Supplementary information

Table S1a: Structure and activity of compounds considered for the studies (QSAR, Pharmacophore and Docking)

Comp code	Structures	Activit y (nm)	pIC ₅₀
	Series A		
A-1	CH ₃ H ₂ C	8	8.10
A-2	CH ₃ H ₂ C	5.7	8.24
A-3	HO HO HO HO HO HO HO HO HO HO HO HO HO H	17.8	7.75
A-4	CH ₃ H ₂ C	2.9	8.54
A-5	HO CH ₃ CH ₃	10	8.00
A-6	H ₃ C CH ₃	7.8	8.11
A-7	HO HO HO HO HO HO HO HO HO HO HO HO HO H	12.7	7.90



B-1	С	N	С	N	Н	Br	228	6.64
B-2	Ν	Ν	С	N	Н	Br	116	6.94



3





	R_1 R_1 R_1 R_1 R_1 R_2 R_3 R_4 R_2 R_1 R_2 R_3 R_4 R_2 R_3 R_4 R_4 R_2 R_3 R_4	×	`R ₂		6.30
	R ₁	R ₂	X		7.89
E-4	3- N	Cl	-SO ₂ -	500	8.52
E-5	4- N 4-	Cl	-SO ₂ -	13	6.50
E-6	4- N 4-	Cl	-CO-	3	5.60
E-7	4- N 4-	Cl	-CH ₂ -	316	7.40
E-8	4- N 4-	OCH ₃	-CO-	2511	7.49
E-9	4-CH ₂ N(CH ₃) ₂	Cl	-CO-	40	7.70
E-10	4-CH ₂ N(CH ₃) ₂	Cl	-SO ₂ -	32	8.22
E-11	4-CH ₂ N(CH ₃) ₂	OCF ₃	-CO-	20	7.49
E-12	4-	Cl	-SO ₂ -	6	7.55
E-13	4- N- N- N- N- N- N- N- N- N- N- N- N- N-	Cl	-CO-	32	7.20
E-14	4- Nrm	Cl	-CO-		



Table S1b: Structure and activity of compounds considered for the studies (QSAR, Pharmacophore and Docking)

Comp code	Structures	Activity (nm)	pIC ₅₀
F-1		19	7.72
F-2	CH ₃ H ₂ C	500	6.30
F-3	CH ₃ H ₂ C	16	7.79









Table S1c: Structure and activity of compounds considered for the studies (Pharmacophore and Docking)





Com p Code	Activi ty	E_oo p	KierA2	DASA	SlogP_ VSA0	E_tor	vsurf_ Wp6	std_di m2	vsurf_ HL1	KierFl ex	SlogP_ VSA2	lip_ don	a_n Cl
A-1	8.10	0.02	8.22	13.47	3.12	10.80	1.25	1.25	0.02	5.13	0	1	0
A-2	8.24	0.03	11.32	50.59	14.12	-0.88	1.25	1.57	0.04	8.38	9.12	1	0
A-3	7.75	0.00	10.50	11.53	39.51	-0.51	1.25	1.44	0.05	7.89	0	2	0
A-4	8.54	0.01	10.89	37.55	14.12	-4.50	1.00	1.18	0.03	8.03	0	1	0
A-5	8.00	0.03	12.30	30.25	39.51	-4.90	1.62	1.75	0.04	9.38	3.98	2	1
A-6	8.11	0.03	12.30	46.84	14.12	-8.96	1.25	1.71	0.02	9.38	3.98	1	1
A-7	7.90	0.06	11.04	29.23	39.51	-5.17	0.50	1.85	0.05	8.32	0	2	0
A-8	8.30	0.07	11.42	27.78	14.12	-6.09	1.50	1.91	0.03	8.46	3.98	1	0
A-9	7.95	0.04	11.89	61.53	28.51	-12.42	1.50	2.19	0.06	9.98	10.62	2	0
A-10	7.54	0.04	10.04	44.04	36.38	-5.41	0.50	2.18	0.07	7.14	30.33	1	1
A-11		0.03	11.99	4.024	93.45	23.78	4.12	2.55	0.18	7.33	45.92	3	0
B-1	6.64	0.07	9.28	9.35	19.91	-0.52	1.37	1.94	0.03	6.48	30.50	1	0
B-2	6.93	0.02	9.24	29.01	3.12	-2.34	0.00	1.69	0.07	6.43	30.50	0	0
B-3	7.24	0.01	6.34	10.48	14.12	6.83	0.62	1.57	0.03	3.82	6.47	1	1
B-4	7.04	0.03	7.56	28.64	0.00	8.31	0.00	1.34	0.07	4.34	11.00	0	0
B-5		0.97	9.47	8.07	19.91	11.49	1.50	1.52	0.03	6.67	6.64	1	2
B-6		0.94	9.80	20.98	19.91	11.40	1.37	1.51	0.03	7.13	6.64	1	1
B-7		0.95	8.96	44.81	19.91	11.60	1.62	1.52	0.03	5.98	15.76	1	1
B-8		0.97	9.56	37.65	19.91	12.30	1.12	1.51	0.04	6.54	6.64	1	1
B-9		0.08	10.31	85.08	19.91	6.99	1.50	1.94	0.03	7.89	30.50	1	0
B-10		0.06	9.25	18.65	19.91	1.62	1.37	1.89	0.05	6.12	39.62	1	0
B-11		0.59	10.27	122.54	3.12	5.73	0.00	1.86	0.07	7.82	30.50	0	0
B-12		0.75	8.95	14.41	0.00	-6.91	0.00	2.06	0.06	6.05	6.64	0	1
B-13		0.77	9.28	36.99	0.00	-7.69	0.00	2.08	0.05	6.48	6.64	0	0

Table S2: Physicochemical descriptor values of the descriptors contributed in the QSAR models

B-14		0.74	8.45	28.25	0.00	-7.45	0.00	2.06	0.07	5.40	15.76	0	0
B-15		0.52	9.45	26.89	0.00	-1.71	0.00	2.13	0.06	6.73	30.50	0	0
C-1		0.05	9.10	113.10	28.51	-9.97	0.75	1.78	0.01	8.21	0	2	0
C-2	8.96	0.05	12.71	117.36	3.12	-9.41	0.00	1.82	0.01	9.93	11.00	1	0
C-3		0.05	12.12	111.56	3.12	-9.47	0.00	1.79	0.01	8.65	11.00	1	0
C-4	8.35	0.06	13.30	124.16	3.12	-4.71	0.00	1.90	0.01	9.45	11.00	1	0
C-5		0.05	14.69	86.32	3.12	-17.09	0.00	1.83	0.01	13.64	11.00	1	0
C-6	9.07	0.02	11.94	104.70	0.00	-11.55	0.00	2.07	0.02	8.89	34.86	0	0
D-1	4.89	0.12	8.30	150.15	32.13	14.06	4.75	2.24	0.01	5.20	0	3	0
D-2	5.85	0.01	6.92	128.91	21.13	2.09	3.87	2.29	0.06	3.95	0	3	0
D-3	4.97	0.01	7.54	81.69	32.13	1.40	2.25	1.94	0.04	4.37	23.86	2	0
D-4	5.51	0.02	7.13	32.94	21.13	1.79	13.37	1.32	0.05	4.60	0	3	1
D-5	5.86	0.05	6.65	19.26	21.13	8.26	3.12	1.36	0.09	4.18	0	2	0
D-6	5.32	0.11	7.16	91.33	18.01	5.88	12.00	1.52	0.05	3.99	0	2	0
D-7	5.30	0.20	9.07	9.57	3.12	-0.66	1.75	2.76	0.07	5.25	40.65	1	0
D-8		0.10	7.58	6.01	18.01	1.23	1.62	2.07	0.11	4.42	16.78	2	1
D-9		0.06	7.85	130.44	21.13	-3.02	5.25	1.85	0.01	5.46	0	3	0
E-1		0.01	8.29	22.16	19.53	-1.45	2.75	1.79	0.04	5.13	6.64	1	0
E-2	7.55	0.01	8.29	16.24	19.53	-1.69	2.37	1.92	0.04	5.13	6.64	1	0
E-3	7.20	0.03	9.88	52.27	19.53	-5.06	4.37	1.71	0.06	6.68	6.64	2	1
E-4	6.30	0.02	8.58	24.31	3.12	-0.33	1.87	1.67	0.04	5.63	6.64	1	1
E-5	7.89	0.01	8.58	26.52	3.12	-0.37	2.00	1.35	0.04	5.63	6.64	1	1
E-6	8.52	0.04	7.77	61.63	3.12	6.89	1.87	2.02	0.05	4.48	0	1	1
E-7	6.50	0.01	8.01	82.80	6.25	2.13	4.00	1.94	0.03	4.79	0	2	1
E-8	5.60	0.02	7.93	147.16	14.12	8.30	2.12	2.35	0.05	4.42	0	1	0
E-9	7.40	0.04	8.16	32.23	6.25	2.89	3.37	2.06	0.03	5.36	0	2	1

E-10	7.49	0.02	8.99	3.41	6.25	-4.49	3.37	1.24	0.02	6.74	6.64	2	1
E-11	7.70	0.07	8.80	3.46	17.25	5.48	3.12	2.50	0.05	5.72	0	2	0
E-12	8.22	0.05	9.47	4.88	9.37	-0.76	3.62	1.33	0.02	6.75	6.64	2	1
E-13	7.49	0.04	7.26	22.69	3.12	1.72	1.75	1.28	0.05	4.14	0	1	1
E-14		0.05	7.26	7.89	3.12	1.69	1.87	1.27	0.04	4.14	0	1	1
E-15		0.02	7.26	14.40	3.12	3.43	3.37	1.24	0.06	4.14	16.66	2	1
E-16		0.04	7.50	9.73	3.12	3.17	2.25	1.94	0.05	4.37	0	1	1
E-17		0.02	7.62	25.44	3.12	3.26	2.25	1.28	0.07	4.51	0	1	1
E-18		0.01	5.99	14.77	3.12	-2.44	2.00	1.31	0.09	3.51	23.86	1	0
F-1	7.72	0.02	8.20	23.40	14.12	8.24	1.75	1.43	0.03	5.47	3.98	1	0
F-2	6.30	0.01	8.62	3.35	14.12	-1.82	1.37	1.27	0.01	5.68	0	1	0
F-3	7.79	0.02	8.22	15.27	3.12	10.30	1.87	1.37	0.02	5.13	0	1	0
F-4	7.01	0.02	9.99	1.78	14.12	4.68	1.50	1.29	0.03	7.12	13.10	1	0
F-5	8.52	0.02	9.42	3.79	14.12	1.16	1.25	1.52	0.03	6.54	0	1	0
F-6	7.54	0.01	8.62	4.33	14.12	-1.73	1.25	1.33	0.01	5.68	0	1	0
F-7	6.36	0.03	7.65	28.15	14.12	18.66	1.37	1.49	0.03	5.03	13.10	1	0
F-8	6.65	0.07	8.44	37.11	14.12	25.89	1.75	2.11	0.03	5.50	3.98	1	0
F-9	8.19	0.03	11.32	49.71	14.12	-1.43	1.12	1.61	0.04	8.38	9.12	1	0
F-10	7.66	0.02	7.47	44.27	14.12	17.90	1.00	1.50	0.03	4.87	3.98	1	0
F-11	7.87	0.01	9.20	28.99	14.12	-0.09	1.50	1.47	0.01	6.45	0	1	0
F-12	6.42	0.01	10.26	44.11	14.12	-5.77	1.00	1.63	0.03	7.14	0	1	0
F-13	6.21	0.01	10.31	27.92	14.12	-4.90	1.12	1.38	0.01	7.21	0	1	0
F-14	8.27	0.02	11.27	26.05	14.12	-2.46	1.25	1.81	0.02	8.31	0	1	0
F-15	6.19	0.04	9.90	27.89	11.00	-7.71	0.00	2.14	0.04	6.65	3.98	0	1
F-16	5.73	0.01	9.15	57.57	14.12	-0.85	1.75	1.47	0.03	6.39	0	1	0
F-17	5.72	0.00	10.89	36.09	14.12	-4.27	1.00	1.56	0.03	8.03	0	1	0

F-18	8.39	0.03	10.97	31.08	14.12	0.39	1.25	1.51	0.02	7.74	11.22	1	0
F-19	7.41	0.01	10.05	1.84	14.12	-5.77	3.37	1.67	0.03	6.86	16.66	2	0
F-20	8.45	0.00	10.64	24.89	14.12	-1.89	1.37	1.96	0.03	7.29	0	1	0
F-21	7.54	0.01	8.75	7.19	14.12	-2.14	1.62	1.79	0.03	5.75	9.12	1	0
F-22	7.71	0.01	10.24	1.75	14.12	-5.76	1.00	1.93	0.02	7.09	0	1	0
F-23	8.54	0.01	10.89	29.28	14.12	-4.09	1.12	1.29	0.03	8.03	0	1	0
F-24	6.62	0.00	8.10	94.12	14.12	-8.86	1.00	1.55	0.03	5.51	0	1	0
F-25	7.95	0.06	10.10	7.96	14.12	-8.01	2.00	2.20	0.02	6.70	3.98	1	1
F-26	7.32	0.02	9.60	76.09	3.12	3.12	1.12	1.38	0.05	6.62	30.57	1	0
F-27	7.15	0.02	10.95	45.74	3.12	-4.39	1.00	1.57	0.04	7.85	26.59	1	0
F-28	7.44	0.03	7.42	0.42	0.00	7.31	0.00	2.04	0.05	4.33	11.00	0	1
G-1		0.00	5.21	36.45	3.12	6.06	0.50	1.37	0.00	3.99	2.77	1	0
G-2		0.00	5.21	54.78	3.12	4.67	0.50	1.37	0.00	3.99	2.77	1	0
G-3		0.00	5.21	57.06	3.12	4.78	0.50	1.33	0.00	3.99	2.77	1	0
G-4		0.02	6.34	21.52	14.12	8.57	0.62	1.36	0.03	3.82	6.47	1	1
G-5		0.02	6.73	41.32	28.51	9.02	1.12	1.45	0.05	4.15	0	2	0
G-6		0.06	6.75	16.13	39.51	10.19	1.50	1.50	0.02	4.25	0	2	0
G-7		0.01	7.22	50.18	28.51	6.69	1.37	1.51	0.02	4.85	0	2	0
G-8		0.00	7.46	20.56	28.51	8.65	1.62	1.43	0.08	5.08	19.55	2	0
G-9		0.04	7.36	89.95	28.51	-7.36	1.37	1.53	0.04	5.08	6.88	2	0
G-10		0.04	6.95	53.33	3.12	7.12	0.50	1.53	0.04	4.22	0	1	0
G-11		0.02	7.56	36.58	0.00	7.78	0.00	1.24	0.06	4.34	11.00	0	0

Table S3: Observed and Predicted activities of the training, test set (test set-1) and inactive compounds

Com	Obs							Predic	ted Ac	tivities						
p. code	erv ed		I	Model	1			I	Model	2			I	Model	3	
	Acti	Pre	LO	LM	BS	Tes	Pre	LO	LM	BS	Tes	Pre	LO	LM	BS	Tes
	vity	d.	0	0		t	d.	0	0		t	d.	0	0		t
A-1*	8.10					7.59					7.08					6.96
A-2	8.24	8.39	8.08	8.01	8.56		7.78	8.74	8.52	8.55		8.31	8.17	8.59	8.15	
A-3	7.75	8.04	7.35	7.54	7.00		7.70	7.81	7.42	7.95		7.41	8.13	7.29	7.69	
A-4	8.54	8.59	8.48	8.04	8.06		8.78	8.25	8.05	8.11		8.46	8.62	8.01	8.05	
A-5*	8.00					8.38					7.90					9.02
A-6*	8.11					8.88					8.74					8.80
A-7	7.90	7.47	8.46	7.45	8.35		7.90	7.89	8.29	7.25		7.63	8.20	7.26	7.54	
A-8	8.30	8.18	8.44	8.66	8.76		8.05	8.58	8.69	8.82		8.54	8.03	8.95	8.95	
A-9	7.95	8.06	7.83	7.07	7.42		8.00	7.89	7.29	8.54		8.10	7.76	8.45	8.39	
A-10	7.54	7.18	7.98	7.85	7.95		7.22	7.95	7.11	7.12		7.86	7.10	7.85	7.39	
A- 11**						7.18					1.73					5.42
B-1	6.64	7.11	6.13	6.92	6.87		7 26	5.89	6.95	6.88		6 5 2	6.78	6.93	6.94	
B-2*	6.94	/.11				7.90	7.50				7.52	0.55				7.48
B-3	7.24	6 51	8.10	7.92	7.36		7 1 5	7.34	7.85	7.54		7.02	7.50	7.63	7.59	
B-4	7.05	7.13	6.95	7.59	7.85		6.89	7.27	7.69	7.71		7.12	6.94	7.01	7.02	
B-5**						-					6.57					9.48
						3.68										
B-6**						- 3.36					6.64					8.74
B-7**						-					6.47					7.80
						3.99										
B-8**						- 3.95					6.39					8.43
B-9**						6 87					6.55					7.26
						0.07					0.00					1.20

B-						7.10					6.96					6.00
10**																
B-						0.67					6.51					8.21
11**																
B-						-					7.80					9.15
12**						0.89										
B-						-					7.91					8.39
13**						1.12										
B-						-					7.74					7.49
14**						1.11										
В-						2.02					7.17					7.64
15**																
C-1**						6.25					8.89					7.58
C-2	8.96	8.54	9.51	8.25	8.26		8 99	8.91	8.39	8.63		9.05	8.85	8.34	8.16	
C_3**						8 3 7	0.77				9.06					8 38
C-5						0.52					9.00					0.50
C-4	8.35	8.66	7.91	8.02	8.66		8.43	8.25	8.01	8.75		8.79	7.83	8.79	8.69	
C-5	9.07	8.72	9.52	9.92	8.51		8.81	9.39	9.85	9.84		8.60	9.73	9.68	9.85	
C-6**						9.77					9.82					10.9
																7
D-1	4.9	4.62	5.41	4.18	5.72		5.17	4.38	4.32	5.49		5.03	4.70	4.59	4.35	
D-2*	5 85					5 68	••••				5 86					5 38
D-3*	4.97					6.14					5.85					4.70
D-4	5.51	6.45	4.44	5.22	5.86		5.56	5.40	5.92	5.12		5.71	5.24	5.99	5.98	
D-5	5.86	5.98	5.72	5.15	5.29		6.04	5.59	5.69	5.44		5.48	6.32	5.36	5.26	
D-6	5.32	4.92	5.85	5.03	5.56		5.09	5.69	4.92	5.78		5.38	5.25	5.01	5.95	
D-7	5.30	5.82	3.74	5.05	5.85		5 87	4.42	5.69	5.98		5 51	4.90	5.99	5.96	
D-8**		0.02				5 97	2.07				6.03	0.01				5 97
<u> </u>						5.71					0.05					5.71
D-9**						5.50					7.33					5.17
E-1**						7.27					7.25					6.71

E-2	7.55	7.34	7.78	7.88	7.85		7.19	7.93	7.96	7.81		6.71	8.50	7.95	7.82	
E-3	7.20	7.58	6.79	6.79	7.84		7.31	7.08	6.85	7.59		7.52	6.83	7.62	7.65	
E-4*	6.30					6.70					6.79					6.96
E-5	7.89	7.72	8.07	7.49	8.29		7.82	7.96	7.12	7.15		7.96	7.80	7.99	7.51	
E-6*	8.52					8.73					8.23					7.60
E-7	6.50	7.01	5.91	6.12	6.91		6.69	6.30	6.95	6.95		6.79	6.17	7.12	6.12	
E-8	5.60	6.09	4.87	5.15	5.95		5.57	5.63	6.12	6.05		6.59	4.39	5.01	5.09	
E-9	7.40	7.08	7.74	7.02	7.89		6.56	8.32	7.92	7.94		7.08	7.75	7.85	7.91	
E-10	7.49	7.96	6.97	7.03	7.02		8.37	6.47	7.98	7.79		7.55	7.43	7.99	7.86	
E-11*	7.70					7.02					7.04					7.28
E-12	8.22	7.79	8.70	7.79	7.94		7.86	8.63	7.85	8.67		7.56	8.98	8.95	8.66	
E-13	7.49	6.82	8.27	7.85	7.95		7.61	7.36	7.97	7.87		7.43	7.58	7.01	7.95	
E- 14**						6.84					7.64					7.43
17																
E- 15**						7.11					7.02					5.83
F_						7.02					6.61					7 55
16**						1.02					0.01					1.55
E- 17**						7.22					7.07					7.62
E- 18**						6.62					7.37					5.23

Pred. = Normal predicted activity

LOO = Leave-one-out

LMO = Leave-many-out

BS = Bootstapping

* Predicted activity of test set compounds (test set-1)

** Predicted activity of experimentally in active or low active compounds

Comp Code	np Code Observed Predicted Activity Activity Model 1 Model 2 Model						
	Activity	Model 1	Model 2	Model 3			
F-1	7.72	7.22	6.99	6.99			
F-2	6.30	6.71	7.09	7.04			
F-3	7.79	7.52	7.87	7.96			
F-4	7.01	7.21	7.57	7.51			
F-5	8.52	7.98	7.72	7.69			
F-6	7.54	7.71	8.05	7.24			
F-7	6.36	6.8	5.89	6.42			
F-8	6.65	6.62	6.38	7.01			
F-9	8.19	8.41	7.82	8.31			
F-10	7.66	7.01	7.04	7.08			
F-11	7.87	7.81	7.16	7.65			
F-12	6.42	7.24	7.14	7.01			
F-13	6.21	6.37	6.86	6.04			
F-14	8.27	8.69	7.86	8.61			
F-15	6.19	6.78	7.04	7.06			
F-16	5.73	6.55	6.09	6.61			
F-17	5.72	6.6	6.33	6.46			
F-18	8.39	8.4	7.89	7.9			
F-19	7.41	8.06	7.88	6.96			
F-20	8.46	8.59	8.57	8.08			
F-21	7.54	7.78	7.71	6.95			
F-22	7.71	8.56	8.13	7.97			
F-23	8.54	8.65	8.6	8.46			

Table S4: Observed and predicted activity of test set (test set-2) compounds

F-24	6.62	6.82	6.82	7.16
F-25	7.95	7.84	7.95	8.61
F-26	7.32	7.66	7.47	6.59
F-27	7.15	7.67	7.61	7.39
F-28	7.44	7.19	6.86	7.1

Table S5: VIF and Durbin-Watson values of the selected models

Models	Descriptors	Tolerance	R-square	VIF	Durbin- Watson
	E_oop	0.986	0.014	1.014	2.357
Model 1	KierA2	0.923	0.077	1.084	
	DASA	0.910	0.089	1.098	
	SlogP_VSA0	0.993	0.007	1.007	
	E_tor	0.849	0.151	1.178	
Model 2	vsurf_Wp6	0.841	0.159	1.189	2.741
	std_dim2	0.940	0.060	1.064	
	vsurf_HL1	0.928	0.071	1.077	
	KierFlex	0.842	0.158	1.188	
Model 3	SlogP_VSA2	0.702	0.298	1.425	2.239
	lip_don	0.693	0.307	1.443	
	a_nCl	0.832	0.168	1.201	

Table S6: Results of virtual screening studies (pharmacophore and docking analysis)

Comp Code	Comp Code	Pharmacophores			Pharmacophore based docking				Normal docking			
		1	2	3	Without water		With water		Without water		With water	
		RMSD	RMSD	RMSD	Score	RMSD	Score	RMSD	Score	RMSD	Score	RMSD

A-1	16-1	0.959		1.222	-	1.819					-	1.679
					10.773						10.251	
A-2	16-2						-	1.669	-	1.329	-8.784	1.804
							13.108		11.709			
A-5	16-5			1.274			-	2.138	-8.170	2.077	-7.641	1.405
							10.952					
A-6	16-6			1.244			-	2.696	-8.220	2.038	-8.423	1.441
							10.776					
A-7	16-7			1.022			-	1.651	-	1.523	-	1.428
							10.997		11.721		12.123	
A-8	16-8			0.899			-	1.727	-	1.704	-9.544	1.765
							11.430		11.205			
A-9	16-9				-9.319	2.016	-8.860	1.769	-6.563	1.487	-7.966	1.149
A-9	16-9						-	1.973	-9.242	1.717	-	1.651
							10.122				11.326	
B-1	3-1				-9.168	1.281					-8.729	1.396
B-2	3-2		1.445						-8.312	1.492	-7.002	1.128
B-3	3-3		0.607						-8.814	0.947	-9.046	1.030
B-4	3-4										-	1.799
											10.180	
B-5	3-5	1.164							-	1.469	-9.533	1.243
									10.961			
B-6	3-6								-	1.397	-9.663	1.264
									10.572			
B-7	3-7								-9.491	0.848	-9.913	1.268
B-8	3-8	1.157					-7.921	1.590	-9.272	1.253	-	1.444
											12.229	
B-9	3-9				-	1.885					-8.302	1.423
					10.177							
B-10	3-10				_	1.860					-	1.681
					10.045						10.204	
B-11	3-11								-8.191	1.440	-8.066	1.237

B-14	3-14										-8.991	1.317
B-15	3-15		1.040									
C-1	5-6								-8.527	1.681	-8.111	1.403
C-2	5-7										-8.802	1.002
C-3	5-8										-9.864	1.324
C-4	5-9										- 10.728	1.532
C-5	5-10										-8.924	1.108
D-1	7-3				- 10.889	1.656	- 12.060	1.584	- 10.227	1.001	-9.712	0.995
D-1	7-3				- 11.228	1.732	- 12.307	1.800	-9.176	1.001	-8.521	0.920
D-2	7-4				-9.113	0.962			- 10.615	1.222	-8.538	1.180
D-3	7-5		0.474	1.584	-8.742	1.071	-7.792	0.943	-8.458	0.923	-8.258	0.991
D-3	7-5				-9.454	1.375	-8.466	1.239	-9.280	1.280	-9.009	1.253
D-4	7-6	1.312	0.797		-8.568	1.232			- 10.539	1.237	-8.724	1.094
D-5	7-7		0.972		-8.690	1.376	-9.903	1.698	-9.091	1.083	-8.882	0.797
D-6	7-8		1.214						- 10.144	1.235	-8.725	1.113
D-7	7-9				- 12.038	2.020	-8.579	1.697	-9.648	1.846	-8.706	1.406
D-9	7-11						- 11.113	1.523	- 10.856	1.627	- 10.018	1.835
D-9	7-11								-8.537	0.885	-8.575	0.969
E-1	9-10		1.106						- 11.298	1.475	-9.488	1.147
E-2	9-11		1.074				7.135	1.666	-9.990	1.226	-8.499	1.292
E-3	9-12			1.326			-9.341	1.600	-8.413	1.899	-9.045	1.713

E-4	9-13										-8.911	1.342
E-5	9-14										-9.503	1.607
E-6	9-15		0.807						-9.701	1.140	-9.035	0.751
E-7	9-16								- 10.347	1.574	-9.242	1.452
E-8	9-17		0.928						- 11.316	1.535	-9.438	1.080
E-9	9-18		0.670	0.771	- 10.092	1.078	- 12.230	1.002	- 12.210	0.928	-9.971	1.160
E-10	9-19	1.076			-7.942	2.627	- 11.690	2.435	- 10.968	1.767	-9.100	1.415
E-11	9-20		0.819		- 11.134	1.866	- 12.553	1.607	- 10.030	1.324	-10.86	1.725
E-12	9-21	0.900									-9.049	1.445
E-13	9-22								-9.637	1.842	-8.594	1.376
E-14	9-23								- 10.571	1.631	-8.038	1.416
E-15	9-24	0.502					-8.339	1.988	-7.698	1.374	-9.087	1.799
E-16	9-25								- 10.018	1.157	-9.181	0.978
E-17	9-26								-8.378	1.531	-8.609	1.455
E-18	9-27								-7.405	1.571	-8.092	1.283
F-1	15-1	0.951							-7.230	1.467	-8.461	1.488
F-2	15-2						- 12.599	2.024	- 10.525	2.207	-8.480	2.209
F-3	15-3	0.987			- 10.728	1.725	- 11.543	1.201	-9.605	1.579	- 10.738	1.664
F-4	15-4	1.089										
F-5	15-5	1.315		0.674	- 10.184	1.721	- 12.380	1.628	- 12.590	1.711	- 10.336	1.603
F-7	15-7	0.810	1.354								-9.393	1.469

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F-8	15-8		0.609	0.888					-	1.667	-9.575	0.984
									10.591			
F-9	15-9								-	1.747	-	2.036
									12.715		10.411	
F-10	15-10	0.825	1.311						-9.038	1.253	-9.203	1.245
F-11	15-11				-9.845	2.031	- 11 403	1.430	-	1.426	-8.293	1.331
							11.105		12.112			
F-12	15-12								-	1.843		
									12.089			
F-14	15-14								-	1.629	-9.335	1.896
									11.943			
F-15	15-15								-8.057	1.127	-7.534	1.007
F-16	15-16	1.201		1.563			-	1.733	-	1.221	-9.178	1.532
							10.403		12.033			
F-17	15-17								-	1.776	-8.202	1.827
									10.523			
F-19	15-19								-	1.902	-8.890	1.991
									13.034			
F-20	15-20								-	1.596	-8.152	2.052
									12.436			
F-21	15-21								-	1.361	-8.306	1.392
									12.690			
F-24	15-24										-	1.751
											10.109	
F-25	15-25		0.984	0.782	-	1.040	-	1.040	-	1.146	-	1.095
					10.225		10.225		10.312		10.792	
F-25	15-25						-	1.463	-	1.445	-	1.139
							10.317		10.477		11.458	
F-27	15-27										-	1.808
											10.273	
F-28	15-28		0.699						-	1.052	-9.167	0.921
									10.011			
G-1	17-10 ^a										-7.787	1.017

G-2	17-										-7.677	0.775
	10B											
G-3	17-										-7.344	0.545
	10C											
G-4	17-13 ^a		0.642						-8.265	0.964	-9.338	0.968
G-5	17-14 ^ª	1.082	0.705		-	1.361			-8.147	1.218	-	0.963
					10.312						10.342	
G-6	17-		1.281		-9.636	1.191			-8.757	0.955	-	1.036
	14 B										10.133	
G-7	17-		1.247		-8.396	0.921	-7.012	1.383	-8.690	1.348	-	1.041
	14C										10.371	
G-8	17-		0.976		-9.981	1.542			-9.673	1.182	-8.978	1.044
	14D											
G-9	17-		0.945	1.380	-7.228	0.881			-9.542	1.112	-	0.817
	14E										10.576	
G-10	17-16		0.758	0.990	-	0.965			-9.822	0.731	-	0.611
					10.109						10.817	
G-11	17-7B										-9.851	1.420

Table S7: Results derived from the virtual screening (docking studies)

S. No	Docking with v	water		Docking without water					
	Comp code	Score	RMSD	Comp Code	S	RMSD			
1	F-22	-12.419	3.720	F-4	-13.630	2.607			
2	B-8	-12.229	1.444	F-20	-13.468	1.447			
3	A-7	-12.137	2.089	F-22	-13.386	1.962			
4	A-8	-12.027	2.250	F-12	-13.191	2.142			
5	A-10	-12.009	2.164	F-21	-13.055	2.042			
6	F-25	-11.975	1.738	F-19	-13.034	1.902			
7	D-9	-11.968	2.901	F-14	-13.023	1.808			
8	A-2	-11.853	3.556	F-1	-12.998	2.433			
9	F-4	-11.824	3.591	F-26	-12.826	2.933			
10	B-10	-11.620	2.747	A-2	-12.696	2.335			

Compound	Ph	Pharmacophore based docking Normal docking				Normal docking				
code	With	water	Witho	ut water	With	water	Witho	ut water		
	Major	Minor	Major	Minor	Major	Minor	Major	Minor		
D-3	Trp581,	Phe696,	Trp581,	Phe696,	Trp387	Phe696,	Trp581,	Phe696,		
	Asp455,	Phe444,	Asp455,	Glu532,		Trp581,	Phe444	Glu532,		
	Phe444	His232	Phe444	His232		Asp455,		Asp455,		
						Phe444,		His232		
-						His232				
E-9	Asp455	Phe696,	Trp581,	Phe696,	Asp455,	Phe696,	Trp581,	Phe696,		
		Trp581,	Asp455,	Tyr503,	H1s232	Trp581,	Asp455,	Tyr503,		
		H1s232	Phe444,	H1s232		Phe444	Phe444,	H1s232		
F 5	Dha606	Trm 5.91	11p387	True 5.91	Dha606	Trm 5.91	11p387	Trm 501		
r-5	Pne090,	1 fp 581, Trm 287	Pne090,	11p581, Terr502	Pheo90, $U_{0}229$	$\frac{110001}{2}$	Pne090,	11p581,		
	Asp455	$11p_{387}, \\ u_{i_8}, 222$	Asp 433 , Dba 144	$1 y_{13} 0_{3}, U_{16} 2_{3} 2_{3}$	110558	Piie444, His222	Asp 433 , Dba 144	П18232		
F_25	Asp455	Phe696	A sp455	Phe696	Trn581	Phe696	A sp455	Phe696		
1-23	Phe 444	Trn581	Phe 444	Glu532	110501	$A \sin 456$	Phe 444	Trn581		
	The FFI,	Glu532	Glv380	Trn581		Phe444	1 no 1 1 1	Glu532		
		His232	GIJS00	His232		Ile338.		His232		
						His232				
G-7	Asp455	Phe696,	Trp581,	Phe696,	His232	Phe696,	His232	Phe696,		
	1	Trp581,	Asp455,	Val453,		Trp581,		Trp581,		
		Phe444,	His232	Phe444		Tyr503,		Asp455,		
		His232				Asp455,		Phe444		
						Phe444				
Nat-1	Ser339	Asn697,	His232	Phe696,	Trp581	Phe696,	Asn697,	Phe696,		
	(water	Phe696,		Trp581,		Phe444,	His232,	Trp581,		
	bridge)	1rp581,		Phe444,		11e338,	Tyr98	Asp455,		
		Phe444,		Asp455		H18232		Phe444		
		HIS232, App 455								
Nat_2	Asn697	Cvs456			Phe696	Trn581	Trn581	Asn697		
1\at-2	Phe696	Phe444			H_2O	Asn455	110501	Phe696		
	Trp581	Tvr98			1120	Cvs456		Asp455		
	Asp455,	-) - > 0				His232		His232,		
	Trp387							Tyr98		
Nat-3	Cys456,	Asn697,	Phe444	Asn697,			Asp455	Asn697,		
	Phe444,	Phe696,		Phe696,			_	Phe696,		
	H_2O	Trp581,		Cys456,				Trp581,		
		Asp455,		Asp455,				Phe444,		
		Trp387,		His232,				His232		
		His232,		Tyr98						
Not 4	T	Tyr98	D1 = 4.4.4	$Dh_{a}(0)$	Court 6	$Dh_{a}(Q)$	Com A5 (A an (07		
INAT-4	1rp581,	Phe 0.96 ,	Pne444,	Pne696, Trn591	Uys456,	Trn591	Cys456,	Asno9/,		
	Asp455	$\frac{110444}{\text{Trn}^{2}87}$	Asp433	$\frac{110001}{2000}$	FIIS232	$\Lambda_{\rm sp}$		Trp 581		
		Hie222		Hie222		Phe///		$\Delta \sin/55$		
		1115232		11152.52		His232		His232		
						1110202		Tvr98		
Nat-5	Val695,	Phe696,	Cys456,	Phe696,	Cys456,	Phe696,	Cys456,	Asn697,		

Table S8: Summary of the amino acid residues responsible for the interactions with the OSC inhibitors

Trp581	Trp581,	Phe444	Trp581,	His232	Trp581,	Phe696,
	Cys456,		Asp455,		Asp455,	Trp581,
	Phe444,		Phe444,		Phe444,	Asp455,
	Trp387,		His232		His232,	His232,
	His232				Tyr98	Tyr98

Figure S1: Graphical representation of docked compounds in the absence of water molecule by pharmacophore based and normal docking methods.

Pharmacophore based docking

Normal docking



Figure S2: Graphical representation of docked compounds in the presence of water molecule by pharmacophore based and normal docking methods.

Pharmacophore

Normal



Figure S3: Binding mode of the reference compound and its structural analogue (compound F-5)



Superimposed structure (F-5) on reference Binding mode of reference compound (with water) compound (with water)

Superimposed structure (F-5) on reference Binding mode of reference compound (without water) water)

Figure S4: Superimposed structures of the natural product compounds (Nat-1 to Nat-5) on reference compound in the X-ray structure





Docking with water

Docking without water



Pharmacophore with water



Pharmacophore without water