



Supporting Information

© Copyright Wiley-VCH Verlag GmbH & Co. KGaA, 69451 Weinheim, 2009

SUPPLEMENTARY DATA

“MOLECULAR MODELING AND RECEPTOR-DEPENDENT (RD) 3D-QSAR APPROACH TO A SET OF ANITUBERCULOSIS DERIVATIVES”

Pasqualoto, Kerly Fernanda Mesquita; Ferreira, Márcia Miguel Castro

Table of Contents:

Table 3. Ligand-receptor complex energy [$E_{LR}(LL,RR,LR)$] and the energy descriptors values (model 8) found for the investigated set.....S2

Table 4. Statistical measures, number of descriptors and number of outliers for the top eight *RD* 3D-QSAR models by using a smoothing factor of 0.7 (N =30).....S3

Table 5. Linear cross-correlation matrix of the residuals of fit for the top eight *RD* 3D-QSAR models (N = 30).....S3

Table 6. Linear cross-correlation matrix of the descriptors found in the optimal *RD* 3D-QSAR (model 8).....S3

Table 7. Internal validation LMO procedure results for the selected best model (model 8; N= 30).....S4

Table 8. Values of LOO q^2 and r^2 found for the ten QSAR models generated with the same data set (N = 30) employing the Y-randomization technique.....S4

Table 9. Test set prediction (N = 6) --- External validation.....S4

Table 10. Random sampling scheme for testing the external predictabilityS5

Table 3

Complex L-R (InhA-adduct or ligand)		$E_{LR}(LL,RR,LR)$	$E_{LR}(LM)$	$E_{LR,el}$	E_{Lel+Hb}	E_{Lbend}	ΔE_{Hb}	pMIC
tb1_A	(InhA-NAD/INH1)	-40105.15	-5.17	-305.13	-126.87	64.32	928.90	4.70
tb90_A	(InhA-NAD/Idv90)	-84183.52	-3.88	-36.58	-226.00	62.71	1373.77	4.22
tb2_A	(InhA-NAD/INHd2)	-39342.31	-3.62	-391.05	-115.81	60.61	1743.44	3.82
tb31_A	(InhA-NAD/INHd31)	-39823.19	-4.19	67.06	-99.99	69.76	1372.96	3.40
tb43_A	(InhA-NAD/INHd43)	-40215.97	-4.82	-164.70	-158.97	66.67	969.04	3.40
tb20_A	(InhA-NAD/INHd20)	-40069.54	-3.68	73.51	-170.91	63.86	1334.70	3.22
tb14_A	(InhA-NAD/INHd14)	-40745.90	-3.13	-162.38	-136.08	59.23	25.64	3.22
tb46_A	(InhA-NAD/INHd46)	-40310.80	-2.58	-71.56	-197.36	61.66	1138.80	2.82
tb128_A	(InhA-NAD/Idv128)	-83453.63	-4.55	-4.44	-198.94	54.02	1745.33	2.82
tb37_A	(InhA-NAD/INHd37)	-40370.96	-5.02	-233.10	-138.66	56.77	846.49	2.70
tb124_A	(InhA-NAD/Idv124)	-84603.51	-4.03	-178.20	-207.79	68.25	1150.56	2.70
tb15_A	(InhA-NAD/INHd15)	-34337.76	-3.72	-104.78	-88.38	64.01	1287.33	2.52
tb23_A	(InhA-NAD/INHd23)	-40275.33	-2.86	53.78	-118.13	62.35	1108.07	2.52
tb29_M	(InhA-NAD/INHd29)	-38951.87	-5.87	9.86	-179.43	59.43	1691.32	2.00
tb131_M	(InhA-NAD/Idv131)	-83899.16	-4.18	-42.84	-146.49	72.15	1446.12	2.00
tb16_M	(InhA-NAD/INHd16)	-39136.88	-2.96	-44.46	-143.25	71.08	1827.88	1.92
tb18_M	(InhA-NAD/INHd18)	-40601.18	-9.14	-319.18	-175.57	56.52	321.48	1.92
tb44_M	(InhA-NAD/INHd44)	-37913.80	-4.10	-223.40	-185.53	72.51	1810.08	1.82
tb25_M	(InhA-NAD/INHd25)	-37063.82	-3.96	-213.66	-177.86	55.20	2155.19	1.92
tb30_M	(InhA-NAD/INHd30)	-30657.54	-7.03	-82.88	-165.94	59.17	1446.83	1.92
tb132_M	(InhA-NAD/Idv132)	-83428.45	-3.73	-104.54	-212.46	81.04	1734.84	1.82
tb130_M	(InhA-NAD/Idv130)	-39466.77	-5.91	-170.08	-129.94	58.30	1953.91	1.70
tb27_M	(InhA-NAD/INHd27)	-40008.02	-4.36	-62.82	-209.23	62.12	886.47	1.52
tb22_M	(InhA-NAD/INHd22)	-40310.18	-4.78	-82.80	-242.62	58.83	719.26	1.52
tb34_M	(InhA-NAD/INHd34)	-39167.80	-4.93	-296.08	-232.15	59.56	1372.88	1.40
tb42_I	(InhA-NAD/INHd42)	-39865.27	-5.33	100.90	-152.13	80.07	1427.16	1.10
tb47_I	(InhA-NAD/INHd47)	-41811.95	-6.90	-129.56	-164.62	64.36	-784.89	1.00
tb107_I	(InhA-NAD/Idv107)	-36130.63	-5.74	7.18	-202.89	60.23	1530.36	0.65
tb45_I	(InhA-NAD/INHd45)	-39805.75	-6.55	95.22	-169.44	64.56	1570.48	0.70
tb126_I	(InhA-NAD/Idv126)	-39629.57	-5.67	-75.26	-179.32	83.49	1685.82	0.60
tb19_I	(InhA-NAD/INHd19)	-40493.02	-8.22	-171.06	-167.14	65.82	466.74	0.52
tb125_I	(InhA-NAD/Idv125)	-39338.28	-3.38	-83.83	-147.12	78.79	2012.03	0.52
tb136_I	(InhA-NAD/Idv136)	-85240.14	-2.06	-153.54	-404.10	91.02	1027.15	0.52
tb41_I	(InhA-NAD/INHd41)	-25799.13	-2.40	-308.74	-200.87	64.84	212.92	0.40
tb49_I	(InhA-NAD/INHd49)	-41497.30	-1.92	-313.54	-266.35	69.42	-191.24	0.22
tb48_I	(InhA-NAD/INHd48)	-39259.56	-4.36	81.50	-214.52	60.83	1667.68	0.22
tb51_I	(InhA-NAD/INHd51)	-83928.67	-3.27	-38.66	-167.78	76.58	1429.53	0.22

The unit of all energy contribution values is kcal/mol. A = active; M = medium activity; I = inactive.

Table 4

Model	No. Descriptors	r^2	q^2	LOF	LSE	No. outliers
1	6	0.81	0.68	0.56	0.24	2
2	5	0.77	0.63	0.56	0.29	2
3	5	0.77	0.63	0.56	0.29	2
4	5	0.77	0.63	0.57	0.29	2
5	5	0.77	0.62	0.57	0.29	2
6	5	0.77	0.61	0.57	0.29	1
7	5	0.77	0.61	0.57	0.30	1
8	5	0.77	0.61	0.58	0.30	0

Table 5

	Mod 1	Mod2	Mod 3	Mod 4	Mod 5	Mod 6	Mod 7	Mod 8
Mod 1	1.00							
Mod 2	0.88	1.00						
Mod 3	0.88	0.99	1.00					
Mod 4	0.88	0.99	1.00	1.00				
Mod 5	0.90	1.00	0.99	0.99	1.00			
Mod 6	0.86	1.00	0.98	0.99	0.99	1.00		
Mod 7	0.86	1.00	0.98	0.99	0.99	1.00	1.00	
Mod 8	0.67	0.84	0.85	0.85	0.84	0.85	0.84	1.00

Table 6

	$E_{LR}(LM)$	$E_{LR,el+Hb}$	$E_{LR,bend}$	$E_{LR,el}$	ΔE_{Hb}
$E_{LR}(LM)$	1.00				
$E_{LR,el+Hb}$	-0.01	1.00			
$E_{LR,bend}$	0.17	0.07	1.00		
$E_{LR,el}$	0.05	0.08	0.24	1.00	
ΔE_{Hb}	0.17	0.19	0.16	0.27	1.00

Table 7

m	q^2_{LMO}
2	0.62
3	0.64
4	0.64
5	0.61
6	0.65
7	0.53
8	0.58
9	0.54
10	0.56

Table 8

q^2_{LOO}	r^2
0.02	0.17
0.02	0.15
0.02	0.19
0.13	0.09
0.02	0.30
0.10	0.00
0.00	0.18
0.00	0.29
0.07	0.08
0.08	0.11

Table 9

Complex	Y_{cal}	Y_{exp}	residuals	SD
tb90q_A	1.10	4.22	-3.12	4.63
tb128q_A	0.72	2.82	-2.10	
tb131q_M	2.28	2.00	0.28	
tb132q_M	-0.02	1.82	-1.84	
tb136q_I	-11.09	0.52	-11.61	
tb51q_I	1.73	0.22	1.51	

SD = standard deviation

Table 10

Complex	Y_{cal}	Y_{exp}	residuals	SD
tb136q_I	0.52	-10.92	11.44	4.72
tb43q_A	3.40	3.25	0.15	
tb1q_A	4.70	4.26	0.44	
tb27q_M	1.52	2.03	-0.51	
tb130q_M	1.70	1.91	-0.21	
tb42q_I	1.10	1.39	-0.29	
tb125q_I	0.52	0.69	-0.17	0.96
tb23q_A	2.52	2.90	-0.38	
tb42q_I	1.10	1.39	-0.29	
tb128q_A	2.82	0.78	2.04	
tb34q_M	1.40	1.92	-0.52	
tb49q_I	0.22	0.30	-0.08	
tb48q_I	0.22	0.79	-0.57	1.39
tb131q_M	2.00	2.30	-0.30	
tb125q_I	0.52	0.69	-0.17	
tb42q_I	1.10	1.39	-0.29	
tb44q_M	1.82	1.75	0.07	
tb90q_A	4.22	1.10	3.12	
tb126q_I	0.60	0.35	0.25	1.05
tb49q_I	0.22	0.30	-0.08	
tb31q_A	3.40	2.45	0.95	
tb37q_A	2.70	3.63	-0.93	
tb128q_A	2.82	0.78	2.04	
tb30q_M	1.92	2.28	-0.36	
tb16q_M	1.92	1.69	0.23	0.80
tb2q_A	3.82	3.85	-0.03	
tb46q_A	2.82	2.18	0.64	
tb27q_M	1.52	2.03	-0.51	
tb1q_A	4.70	4.26	0.44	
tb132q_M	1.82	-0.02	1.84	
tb2q_A	3.82	3.85	-0.03	4.81
tb37q_A	2.70	3.63	-0.93	
tb49q_I	0.22	0.30	-0.08	
tb136q_I	0.52	-10.92	11.44	
tb27q_M	1.52	2.03	-0.51	
tb44q_M	1.82	1.75	0.07	

Table 10 – cont.

Complex	Y_{cal}	Y_{exp}	residuals	SD
tb30q_M	1.92	2.28	-0.36	0.67
tb44q_M	1.82	1.75	0.07	
tb23q_A	2.52	2.90	-0.38	
tb49q_I	0.22	0.30	-0.08	
tb51q_I	0.22	1.74	-1.52	
tb1q_A	4.70	4.26	0.44	
tb22q_M	1.52	1.00	0.52	1.14
tb15q_A	2.52	2.92	-0.40	
tb42q_I	1.10	1.39	-0.29	
tb2q_A	3.82	3.85	-0.03	
tb19q_I	0.52	3.03	-2.51	
tb46q_A	2.82	2.18	0.64	
tb126q_I	0.60	0.35	0.25	0.69
tb27q_M	1.52	2.03	-0.51	
tb1q_A	4.70	4.26	0.44	
tb130q_M	1.70	1.91	-0.21	
tb51q_I	0.22	1.74	-1.52	
tb125q_I	0.52	0.69	-0.17	
tb34q_M	1.40	1.92	-0.52	1.02
tb130q_M	1.70	1.91	-0.21	
tb42q_I	1.10	1.39	-0.29	
tb37q_A	2.70	3.63	-0.93	
tb29q_M	2.00	1.52	0.48	
tb19q_I	0.52	3.03	-2.51	
