Supplementary Information

The Pivotal role of Carbonyl Group in Methoxy Chalcones: Comprehensive Analyses of Structure and Computational Insights into Binding Affinity with Monoamine Oxidase Enzymes

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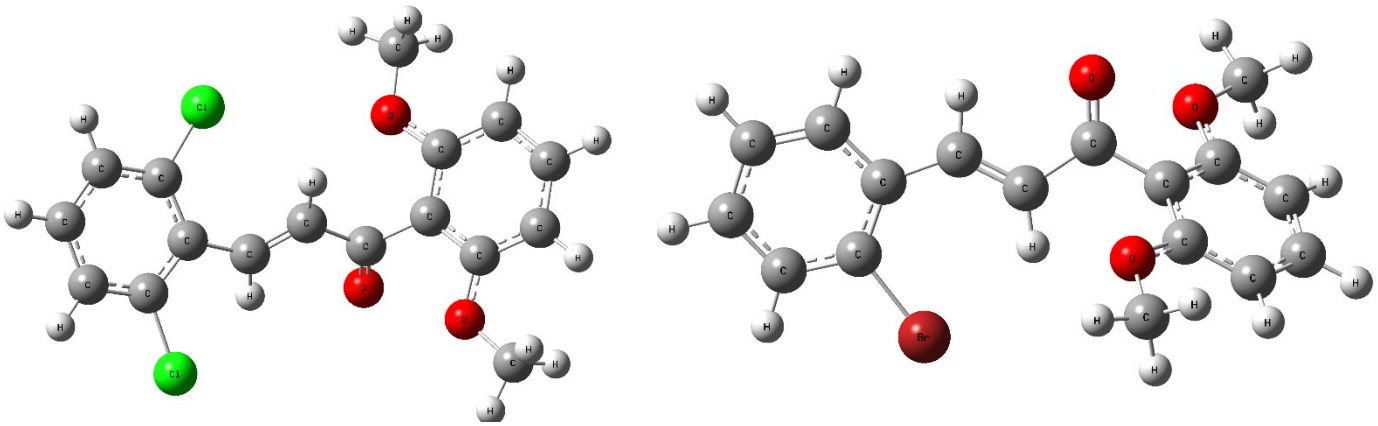


Figure S1: Optimized electronic structures of HK1 and HK2

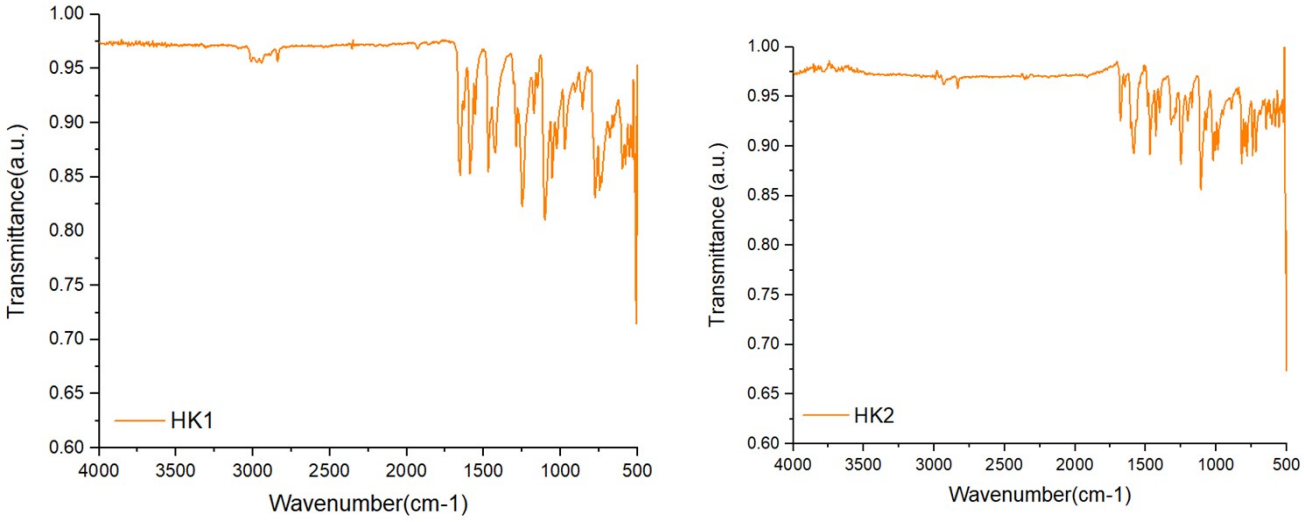


Figure S2: The FTIR spectra for HK1 and HK2

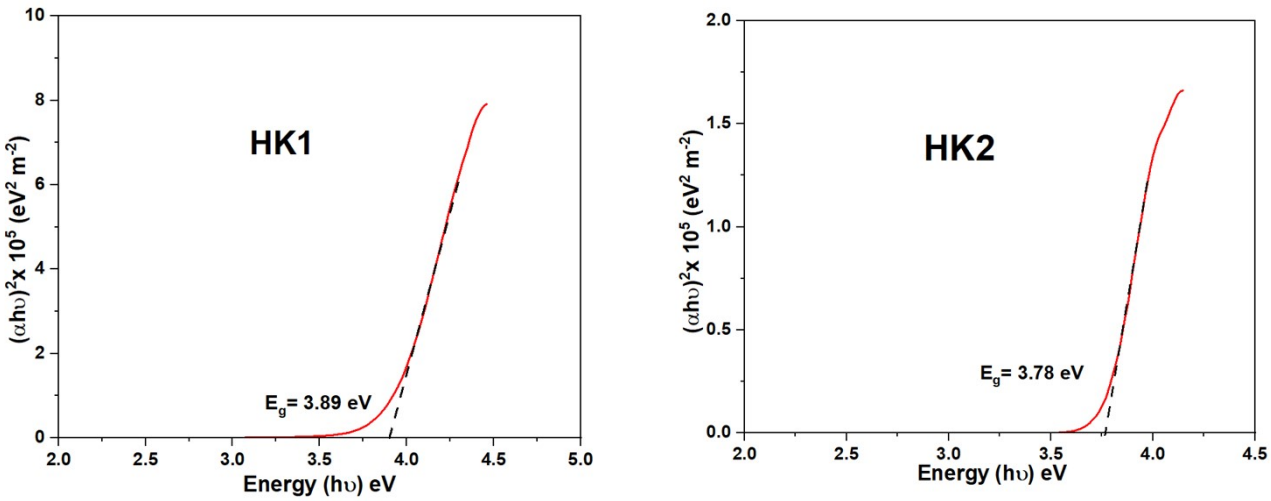


Figure S3: The experimental band gap obtained from Tauc plot via UV-Vis spectroscopy for HK1 and HK2

Table S1: Comparison of geometrical bond lengths of HK1 and HK2

Compound HK1

Atoms	Bond Length (Å)		Atoms	Bond Length(Å)		Atoms	Bond Length (Å)	
	XRD	DFT		XRD	DFT		XRD	DFT
C1A-Cl1A	1.736(5)	1.795	**C14A-C15A**	1.386(7)	1.398	**C7A-C6A**	1.466(6)	1.470
C5A-Cl2A	1.723(5)	1.758	**C4A-C5A**	1.381(7)	1.388	**C5A-C6A**	1.407(6)	1.413
C15A-O3A	1.366(5)	1.364	**C12A-C11A**	1.384(7)	1.400	**C1A-C6A**	1.386(6)	1.411
C16A-O3A	1.422(5)	1.422	**C2A-C1A**	1.369(6)	1.391	**H7A-C7A**	0.9290	1.081
C9A-O1A	1.207(4)	1.215	**H14A-C14A**	0.9300	1.081	**C8A-C7A**	1.311(6)	1.340
C11A-O2A	1.361(5)	1.357	**C13A-C14A**	1.367(9)	1.391	**H8A-C8A**	0.9300	1.081
C17A-O2A	1.429(6)	1.421	**H13A-C13A**	0.9300	1.084	**H17G-C17A**	0.9600	1.095
C10A-C9A	1.505(5)	1.509	**C12A-C13A**	1.375(9)	1.391	**H17I-C17A**	0.9600	1.095
C8A-C9A	1.478(6)	1.491	**H12A-C12A**	0.9300	1.081	**H4A-C4A**	0.9300	1.082
C15A-C10A	1.390(6)	1.402	**H2A-C2A**	0.9310	1.082	**C3A-C4A**	1.361(9)	1.391
C11A-C10A	1.392(6)	1.405	**C3A-C2A**	1.374(7)	1.390	**H3A-C3A**	0.9300	1.083
H16E-C16A	0.9600	1.088	**H16F-C16A**	0.9600	1.095	**H17H-C17A**	0.9600	1.095

Compound HK2

Atoms	Bond Length (Å)		Atoms	Bond Length(Å)		Atoms	Bond Length (Å)	
	XRD	DFT		XRD	DFT		XRD	DFT
C1- Br1A	1.900(4)	1.924	**C11A-C10A**	1.377(6)	1.405	**H8A-C8A**	0.9300	1.087
C9A-O1A	1.226(5)	1.216	**C7A-C6A**	1.454(5)	1.464	**H14A-C14A**	0.9300	1.081
C15A-O3A	1.348(5)	1.364	**C1A-C6A**	1.394(6)	1.418	**C13A-C14A**	1.375(6)	1.391
C16A-O3A	1.436(4)	1.422	**C5A-C6A**	1.399(6)	1.392	**C2A-C1A**	1.371(6)	1.395
C11A-O2A	1.367(5)	1.358	**H4A-C4A**	0.9300	1.084	**H5A-C5A**	0.9300	1.084
C11A-O2A	1.418(5)	1.358	**C5A-C4A**	1.371(6)	1.366	**H12A-C12A**	0.9310	1.081
C10A-C9A	1.496(6)	1.510	**C3A-C4A**	1.385(7)	1.393	**C13A-C12A**	1.374(7)	1.391
C8A-C9A	1.447(5)	1.490	**C12A-C11A**	1.380(6)	1.400	**H16A-C16A**	0.9600	1.095
C10A-C15A	1.398(5)	1.402	**H7A-C7A**	0.9300	1.087	**H16B-C16A**	0.9600	1.089
C14A-C15A	1.379(6)	1.398	**C8A-C7A**	1.320(6)	1.344	**H16C-C16A**	0.9600	1.095
H13A-C13A	0.9290	1.082	**H2A-C2A**	0.9300	1.082	**C3A-C2A**	1.383(7)	1.393
H17A-C17A	0.9590	1.095	**H17B-C17A**	0.9600	1.095	**H17C-C17A**	0.9600	1.095
H3A-C3A	0.9300	1.084						

Table S2: Comparison of geometrical bond angles of HK1 and HK2

Compound HK1

Atoms	Bond Angles ()		Atoms	Bond Angles ()	
	XRD	DFT		XRD	DFT
C15A-O3A-C16A	118.2(3)	119.11	**Cl2A-C5A-C4A**	117.2(4)	117.15
C11A-O2A-C17A	118.5(4)	119.13	**C6A-C5A-C4A**	121.7(4)	123.18
O1A-C9A-C10A	120.9(3)	121.08	**O2A-C11A-C10A**	115.0(4)	115.83
O1A-C9A-C8A	120.8(4)	122.42	**O2A-C11A-C12A**	124.8(4)	123.76
C10A-C9A-C8A	118.3(3)	116.47	**C10A-C11A-C12A**	120.2(4)	120.37
C9A-C10A-C15A	119.9(3)	120.37	**Cl1A-C1A-C6A**	119.6(3)	121.25
C9A-C10A-C11A	120.0(3)	120.58	**Cl1A-C1A-C2A**	116.8(3)	116.16
C15A-C10A-C11A	120.1(4)	119.01	**C6A-C1A-C2A**	123.5(4)	122.54
C7A-C6A-C5A	124.6(3)	119.43	**C15A-C14A-H14A**	120.4	121.23
C7A-C6A-C1A	120.0(3)	125.31	**C15A-C14A-C13A**	119.1(5)	118.75
C5A C6A C1A	115.4(4)	115.21	**H14A-C14A-C13A**	120.4	120.00
C6A-C7A-H7A	115.0	115.73	**C14A-C13A-H13A**	118.7	119.19
C6A-C7A-C8A	130.1(4)	127.69	**C14A-C13A-C12A**	122.6(5)	121.63
H7A-C7A-C8A	115.0	116.49	**H13A-C13A-C12A**	118.7	119.17
C9A-C8A-C7A	123.9(4)	120.04	**C11A-C12A-C13A**	118.4(5)	119.23
C9A-C8A-H8A	118.1	117.31	**C11A-C12A-H12A**	120.8	120.96
C7A-C8A-H8A	118.1	122..57	**C13A-C12A-H12A**	120.8	119.80
O3A-C15A-C10A	115.1(4)	115.11	**C1A-C2A-H2A**	120.5	119.32
O3A-C15A-C14A	125.3(4)	123.88	**C1A-C2A-C3A**	119.0(4)	119.81
C10A-C15A-C14A	119.6(4)	120.98	**H2A-C2A-C3A**	120.5	120.58
Cl2A-C5A-C6A	121.1(3)	119.64	**C5A-C4A-H4A**	120.0	119.64
C5A-C4A-C3A	120.0(5)	119.23	**H4A-C4A-C3A**	120.1	121.12
C2A-C3A-C4A	120.5(5)	120.00	**C2A-C3A-H3A**	119.7	119.95
C4A-C3A-H3A	119.8	120.03	**O3A-C16A-H16D**	109.5	111.44
O3A C16A H16E	109.4	105.66	**O3A-C16A-H16F**	109.4	111.19
H16D C16A H16E	109.5	109.43	**H16D-C16A-H16F**	109.5	109.62
H16E C16A H16F	109.5	109.43	**O2A-C17A-H17G**	109.5	111.30
O2A C17A H17H	109.5	105.58	**O2A-C17A-H17I**	109.5	111.49
H17G C17A H17H	109.5	109.35	**H17G-C17A-H17I**	109.4	109.64
H17H C17A H17I	109.5	109.64			

Compound HK2

Atoms	Bond Angles () XRD	DFT	Atoms	Bond Angles () XRD	DFT
C15A-O3A-C16A	117.7(3)	119.10	**Br1A-C1A-C6A**	120.0(3)	122.96
C11A-O2A-C17A	118.0(3)	119.10	**Br1A-C1A-C2A**	117.7(3)	115.18
O1A-C9A-C10A	120.5(3)	120.83	**C6A-C1A-C2A**	122.2(4)	121.12
O1A-C9A-C8A	120.4(4)	120.83	**C6A-C5A-C4A**	123.5(4)	129.55
C10A-C9A-C8A	119.1(3)	119.53	**C6A-C5A-H5A**	118.2	117.12
O3A-C15A-C10A	115.0(3)	115.17	**C4A-C5A-H5A**	118.2	117.32
O3A-C15A-C14A	125.1(4)	123.81	**C11A-C12A-H12A**	120.8	127.47
C10A-C15A-C14A	119.9(4)	120.09	**C11A-C12A-C13**	118.5(4)	119.23
C9A-C10A-C15A	119.7(3)	120.42	**H12A-C12A-C13A**	120.7	119.81
C9A-C10A-C11A	120.6(3)	120.58	**O3A-C16A-H16A**	109.5	111.22
C15A-C10A-C11A	119.7(4)	118.96	**O3A-C16A-H16B**	109.5	111.43
C7A-C6A-C1A	123.2(4)	131.11	**O3A-C16A-H16C**	109.5	105.67
C7A-C6A-C5A	120.7(4)	116.70	**H16A-C16A-H16B**	109.5	109.38
C1A-C6A-C5A	116.1(4)	112.18	**H16A-C16A-H16C**	109.5	109.61
H4A-C4A-C5A	121.3	122.62	**H16B-C16A-H16C**	109.4	109.40
H4A-C4A-C3A	121.3	121.80	**C14A-C13A-C12A**	122.3(4)	121.59
C5A-C4A-C3A	117.5(4)	115.56	**C14A-C13A-H13A**	118.8	119.20
O2A-C11A-C10A	114.7(3)	115.85	**C12A-C13A-H13A**	118.9	120.00
O2A-C11A-C12A	124.6(4)	123.69	**C1A-C2A-H2A**	120.5	119.00
C10A-C11A-C12A	120.7(4)	120.42	**C1A-C2A-C3A**	119.0(4)	121.12
C6A-C7A-H7A	116.8	112.89	**H2A-C2A-C3A**	120.5	119.85
C6A-C7A-C8A	126.5(4)	131.73	**O2A-C17A-H17A**	109.5	111.51
H7A-C7A-C8A	116.7	112.89	**O2A-C17A-H17B**	109.4	105.59
C9A-C8A-C7A	124.0(4)	131.73	**O2A-C17A-H17C**	109.5	111.30
C9A-C8A-H8A	118.0	117.12	**H17A-C17A H17B**	109.5	109.35
C7A-C8A-H8A	118.0	123.33	**H17A-C17A-H17C**	109.5	109.61
C15A-C14A-H14A	120.6	121.21	**H17B-C17A-H17C**	109.4	109.34
C15A-C14A-C13A	118.8(4)	118.78	**C4A-C3A-C2A**	121.5(4)	119.73
H14A-C14A-C13A	120.5	120.00	**C4A-C3A-H3A**	119.3	120.43
C2A-C3A-H3A	119.2	121.80			

Table S3: Comparison of geometrical torsion angles of HK1 and HK2

Compound HK1

Atoms	Torsion Angles () XRD	DFT	Atoms	Torsion Angles () XRD	DFT
C16A-O3A-C15A-C10A	172.6(4)	-178.25	**C5A-C6A-C1A-C2A**	-0.3(6)	0.55
C16A-O3A-C15A-C14A	-8.6(6)	0.420	**C6A-C7A-C8A-C9A**	177.2(4)	176.79
C15A-O3A-C16A-H16D	-57.7	-61.84	**C6A-C7A-C8A-H8A**	-2.8	-0.11
C15A-O3A-C16A-H16E	-177.8	179.37	**H7A-C7A-C8A-C9A**	-2.8	0.12
C15A-O3A-C16A-H16F	62.3	60.79	**H7A-C7A-C8A-H8A**	177.2	-176.78
C17A-O2A-C11A-C10A	178.6(4)	177.47	**O3A-C15A-C14A-H14A**	2.5	0.596
C17A-O2A-C11A-C12A	-2.0(7)	-4.35	**O3A-C15A-C14A-C13A**	-177.5(5)	-178.89
C11A-O2A-C17A-H17G	-61.8	-59.26	**C10A-C15A-C14A-H14A**	-178.8	179.19
C11A-O2A-C17A-H17H	178.2	-177.82	**C10A-C15A-C14A-C13A**	1.3(7)	-0.263
C11A-O2A-C17A-H17I	58.2	63.50	**Cl2A-C5A-C4A-H4A**	-0.7	-0.64
O1A-C9A-C10A-C15A	104.9(4)	117.54	**Cl2A-C5A-C4-C3A**	179.3(4)	179.19
O1A-C9A-C10A-C11A	-73.7(5)	-60.57	**C6A-C5A-C4A-H4A**	-178.6	-179.24
C8A-C9A-C10A-C15A	-75.1(5)	-63.94	**C6A-C5A-C4A-C3A**	1.5(7)	0.59
C8A-C9A-C10A-C11A	106.3(4)	117.92	**O2- C11A-C12A-C13A**	-178.5(5)	-178.27
O1A-C9A-C8A-C7A	-175.2(4)	9.28	**O2A-C11A-C12A-H12A**	1.6	1.5
O1A-C9A-C8A-H8A	4.8	-173.65	**C10A-C11A-C12A-C13A**	0.8(7)	-0.16
C10A-C9A-C8A-C7A	4.8(6)	-169.19	**C10A-C11A-C12A-H12A**	-179.1	179.62
C10A-C9A-C8A-H8A	-175.2	7.86	**Cl1A-C1A-C2A-H2A**	-0.9	-1.68
C9A-C10A-C15A-O3A	-1.6(5)	1.06	**Cl1A-C1A-C2A-C3A**	179.0(4)	177.83
C9A-C10A-C15A-C14A	179.6(4)	-177.64	**C6A-C1A-C2A-H2A**	-178.8	-179.45
C11A-C10A-C15A-O3A	177.0(4)	179.22	**C6A-1A-C2A-C3A**	1.2(7)	0.07
C11A-C10A-C15A-C14A	-1.8(6)	0.50	**C15A-C14A-C13A-H13A**	-179.6	179.90
C9A-C10A-C11A-O2A	-1.2(5)	-3.87	**C15A-C14A-C13A-C12A**	0.3(8)	-0.16
C9A-C10A-C11A-C12A	179.4(4)	177.88	**H14A-C14A-C13A-H13A**	0.4	0.40
C15A-C10A-C11A-O2A	-179.9(4)	177.97	**H14A-C14A-C13A-C12A**	-179.6	-179.66
C15A-C10A-C11A-C12A	0.7(6)	-0.26	**C14A-C13A-C12A-C11A**	-1.4(9)	0.40
C5A-C6A-C7A-H7A	-138.6	36.67	**C14A-C13A-C12A-H12A**	178.5	-179.40
C5A-C6A-C7A-C8A	41.4(6)	-140.01	**H13A-C13A-C12A-C11A**	178.6	-179.66
C1A-C6A-C7A-H7A	37.9	-141.14	**H13A-C13A-C12A-H12A**	-2	0.52
C1A-C6A-C7A-C8A	-142.1(4)	42.16	**C1A-C2A-C3A-C4A**	-0.7(7)	-0.41
C7A-C6A-C5A-Cl2A	-2.1(6)	2.49	**C1A-C2A-C3A-H3A**	179.2	179.87
C7A-C6A-C5A-C4A	175.7(4)	-178.93	**H2A-C2A-C3A-C4A**	179.2	179.09
C1A-C6A-C5A-Cl2A	-178.8(3)	-179.46	**H2A-C2A-C3A-H3A**	-0.8	-0.6
C1A-C6A-C5A-C4A	-1.0(6)	-0.89	**C5A-C4A-C3A-C2A**	-0.6(8)	0.09
C7A-C6A-C1A-Cl1A	5.0(5)	0.80	**C5A-C4A-C3A-H3A**	179.5	179.80
C7A-C6A-C1A-C2A	-177.2(4)	178.46	**H4A-C4A-C3A-C2A**	179.5	179.93
C5A-C6A-C1A-Cl1A	-178.1(3)	-177.09	**H4A-C4A-C3A-H3A**	-0.4	-0.351

Compound HK2

Atoms	Torsion Angles ()		Atoms	Torsion Angles ()	
	XRD	DFT		XRD	DFT
C16A-O3A-C15A-C10A	-167.5(3)	-179.36	**C7A-C6A-C1A-Br1A**	-0.8(6)	-0.11
C16A-O3A-C15A-C14A	12.3(5)	-0.65	**C7A-C6A-C1A-C2A**	179.8(4)	-179.91
C15A-O3A-C16A-H16A	-70.9	61.81	**C5A-C6A-C1A-Br1A**	179.6(3)	179.84
C15A-O3A-C16A-H16B	169.1	-179.57	**C5A-C6A-C1A-C2A**	0.1(6)	0.04
C15A-O3A-C16A-H16C	49.2	-60.83	**C7A-C6A-C5A-C4A**	-177.6(4)	179.99
C17A-O2A-C11A-C10A	-177.3(4)	177.15	**C1A-C6A-C5A-C4A**	2.1(6)	0.02
C17A-O2A-C11A-C12A	4.4(6)	-4.75	**C1A-C6A-C5A-H5A**	-177.9	179.69
C11A-O2A-C17A-H17A	-67.7	63.40	**H4A-C4A-C5A-C6A**	176	179.95
C11A-O2A-C17A-H17B	172.3	-177.91	**C3A-C4A-C5A-C6A**	-4.1(7)	-0.05
C11A-O2A-C17A-H17C	52.4	-59.35	**H4A-C4A-C3A-C2A**	-176.1	179.99
O1A-C9A-C10A-C15A	-97.2(5)	117.91	**H4A-C4A-C3A-H3A**	3.8	0.02
O1A-C9A-C10A-C11A	81.7(5)	-60.36	**C5A-C4A-C3A-C2A**	3.9(7)	0.01
C8A-C9A-C10A-C15A	83.2(5)	-63.31	**C5A-C4A-C3A-H3A**	-176.1	-179.96
C8A-C9A-C10A-C11A	-97.9(5)	118.40	**O2A-C11A-C12A-H12A**	-1	1.58
O1A-C9A-C8A-C7A	169.4(4)	4.00	**O2A-C11A-C12A-C13A**	179.0(4)	-178.16
O1A-C9A-C8A-H8A	-10.6	-176.96	**C10A-C11A-C12A-H12A**	-179.3	179.59
C10A-C9A-C8A-H8A	169	4.29	**C10A-C11A-C12A-C13A**	0.7(6)	-0.16
O3A-C15A-C10A-C9A	-0.7(5)	1.00	**C6A-C7A-C8A-C9A**	-179.6(4)	178.92
O3A-C15A-C10A-C11A	-179.6(3)	179.31	**C6A-C7A-C8A-H8A**	0.4	-0.03
C14A-C15A-C10A-C9A	179.5(4)	-177.74	**H7A-C7A-C8A-C9A**	0.4	-1.21
C14A-C15A-C10A-C11A	0.6(6)	0.56	**H7A-C7A-C8A-H8A**	-179.6	179.82
O3A-C15A-C14A-H14A	0.6	179.31	**C15A-C14A-C13A-C12A**	-0.8(7)	-0.13
C10A-C9A-C8A-H8A	169	4.29	**C15A-C14A-C13A-H13A**	179.2	179.93
O3A-C15A-C14A-C13A	-179.4(4)	-178.98	**H14A-C14A-C13A-C12A**	179.2	-179.63
C10A-C15A-C14A-H14A	-179.6	179.14	**H14A-C14A-C13A-H13A**	-0.8	0.43
C10A-C15A-C14A-C13A	0.4(6)	-0.34	**Br1A-C1A-C2A-H2A**	0.4	-179.90
C9A-C10A-C11A-O2A	1.5(5)	-3.84	**Br1A-C1A-C2A-C3A**	-179.6(4)	-179.90
C9A-C10A-C11A-C12A	180.0(4)	178.00	**C6A-C1A-C2A-H2A**	179.8	179.89
C15A-C10A-C11A-O2A	-179.6(3)	177.85	**C7A-C6A-C1A-Br1A**	-0.8(6)	-0.11
C15A-C10A-C11A-C12A	-1.1(6)	-0.30	**C7A-C6A-C1A-C2A**	179.8(4)	-179.91
C1A-C6A-C7A-H7A	-30.4	179.33	**H12A-C12A-C13A-C14A**	-179.7	-179.36
C1A-C6A-C7A-C8A	149.6(4)	-0.80	**H12A-C12A-C13A-H13A**	0.3	0.55
C5A-C6A-C7A-H7A	149.2	-0.63	**C1A-C2A-C3A-C4A**	-1.9(7)	0.05
C5A-C6A-C7A-C8A	-30.8(6)	-179.22			
C6A-C1A-C2A-C3A	-0.2(7)	-0.09			
C11A-C12A-C13A-C14A	0.3(7)	0.38			
C11A-C12A-C13A-H13A	-179.7	-179.68			
H2A-C2A-C3A-C4A	178.1	-179.93			

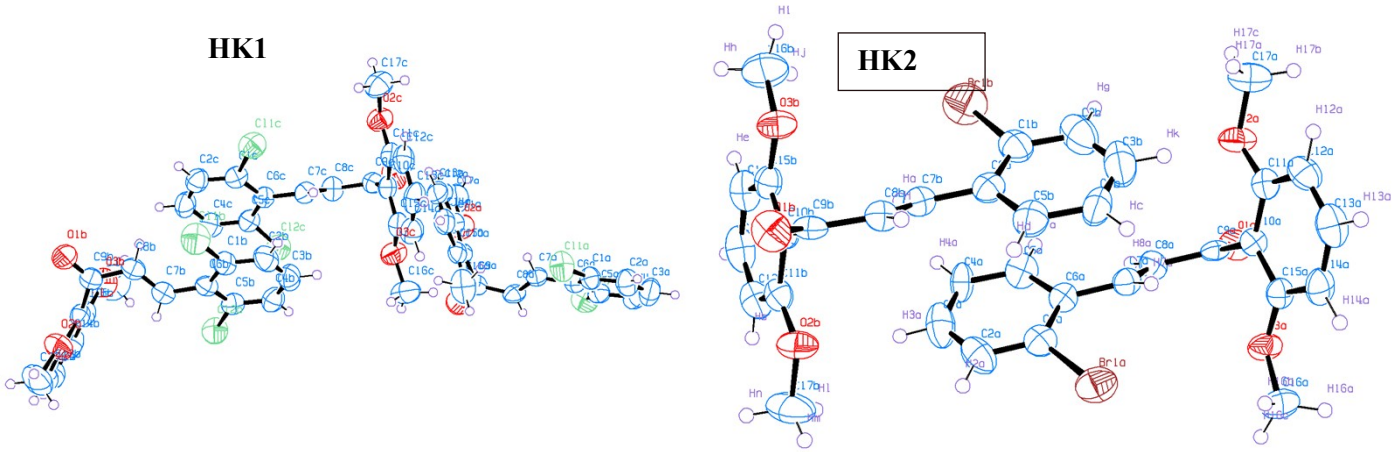
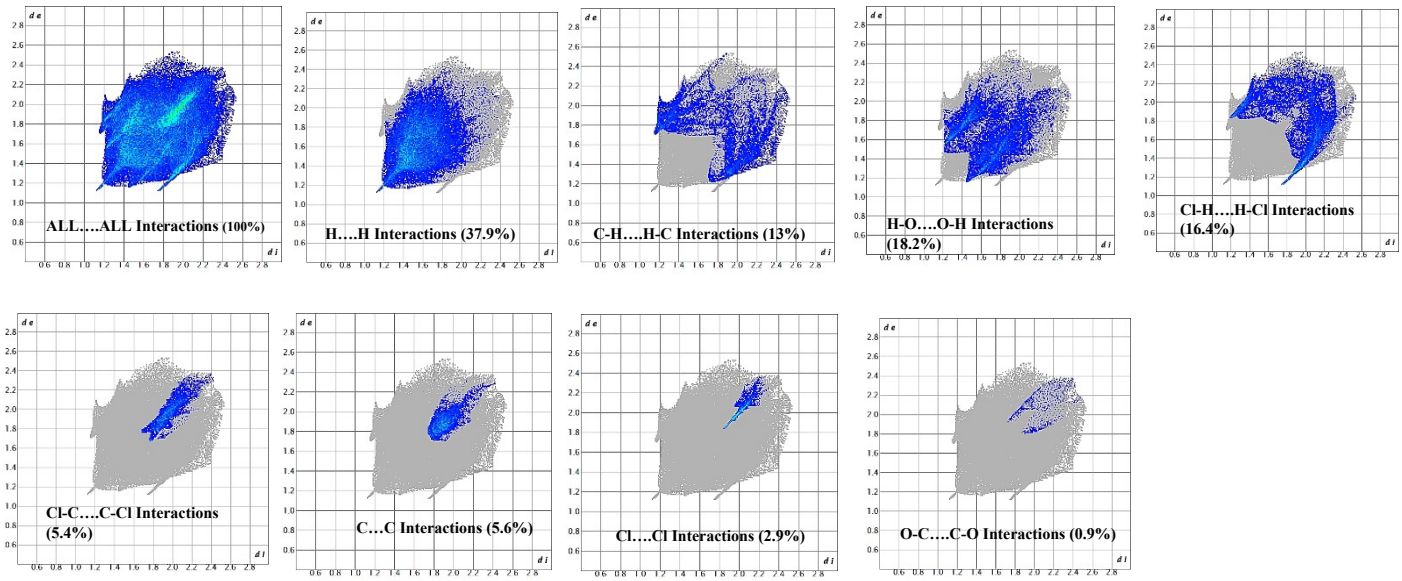


Figure S4: Anisotropic displacement parameter (ADP) plot for HK1and HK2 strucutres

HK1



HK2

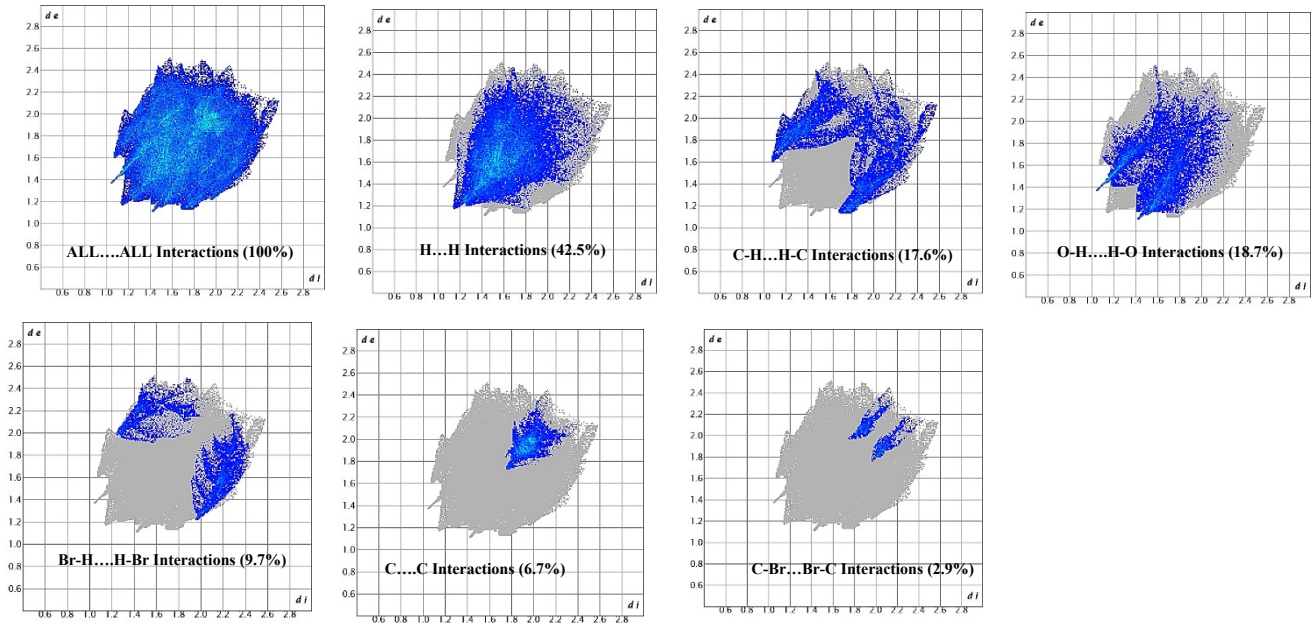


Figure S5: The 2D fingerprint plots representation of Hirshfeld surface interaction for HK1 and HK2

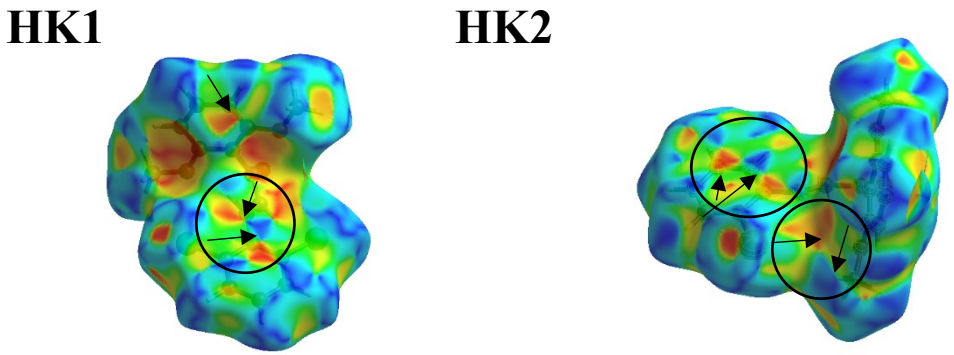


Figure S6: Shape Index map for HK1and HK2 indicating pi-pi interactions with the formation of blue and red triangles, which is encircled in black colour

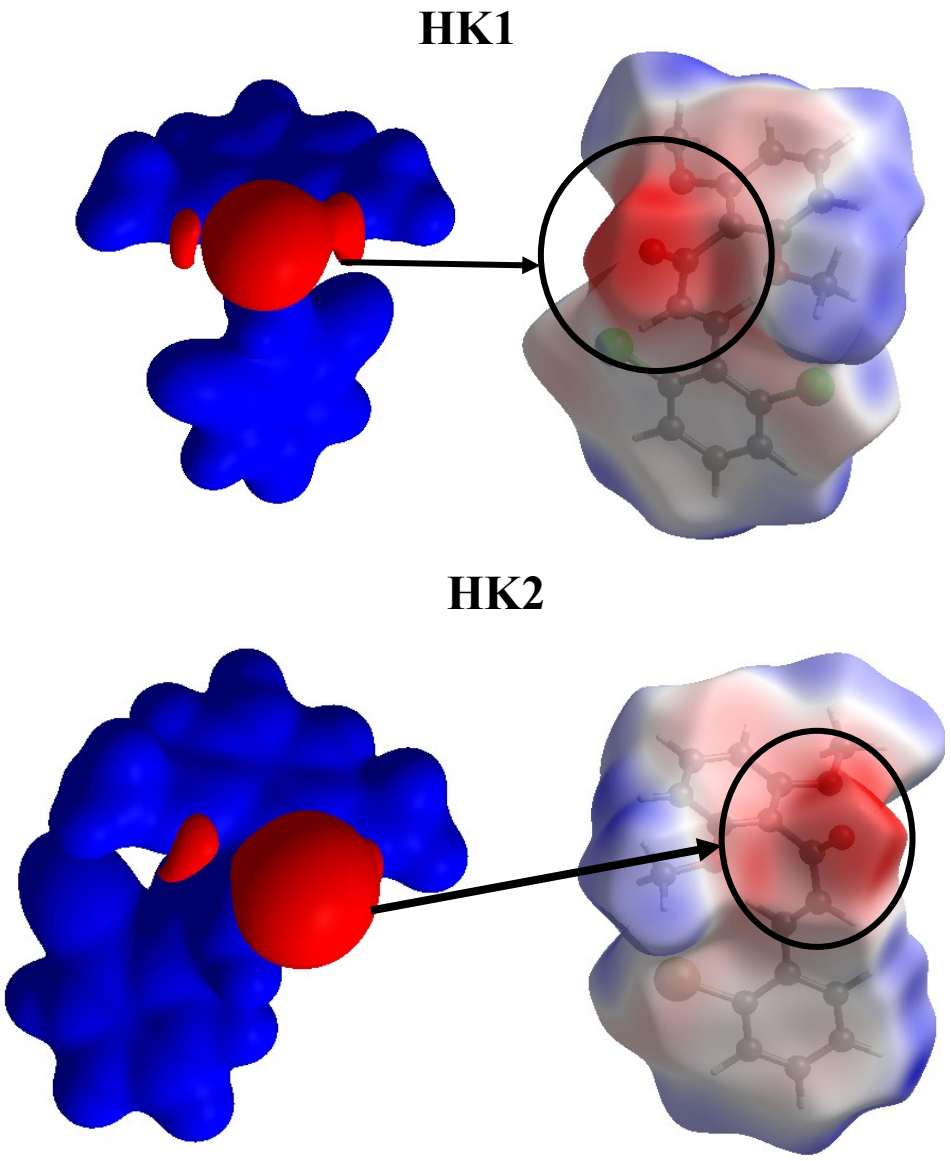


Figure S7: Electrostatic potential surface plot of HK1 and HK2 indicating nucleophile attack regions

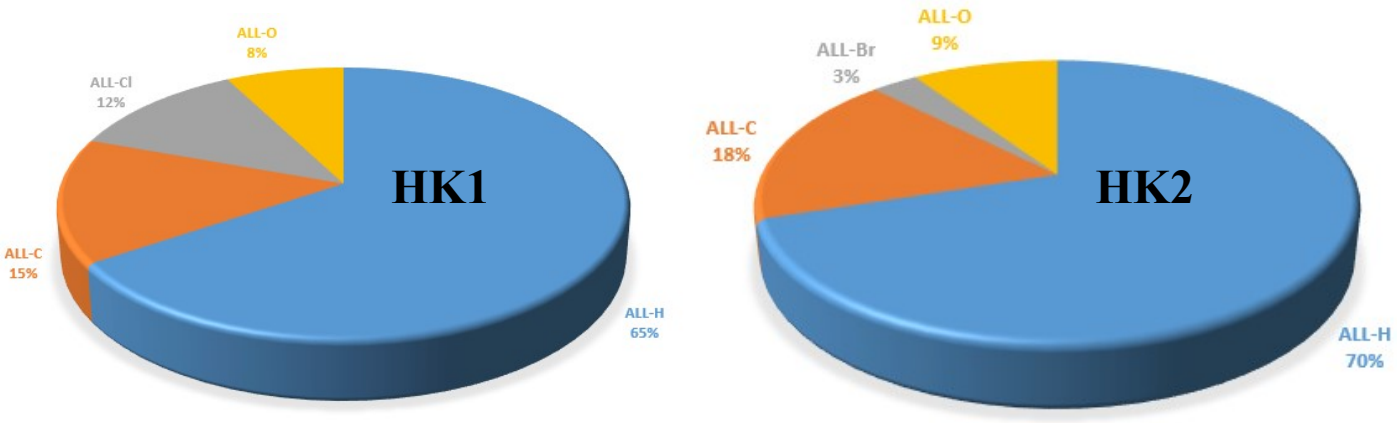


Figure S8: The 3-D pie chart representation of fingerprint plot interaction with respect to elements present in a molecule

Table S4: Hirshfeld surface contacts (actual and random) along with enrichment ratios for HK1 and HK2 structures

HK1					**HK2**				
Inside Atoms	**Outside Atoms**				**Inside Atoms**	**Outside Atoms**			
	H	**C**	**O**	**Cl**		**H**	**C**	**O**	**Br**
Actual Contacts (C_{XX} and C_{XY})									
H	37.9	-	-	-	**H**	42.5	-	-	-
C	13	5.6	-	-	**C**	17.6	6.7	-	-
O	18.2	0.9	0.0	-	**O**	18.7	0.0	0.0	-
Cl	16.4	5.3	0.0	2.9	**Br**	9.7	2.9	1.8	0.0
Total Observed % Contribution	85.5	8.8	0.0	2.9	**Total Observed %Contribution**	88.5	9.6	18	0.0
Surface % (S_X)	61.7	15.2	9.5	13.75	**Surface % (S_X)**	65.5	16.95	10.25	7.2
Random Contacts % (R_{XX} and R_{xy})									
H	38.06	-	-	-	**H**	42.90	-	-	-
C	18.75	2.31	-	-	**C**	22.20	2.87	-	-
O	11.72	2.88	0.90	-	**O**	13.42	3.47	1.05	-
Cl	16.96	4.18	2.61	1.89	**Br**	9.42	2.44	1.42	0.51
Enrichment Ratio E (E_{XX} and E_{XY})									
H	0.99	-	-	-	**H**	0.99	-	-	-
C	0.69	**2.42**	-	-	**C**	0.79	**2.33**	-	-
O	**1.55**	0.31	0.00	-	**O**	**1.39**	0.0	0.0	-
Cl	0.96	**1.29**	-	**1.53**	**Br**	**1.02**	**1.18**	**1.26**	0.0

Table S5: Second order natural bond orbital perturbation theory analysis corresponding to fock matrix revealing Lewis and non-Lewis interactions

Donor (i)	**ED (i)(e)**	**Acceptor(j)**	**ED (j)(e)**	**E^2 kJ/mol**	**$\Delta E^{a.}$**	**F(i,j)[b] a.u.**
		HK1				
π(C15A-C14A)	1.652	π*(C13A-C12A)	0.373	109.36	0.28	0.077
		π*(C11A-C10A)	0.411	64.72	0.29	0.060
σ(C14A-C13A)	1.974	σ* (C17A-H17G)	0.018	36.52	3.42	0.154
π(C13A-C12A)	1.708	π*(C15A-C14A)	0.408	59.87	0.28	0.058
		π*(C11A-C10A)	0.411	101.71	0.28	0.076
σ(C13A-H13A)	1.978	σ* (C17A-H17H)	0.009	43.72	3.04	0.160
π(C11A-C10A)	1.657	π*(C15A-C14A)	0.408	103.63	0.28	0.076
		π*(C13A-C12A)	0.373	65.605	0.28	0.060
π(C8A-C7A)	1.853	π*(C9A-O1A)	0.138	75.89	0.31	0.067
π(C4A-C5A)	1.979	π*(C17A-H17C)	0.018	34.51	3.45	0.151
LP(3) Cl 1A	1.922	π*(C1A-C2A)	0.377	53.05	0.32	0.062
π(C6A-C5A)	1.652	π*(C1A-C2A)	0.390	78.11	0.28	0.065
		π*(C3A-C4A)	0.297	81.67	0.30	0.068
π(C1A-C2A)	1.683	π*(C6A-C5A)	0.429	80.58	0.28	0.068
		π*(C3A-C12A)	0.297	79.16	0.30	0.067
π(C3A-C4A)	1.656	π*(C6A-C5A)	0.429	89.49	0.27	0.069

		π*(C1A-C2A)	0.390	87.52	0.27	0.068
LP(2)O1A	1.879	σ* (C10A-C9A)	0.065	85.77	0.67	0.106
		σ* (C9A-C8A)	0.063	80.41	0.69	0.104
LP(2)O3A	1.960	σ* (C15A-C14A)	0.027	28.07	1.10	0.077
		π*(C15A-C14A)	0.408	133.38	0.33	0.098
		σ* (C16A-H16F)	0.018	21.88	0.68	0.055
		σ*(C16A-H16E)	0.019	23.38	0.68	0.057
LP(1)O2A	1.959	σ*(C12A-C11A)	0.027	24.65	1.10	0.076
LP(3) Cl 2A	1.924	π*(C6A-C5A)	0.429	53.80	0.32	0.063
LP(2)O2A	1.840	π*(C11A-C10A)	0.411	117.61	0.35	0.094

Donor (i)	**ED (i)(e)**	**Acceptor(j)**	**ED (j)(e)**	**E^2 kJ/mol**	**$\Delta E^{a.}$**	**F(i,j)[b] a.u.**
		HK2				
π(C11A-C12A)	0.826	π*(C13A-C14A)	0.033	58.15	0.28	0.077
		π*(C15A-C10A)	0.013	32.38	0.29	0.060
π(C13A-C14A)	0.854	π*(C11A-C12A)	0.013	30.04	0.28	0.058
		π*(C15A-C10A)	0.013	50.50	0.28	0.076
π(C15A-C10A)	0.826	π*(C11A-C12A)	0.013	51.50	0.28	0.076
		π*(C13A-C14A)	0.007	33.17	0.28	0.060
π(C8A-C7A)	0.927	π*(C9A-O1A)	0.007	40.29	0.30	0.069
		π*(C6A-C1A)	0.018	27.82	0.26	0.057
π(C6A-C1A)	0.975	π*(C5A-C4A)	0.005	45.31	0.32	0.076
		π*(C3A-C2A)	0.009	24.09	0.53	0.070
π(C5A-C4A)	0.819	π*(C6A-C1A)	0.018	37.36	0.26	0.062
		π*(C3A-C2A)	0.005	28.28	0.51	0.075
π(C3A-C2A)	0.833	π*(C6A-C1A)	0.018	48.82	0.26	0.073
		π*(C5A-C4A)	0.005	26.10	0.31	0.057
σ (C1A-Br1A)	0.988	σ*(O2A-C17A)	0.016	28.07	1.31	0.121
LP(2)O1A	0.939	σ* (C10A-C9A)	0.0413	42.96	0.67	0.106
		σ* (C9A-C8A)	0.032	39.95	0.69	0.104
LP(2)O2A	0.917	π*(C11A-C12A)	0.013	66.35	0.34	0.099
LP(2)O3A	0.920	π*(C15A-C10A)	0.013	58.61	0.35	0.094
LP(3Br 35	0.965	π*(C10-C15)	0.018	21.42	0.30	0.055

$E^{(2)}$ is the stabilization energy in kJ/mol.

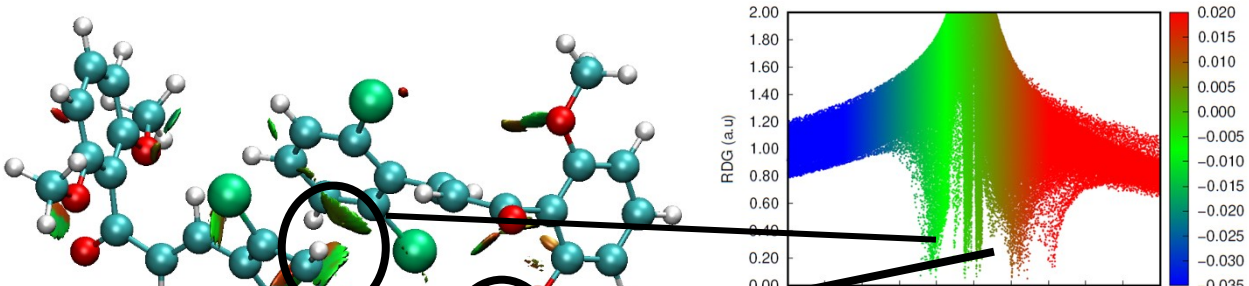
[a] Energy difference between donor orbital (i)and acceptor (j) orbital $\Delta E = E(i)-E(j)$ a.u.

[b] F(i,j) is the Fock matrix element between i^{th} and j^{th} NBO orbitals in a.u. unit

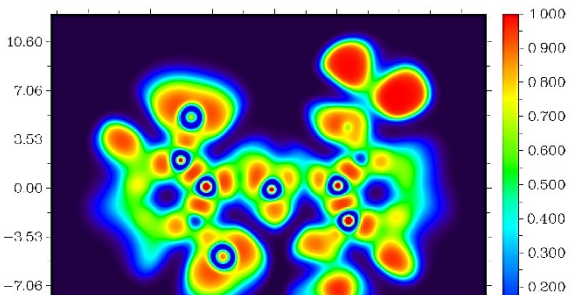
Table S6: Quantum theory of atoms in molecules (QTAIM)derived topological analysis with respective bond critical points for the studied compounds

Where, ρ_{BCP} = Electron Density ; G(r)= Lagrangian Kinetic Energy; K(r)= Hamiltonian Kinetic Energy ; V(r)= Potential Energy Density; E(r)= Energy Density; $\nabla^2\rho$= Laplacian of Electron Density; ESP= Electrostatic potential; B.E= Binding Energy

Molecules	**HK1**	
Interactions	C8-H29•••Cl28	C8
BCP	45	
BCP type	(3,-1)	
ρ_{BCP} (a.u.)	0.0106	
G(r) (a.u.):	0.00827	
K(r) (a.u.):	-0.00192	
V(r) (a.u.):	-0.00629	
-G(r)/ V(r):	1.314	
$\lvert\lambda_1\rvert/\lambda_3$	0.064	
E(r)	0.00198	
$\nabla^2\rho$ (a.u.)	0.0410	
Total ESP (a.u.)	0.0299	
Eigenvalues ($\lambda_3 > 0, \lambda_2 < 0, \lambda_1 < 0$)	0.0525,-0.00815 ,-0.00336	0.0685
Ellipticity of electron density(ε)	1.42	
H-bond B.E (kJ/mol):	-12.97	



ELF


10.60
7.06
3.53
0.00
−3.53
−7.06
1.000
0.900
0.800
0.700
0.600
0.500
0.400
0.300
0.200

LOL

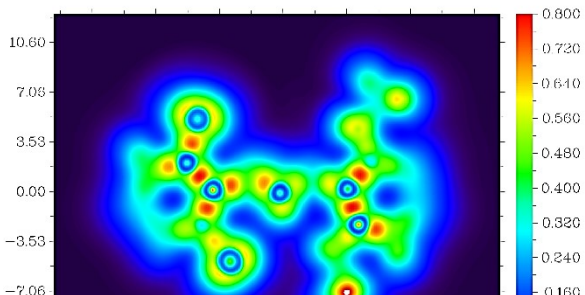

10.60
7.06
3.53
0.00
−3.53
−7.06
0.800
0.720
0.640
0.560
0.480
0.400
0.320
0.240
0.160

Table S7: Evaluation of physicochemical and ADME-T descriptor parameters

Descriptor P		
Mol. Weigh		
Rotatable		
H-bond Ac		
H-bond I		
Molar Refi		
Polar Surface		
Lipinski Rule		
M log		
Water Solubility(l		
Caco2 pern		
(log Papp in		
Intestinal abs		
Skin Permeabi		
P-glycoprotei		
P-glycoprotein I inhibitor	Yes	No
P-glycoprotein II inhibitor	No	No
Distribution		
VDss (log L/kg)	0.077	0.092
T		
AMES	No	No
Oral Rat Acute Toxicity (LD50)(mol/kg)	2.604	2.349
Oral Rat Chronic Toxicity (LOAEL) (log mg/kg_bw/day)	1.271	2.039
hERG I inhibitor	No	No
hERG II inhibitor	No	No
Hepatotoxicity	No	No
Skin Sensitisation	No	No
T. Pyriformis (log ug/L)	1.118	1.147
Minnow (log mM)	-2.158	-1.99
Druglikeliness		
Bioavailability score	0.55	0.55
Synthetic accessibility	2.88	2.81
Lead likeliness (1 violation)	XLOGP3> 3.5	XLOGP3> 3.5
Pains	0	0

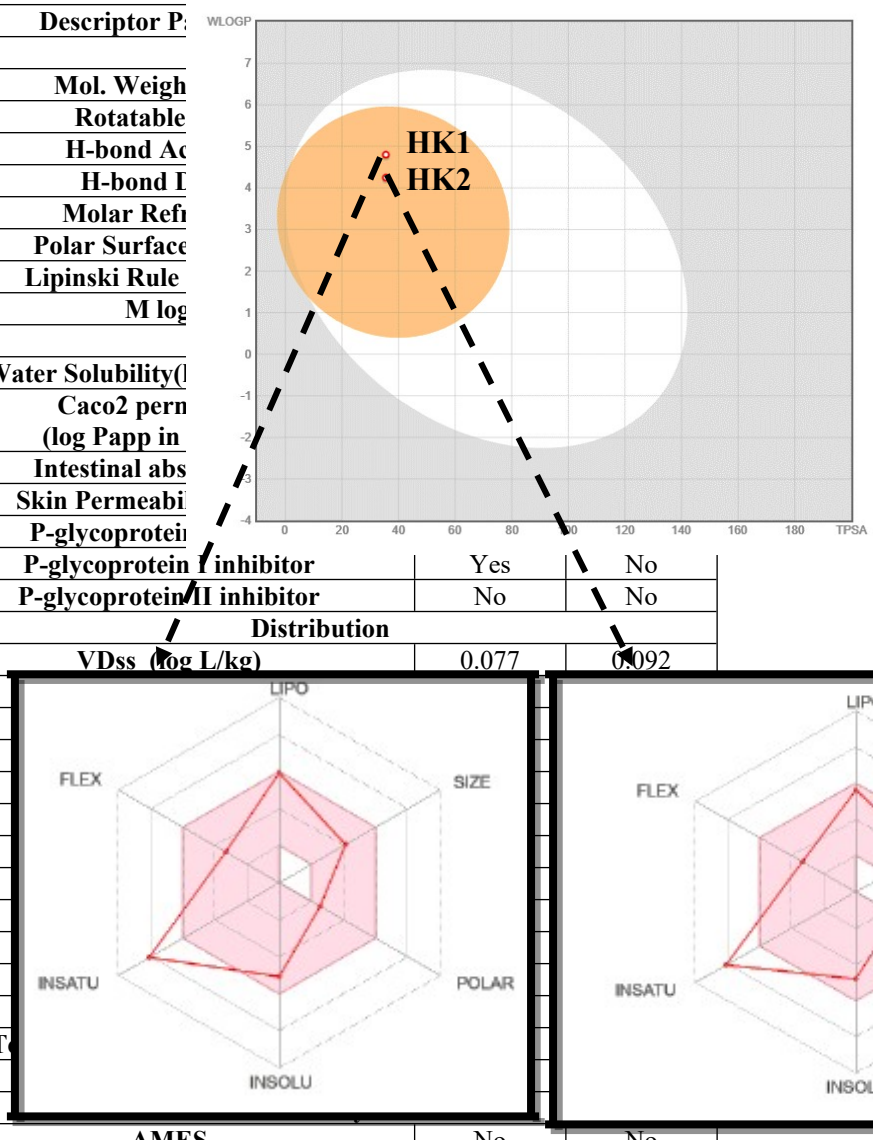


Figure S11. Boiled-egg model illustrating the permeability of the blood-brain barrier along with the Swiss ADME physicochemical property radars for HK1and HK2

Table S8: Comparison of docking results showing similar interacting residues with the reported literature (Residues bolded in black for MAO-B and bolded red for MAO-A)

Ligand	Target	Interacting Amino Acid Residues	Binding	Referen

ID			Energy (kcal/mol)	ce
HK1	MAO-A	**TYR69,**ALA68,MET445,**TYR444**,GLY443,VAL303,**TYR197,**ASN181,**ILE180**,GLU67,GLY66,LYS305,ARG51	-9.76	Present Work
	MAO-B	SER59.**TYR60,TYR398,**GLY434,**TYR435,**MET436,ARG42,THR43,**GLN206**,CYS397,**LEU171, CYS172**, **ILE198**, **TYR188**	-9.50	
HK2	MAO-A	**TYR69**,ALA68,MET445,**TYR444,GLY443**,VAL303,**TYR197,ASN181,ILE180,**GLY67,GLY66,LYS305,ARG51,VAL70,**GLN215**,**PHE352**,CYS406,**TYR407**	-10.55	
	MAO-B	**TYR60**,SER59,TRP388,**TYR435,**GLY434,MET436,ARG42,THR43,**GLN206**,CYS397,**LEU171, CYS172,ILE198,TYR188**,**TYR398,**VAL294,LYS296,GLY58,GLY57	-9.88	
AC4	MAO-B	LEU88, PHE99, PRO104, TRP119, LEU164, LEU167, PHE168, **LEU171**, **ILE198**, ILE199, ILE316, TYR326, LEU328, PHE343, **TYR398, TYR435**	-9.5	107
O23	MAO-A	**TYR444**,**TYR407**	-8.593	38
	MAO-B	**TYR435,TYR398**,ILE199	-10.220	
E7	MAO-A	PHE208,**TYR444,TYR407**	-7.914	39
	MAO-B	ILE199,ILE316,**LEU171,TYR435,TYR398**	-10.032	
TB8	MAO-A	PHE352,**TYR407,TYR444,ILE180**,ILE335,LEU337,PHE352, GLY 74, ILE207, PHE208,GLU216, TRP441	Not mentioned	108
	MAO-B	ILE199		
51	MAO-B	**TYR435,TYR398,TYR60**,TYR326,PHE168,ILE199,**LEU171,ILE198**,**CYS172, GLN206**,PHE343,TYR398	-8.8	109
52	MAO-A	CYS323,THR336,**ILE180,**PHE208,ILE207,ASN181,**TYR444**,**TYR407,GLN215**,LEU337,VAL210,ILE335	+2.3	109
	MAO-B	**TYR326**,TRP119,**LEU171**,PHE168,**ILE198**,**GLN206,TYR398,TYR435**,PHE343,ILE316,LEU167,ILE199,LEU164	-10.3	
Thiophene and furan Chalcones	MAO-B	**TYR435,TYR398**	Not mentioned	110,111
(R)-**P5**	MAO-B	**TYR398,TYR435**,**LEU171,CYS172**,ILE199,TYR362,PHE103, PRO104, TRP119, ILE316	Not mentioned	35
(S)-**P5**	MAO-B	**TYR398 ,TYR435**,**LEU171**, **CYS172,** ILE199, TYR362,PHE103, PRO104, TRP119, ILE316	Not mentioned	
MHC5	MAO-B	**TYR326,TYR60,** PHE99, PRO102, PHE103, PHE104, TRP119, LEU164, LEU167, PHE168, **LEU171, CYS172, TYR188**, **ILE198**, ILE199, **GLN206, TYR398, TYR435,** ILE316, LEU328, PHE343	-10.915	112
MHC4	MAO-B	**TYR326,TYR60**, PHE99, PRO102, PHE103, PHE104, TRP119, LEU164, LEU167, PHE168, **LEU171, CYS172, TYR188, ILE198,** ILE199,	-10.643	112

		GLN206, TYR398, TYR435, ILE316, LEU328, PHE343		
4b	MAO-A	PRO102,GLU84,TYR326,TRP119,PHE103 **TYR197,TYR444,GLY443,ASN181,ILE180,**LEU 337,ILE335,VAL91,PHE108,GLY110,ALA111,V AL210,SER209,PHE208,ILE207,**TYR69**,MET350, **PHE352,**LEU354,LEU97	-9.75	113
4a	MAO-A	TYR326,TRP119,PHE103,**TYR197,TYR444,GLY 443,ASN181,ILE180,**LEU337,ILE335,VAL91,PH E108,GLY110,ALA111,VAL210,SER209,PHE208 ,ILE207,**TYR69,**MET350,**PHE352,**LEU354,LEU9 7	-9.52	113
4d	MAO-A	TYR326,TRP119,PHE103,**TYR197,TYR444**,**GLY 443**,**ASN181,ILE180**,LEU337,ILE335,VAL91,PH E108,GLY110,ALA111,VAL210,SER209,PHE208 ,ILE207,**TYR69,**MET350,**PHE352,**LEU354,LEU9 7	-9.46	113
5-HT	MAO-A	**TYR444, TYR407,GLN215**,**ILE180**	Not mentioned	114
	MAO-B	**TYR435,TYR398,GLY206,LEU171**	Not mentioned	114
1	MAO-A	LEU97, PHE108, ALA111, **ILE180**, ILE325, **TYR69, TYR197, TYR407,TYR444**,	-11.66	115
4 and 6	MAO-B	**TYR60,PHE343,TYR398**,**TYR435,CYS172**,**GLN 206,**TYR188,LEU164,LEU167,PHE168,ILE199,IL E316,**TYR326**	-9.66,-10.56	115

Table S9: Comparison of dynamics results having similar interacting residues with the reported literature (Residues bolded in black for MAO-B)

Ligand ID	Target	Interacting Amino Acid Residues			Ligand RMSD (Å)	Protein RMSD (Å)	Ref.
		H-bond	Hydrophobic	Water bridge			
HK1	MAO-A	LYS305, GLY66	TYR69,ILE180,VAL303,ILE335,PHE352,TRP397,TYR407,TYR444	ALA68,TYR69,LYS218,VAL303, LYS305,TYR407	2.5	5	Present
HK1	MAO-B	MET436	**ILE198,ILE199,PHE343,**TRP388,**TYR398,TYR435**	**SER59,TYR60**,**GLN206**	1.4	2.5	Present
HK2	MAO-A	GLY67, LYS305	ARG51,GLY67,TYR69, LYS305,GLY443,MET445	TYR69,TYR197,ILE207,LYS305,PHE352,TRP397,TYR407,GLY443, TYR444	3.3	5	Present
HK2	MAO-B	**SER59**,**TYR60**,**GLN206**	GLY58,**SER59**,**TYR60**,**ILE199**,VAL294,LYS296,**TYR326,**LEU328,**MET341**,**PHE343**,TRP388, CYS397,**TYR398,TYR435**	GLY58,**SER59,TYR60,GLN206,**LYS296,**GLY434,** MET436	4.8	2.8	Present
AC4	MAO-B	CYS172, **TYR435**	LEU88, PHE99,PRO104,LEU164,PHE168,LEU171,**ILE198,ILE199,**ILE316,**TYR326,**LEU328,**PHE343**, **TYR398,TYR435**	**TYR435**	3.5	4	107
MHC5	MAO-B	**TYR398**, CYS172, **TYR435**	PRO104,LEU164,LEU167,PHE168,LEU171,**ILE198**,**ILE199,**ILE316,**TYR326**,**PHE343,TYR398**	HIS90,CYS172,TYR188,**ILE198**,**ILE199,GLN206, TYR398,TYR435**	3.5	-	113
MHC4	MAO-B	**GLN206,**CYS172 **TYR435**	**TYR60**,PRO104,LEU164,LEU167,LEU171,**ILE199,ILE198**,ILE316,**TYR326**,**PHE343,TYR398**	HIS90,**GLN206, TYR435**	2.5	-	113
RAS	MAO-B	**GLN206,TYR435,TYR398,**LEU171,**TYR60**,CYS172,**PHE343**,**ILE198**,**GLY434,**LEU328,**TYR326,**THR399,VAL173,GLY205,**MET341**,GLN191,ARG42,TYR188,**ILE199,SER59**			-	-	116
SEL	MAO-B	**GLN206,TYR435,TYR398,**LEU171,**TYR60,**CYS172,**PHE343**,ILE198,**GLY434,**LEU328,**TYR326,**THR399,VAL173,GLY205,**MET341,**GLN191,ARG42,TYR188,**ILE199,SER59**			-	-	116

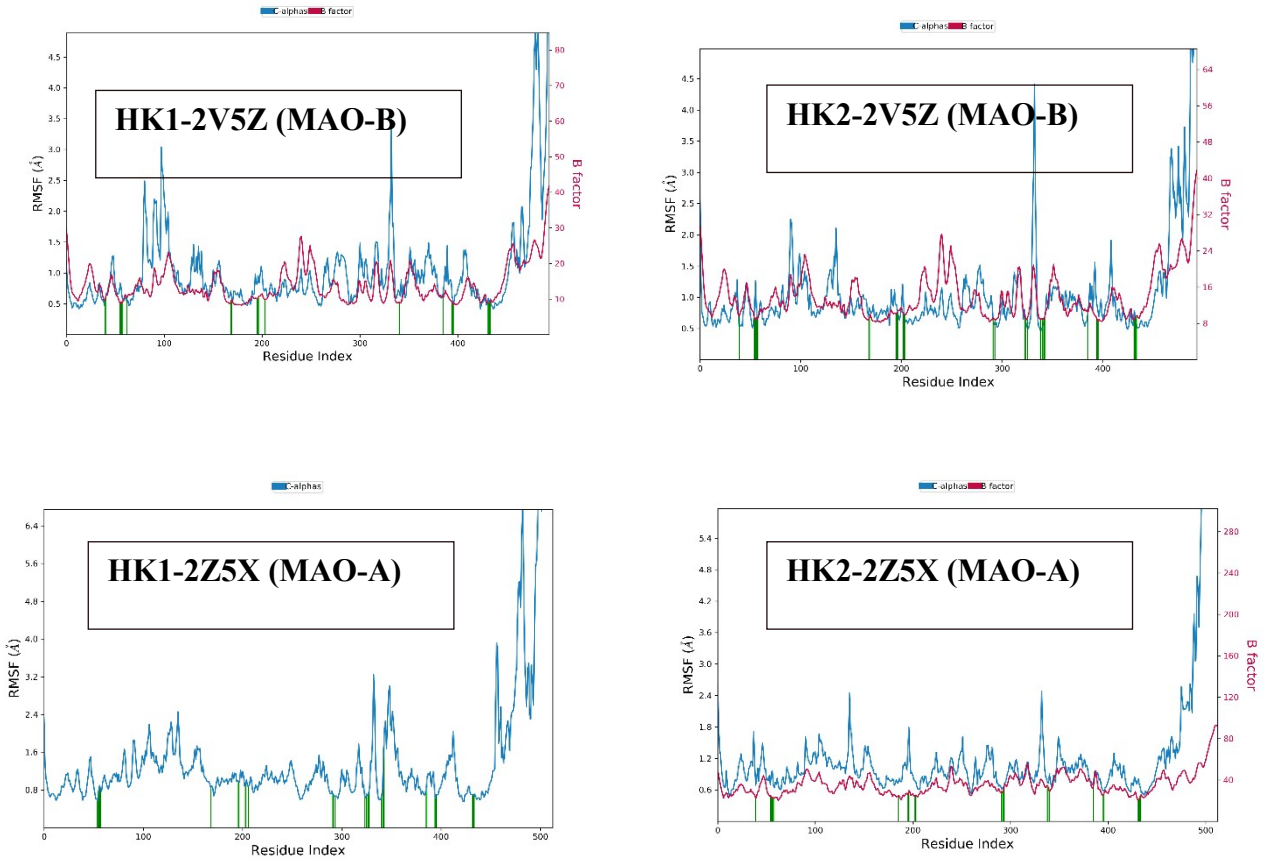


Figure S12: Root mean square fluctuation (RMSF) plot of MAO protein