SUPPORTING DATA

Synthesis, Pharmacokinetic, Molecular Docking, and Molecular Dynamics Simulation of 2-Styrylchromone Derivatives as Potential Inhibitor of Human Kinesin Eg5

Tables:

Table S1. Drug-likeness properties.

Rules	G7X	DM2	MT-1	MT-2	MT-3
Lipinski	No; 2 violations	No; 3 violations	Yes; 0 violation	Yes; 0 violation	Yes; 0 violation
Ghose	No; 2 violations	No; 2 violations	Yes; 0 violation	Yes; 0 violation	Yes; 0 violation
Veber	Yes; 0 violation	No; 1 violation	Yes; 0 violation	Yes; 0 violation	Yes; 0 violation
Egan	Yes; 0 violation	No; 1 violation	Yes; 0 violation	Yes; 0 violation	Yes; 0 violation
Muegge	No; 1 violation	No; 3 violations	Yes; 0 violation	No; 1 violation	Yes; 0 violation
Bioavailability	0.17	0.17	0.55	0.55	0.55

Lipinski: MW ≤ 500 (g/mol), MlogP ≤ 4.15, ∑ HBA ≤ 10, and ∑ HBD ≤ 5, Ghose: 160 ≤ MW ≤ 480 (g/mol), -0.4 ≤ WlogP ≤ 5.6, 40 ≤ MR ≤ 130, and 20 ≤ atoms ≤ 70, Veber: ∑ Rotatable bonds ≤ 10 and TPSA ≤ 140 $Å^2$, Egan: WlogP ≤ 5.88 and TPSA ≤ 131.6 $Å^2$, and Muegge: 200 ≤ MW ≤ 600 (g/mol), -2 ≤ XlogP3 ≤ 5, TPSA ≤ 150 $Å^2$, ∑ Rings ≤ 7, ∑ Carbon > 4, ∑ Heteroatoms > 1, ∑ Rotatable bonds ≤ 15, ∑ HBA ≤ 10, and ∑ HBD ≤ 5.

Table S2. Results of ADMET properties using pkCSM server.

Parameters	G7X	DM2	MT-1	MT-2	MT-3
Absorption					
Intestinal Absorption-Human (% Absorbed)	93.28	62.37	94.68	92.86	97.07
Distribution					
BBB Permeability (log BB)	-0.10	-1.37	0.32	0.28	0.26
Metabolism					
CYP2D6 Inhibitor	No	No	No	No	No
CYP3A4 Inhibitor	Yes	No	No	No	No
Excretion					
Renal OCT2 Substrate	Yes	No	No	No	No
Toxicity					
AMES Toxicity	No	No	No	Yes	No
Skin Sensitisation	No	No	No	No	No

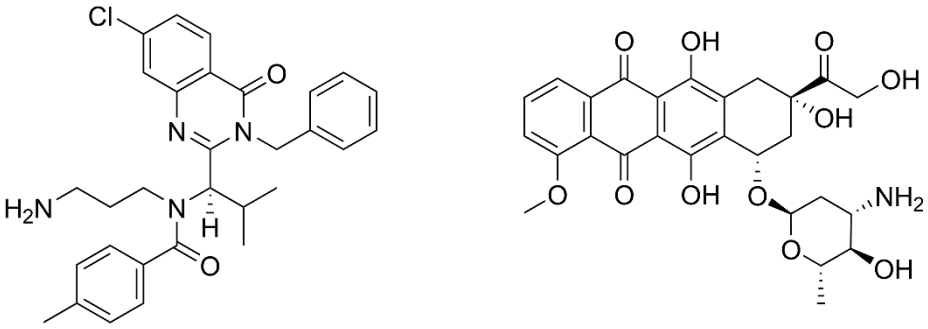
Intestinal Absorption-Human (+): HIA > 30% and Intestinal Absorption-Human (-): HIA < 30%. BBB Permeability (+): log BB > 0.3 and BBB Permeability (-): log BB < -1.0.

Tabel S3. Hydrogen bonding analysis using the last 20 ns trajectories (cutoff value: distance < 3.5 Å and angle > 120^{o}).

Contact	Frame	Fraction (%)	Avg-Dist (Å)	Avg-Ang (^{o})
G7X-Eg5				
ND	ND	ND	ND	ND
DM2-Eg5				
(E102)OE1…H12-O12	1005	50.25	2.72	160.76
O4…HH12-N(R205)	996	49.80	2.96	150.70
(E102)OE2…H12-O12	770	38.50	2.74	160.04
(E100)OE2…HN31-N3	605	30.25	2.88	148.80
(E100)OE1…HN31-N3	580	29.00	2.91	147.32
(E100)OE2…HN33-N3	552	27.60	2.87	150.68
(E102)OE1…HO14-O14	522	26.10	2.70	162.59
(E102)OE2…HO14-O14	518	25.90	2.69	162.98
(E100)OE2…HN32-N3	510	25.55	2.88	149.76
(E100)OE1…HN33-N3	499	24.95	2.91	145.32
(E100)OE1…HN32-N3	492	24.60	2.91	147.30
(E199)OE2…H17-O17	451	22.55	3.12	127.82
(T206)OG1…H8-O8	429	21.45	3.01	128.77
O14…H-N(R103)	260	13.00	3.17	152.96
MT-1-Eg5				
ND	ND	ND	ND	ND
MT-2-Eg5				
ND	ND	ND	ND	ND
MT-3-Eg5				
C=O…HH-OH(Y195)	556	27.80	2.81	161.40

*ND: Undetected H-bond with fraction > 10 %.

Figures:



Ispinesib (**G7X**) Doxorubicin (**DM2**)

Fig. S1 Chemical structure of G7X and DM2 as control.

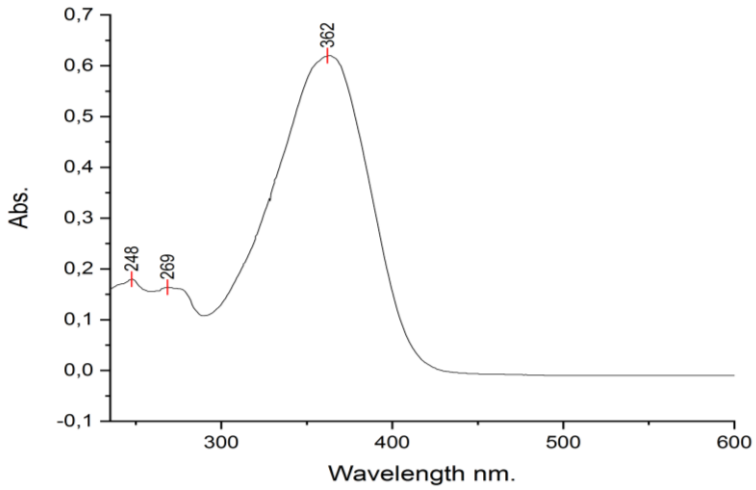


Fig. S2 UV-Vis spectrum of 2-styrylchromone derivative **(MT-1)**.

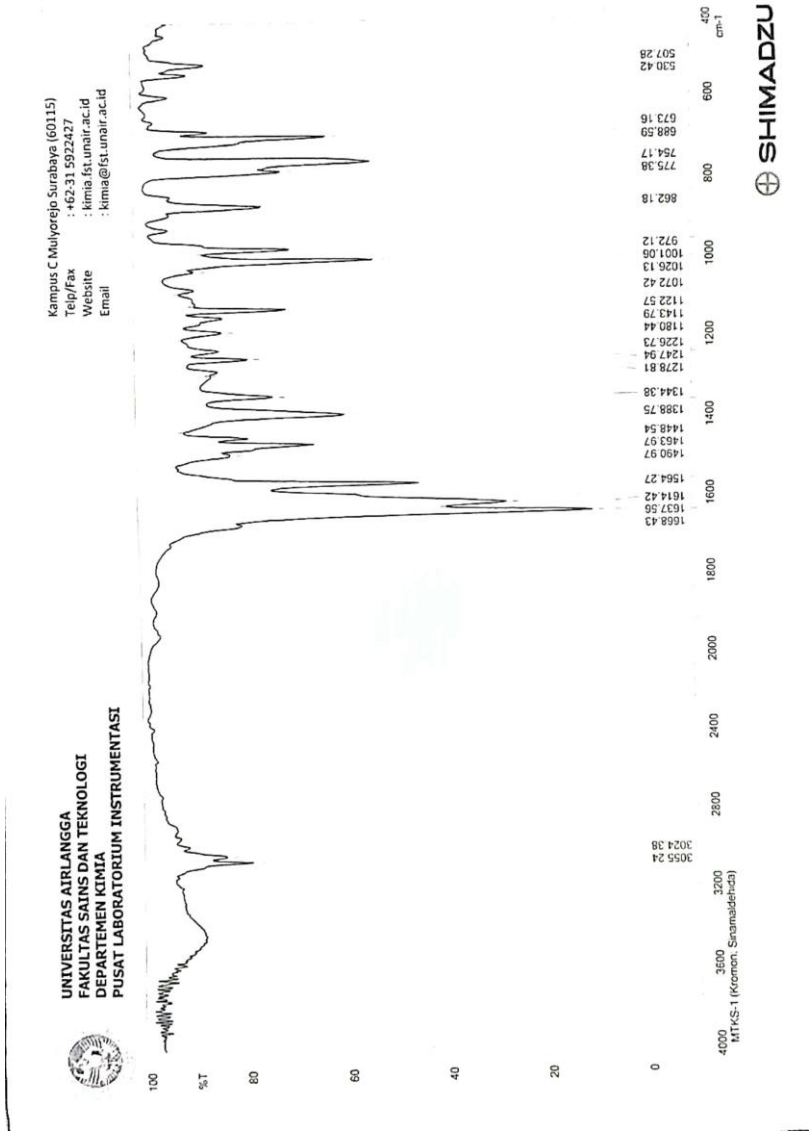


Fig. S3 FTIR spectrum of 2-styrylchromone derivative **(MT-1)**.

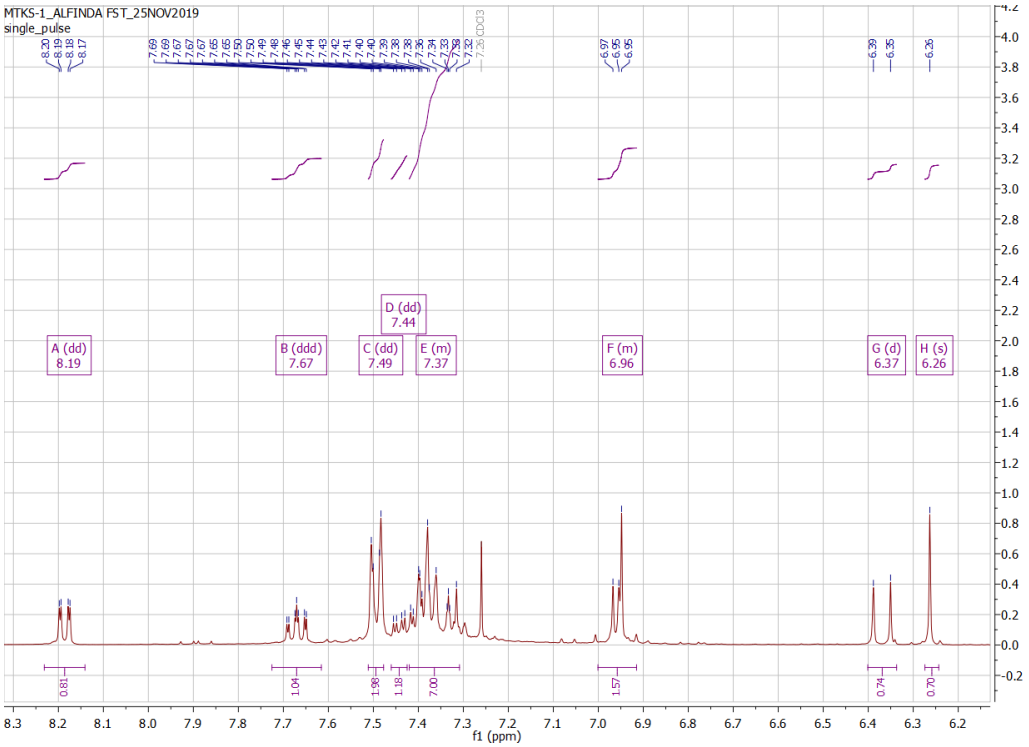


Fig. S4 ^{1}H-NMR spectrum of 2-styrylchromone derivative **(MT-1)**.

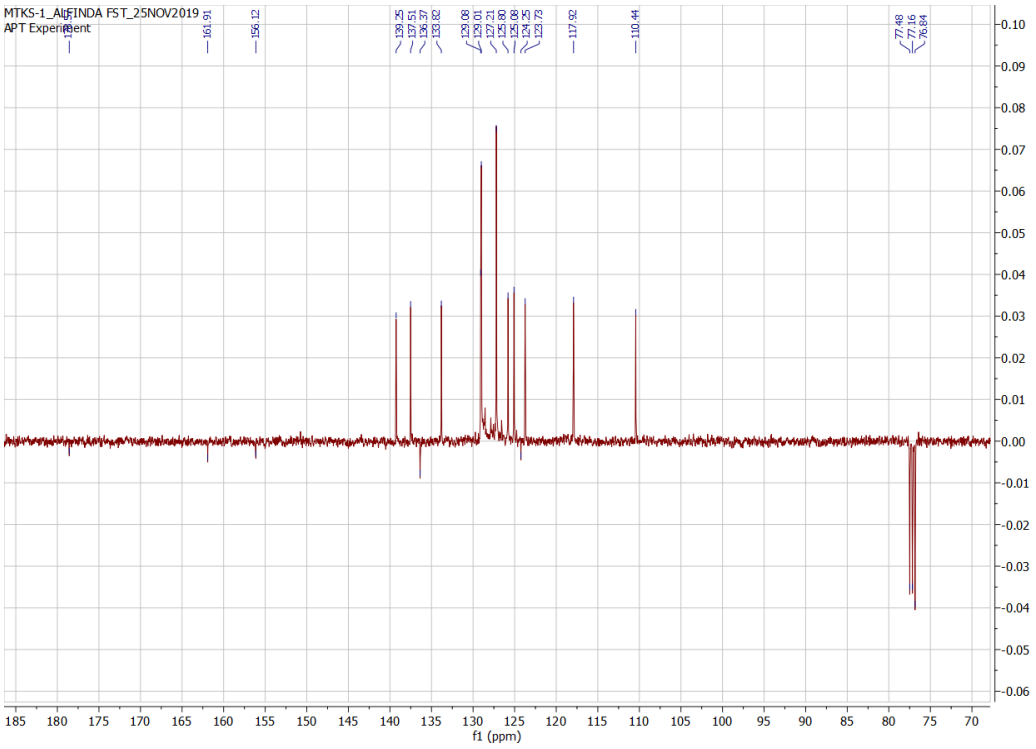


Fig. S5 ^{13}C-NMR spectrum of 2-styrylchromone derivative **(MT-1)**.

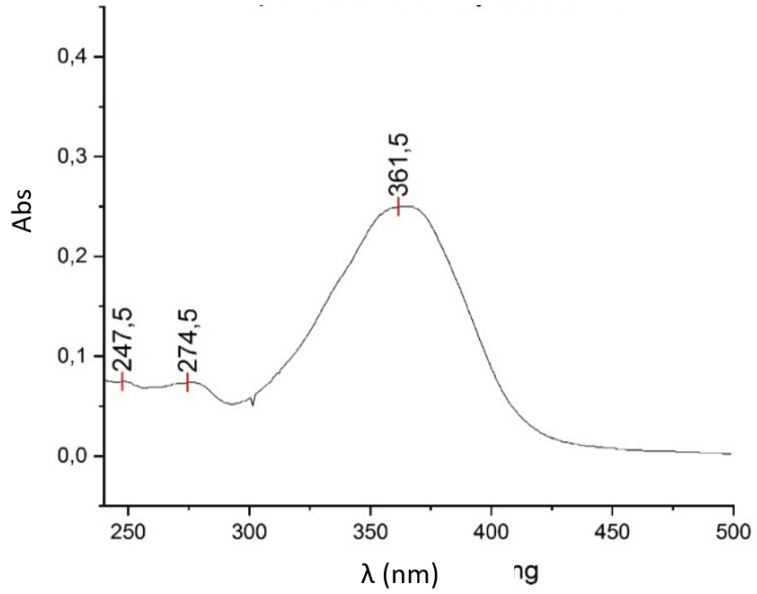


Fig. S6 UV-Vis spectrum of 2-styrylchromone derivative **(MT-2)**.

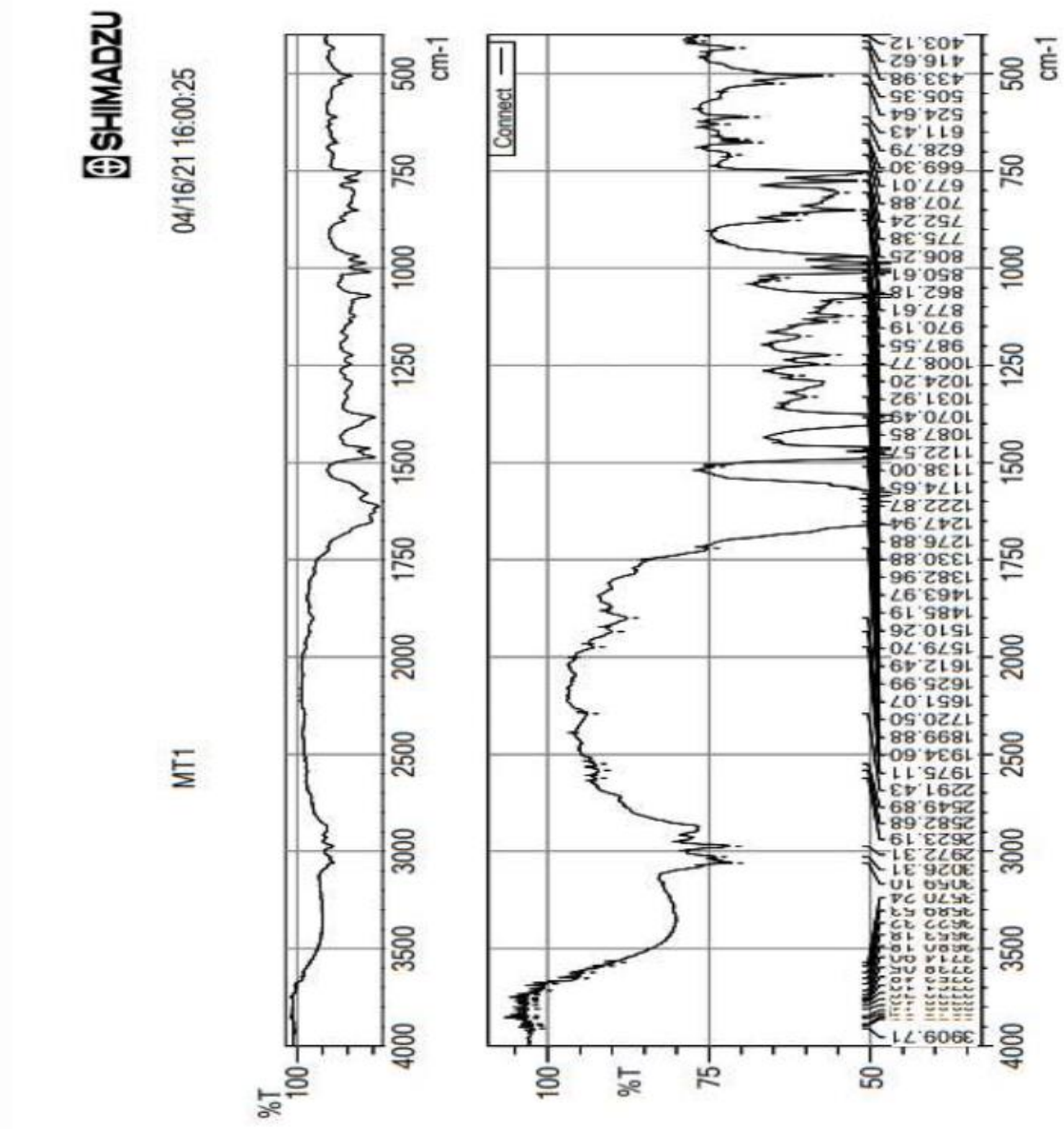


Fig. S7 FTIR spectrum of 2-styrylchromone derivative **(MT-2)**.

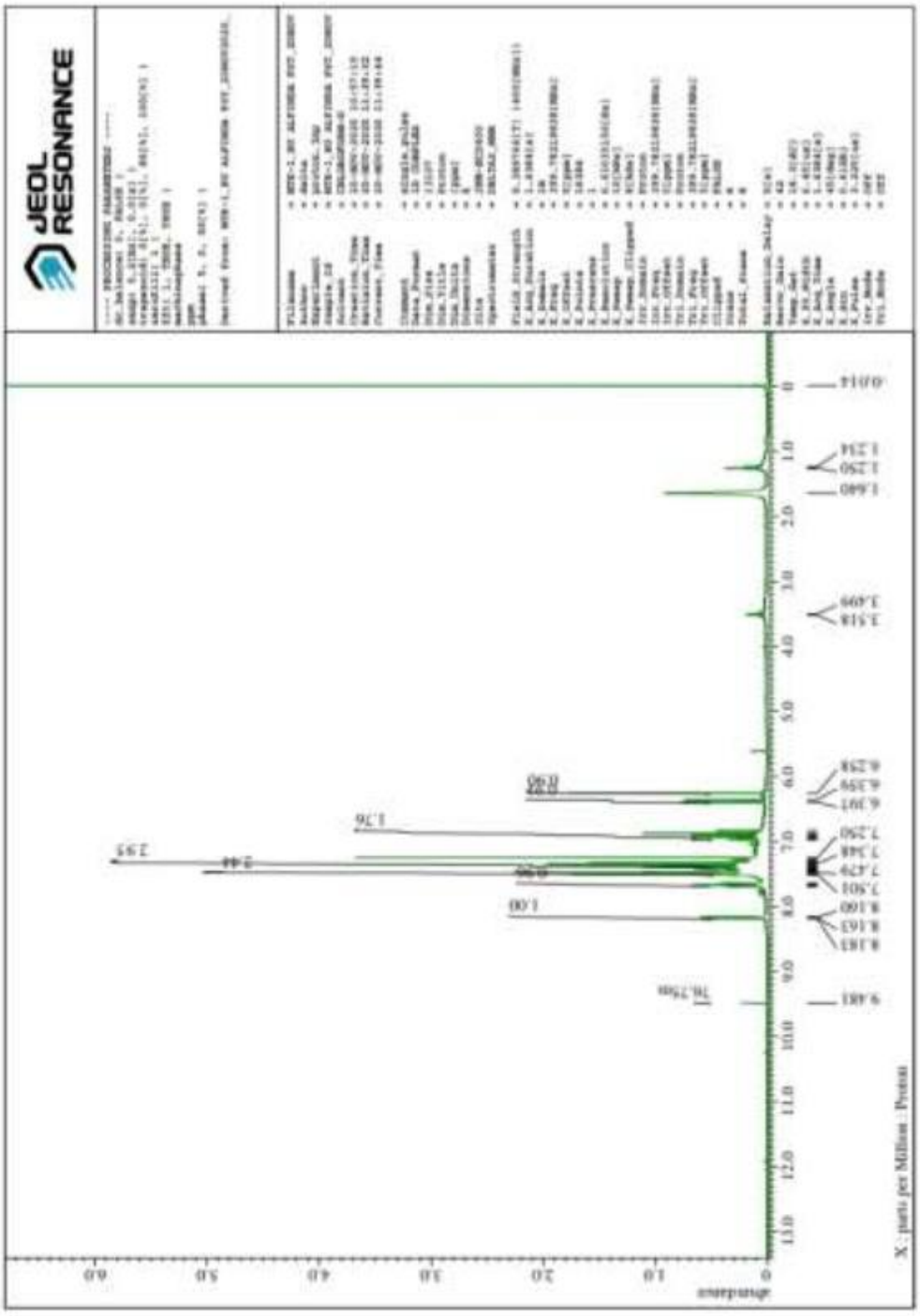


Fig. S8 [1]H-NMR spectrum of 2-styrylchromone derivative **(MT-2)**.

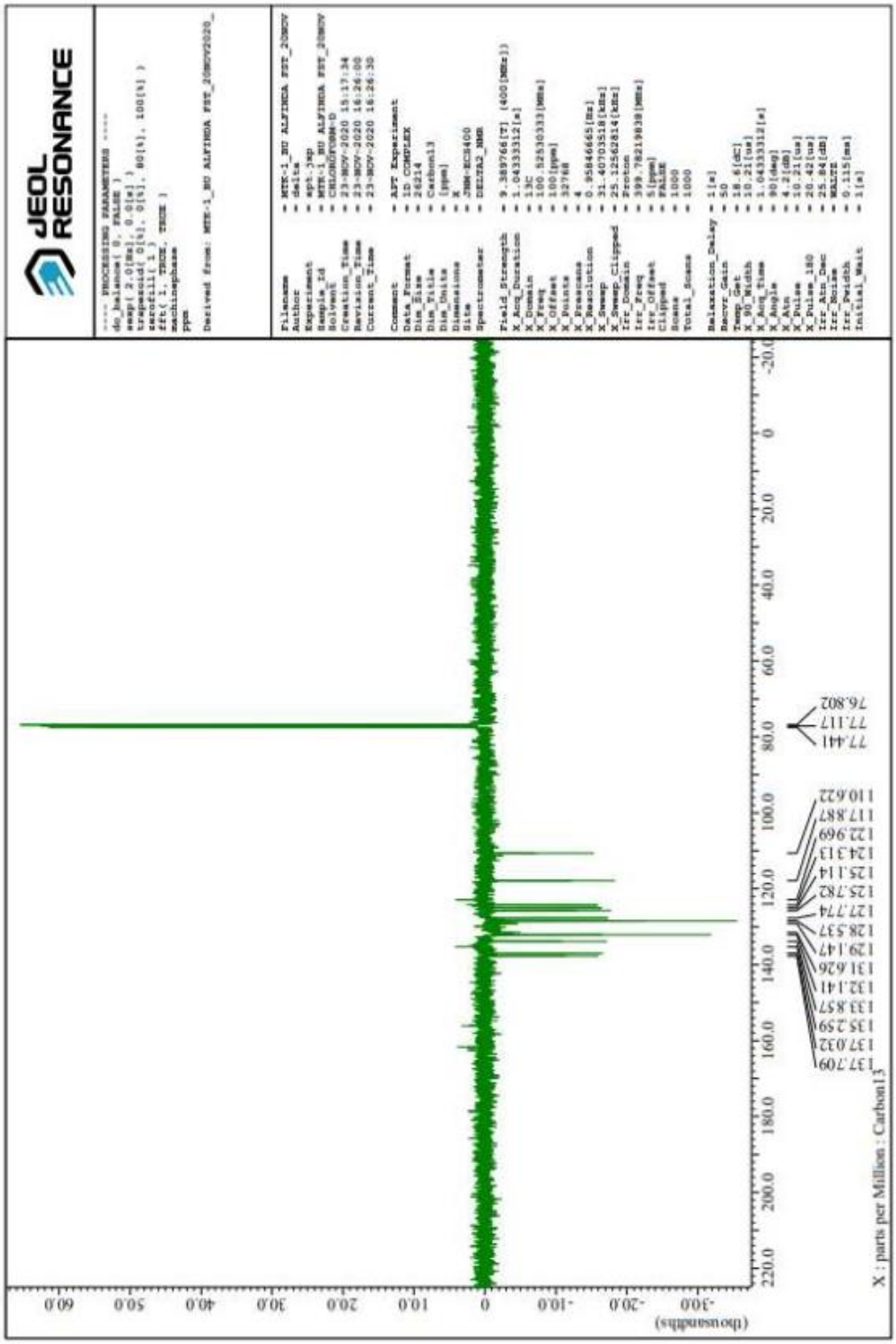


Fig. S9 ^{13}C-NMR spectrum of 2-styrylchromone derivative **(MT-2)**.

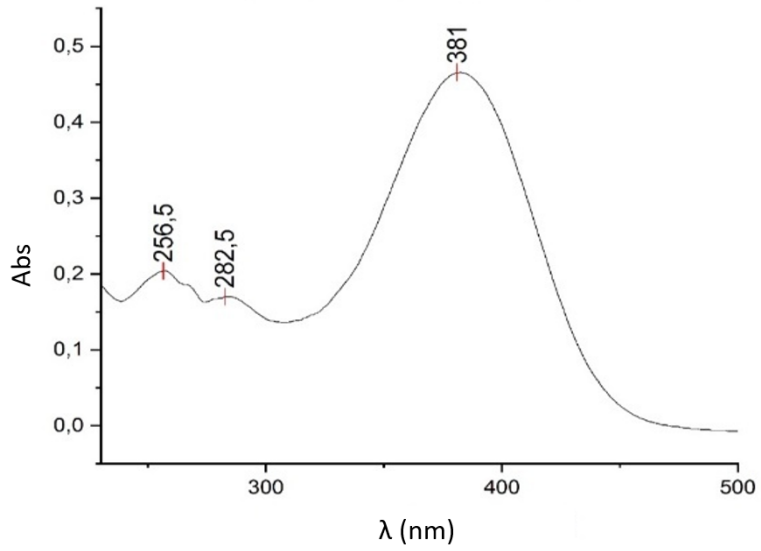


Fig. S10 UV-Vis spectrum of 2-styrylchromone derivative **(MT-3)**.

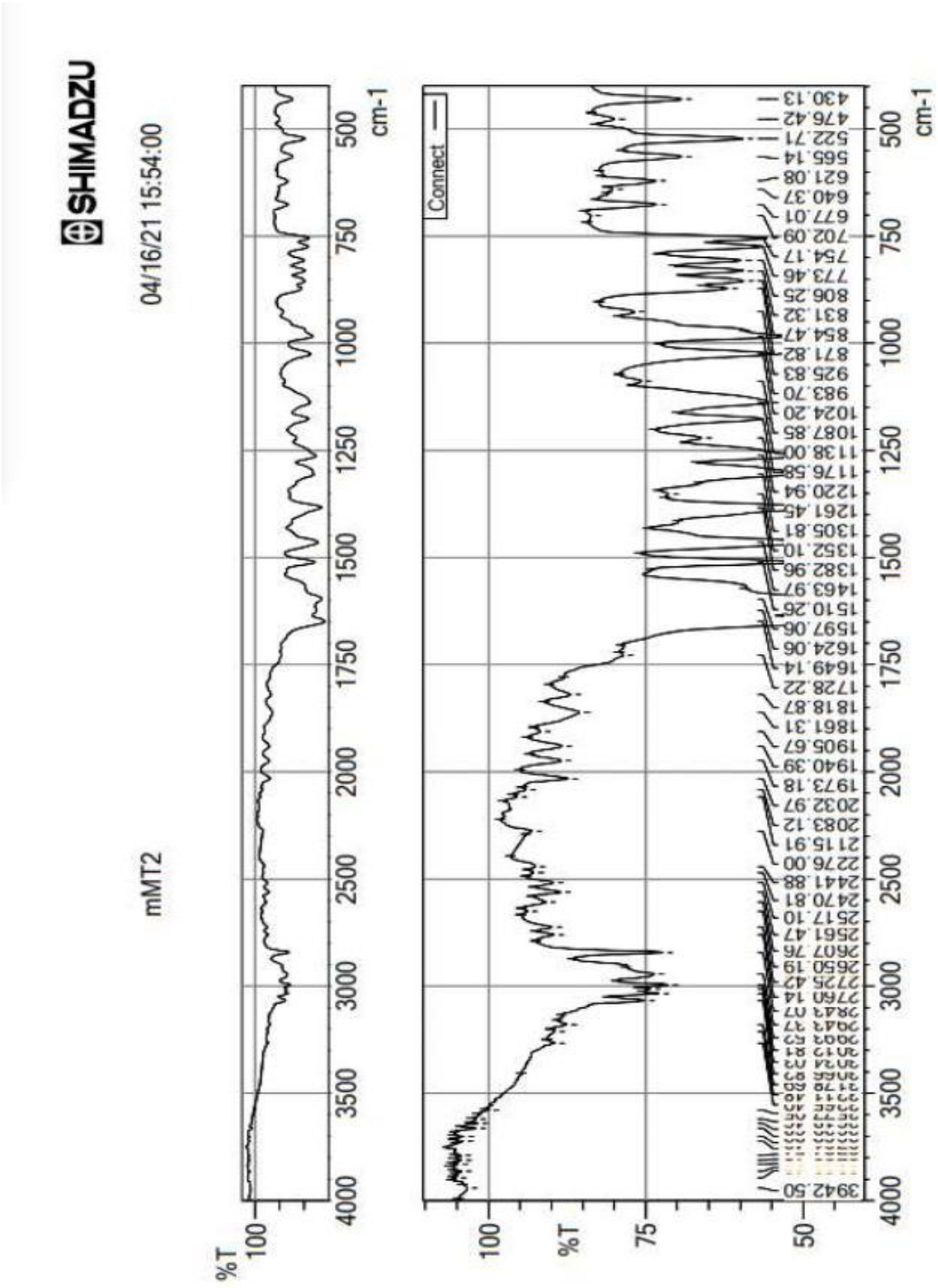


Fig. S11 FTIR spectrum of 2-styrylchromone derivative **(MT-3)**.

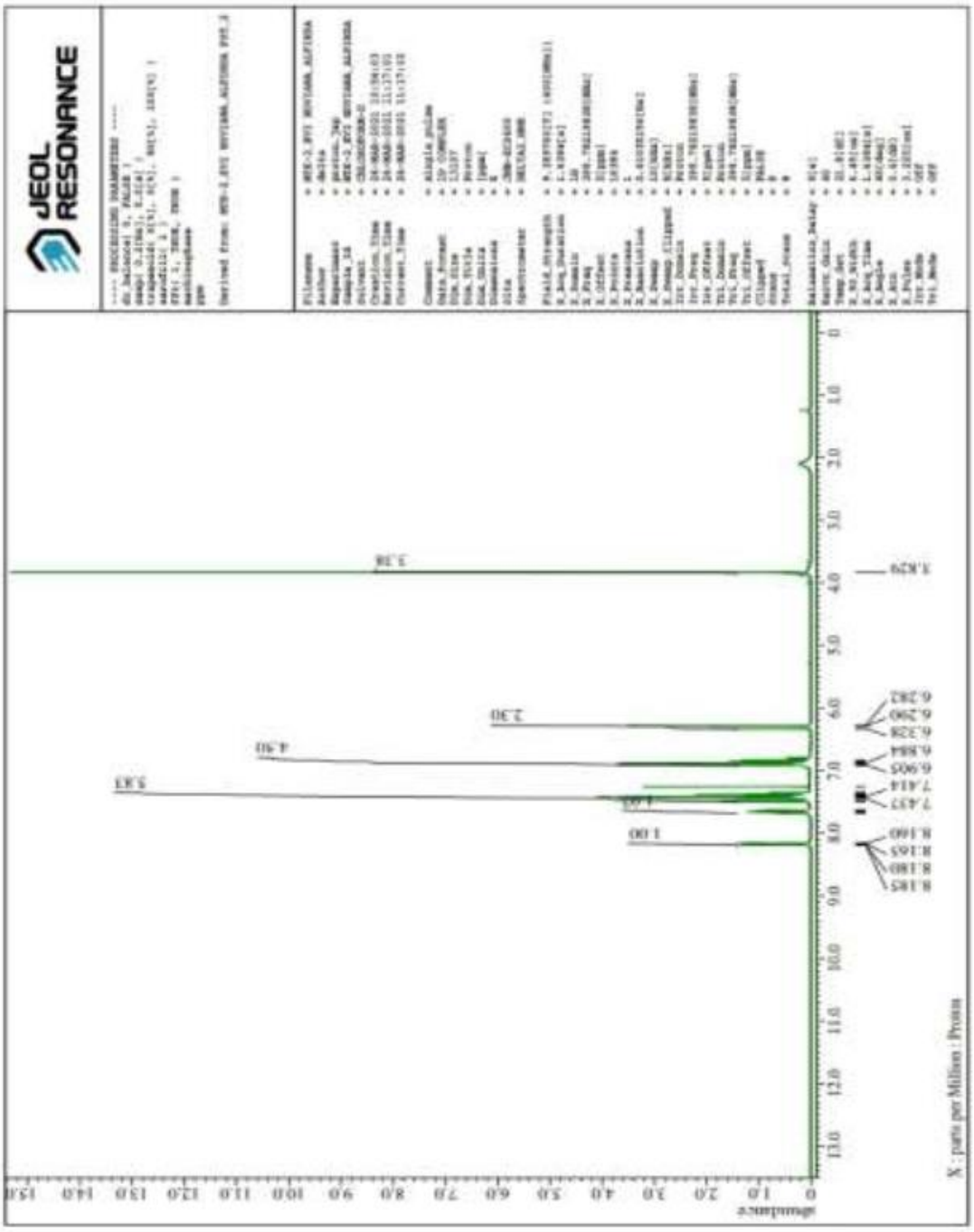


Fig. S12 ^{1}H-NMR spectrum of 2-styrylchromone derivative **(MT-3)**.

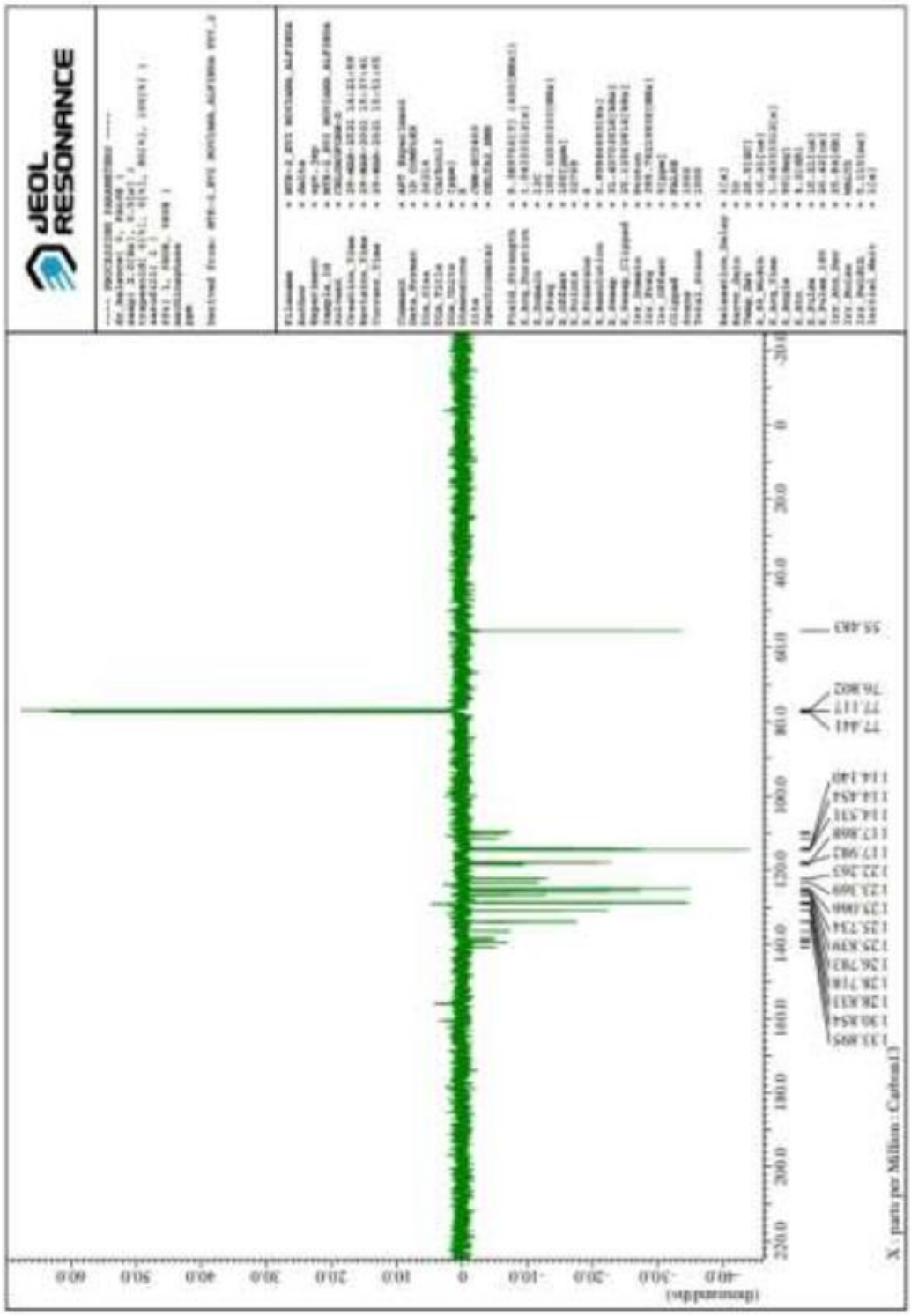


Fig. S13 ^{13}C-NMR spectrum of 2-styrylchromone derivative **(MT-3)**.