions within the binding pocket; (B) 2D interaction diagram depicting key amino acid residues and specific interaction types; (C) Receptor surface maps illustrating the physicochemical properties of the binding site, including Hydrogen Bonds (Donor/Acceptor), Hydrophobicity, Interpolated Charge, and Ionizability.