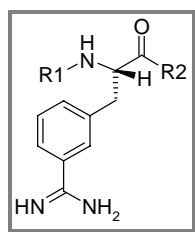


Supporting Information

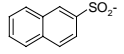

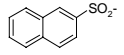
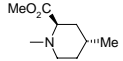
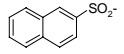

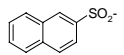

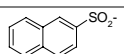

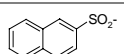
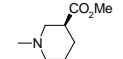
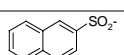
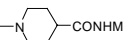
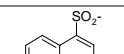

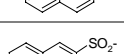
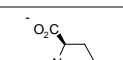
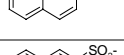
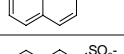
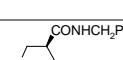
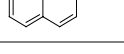

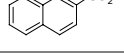

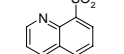

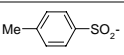

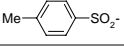
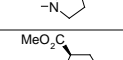
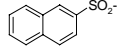

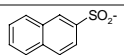
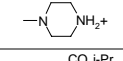
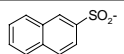
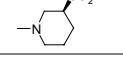
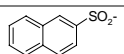
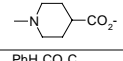
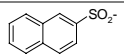
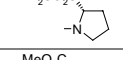
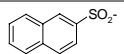
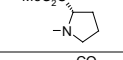
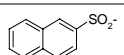

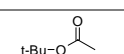
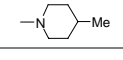
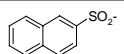
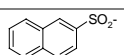
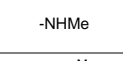
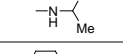

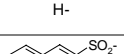
“COMBINE analysis considering multiple receptors: a step towards 3D-QSAR models for multiple targets” by Marta Murcia, Antonio Morreale and Angel R. Ortiz.

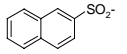
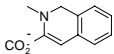
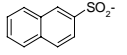
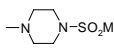
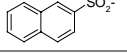
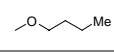
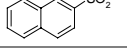
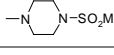
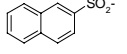
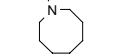
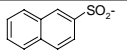
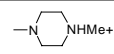
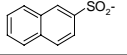
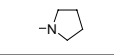
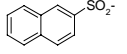
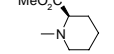
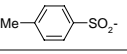
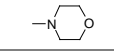
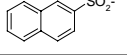
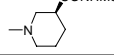
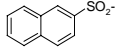
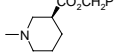
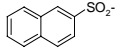
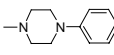
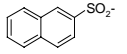
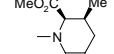
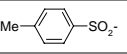

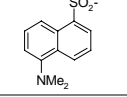
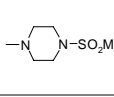
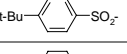
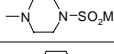
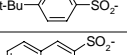
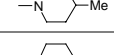
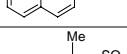
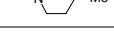
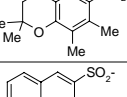
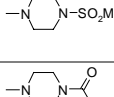
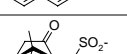
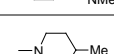
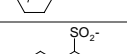
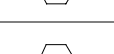
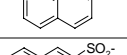
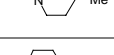
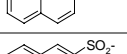
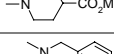
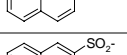
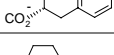
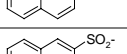
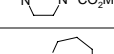
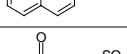
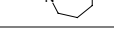
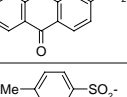
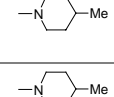


Contents: Compound description, receptor, experimental and predicted (*LOO*) activities multi-receptor and the corresponding one-receptor based COMBINE regression models shown (**Table 1**). Different conditions and results for the derivation of COMBINE models studied in this paper, Trp+Thr+Fxa, Thr+Fxa, Thr+Trp, Fxa+Trp, and the individual receptor-based ones (1 to 10 latent variables regression models) (**Table2**).

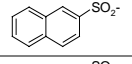
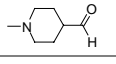
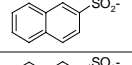
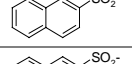
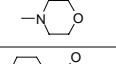
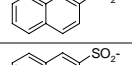
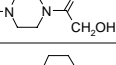
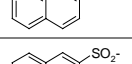
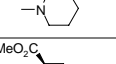
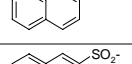
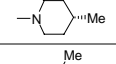
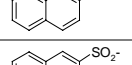
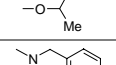
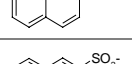
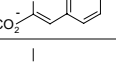
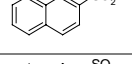
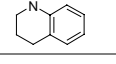
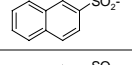
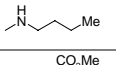
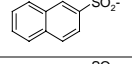
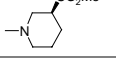
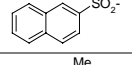
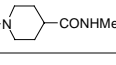
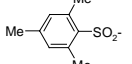
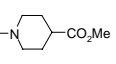
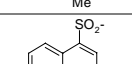
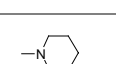
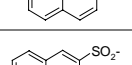
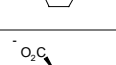
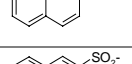
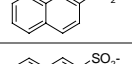
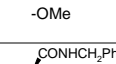
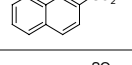
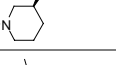
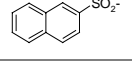
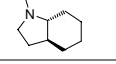
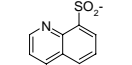
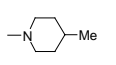
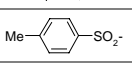
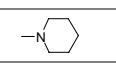
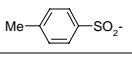
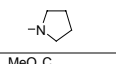
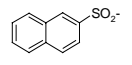
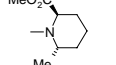
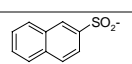
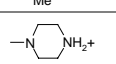
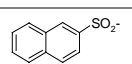
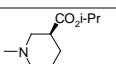
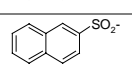
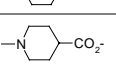
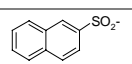
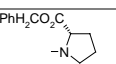
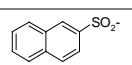
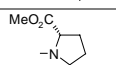
Table 1. Compound description, binding receptor, name of the PDB file with the modeled structure of the complex, and experimental and predicted (*LOO*) activities for the 4 multi-receptor and the corresponding one-receptor based COMBINE regression models (files available upon request. Contact the corresponding author: aro@cbm.uam.es).



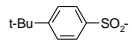
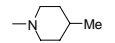
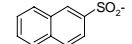
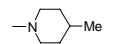
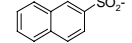
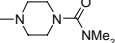
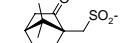
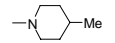
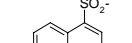
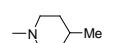
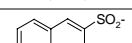
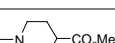
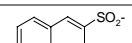
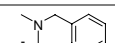
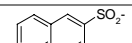
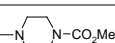
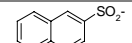
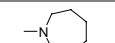
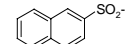
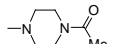
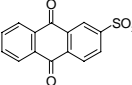
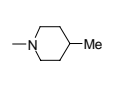
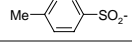
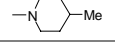
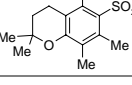
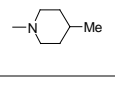
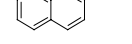
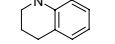
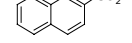
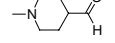
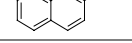
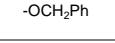
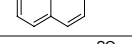
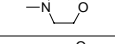
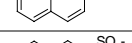
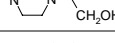
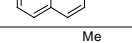
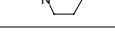
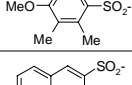
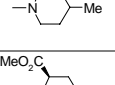
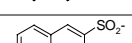
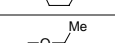
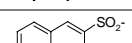
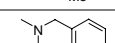
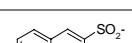
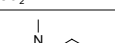
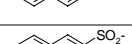
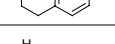

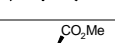
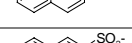
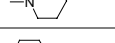
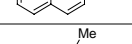
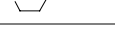
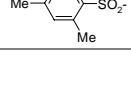
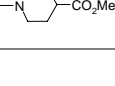
Compound description				Receptor PDB ID	exp p <i>K_i</i>	Predicted (cross validated) p <i>K_i</i>				
Num	R1	R2	Charge			Trp+Thr+Fxa	Thr+Fxa	Thr+Trp	Fxa+Trp	One R
1			+1	Thrombin 1ets	8.38	7.05	7.20	7.12	-	7.21
2			+1	Thrombin 1ets	8.37	8.03	8.06	8.70	-	8.96
3			+1	Thrombin 1ets	8.30	7.24	7.15	7.44	-	7.19
4			+1	Thrombin 1ets	8.21	7.02	7.04	6.96	-	6.66
7			+1	Thrombin 1ets	7.85	7.41	7.29	7.47	-	7.71
9			+1	Thrombin 1ets	7.77	7.83	7.70	7.91	-	7.79
11			+1	Thrombin 1ets	7.72	6.69	6.95	6.57	-	6.24
12			+1	Thrombin 1ets	7.68	7.39	7.33	7.09	-	7.31
14			+1	Thrombin 1ets	7.59	8.40	8.47	8.07	-	8.80
15			+1	Thrombin 1ets	7.59	7.05	6.94	7.22	-	7.31
16			+1	Thrombin 1ets	7.50	6.67	6.54	6.59	-	7.28
18			+1	Thrombin 1ets	7.43	6.39	6.45	6.62	-	7.63
19			+1	Thrombin 1ets	7.43	7.59	7.52	7.63	-	7.76
20			+1	Thrombin 1ets	7.38	7.49	7.56	7.17	-	6.75
21			+1	Thrombin 1ets	7.38	6.93	6.85	6.82	-	6.78
22			+1	Thrombin 1ets	7.24	7.75	7.96	8.26	-	8.80

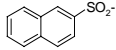
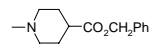
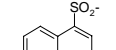

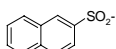

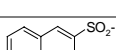
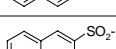
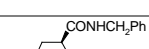
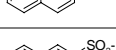

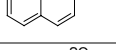

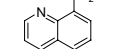

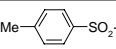

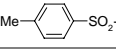

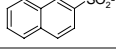
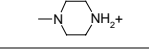
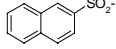

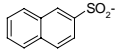
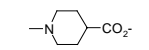
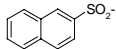

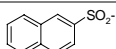

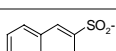

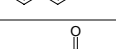

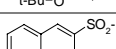

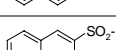


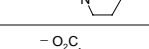
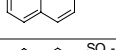
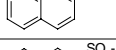


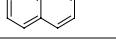

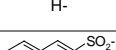

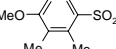
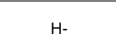

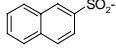
24			+1	Thrombin lets	7.19	7.14	7.09	6.91	-	7.15
27			+1	Thrombin lets	7.02	7.38	7.55	7.60	-	7.79
28			+1	Thrombin lets	6.96	5.16	5.08	4.97	-	5.01
30			+1	Thrombin lets	6.92	6.60	6.45	6.50	-	6.45
31			+1	Thrombin lets	6.92	6.73	6.57	7.11	-	7.74
32			+1	Thrombin lets	6.82	6.80	6.70	6.85	-	6.88
34			+1	Thrombin lets	6.80	7.55	7.45	7.15	-	7.02
38			+1	Thrombin lets	6.64	6.87	6.80	6.50	-	6.44
40			0	Thrombin lets	6.59	6.64	6.60	6.89	-	6.40
41		-OMe	+1	Thrombin lets	6.55	5.82	5.73	6.19	-	6.48
42			+1	Thrombin lets	6.55	6.31	6.31	6.53	-	6.33
43			+1	Thrombin lets	6.50	6.62	6.78	6.40	-	6.40
44			+1	Thrombin lets	6.47	7.27	7.26	7.29	-	7.63
45			+1	Thrombin lets	6.47	6.57	6.57	6.28	-	6.48
46			+1	Thrombin lets	6.46	6.21	6.36	5.90	-	5.82
47			+1	Thrombin lets	6.38	7.49	7.43	7.08	-	6.93
48			+2	Thrombin lets	6.30	7.14	6.98	7.00	-	7.17
49			+1	Thrombin lets	6.29	6.45	6.44	6.67	-	6.44
50			0	Thrombin lets	6.24	7.40	7.39	7.27	-	6.00
51			+1	Thrombin lets	6.20	6.98	7.05	6.63	-	6.55
52			+1	Thrombin lets	6.18	5.87	5.95	6.31	-	6.19
55			0	Thrombin lets	5.96	6.33	6.17	6.58	-	6.68
56			+1	Thrombin lets	5.92	6.23	6.18	5.91	-	6.21
60			0	Thrombin lets	5.54	6.76	6.81	6.77	-	6.46
63		-NHMe	+1	Thrombin lets	5.24	5.69	5.58	5.73	-	5.42
64			+1	Thrombin lets	5.21	5.63	5.43	5.40	-	5.47
66	H-		+2	Thrombin lets	4.89	6.48	6.64	6.49	-	5.92
69	H-		+2	Thrombin lets	4.57	4.82	5.01	4.28	-	4.82
70		-CO ₂ ⁻	0	Thrombin lets	4.52	5.44	5.64	5.43	-	5.52

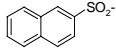
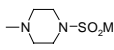
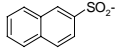
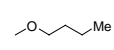
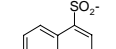
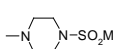
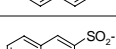
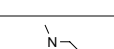
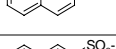
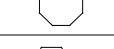
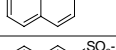
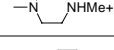
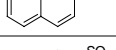
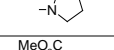
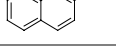
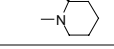
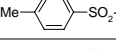
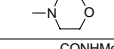
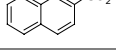
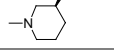
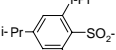
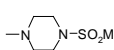
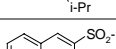
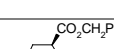
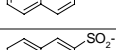
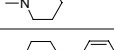
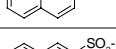
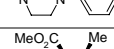
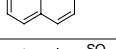
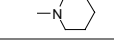
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73			+1	Thrombin lets	8.48	7.69	7.59	7.89	-	7.43
74			+1	Thrombin lets	7.89	6.39	6.37	6.59	-	6.73
75			+1	Thrombin lets	7.59	8.20	8.10	8.19	-	7.53
76			+1	Thrombin lets	7.52	6.51	6.53	7.08	-	7.41
77			+2	Thrombin lets	7.44	7.52	7.32	7.70	-	7.74
78			+1	Thrombin lets	7.28	6.78	6.92	6.89	-	7.23
79			+1	Thrombin lets	7.16	7.36	7.37	7.05	-	7.22
80			+1	Thrombin lets	6.77	6.57	6.35	6.53	-	6.30
81			+1	Thrombin lets	6.59	6.36	6.37	6.64	-	6.84
83			+1	Thrombin lets	6.52	6.51	6.49	6.66	-	6.77
84			+1	Thrombin lets	6.28	7.31	7.17	7.09	-	7.33
85			+1	Thrombin lets	6.28	6.21	6.23	6.58	-	5.65
88			+1	Thrombin lets	4.75	5.39	5.22	5.25	-	5.09
1			+1	FXa 1hcg	5.41	4.88	4.49	-	4.85	4.69
2			+1	FXa 1hcg	5.17	4.85	4.92	-	4.75	4.89
3			+1	FXa 1hcg	4.92	4.59	4.52	-	5.01	4.65
4			+1	FXa 1hcg	4.39	4.54	4.41	-	4.82	4.65
5			+1	FXa 1hcg	4.13	5.31	5.00	-	5.03	4.74
6			+1	FXa 1hcg	4.62	5.06	4.92	-	4.67	4.66
7			+1	FXa 1hcg	4.85	4.04	4.32	-	4.18	4.28
8			+1	FXa 1hcg	4.38	4.11	4.11	-	4.27	4.21
9			+1	FXa 1hcg	4.37	4.86	4.72	-	4.59	4.59
10			0	FXa 1hcg	4.38	4.11	4.02	-	4.36	4.51
11			+1	FXa 1hcg	4.11	4.87	4.70	-	4.72	4.66
12			+1	FXa 1hcg	4.59	4.57	4.40	-	4.72	4.50
14			+1	FXa 1hcg	5.64	5.01	5.04	-	4.99	4.76
15			+1	FXa 1hcg	4.15	4.40	4.27	-	4.55	4.49

19			+1	FXa 1hcg	4.72	4.60	4.46	-	4.63	4.63
20		-OCH ₂ Ph	+1	FXa 1hcg	5.66	4.37	4.56	-	4.51	4.57
21			+1	FXa 1hcg	4.80	4.51	4.52	-	4.39	4.50
22			+1	FXa 1hcg	4.46	5.05	4.76	-	4.69	4.67
24			+1	FXa 1hcg	4.42	4.49	4.54	-	4.40	4.54
27			+1	FXa 1hcg	4.24	5.19	5.18	-	4.88	4.63
28			+1	FXa 1hcg	5.46	4.25	4.24	-	4.19	4.20
29			0	FXa 1hcg	4.27	4.70	4.77	-	4.78	4.72
30			+1	FXa 1hcg	5.64	4.64	4.58	-	4.94	4.64
31			+1	FXa 1hcg	4.33	4.73	4.82	-	5.00	4.64
32			+1	FXa 1hcg	4.75	4.63	4.79	-	4.66	4.69
34			+1	FXa 1hcg	4.12	4.86	4.71	-	4.38	4.65
35			+1	FXa 1hcg	4.08	3.88	3.98	-	3.83	4.32
38			+1	FXa 1hcg	4.77	4.38	4.62	-	4.23	4.38
40			0	FXa 1hcg	4.42	4.30	4.19	-	4.26	4.54
41		-OMe	+1	FXa 1hcg	5.60	4.80	4.70	-	4.71	4.32
42			+1	FXa 1hcg	4.77	4.17	4.16	-	4.95	4.92
43			+1	FXa 1hcg	4.89	4.96	4.96	-	5.12	4.67
44			+1	FXa 1hcg	3.75	4.74	5.06	-	4.59	4.52
45			+1	FXa 1hcg	4.82	4.23	4.13	-	4.38	4.33
46			+1	FXa 1hcg	4.12	4.18	4.26	-	4.05	4.31
47			+1	FXa 1hcg	5.50	4.91	4.71	-	4.79	4.33
48			+2	FXa 1hcg	4.68	4.45	4.44	-	4.44	4.46
49			+1	FXa 1hcg	4.80	4.60	4.78	-	4.55	4.72
50			0	FXa 1hcg	4.36	4.43	4.40	-	4.71	4.58
51			+1	FXa 1hcg	4.70	4.67	5.01	-	4.48	4.74
52			+1	FXa 1hcg	3.96	4.70	4.72	-	4.69	4.79
55			0	FXa 1hcg	4.36	4.47	4.47	-	4.72	4.70

56			+1	FXa 1hcg	4.19	4.44	4.46	-	4.36	4.17
58			+1	FXa 1hcg	5.12	4.70	4.13	-	4.03	4.06
59			+1	FXa 1hcg	4.24	5.05	5.00	-	4.87	4.41
60			0	FXa 1hcg	3.89	4.62	4.47	-	4.70	4.71
61			+1	FXa 1hcg	4.46	5.43	5.20	-	5.36	4.90
63			+1	FXa 1hcg	4.59	4.72	4.87	-	4.71	4.48
64			+1	FXa 1hcg	3.44	3.55	4.51	-	3.78	4.28
66	H-		+2	FXa 1hcg	3.00	3.50	3.48	-	3.23	4.45
67			+2	FXa 1hcg	4.66	4.71	4.59	-	4.72	4.64
68			+1	FXa 1hcg	3.72	4.80	4.99	-	4.75	4.29
69	H-		+2	FXa 1hcg	3.64	3.02	2.99	-	3.35	4.14
70			0	FXa 1hcg	3.89	4.45	4.71	-	4.46	4.52
71			0	FXa 1hcg	4.39	4.45	4.29	-	4.88	4.71
73			+1	FXa 1hcg	4.66	4.25	4.29	-	4.19	4.59
74			+1	FXa 1hcg	5.51	4.68	4.89	-	4.60	4.56
75			+1	FXa 1hcg	5.01	4.36	4.12	-	4.18	4.57
76			+1	FXa 1hcg	4.66	4.69	4.38	-	4.91	4.59
77			+2	FXa 1hcg	4.52	4.57	4.53	-	4.41	4.66
78			+1	FXa 1hcg	4.30	4.54	4.70	-	4.32	4.50
79			+1	FXa 1hcg	4.34	5.07	5.04	-	5.13	4.65
80			+1	FXa 1hcg	4.28	4.31	4.16	-	4.39	4.44
81			+1	FXa 1hcg	4.48	4.66	4.75	-	4.53	4.66
83			+1	FXa 1hcg	5.07	4.42	4.81	-	4.71	4.77
84			+1	FXa 1hcg	4.57	4.85	4.86	-	4.31	4.55
85			+1	FXa 1hcg	4.44	4.94	4.92	-	4.81	4.64
86			+1	FXa 1hcg	4.60	4.63	4.50	-	4.76	4.56
88			+1	FXa 1hcg	4.40	4.44	4.50	-	4.46	4.25
1			+1	Trypsin 1pph	6.77	6.65	-	6.54	6.50	6.97
2			+1	Trypsin 1pph	6.80	6.40	-	6.45	6.39	7.08

3			+1	Trypsin 1pph	6.70	6.16	-	5.93	6.15	5.85
4			+1	Trypsin 1pph	6.85	6.15	-	6.28	6.04	6.14
6			+1	Trypsin 1pph	6.77	6.33	-	6.48	6.21	6.45
7			+1	Trypsin 1pph	6.20	5.89	-	5.97	5.59	5.38
8			+1	Trypsin 1pph	6.20	5.58	-	5.71	5.58	5.45
9			+1	Trypsin 1pph	7.44	6.58	-	6.65	6.63	6.59
10			0	Trypsin 1pph	6.89	4.98	-	5.12	5.35	6.25
11			+1	Trypsin 1pph	7.70	5.98	-	6.11	5.89	6.13
12			+1	Trypsin 1pph	6.26	5.62	-	5.32	5.62	5.26
13			+1	Trypsin 1pph	6.85	6.07	-	6.39	5.98	5.99
14			+1	Trypsin 1pph	7.13	6.16	-	5.90	5.98	6.20
15			+1	Trypsin 1pph	6.28	5.94	-	5.79	6.06	5.92
17			+1	Trypsin 1pph	6.14	6.10	-	6.06	6.09	5.97
18			+1	Trypsin 1pph	6.59	6.24	-	6.39	6.34	6.14
19			+1	Trypsin 1pph	6.66	6.49	-	6.54	6.50	6.44
20			+1	Trypsin 1pph	6.28	6.14	-	6.03	6.23	6.07
21			+1	Trypsin 1pph	6.68	6.23	-	6.37	6.16	6.25
22			+1	Trypsin 1pph	5.96	6.14	-	6.24	6.14	6.35
24			+1	Trypsin 1pph	6.48	6.23	-	6.40	6.11	6.20
26			+1	Trypsin 1pph	6.11	5.41	-	5.74	5.45	6.00
27			+1	Trypsin 1pph	5.66	6.18	-	6.24	6.51	6.53
28			+1	Trypsin 1pph	5.85	5.65	-	5.78	5.56	5.72
29			0	Trypsin 1pph	5.35	5.25	-	5.48	5.55	6.21
30			+1	Trypsin 1pph	5.82	6.00	-	5.98	6.11	6.12
31			+1	Trypsin 1pph	5.40	6.13	-	6.33	6.11	6.04
32			+1	Trypsin 1pph	6.41	6.32	-	6.36	6.33	6.22
34			+1	Trypsin 1pph	6.80	6.84	-	6.94	6.89	6.83
35			+1	Trypsin 1pph	6.00	5.53	-	5.34	5.74	5.71

37			+1	Trypsin 1pph	7.17	7.26	-	6.98	7.24	6.41
38			+1	Trypsin 1pph	6.22	6.20	-	6.19	6.05	5.55
40			0	Trypsin 1pph	6.20	5.94	-	6.27	6.03	6.33
41		-OMe	+1	Trypsin 1pph	5.60	5.44	-	5.56	5.18	5.32
42			+1	Trypsin 1pph	6.92	6.69	-	6.68	6.77	6.74
43			+1	Trypsin 1pph	5.92	5.99	-	5.92	6.07	5.91
44			+1	Trypsin 1pph	5.44	6.46	-	6.58	6.36	5.84
45			+1	Trypsin 1pph	5.92	5.72	-	5.61	5.71	5.57
46			+1	Trypsin 1pph	5.66	5.58	-	5.65	5.45	5.38
48			+2	Trypsin 1pph	6.66	6.30	-	6.43	6.33	6.29
49			+1	Trypsin 1pph	6.37	6.56	-	6.46	6.51	6.33
50			0	Trypsin 1pph	6.24	5.52	-	5.81	5.28	5.70
51			+1	Trypsin 1pph	6.00	6.16	-	5.94	6.16	5.52
52			+1	Trypsin 1pph	5.09	6.01	-	5.97	6.02	6.12
55			0	Trypsin 1pph	6.36	6.33	-	6.49	6.32	6.34
56			+1	Trypsin 1pph	4.85	5.78	-	5.62	5.66	4.93
58			+1	Trypsin 1pph	7.10	7.27	-	6.60	7.24	6.40
59			+1	Trypsin 1pph	5.10	5.58	-	5.59	5.48	5.88
60			0	Trypsin 1pph	4.80	6.07	-	6.22	6.02	6.09
61			+1	Trypsin 1pph	6.57	7.93	-	7.68	7.80	7.31
63		-NHMe	+1	Trypsin 1pph	4.60	5.55	-	5.63	5.36	5.45
64			+1	Trypsin 1pph	4.80	5.66	-	5.31	5.60	5.44
66	H-		+2	Trypsin 1pph	4.54	4.32	-	4.24	4.62	5.32
67			+2	Trypsin 1pph	6.00	7.17	-	7.21	7.40	7.01
68		-NHMe	+1	Trypsin 1pph	3.85	5.30	-	5.17	5.39	5.52
69	H-		+2	Trypsin 1pph	4.54	4.02	-	3.71	4.23	4.33
70		-CO ₂ ⁻	0	Trypsin 1pph	3.93	5.51	-	5.69	5.35	5.60
71			0	Trypsin 1pph	4.51	5.52	-	5.56	5.64	6.18
72		-NHMe	+1	Trypsin 1pph	3.00	5.19	-	5.26	5.17	5.22

73			+1	Trypsin 1pph	6.72	6.13	–	6.01	6.14	6.36
74			+1	Trypsin 1pph	6.59	6.03	–	6.18	5.94	5.92
75			+1	Trypsin 1pph	6.50	5.94	–	6.05	5.91	6.46
76			+1	Trypsin 1pph	6.22	6.30	–	6.52	6.25	6.19
77			+2	Trypsin 1pph	5.89	6.47	–	6.70	6.54	6.84
78			+1	Trypsin 1pph	6.36	6.05	–	6.20	5.91	5.80
79			+1	Trypsin 1pph	5.72	6.11	–	5.77	6.76	6.57
80			+1	Trypsin 1pph	6.15	5.90	–	5.82	6.06	5.91
81			+1	Trypsin 1pph	6.51	6.21	–	6.25	6.23	6.33
82			+1	Trypsin 1pph	6.01	4.72	–	4.70	4.25	4.60
83			+1	Trypsin 1pph	6.80	6.76	–	6.59	6.91	6.61
84			+1	Trypsin 1pph	7.57	6.81	–	7.08	6.80	6.97
85			+1	Trypsin 1pph	5.75	6.14	–	6.20	6.31	6.47
86			+1	Trypsin 1pph	7.64	7.05	–	7.12	7.07	7.00
88			+1	Trypsin 1pph	4.34	5.39	–	5.44	5.21	5.14

^aAbbreviations: *Num*, number of the compound at it appears in reference (1). Data shown in Figure 3 in the main text are highlighted with bold characters.

Table 2. Different conditions for the derivation of COMBINE models studied in this paper (for the 4 cases: Trp+Thr+Fxa, Thr+Fxa, Thr+Trp, Fxa+Trp, and the individual one-receptor models)^a.

diel. model	additional variables	LVs																				
		1		2		3		4		5		6		7		8		9		10		
		R ²	Q ²	R ²	Q ²	R ²	Q ²	R ²	Q ²	R ²	Q ²	R ²	Q ²	R ²	Q ²	R ²	Q ²	R ²	Q ²	R ²	Q ²	
Trp+Thr+Fxa 202	4	none	0.466	0.442	0.484	0.450	0.505	0.465	0.664	0.596	0.707	0.636	0.743	0.654	0.775	0.679	0.797	0.687	0.807	0.689	0.815	0.695
		RL_DelPhi	0.470	0.446	0.491	0.458	0.527	0.485	0.674	0.620	0.716	0.647	0.739	0.651	0.767	0.669	0.785	0.672	0.804	0.676	0.818	0.680
		RL_ISM	0.467	0.442	0.487	0.452	0.518	0.472	0.642	0.570	0.697	0.621	0.728	0.633	0.757	0.652	0.780	0.664	0.799	0.675	0.809	0.678
	d _{ij}	none	0.371	0.316	0.514	0.425	0.634	0.538	0.663	0.585	0.697	0.619	0.732	0.646	0.752	0.645	0.775	0.658	0.790	0.664	0.802	0.660
		RL_DelPhi	0.396	0.343	0.561	0.480	0.659	0.580	0.679	0.609	0.706	0.623	0.734	0.638	0.751	0.632	0.774	0.645	0.785	0.646	0.802	0.647
		RL_ISM	0.376	0.318	0.529	0.432	0.637	0.529	0.673	0.579	0.718	0.640	0.732	0.646	0.753	0.627	0.770	0.642	0.784	0.632	0.792	0.644
	gf	none	0.454	0.417	0.582	0.532	0.687	0.611	0.703	0.625	0.763	0.667	0.783	0.687	0.795	0.693	0.801	0.695	0.816	0.688	0.826	0.676
		RL_DelPhi	0.490	0.457	0.631	0.584	0.676	0.615	0.707	0.627	0.734	0.638	0.762	0.658	0.785	0.676	0.796	0.679	0.804	0.685	0.818	0.682
		RL_ISM	0.440	0.400	0.579	0.517	0.657	0.585	0.689	0.611	0.724	0.639	0.744	0.648	0.775	0.668	0.787	0.677	0.800	0.673	0.810	0.689
	ISM	none	0.558	0.538	0.644	0.616	0.690	0.642	0.728	0.672	0.745	0.682	0.752	0.690	0.754	0.692	0.758	0.684	0.767	0.672	0.773	0.662
		RL_DelPhi	0.537	0.516	0.634	0.605	0.664	0.622	0.693	0.634	0.731	0.656	0.744	0.670	0.756	0.685	0.759	0.684	0.762	0.681	0.772	0.668
		RL_ISM	0.399	0.371	0.618	0.585	0.663	0.627	0.683	0.639	0.704	0.643	0.727	0.660	0.747	0.673	0.754	0.678	0.759	0.679	0.766	0.671
RL_ISM_res		0.487	0.466	0.629	0.599	0.680	0.648	0.709	0.661	0.749	0.674	0.762	0.683	0.771	0.689	0.780	0.687	0.784	0.681	0.794	0.652	
Thr+Fxa 128	4	none	0.590	0.562	0.655	0.496	0.744	0.664	0.778	0.709	0.817	0.722	0.835	0.739	0.848	0.729	0.860	0.715	0.867	0.710	0.874	0.712
		RL_DelPhi	0.593	0.566	0.692	0.512	0.767	0.704	0.793	0.727	0.826	0.735	0.841	0.751	0.854	0.735	0.863	0.730	0.869	0.722	0.876	0.721
		RL_ISM	0.593	0.565	0.680	0.498	0.748	0.663	0.779	0.708	0.810	0.714	0.824	0.709	0.837	0.719	0.846	0.721	0.856	0.716	0.869	0.714
	d _{ij}	none	0.504	0.436	0.660	0.543	0.760	0.666	0.795	0.727	0.820	0.723	0.828	0.717	0.837	0.727	0.843	0.722	0.852	0.703	0.862	0.690
		RL_DelPhi	0.527	0.463	0.699	0.597	0.779	0.703	0.807	0.731	0.824	0.736	0.833	0.723	0.843	0.729	0.852	0.723	0.858	0.706	0.867	0.704
		RL_ISM	0.525	0.458	0.690	0.570	0.777	0.676	0.809	0.735	0.818	0.730	0.828	0.709	0.837	0.713	0.845	0.708	0.853	0.689	0.860	0.692
	gf	none	0.611	0.571	0.708	0.650	0.790	0.722	0.828	0.747	0.840	0.742	0.849	0.725	0.855	0.725	0.866	0.706	0.878	0.701	0.890	0.697
		RL_DelPhi	0.643	0.608	0.750	0.703	0.784	0.728	0.814	0.738	0.838	0.738	0.850	0.738	0.858	0.744	0.866	0.735	0.878	0.715	0.887	0.710
		RL_ISM	0.647	0.606	0.725	0.646	0.786	0.705	0.803	0.732	0.817	0.717	0.837	0.725	0.847	0.721	0.856	0.724	0.866	0.718	0.881	0.705
	ISM	none	0.723	0.707	0.766	0.724	0.796	0.728	0.807	0.732	0.814	0.729	0.818	0.721	0.825	0.715	0.833	0.696	0.840	0.689	0.843	0.687
		RL_DelPhi	0.699	0.680	0.754	0.726	0.782	0.729	0.813	0.733	0.822	0.740	0.830	0.744	0.833	0.742	0.841	0.728	0.847	0.713	0.851	0.710
		RL_ISM	0.672	0.650	0.746	0.716	0.764	0.719	0.781	0.713	0.806	0.711	0.815	0.725	0.821	0.725	0.828	0.719	0.833	0.713	0.839	0.706
RL_ISM_res		0.713	0.695	0.760	0.722	0.780	0.736	0.820	0.726	0.832	0.733	0.842	0.736	0.850	0.732	0.856	0.717	0.864	0.697	0.868	0.689	
Thr+Trp 133	4	none	0.130	0.083	0.256	0.011	0.472	0.287	0.584	0.464	0.636	0.443	0.700	0.539	0.732	0.566	0.748	0.572	0.767	0.580	0.779	0.575
		RL_DelPhi	0.133	0.086	0.348	0.038	0.454	0.315	0.569	0.451	0.634	0.432	0.689	0.514	0.736	0.543	0.752	0.557	0.770	0.567	0.784	0.570
		RL_ISM	0.136	0.090	0.338	0.007	0.390	0.245	0.517	0.352	0.594	0.432	0.685	0.461	0.708	0.500	0.735	0.540	0.758	0.567	0.773	0.566
	d _{ij}	none	0.138	0.056	0.257	0.104	0.410	0.172	0.532	0.357	0.606	0.423	0.638	0.420	0.703	0.502	0.724	0.514	0.749	0.543	0.763	0.561
		RL_DelPhi	0.156	0.075	0.305	0.159	0.434	0.226	0.535	0.352	0.596	0.390	0.635	0.395	0.706	0.494	0.731	0.490	0.750	0.528	0.763	0.548
		RL_ISM	0.172	0.097	0.312	0.162	0.439	0.219	0.540	0.395	0.587	0.386	0.614	0.423	0.674	0.453	0.714	0.464	0.744	0.500	0.765	0.526
	gf	none	0.163	0.105	0.492	0.282	0.587	0.460	0.646	0.483	0.697	0.523	0.726	0.562	0.740	0.574	0.765	0.577	0.775	0.579	0.787	0.570
		RL_DelPhi	0.198	0.139	0.450	0.307	0.508	0.359	0.588	0.403	0.662	0.466	0.703	0.500	0.735	0.559	0.752	0.568	0.777	0.566	0.786	0.578
		RL_ISM	0.208	0.155	0.445	0.245	0.510	0.356	0.558	0.399	0.612	0.429	0.688	0.476	0.724	0.541	0.746	0.556	0.765	0.576	0.780	0.587
	ISM	none	0.303	0.264	0.481	0.416	0.587	0.488	0.623	0.525	0.631	0.525	0.635	0.521	0.647	0.490	0.656	0.465	0.663	0.459	0.671	0.457
		RL_DelPhi	0.327	0.279	0.442	0.372	0.507	0.402	0.592	0.465	0.628	0.506	0.637	0.521	0.642	0.508	0.654	0.475	0.664	0.447	0.671	0.452

	<i>RL_ISM</i>	0.248 0.214	0.487 0.394	0.522 0.452	0.576 0.451	0.612 0.487	0.636 0.517	0.641 0.512	0.650 0.498	0.661 0.462	0.668 0.446	
	<i>RL_ISM_res</i>	0.238 0.203	0.481 0.403	0.515 0.427	0.613 0.452	0.636 0.486	0.658 0.479	0.669 0.484	0.679 0.467	0.703 0.418	0.714 0.421	
FXa+Trp 143	<i>4</i>	<i>none</i>	0.410 0.390	0.447 0.413	0.636 0.572	0.692 0.593	0.740 0.623	0.767 0.636	0.784 0.649	0.793 0.654	0.803 0.654	0.817 0.646
		<i>RL_DelPhi</i>	0.413 0.392	0.454 0.420	0.649 0.589	0.680 0.589	0.737 0.601	0.757 0.623	0.783 0.647	0.794 0.637	0.800 0.635	0.815 0.637
		<i>RL_ISM</i>	0.410 0.389	0.446 0.412	0.638 0.561	0.666 0.585	0.722 0.604	0.752 0.614	0.778 0.640	0.788 0.630	0.796 0.637	0.802 0.631
	<i>d_y</i>	<i>none</i>	0.440 0.398	0.542 0.471	0.616 0.529	0.656 0.567	0.696 0.591	0.731 0.599	0.759 0.607	0.777 0.617	0.803 0.629	0.816 0.641
		<i>RL_DelPhi</i>	0.457 0.414	0.569 0.497	0.639 0.553	0.674 0.588	0.697 0.601	0.735 0.594	0.756 0.592	0.773 0.607	0.800 0.622	0.817 0.641
		<i>RL_ISM</i>	0.422 0.380	0.539 0.460	0.625 0.526	0.665 0.570	0.691 0.591	0.729 0.594	0.752 0.592	0.780 0.616	0.795 0.627	0.809 0.633
	<i>gf</i>	<i>none</i>	0.531 0.502	0.623 0.556	0.662 0.590	0.724 0.617	0.753 0.639	0.774 0.646	0.793 0.652	0.807 0.649	0.818 0.646	0.827 0.637
		<i>RL_DelPhi</i>	0.563 0.533	0.635 0.570	0.663 0.587	0.707 0.604	0.730 0.619	0.762 0.629	0.778 0.638	0.794 0.635	0.814 0.638	0.821 0.636
		<i>RL_ISM</i>	0.456 0.423	0.613 0.549	0.653 0.586	0.695 0.605	0.734 0.624	0.750 0.635	0.770 0.636	0.787 0.630	0.802 0.621	0.815 0.620
	<i>ISM</i>	<i>none</i>	0.618 0.596	0.658 0.615	0.705 0.620	0.713 0.625	0.722 0.642	0.730 0.615	0.733 0.619	0.738 0.596	0.742 0.591	0.753 0.576
		<i>RL_DelPhi</i>	0.621 0.593	0.661 0.619	0.683 0.613	0.705 0.605	0.713 0.621	0.720 0.620	0.726 0.624	0.733 0.609	0.739 0.591	0.751 0.556
		<i>RL_ISM</i>	0.355 0.323	0.616 0.576	0.669 0.623	0.685 0.626	0.700 0.627	0.710 0.622	0.724 0.616	0.729 0.615	0.737 0.604	0.741 0.592
		<i>RL_ISM_res</i>	0.525 0.499	0.644 0.608	0.675 0.620	0.712 0.618	0.723 0.621	0.735 0.613	0.749 0.614	0.761 0.599	0.771 0.606	0.783 0.592

Table 2. Continuation.

diel. model	additional variables	LVs																				
		1		2		3		4		5		6		7		8		9		10		
		R^2	Q^2	R^2	Q^2	R^2	Q^2	R^2	Q^2	R^2	Q^2	R^2	Q^2	R^2	Q^2	R^2	Q^2	R^2	Q^2	R^2	Q^2	
Thr 59	4	none	0.039	-0.086	0.269	0.079	0.589	0.269	0.683	0.409	0.735	0.406	0.775	0.450	0.790	0.491	0.813	0.493	0.830	0.460	0.842	0.464
		RL_DelPhi	0.043	-0.075	0.333	0.155	0.576	0.307	0.685	0.454	0.732	0.451	0.771	0.467	0.802	0.499	0.821	0.515	0.842	0.554	0.856	0.554
		RL_ISM	0.047	-0.071	0.336	-0.013	0.508	0.237	0.585	0.265	0.692	0.327	0.756	0.364	0.774	0.406	0.793	0.464	0.815	0.462	0.827	0.464
	d_{ij}	none	0.167	-0.356	0.262	-0.144	0.591	0.257	0.624	0.290	0.676	0.394	0.736	0.356	0.748	0.390	0.790	0.355	0.811	0.370	0.834	0.355
		RL_DelPhi	0.225	-0.372	0.328	-0.080	0.603	0.297	0.634	0.334	0.696	0.424	0.732	0.385	0.781	0.424	0.802	0.474	0.826	0.501	0.841	0.501
		RL_ISM	0.287	-0.394	0.362	-0.116	0.518	0.240	0.611	0.270	0.629	0.306	0.655	0.269	0.724	0.286	0.772	0.265	0.803	0.306	0.827	0.306
	gf	none	0.151	-0.066	0.463	0.077	0.606	0.359	0.686	0.371	0.767	0.442	0.790	0.496	0.812	0.515	0.850	0.527	0.874	0.545	0.887	0.545
		RL_DelPhi	0.279	-0.063	0.469	0.236	0.598	0.365	0.694	0.408	0.734	0.478	0.787	0.480	0.815	0.519	0.836	0.543	0.868	0.579	0.901	0.579
		RL_ISM	0.239	-0.141	0.411	0.125	0.503	0.170	0.589	0.261	0.701	0.318	0.758	0.398	0.790	0.444	0.810	0.490	0.863	0.527	0.880	0.527
	ISM	none	0.452	0.279	0.581	0.350	0.648	0.375	0.676	0.408	0.697	0.410	0.714	0.403	0.721	0.382	0.725	0.394	0.728	0.361	0.731	0.355
		RL_DelPhi	0.380	0.214	0.528	0.295	0.644	0.426	0.681	0.449	0.726	0.484	0.747	0.502	0.767	0.529	0.780	0.507	0.785	0.509	0.789	0.507
		RL_ISM	0.178	0.092	0.460	0.250	0.630	0.312	0.665	0.357	0.699	0.426	0.714	0.456	0.742	0.458	0.752	0.447	0.759	0.452	0.762	0.452
RL_ISM_res		0.206	0.127	0.470	0.281	0.620	0.284	0.693	0.326	0.732	0.391	0.752	0.424	0.779	0.439	0.793	0.410	0.800	0.425	0.809	0.425	
FXa 69	4	none	0.116	-0.113	0.226	0.032	0.307	-0.221	0.392	-0.347	0.424	-0.384	0.510	-0.442	0.535	-0.455	0.565	-0.440	0.596	-0.396	0.617	-0.396
		RL_DelPhi	0.181	-0.147	0.249	0.084	0.320	-0.037	0.368	-0.147	0.421	-0.340	0.488	-0.542	0.514	-0.575	0.538	-0.417	0.552	-0.366	0.592	-0.366
		RL_ISM	0.175	-0.157	0.252	0.039	0.309	0.033	0.364	-0.104	0.435	-0.240	0.497	-0.417	0.527	-0.450	0.562	-0.329	0.584	-0.293	0.596	-0.293
	d_{ij}	none	0.192	-0.144	0.251	-0.034	0.276	-0.067	0.314	-0.208	0.383	-0.423	0.487	-0.704	0.519	-0.710	0.574	-0.584	0.599	-0.333	0.615	-0.333
		RL_DelPhi	0.224	-0.084	0.285	0.017	0.316	-0.025	0.357	-0.101	0.392	-0.202	0.489	-0.575	0.539	-0.597	0.563	-0.576	0.569	-0.435	0.596	-0.435
		RL_ISM	0.237	-0.093	0.322	0.032	0.346	0.022	0.374	-0.025	0.471	-0.364	0.517	-0.397	0.565	-0.419	0.579	-0.401	0.597	-0.315	0.605	-0.315
	gf	none	0.200	-0.132	0.265	-0.014	0.350	-0.111	0.422	-0.236	0.469	-0.264	0.537	-0.258	0.557	-0.280	0.577	-0.246	0.607	-0.304	0.619	-0.304
		RL_DelPhi	0.241	0.004	0.282	0.047	0.348	-0.033	0.396	-0.121	0.483	-0.385	0.526	-0.377	0.546	-0.341	0.558	-0.195	0.581	-0.178	0.605	-0.178
		RL_ISM	0.177	-0.037	0.278	0.056	0.347	0.008	0.391	-0.029	0.444	-0.120	0.515	-0.260	0.547	-0.298	0.567	-0.242	0.581	-0.228	0.604	-0.228
	ISM	none	0.124	-0.022	0.298	-0.303	0.358	-0.142	0.384	-0.141	0.410	-0.152	0.428	-0.194	0.439	-0.224	0.453	-0.253	0.467	-0.377	0.485	-0.377
		RL_DelPhi	0.217	0.078	0.278	0.014	0.327	-0.066	0.385	-0.107	0.418	-0.183	0.435	-0.175	0.447	-0.136	0.464	-0.223	0.477	-0.248	0.505	-0.248
		RL_ISM	0.126	0.016	0.206	-0.014	0.289	-0.075	0.352	-0.080	0.416	-0.054	0.435	-0.149	0.448	-0.119	0.457	-0.122	0.473	-0.214	0.492	-0.214
RL_ISM_res		0.152	-0.040	0.225	-0.090	0.388	-0.241	0.426	-0.115	0.490	-0.047	0.505	-0.196	0.524	-0.181	0.539	-0.189	0.582	-0.353	0.611	-0.353	
Trp 74	4	none	0.029	0.013	0.525	0.316	0.622	0.429	0.704	0.461	0.731	0.496	0.752	0.520	0.776	0.518	0.790	0.463	0.807	0.428	0.820	0.428
		RL_DelPhi	0.043	0.027	0.471	0.280	0.575	0.368	0.674	0.366	0.709	0.444	0.737	0.483	0.760	0.467	0.780	0.449	0.789	0.425	0.809	0.425
		RL_ISM	0.040	0.015	0.415	0.232	0.559	0.336	0.631	0.354	0.718	0.421	0.739	0.482	0.761	0.521	0.778	0.503	0.784	0.490	0.801	0.490
	d_{ij}	none	0.457	-0.116	0.526	0.258	0.565	0.397	0.653	0.444	0.692	0.456	0.758	0.519	0.775	0.538	0.792	0.544	0.810	0.531	0.821	0.531
		RL_DelPhi	0.463	-0.043	0.517	0.292	0.549	0.370	0.636	0.419	0.700	0.426	0.737	0.448	0.773	0.488	0.789	0.504	0.809	0.479	0.821	0.479
		RL_ISM	0.439	-0.113	0.475	0.278	0.595	0.414	0.635	0.346	0.680	0.455	0.722	0.461	0.767	0.516	0.781	0.529	0.796	0.525	0.805	0.525
	gf	none	0.358	0.174	0.502	0.332	0.640	0.386	0.714	0.438	0.742	0.501	0.776	0.573	0.790	0.532	0.806	0.461	0.815	0.470	0.824	0.470
		RL_DelPhi	0.382	0.202	0.469	0.287	0.589	0.328	0.680	0.320	0.718	0.410	0.754	0.492	0.779	0.496	0.789	0.488	0.807	0.388	0.817	0.388
		RL_ISM	0.375	0.177	0.478	0.333	0.533	0.307	0.629	0.330	0.729	0.407	0.751	0.483	0.770	0.561	0.788	0.560	0.802	0.528	0.813	0.528
	ISM	none	0.440	0.355	0.516	0.263	0.533	0.274	0.556	0.363	0.576	0.308	0.601	0.256	0.605	0.279	0.617	0.242	0.634	0.175	0.647	0.175
		RL_DelPhi	0.417	0.327	0.453	0.306	0.489	0.264	0.516	0.237	0.541	0.228	0.575	0.224	0.602	0.132	0.608	0.187	0.614	0.159	0.624	0.159
		RL_ISM	0.356	0.278	0.454	0.346	0.486	0.275	0.518	0.234	0.531	0.253	0.574	0.294	0.593	0.206	0.612	0.193	0.622	0.214	0.640	0.214
RL_ISM_res		0.428	0.335	0.460	0.327	0.500	0.258	0.550	0.181	0.577	0.233	0.630	0.214	0.649	0.177	0.682	0.213	0.688	0.194	0.714	0.194	

^a Abbreviations: *diel model*, dielectric models used for the computation of electrostatic energy contributions in the interaction inhibitor-enzyme: coulombic with uniform dielectric constant of $\epsilon=4.0$ or distance dependent dielectric constant $\epsilon=\epsilon_{ij}$, where ϵ_{ij} is the interatomic distance, the images method of Goodford²⁷, and the screened electrostatic interactions calculated with our ISM (Gonzalez-Ruiz & Ortiz, in preparation)- entries labeled *4*, *d_{ij}*, *gf*, and *ISM* respectively; *additional variables*, incorporation of desolvation energies as external additional variables: none, desolvation of the receptor and the ligand calculated with DelPhi²⁸ or ISM(Gonzalez-Ruiz & Ortiz, in preparation), either taking both as global values, or decomposing the receptor desolvation energy value per residue- *none*, *RL_DelPhi*, *RL_ISM*, and *RL_ISM_res* labeled entries; *LVs*, latent variables; *R²*, correlation coefficient (fitting performance given by $R^2 = 1 - \frac{\sum (y_{\text{exp}(i)} - y_{\text{fit}(i)})^2}{\sum (y_{\text{exp}(i)} - \langle y_{\text{exp}} \rangle)^2}$ where $y_{\text{fit}(i)}$ corresponds to the value of the quantity fitted with the model for complex i , $y_{\text{exp}(i)}$ is the experimental value of the quantity for complex i , and $\langle y_{\text{exp}} \rangle$ is the average experimental value of the quantity for the complete set of n complexes); *Q²*, predictive correlation coefficient (the equivalent of *R²* calculated for the cross-validated predictive performance). The number of complexes included in the training set is indicated in the left hand side of the table, together with the corresponding set of considered receptors. Cells corresponding to the optimal number of latent variables (best *Q²*) appear shaded in gray color. Statistics for the discussed models (entries *ISM* and *RL_ISM_res* -Table 1 in the communication) are shown in bold characters.

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