Stability of Complexes of Aromatic Amides with Bromide Anion: Quantitative Structure—Property Relationships

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Most of the theoretical studies published to-date on the structural and electronic properties of supramolecules have been devoted to the neutral or cationic complexes, while little is known about anionic systems. A detailed theoretical study of the interaction between simple aromatic amides and the bromide anion has recently been published (Čajan, M.; Stibor, I.; Koča, J. *J. Phys. Chem. A* **1999**, *103*, 3778). The present work focuses on the structural and physicochemical parameters of simple aromatic amides related to their ability to form the 1:1 complex with a bromide anion. A quantitative structure—property relationships (QSPR) model for the prediction of association constants is proposed. The model based on 22 complexes and nine molecular descriptors explained 96% (84% cross-validated) of the variance in association constants. The descriptors employed in this model included parameters for the characterization of conformational behavior and the 3D structure of amide molecules, distribution of electron density on the amidic functional group, and parameters for substitution on aromatic units. The quantitative structure—property relationship approach predicted the association constants with comparable quality, but significantly lower computational demand, than molecular modeling or standard quantum chemistry calculations.

1. INTRODUCTION

Theoretical studies of supramolecular complexes provide insight into the structure, conformation, and electronic properties of these interesting chemical species. The study of electron-deficient abiotic receptor molecules designed for noncovalent binding of anion guest species is an area of ever increasing research activity.^{1,2}

Anions play numerous fundamental roles in biological and chemical processes.³ For example, a number of enzymes bind anions as either substrates or cofactors. An understanding of the structural rules underlying the engineering of these anion binding sites is of paramount importance. It can have a considerable impact on the design of molecules that may find application as therapeutic agents. For example, in phosphate binding protein, there are as many as 12 distinct hydrogen bonds fixing the position of the anion in the binding site.⁴

We have initiated a research project aimed at the understanding of factors governing the ability of the simple secondary amide bond to form 1:1 complexes with anions and designing the abiotic receptors with several amide bonds cooperating in the anion binding event.⁵ We have recently published a detailed theoretical study of these important phenomena.⁶

Association constants were measured for bromide ions and amides substituted on both sides of the amidic bond by an aromatic group bearing different substituents. Subsequently, the models of amide-bromide complexes were investigated

by molecular mechanics and quantum mechanics calculations to understand the structural determinants of complexation and to predict stabilities. The computational study of the complexes with the anions was found to be complicated due to the requirements for the methodology and the hardware. Molecular mechanics (CVFF) methods and semiempirical quantum mechanics methods (AM1, PM3) provided incorrect results, while calculations with quantum mechanics methods based on DFT and the Møller—Plesset perturbation theory were computationally very demanding.⁶ The use of such calculations for predictive purposes is therefore limited.

The structural formula of an organic compound, in principle, contains all of the information, which predetermines the chemical, biological, and physical properties of that compound⁷ or its behavior to different ambience or phenomena. Here we describe the application of quantitative structure—properties relationships (QSPR) for the prediction of the property of supramolecular species from their chemical structure. Employing a QSPR model, we will attempt to explain the stability of 22 [amide][anion] complexes based on their electronic and steric properties. We will attempt to demonstrate that the QSPR methodology provides a robust and relatively fast tool for the prediction of association constants of such complexes.

2. METHODS

2.1. Association Constants of [Amide]Br⁻ **Complexes (Variable y).** Association constants for 1:1 complexes [amide]Br⁻ were determined by titration ¹H NMR of the solution of the corresponding amide with the addition of (ⁿBu)₄N⁺Br⁻.⁵ Stability constants were determined for 22 complexes of aromatic amides with the general structure shown in Scheme 1. The studied amides are listed in Table 1 together with the experimentally obtained stability constants.

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Scheme 1: General Formula for the Set of Studied Amidesa

$$R^{1}$$
, R^{2} .

 R^{1} , R^{2} .

 R^{2} .

 R^{1} , R^{2} .

 R^{2} .

^a The substituents R¹ and R² mean one of the following functional groups: phenyl, fluorophenyl, perfluorophenyl and pyridil.

2.2. Amide Property Data (Variables *x***).** Descriptors used for QSPR analysis can be conveniently divided into three categories: (2.2.1) steric parameters, (2.2.2) electronic parameters, and (2.2.3) parameters for the description of substitution pattern. The annotation and the sources of descriptors are summarized in Table 2, while the values are summarized in Table 3. The steric and electronic descriptors are illustrated in Figure 1 and discussed in the text below.

2.2.1. Steric Descriptors. The steric descriptors were calculated for the most stable conformer of each molecule. All amides were optimized by the DFT method on B3LYP/ dzvd level^{8,9} prior to calculation of the descriptors. All DFT calculations were performed with TURBOMOLE v95.0/3.0.0 (Biosym/MSI, USA). The driving force to create the complex is the interaction between the bromide anion and the amidic hydrogen. The strength of this interaction is influenced by the volume and electron affinity of the ortho substituents on both aromatic moieties. This effect is stronger for the C aromatic substituent than for the N substituent of the amidic group. It was included in **D(XH)**, **D(XY)**, **Dsum**, and **Tor** descriptors. On the other hand, the distance **D(YH)** (-NH---Y-) was not used as a descriptor because it is similar in all complexes. The amidic group with the NH-ring system is nonplanar only in one case (molecule 8), and this effect is incorporated in the descriptor D(XY). MM, MS, MV, EV, IM1s, IM2s, IM3s, IM1l, IM2l, IM3l, Sim, SimQ, SimS, Rtop, Btop, Wtop, and FI are the global descriptors of amide molecules, which were calculated using TSAR v3.1 (Oxford Molecular, UK). For an explanation of the abbreviations see Table 2.

2.2.2. Electronic Descriptors. The distribution of electron density in the amide and its influence on amide-anion interactions was characterized by a set of electronic descriptors. Electron density was expressed by the partial charges on the atoms around the binding site for the anion (i.e., around the amidic hydrogen) and by the selected bond orders of the central amidic group. Four population analyses were tested for the calculation of partial charges: Mulliken, 10 Löwdin, 11,12 Roby-Davidson, 13 and ESP. 14 The charges for QSPR analysis were finally derived from ESP population analysis, which gave the best results. The partial charges qX, qY, qH, the sum of these charges Q, and the total dipole **Tdip** were used for the description of the influence of electron density and the respective repulsive or attractive forces of atoms interacting with the bromide anion on the stability of the complex.

The substituents on both the aromatic moieties can activate or deactivate the amidic group through the π -electron system.

The electron density on the amidic group regulates the electronic properties of the amidic hydrogen. So, the bond orders of all bonds on the amidic group are dependent on the substitution of the aromatic moieties and on the 3D structure of the molecule. Bond orders of selected bonds, μ -C_{Ar}, μ -N_{Ar}, μ -NH, μ -CO, μ -CN, and their sums, $\Sigma \mu_{Ar}$, $\Sigma \mu$, were used to include the electron density distribution on the amidic functional group.¹⁵ Mayer bond orders¹⁶ were computed on the B3LYP/dzvd/iii_iglo level by DEMON v1.0.¹⁷

2.2.3. Empirical Descriptors of the Substitution Pattern.

The properties arising from the different substitution patterns were quantified by the Hammett (σ) and Taft (E_S) constants. ¹⁸ The Hammett constants for substituents in *meta* and *para* positions on both the aromatic moieties consist of σ -NH, σ -CO, and σ -tot. The steric and electronic effects of substituents in *ortho* positions are characterized by the Taft constants E_S-NH, E_S-CO, and E_S-tot. The sums of constants on both the aromatic moieties and the total sum of σ and E_S (-tot) were used to simplify the models. All E_S substituent constants have odd distributions. E_S-tot has only four different values (two of them are unique), E_S-CO has only three, and E_S-NH is essentially an indicator variable for compounds 1 and 8. Despite this fact, the incorporation of these descriptors in the modeling could be necessary for description of nonbonding interactions in binding site.

2.3. Data Analysis. 2.3.1. Partial Least-Squares Projection to Latent Structures (PLS). Partial Least-Squares Projection to Latent Structures¹⁹ analysis was used to select the most appropriate descriptors for the prediction of association constants. It correlates the systematic variation of the matrix of dependent variables Y to the systematic variation in the independent variables X. PLS finds combinations of independent variables (here descriptors) that can predict dependent variables (here the association constant) and at the same time approximates the matrix X accurately. Autoscaled and centered data were used in the PLS analysis. The importance of every descriptor in the model was accessed using the VIP parameter (variable importance in the projection) and plots of the PLS variable weights (loading plots). All statistical analyses described in this article were conducted using SIMCA-S v6.1 (UmeTri, Sweden).

2.3.2. Validation. The internal validation was employed to access the quality and validity of the developed PLS models. Cross-validation routine and permutation testing secured internal validation. During the cross-validation procedure, parts of the Y data are kept out of the model development, predicted by the model, and compared with the actual values, providing the cross-validated Q^2 . This gives a more realistic value for the predictive power than the squared multiple regression coefficient (R^2). In the permutation testing, the model was recalculated with a randomly reordered dependent variable.

3. RESULTS

3.1. MODEL I. The PLS analysis was applied to the data matrix composed of the training set of 22 amides and 32 descriptors. The values of the dependent variable were logarithmically transformed to improve data distribution. One-component PLS model (**MODEL I**) was established explaining 41% of the variance in the stability of complexes

Table 1: Studied Molecules and Their Experimentally Determined Association Constants

no.	compound	$K_{\rm ass} [\mathrm{M}^{-1}]$	no.	compound	$K_{\rm ass}~[{ m M}^{-1}]$
1	C ₆ F ₅ -CONH-o-F-C ₆ H ₄	62 ± 16	12	p-F-C ₆ H ₄ -CONH-p-F-C ₆ H ₄	880 ± 28
2	o-F-C ₆ H ₄ -CONH-C ₆ H ₅	64 ± 18	13	p-F-C ₆ H ₄ -CONH-m-F-C ₆ H ₄	930 ± 38
3	C_6H_5 -CONH- C_6H_5	145 ± 12	14	C_6F_5 -CONH- C_6H_5	1320 ± 121
4	m-F-C ₆ H ₄ -CONH-C ₆ H ₅	210 ± 25	15	4-pyridyl-CONH-C ₆ H ₅	1650 ± 148
5	3-pyridyl-CONH-C ₆ H ₅	258 ± 22	16	C ₆ F ₅ —CONH-3-pyridyl	1680 ± 174
6	C_6H_5 -CONH- p -F- C_6H_4	297 ± 10	17	C_6F_5 -CONH- p -F- C_6H_4	1687 ± 182
7	C_6H_5 -CONH- m -F- C_6H_4	340 ± 15	18	C_6F_5 -CONH- m -F- C_6H_4	2305 ± 134
8	C_6H_5 -CONH- C_6F_5	368 ± 9	19	C ₆ F ₅ —CONH-4-pyridyl	2684 ± 153
9	p-F-C ₆ H ₄ -CONH-C ₆ H ₅	434 ± 30	20	C ₆ F ₅ -CONH-2-pyridyl	3200 ± 187
10	C ₆ H ₅ -CONH-2-pyridyl	530 ± 36	21	C_6F_5 -CONH-3,5- F_2 - C_6H_3	4750 ± 158
11	m-F-C ₆ H ₄ -CONH- m -F-C ₆ H ₄	700 ± 29	22	4 -pyridyl-CONH- 3 , 5 - F_2 - C_6 H $_3$	5400 ± 298

Table 2: Molecular Descriptors—Description, Annotation and Source

	descriptor	source		descriptor	source
MM	molecular mass	TSAR	Q	sum of charges on X, Y, H	DFT
MS	molecular surface area	TSAR	Ď	interatomic distance between Y and H	DFT
MV	molecular volume	TSAR	Tor	torsion angle for description of nonplanarity of amide	DFT
\mathbf{EV}	ellipsoidal volume	TSAR	D(XY)	interatomic distance between X and Y	DFT
IM1s	inertia moment 1 size	TSAR	Dsum	sum of distances between X, Y, H	DFT
IM2s	inertia moment 2 size	TSAR	Tdip	dipole moment	DFT
IM3s	inertia moment 3 size	TSAR	σ -CO	sum of σ -constants of m,p-substituents on CO ring	empirical
IM1l	inertia moment 1 length	TSAR	σ -NH	sum of σ -constants of m,p-substituents on NH ring	empirical
IM2l	inertia moment 2 length	TSAR	σ -tot	sum of σ -constants of all m,p-substituents	empirical
IM3l	inertia moment 3 length	TSAR	E_s -CO	sum of E _s -constants of o-substituents on CO ring	empirical
Sim	combined similarity vs molecule 3	TSAR	E_s -NH	sum of E _s -constants of o-substituents on NH ring	empirical
SimQ	charge similarity vs molecule 3	TSAR	$\mathbf{E_{s}}$ -tot	sum of E _s -constants of all o-substituents	empirical
SimS	shape similarity vs molecule 3	TSAR	μ-CO	bond order on amidic carbonyl group	DFT
Rtop	Randic topological index	TSAR	μ-NH	bond order on amidic -NH bond	DFT
Btop	Balaban topological index	TSAR	μ - C_{Ar}	bond order on bond between amidic group and NH ring	DFT
Wtop	Wiener topological index	TSAR	μ -N _{Ar}	bond order on bond between amidic group and CO ring	DFT
FI -	molecular flexibility	TSAR	μ-NC	bond order on amidic OC-NH bond	DFT
$\mathbf{q}\mathbf{Y}$	partial charge on atom Y	DFT	$\Sigma \mu$	sum of bond orders of all bonds on amidic group	DFT
$\bar{\mathbf{q}}\mathbf{X}$	partial charge on atom X	DFT	$\Sigma \mu_{ m Ar}$	sum of bond orders on bonds between amidic functional	DFT
qΉ	partial charge on amidic hydrogen	DFT	-	group and both aromatic moieties	

 $(R^2 = 0.41)$. The predictive power of **MODEL I**, quantified by cross-validated explained variance, was 25% ($Q^2 = 0.25$). The graph of correlation between the experimentally observed and predicted values of association constants is shown in Figure 2.

Two outliers, i.e., molecules 21 and 22, strongly affected the model predictivity. The association constants of the compounds 21 and 22 are of extremely high value ($\sim 5000 \text{ M}^{-1}$) compared to the rest of the compounds in the analysis. In further analyses we decided to (i) construct a new model (MODEL II) only for compounds showing association contacts lower than 3000 M⁻¹ and (ii) employ the additional descriptors for the modeling of the data altogether (MODEL III).

3.2. MODEL II. The new matrix for PLS analysis was restricted in terms of the number of compounds (amides 21 and 22 have been eliminated) but used the same number of descriptors as in MODEL I. A two component PLS model with 32 descriptors was established which was characterized by $R^2 = 0.89$ and $Q^2 = 0.52$. There are a number of variables containing little or no information about amide ability for complexation of the anion. Variable selection based on VIP (variable importance in the projection) values and the position of descriptors on the plots of PLS variable weights resulted in a **MODEL II** with improved statistical quality, $R^2 = 0.91$ and $Q^2 = 0.75$. This model is based on eight descriptors. Derived PLS model can be expressed by the regression equation as follows:

$$\begin{split} \log K_{assoc} &= 0.1396MV + 0.0514Sim - 0.3462H + \\ &0.4348Q + 0.2987Tor + 0.5535D(XY) + \\ &0.4963\sigma_{m,p}Tot + 0.3877E_{\rm S}NH + 5.4251 \end{split}$$

Experimentally observed association constants are plotted against the predicted values of association constants in Figure 3. PLS variable weights are shown in Figure 4. Ten fixed permutations were used for the model validation. The validation plot for **MODEL II** is shown in Figure 5.

3.3. MODEL III. MODEL II provides good predictions for the complexation ability of amides that interact with the anion with association constants from 0 to about 3000 M^{-1} . However, the most stable complexes can be the most interesting ones, thus an attempt has been made to find a model for the prediction of the complexation abilities of all 22 amides. Bond orders μ -C_{Ar}, μ -N_{Ar}, μ -NH, μ -CO, and their combinations $\Sigma \mu_{Ar}$, $\Sigma \mu$ for selected bonds were used as new descriptors to characterize the distribution of electron density on the amidic group.

The matrix for PLS analysis was extended in terms of these new descriptors and included 22 amides as the training set. The variable selection resulted in **MODEL III** with R^2 0.92 and $Q^2 = 0.70$. This model is based on nine descriptors. Obtained PLS model can be expressed by the regression equation

$$\begin{split} \log K_{assoc} &= 0.1107MV - 0.0096Sim - 0.3096H + \\ &0.3546Q + 0.2446Tor + 0.4597D(XY) + \\ &0.4772\sigma_{m,p}Tot + 0.3096E_{\rm S}NH - 0.2344\sum\mu + 5.1047 \end{split}$$

The correlation plot of experimentally observed and predicted association constants is shown in Figure 6. The PLS variable weights (Figure 7) were calculated for important descriptors. **MODEL III** was validated with 10 fixed permutations, and the results are shown in Figure 8.

Table 3: Molecular Descriptors — Values

Table	e 3. 1010	iccuiai L	escriptors	v aiu	CS .									
D	MM	I MS	$S[Å^2]$	$MV [\mathring{A}^3]$	IM1s	IM2s	IM3s	IM11	IM21	IM31	EV [Å	Å ³] FI	Rtop	Btop
1	305.1	9 23	39.91	189.94	129.20	555.1	1 655.28	12.03	2.80	2.37	335.0	06 3.99	11.93	2.05
2	215.2		12.03	144.49	55.35	326.9		14.60	2.47	2.13	321.2		11.93	
3	197.2)5.65	137.62	41.81	316.8		20.44	2.70	2.39	552.4		11.93	
4	215.2		18.07	150.31	61.48	365.5		16.17	2.72	2.37	436.3		11.93	
5	198.2		11.19	137.14	41.87	315.5	3 354.89	18.22	2.42	2.15	396.6	60 2.85	11.50	
6	215.2		13.64	144.91	41.79	418.3		26.89	2.67	2.45	741.4		11.93	
7	215.2		14.36	147.46	56.34	382.1		19.84	2.93	2.57	625.4		11.93	
8	287.2		12.50	186.52	110.25	526.6		14.71	3.08	2.70	512.9	99 3.80	11.93	2.05
9	215.2		12.33	148.95	44.11	414.4		23.77	2.53	2.31	582.4		11.93	2.05
10	198.2		08.47	138.45	42.00	311.2	5 349.11	20.07	2.71	2.41	549.9	99 2.85	11.50	
11	233.2		20.31	154.15	79.17	433.7	8 507.50	14.63	2.67	2.28	373.4	48 3.25	11.93	2.05
12	233.2	23 22	23.25	151.90	43.65	534.6		30.15	2.46	2.28	709.0		11.93	
13	233.2	23 22	23.94	153.95	60.20	491.2		21.25	2.65	2.34	541.6		11.93	
14	287.2	20 24	10.13	185.01 139.81	111.94	524.6	0 609.21	13.50	2.88	2.48	404.3	30 3.80	11.93	2.05
15	198.2		10.02	139.81	41.62	319.3	5 355.71	20.08	2.62	2.35	517.5	58 2.85	11.50	2.22
16	288.1	.9 24	13.60	182.89	112.18	525.1	4 607.19	12.81	2.74	2.37	347.8	87 3.75	11.50	
17	305.1	.9 24	13.60	192.24	112.32	673.7		16.39	2.73	2.43	455.5		11.93	
18	305.1		38.66	194.74	129.32	633.8	4 712.20	13.78	2.81	2.50	406.4	43 3.99	11.93	
19	288.1	9 23	36.63	185.30	112.06	530.8	2 605.38	13.56	2.86	2.51	407.9	98 3.75	11.50	2.12
20	290.2		37.07	186.62	114.28	530.8		13.90	2.99	2.64	460.0		12.26	
21	323.1		53.94	203.13	147.11	724.7	0 806.60	14.14	2.87	2.58	438.4		11.93	2.05
22	234.2	22 22	21.02	153.76	75.46	432.0	7 501.04	15.80	2.76	2.38	434.7	79 3.20	11.50	2.02
											0	0		
D	Wtop	Sim	SimQ	SimS	qX [au]	qH [au]	qY [au]	Q [au]	D(XH) [Å			Dsum [Å]	Tor [°]	Tdip [Db]
1	1519	0.4876	0.1170	0.8583	-0.1453	0.3748	-0.2027	0.0268	2.27	3.9	2	8.41	41.00	2.6879
2	1519	0.9235	0.8795	0.9675	-0.2313	0.3651	0.1708	0.3046	1.95	3.7	4	7.96	11.59	2.8896
3	1519	1.0000	1.0000	1.0000	0.1287	0.2967	0.1774	0.6028	1.99 2.12	3.8	2	8.07	16.20	3.4358
4	1519	0.8610	0.7954	0.9267	0.1714	0.3100	0.1748	0.6562	2.12	3.9 3.8	8	8.37	25.06	1.9716
5	1380	0.8406	0.7140	0.9673	0.0242	0.3174	0.1819	0.5235	2.05	3.8	7	8.19	21.59	1.4384
6	1519	0.9384	0.8973	0.9795	0.1265	0.2814	0.1914	0.5993	1.99	3.8	4	8.11	16.35	4.4058
7	1519	0.8959	0.8541	0.9377	0.1239	0.2879	0.2352	0.6470	2.07	3.9	1	8.28	23.92	2.9597
8	1519	0.5924	0.3692	0.8156	0.1250	0.2612	-0.1380	0.2482	2.16	4.5	7	9.24	23.25	4.9407
9	1519	0.8879	0.8409	0.9350	0.1316	0.3111	0.1749	0.6176	2.11	3.9	7	8.35	25.02	2.9063
10	1394	0.8144	0.6715	0.9573	0.1257	0.3094	-0.6641	-0.2290	2.11	4.2	2	8.66	25.87	1.6131
11	1519	0.8613	0.7466	0.9760	0.1742	0.3018	0.2228	0.6988	2.07	3.9	2	8.29	21.78	1.6787
12	1519	0.8974	0.8239	0.9708	0.1362	0.2863	0.1903	0.6128	2.00	3.8	5	8.12	15.78	3.1549
13	1519	0.8928	0.8016	0.9840	0.1337	0.3008	0.2211	0.6556	2.05 2.38	3.9	1	8.26	20.79	1.5434
14	1519	0.6317	0.3966	0.8668	-0.1494	0.3696	0.1592	0.3794	2.38	4.2	1	8.87	46.91	3.3795
15	1366	0.8370	0.7239	0.9501	0.1721	0.3012	0.1806	00.6539	2.19	4.0	0	8.46	31.20	3.2446
16	1380	0.5571	0.2434	0.8707	-0.1511	0.3787	0.0565	0.2841	2.48	4.2	. /	9.04	51.98	0.9025
17	1519	0.6300	0.3581	0.9018	-0.1548	0.3725	0.1712	0.3889	2.41	4.2	.2	8.91	48.79	2.865
18	1519	0.5469	0.2568	0.8371	-0.1528	0.3722	0.2079	0.4273	2.54	4.3	/	9.22	54.69	1.5954
19	1366	0.5529	0.2475	0.8582	-0.1484	0.4153	0.2146	0.4815	2.67	4.4	9	9.49	51.70	3.0044
20	1660	0.6150	0.3846	0.8454	-0.1448	0.3801	-0.6713	-0.4360	2.76	4.6		9.78	61.81	3.0761
21	1519	0.5686	0.2768	0.8605	-0.1547	0.3698	0.2250	0.4401	2.65	4.4	3	9.39	60.05	2.8188
22	1366	0.7733	0.5909	0.9557	0.1734	0.2867	0.2399	0.7000	2.18	4.0	4	8.53	30.37	2.6273
D	σ-СО	<i>σ</i> -N	H σ-to	ot E _s -	CO E _s -1	NH Es	-tot μ-N	Η μ-C	μ -l	N _{Ar} μ	-CN	μ-СО	Σμ	$\Sigma \mu_{Ar}$
1	0.46	0	0.4	6 -0	0.92 -0.	.46 –0	0.14 0.92				2080	1.9361	6.0065	1.9379
2	0	0	0		0.46	-(0.46 0.92				1848	1.8334	5.9683	2.0244
3	0	0	0	0	0	(0.95	85 1.07	23 0.9	726 1.	1675	1.8585	6.0293	2.0449
4	0.06	0	0.0	6 0	0	(0.95	51 1.04	68 0.9	584 1.	1787	1.8611	6.0000	2.0052
5	0.73		0.7	3 0	0	(0.95			574 1.	1804	1.8773	6.0398	2.0285
6	0	0.3	4 0.3	4 0	0	(0.949			616 1.	1559	1.8598	6.0074	2.0418
7	0	0.0	6 0.0	6 0			0.94			412 1.	1606	1.8707	5.9974	2.0205
8	0	0.4	6 0.4	6 0	-0.	.92 –(0.92 0.96			961 1.	1119	1.9220	5.9661	1.9712
9	0.34	0	0.3			(0.95			610 1.	1746	1.8600	6.0301	2.0383
10	0	0.9					0.92				1737	1.8521	5.9910	2.0380
11	0.06						0.95				1537	1.8675	5.9788	2.0013
12	0.34	0.3					0.95				1540	1.8379	5.9903	2.0471
13	0.34	0.0					0.95				1462	1.8692	6.0087	2.0373
14	0.46		0.4		0.92 0		0.92 0.95				2228	1.9623	6.1024	1.9630
15	0.83	0	0.8				0.94				1863	1.8909	6.0031	1.9818
16	0.46				0.92 0		0.92 0.95				2153	1.9775	6.1204	1.9772
17	0.46	0.3	4 0.8		0.92 0		0.92 0.94	34 0.99	0.9		2108	1.9497	6.0454	1.9416
18	0.46				0.92 0		0.92 0.93				2040	1.9526	6.0383	1.9437
19	0.46				0.92 0		0.92 0.95	14 1.00	0.9	902 1.	1957	1.9902	6.1308	1.9935
20	0.46				0.92 0		0.92 0.92				2231	1.9385	6.0281	6.0281
2.1	0.46	0.1			0.92 0		0.92 0.939				2024	1.9407	5.0842	1.9410
21 22	0.83	0.1	2 0.9		0		0.94	84 1.02	0.0	253 1.	1727	1.8991	5.0263	1.9545

4. DISCUSSION

The concept of quantitative structure—property relationships (QSPR) is to transform searches for compounds with desired properties using chemical intuition and experience into a mathematically quantified and computerized form. ¹⁵ QSPR requires a set of descriptors, which gives information about the investigated properties. Such information may not

only lead to a better understanding of the system but may also allow for transferring information and predictions from one series of compounds to another.²⁰ This work presents a description and prediction of the stability of 1:1 complexes of the aromatic amides with bromide anion focused on the prediction of their stability. Theoretical chemistry tools and descriptors are employed in the constructed QSPR models.

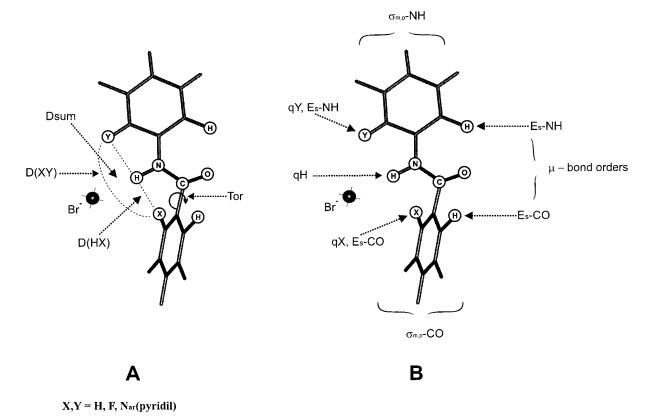


Figure 1. Graphical interpretation of selected descriptors: (A) steric descriptors of geometrical properties of the amide binding site and (B) electronic descriptors of the amide binding site and empirical descriptors of the substituents on both aromatic rings.

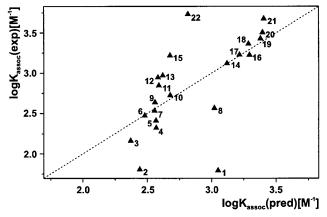


Figure 2. Plot of experimentally observed versus predicted association constants. MODEL I based on 32 descriptors was used for predictions (one component, n = 22, $R^2 = 0.4\hat{1}$, $Q^2 = 0.25$).

The computing of interaction energies or even association constants for such complexes, using molecular modeling or standard quantum chemistry methods, is a considerable problem. The QSPR approach can provide results of comparable quality but significantly lower computational demand. The objective of this study was to find the structural and physicochemical parameters of aromatic amides related to their ability to form a complex with bromide anion and to construct a QSPR model for the prediction of association constants.

Overall 39 descriptors were applied in QSPR. These descriptors were designed according to the knowledge of the structure and properties of the complexes.^{5,6,21} Three models were developed for the description of association constants for [amide]Br⁻ complexes. The initial model, **MODEL I**, served for the characterization and classification of the input

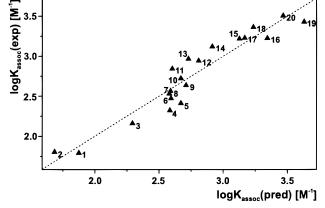


Figure 3. Plot of experimentally observed versus predicted association constants. MODEL II based on eight descriptors was used for predictions (two components, n = 20, $R^2 = 0.91$, $Q^2 =$ 0.75).

data. This model, characterized by $R^2 = 0.41$ and $Q^2 = 0.25$ for 22 compounds and 32 descriptors, was further refined and resulted in MODELS II and III.

The later two models attempted to eliminate redundant descriptors and to deal with the outlying compounds 21 and **22** (Figure 2). **MODEL II** eliminated the outliers from the training set, while new descriptors have been included to MODEL III in order to keep all compounds in the model. The descriptors used in **MODEL I** and **MODEL II** primarily described global properties of the anion binding site and the properties of the amidic hydrogen. Amides 21 and 22 have similar structural properties to other molecules but show very high association constants. Extreme complexation of these compounds with bromide anions is probably related to the electronic properties of the aromatic rings. The predictive

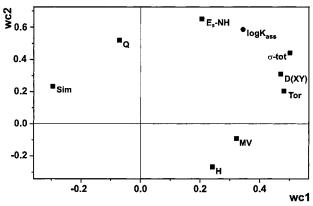


Figure 4. Loading plot of the first two components from PLS analysis applied to descriptors fixed in **MODEL II**.

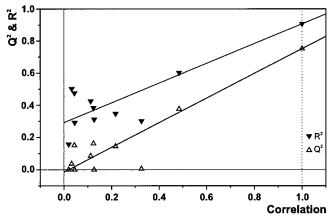


Figure 5. Validation plot of **MODEL II**. Ten fixed permutations were used for validation. The *Y*-axis represents R^2 (filled triangles) and Q^2 (empty triangles) for the original model (right-hand part of the plot) and every model with permuted *y*. *X*-axis designates the correlation coefficient between original and permuted *y*. Good models have the R^2 -intercept below 0.4 and Q^2 -intercept below 0.05.

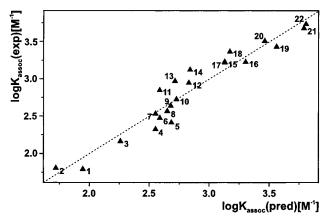


Figure 6. Plot of experimentally observed versus predicted association constants. **MODEL III** based on 10 descriptors was used for prediction (two components, n = 22, $R^2 = 0.92$, $Q^2 = 0.70$).

power of **MODEL II** is characterized by $R^2 = 0.91$ and $Q^2 = 0.75$, for 20 compounds and eight descriptors. This model provided good predictions for compounds with association constants below 3000 M⁻¹. **MODEL III** used the same descriptors as **MODEL II** and employed one additional descriptor to characterize the electronic properties of the central amidic group. **MODEL III** showed $R^2 = 0.92$ and $Q^2 = 0.70$ (22 compounds, nine descriptors).

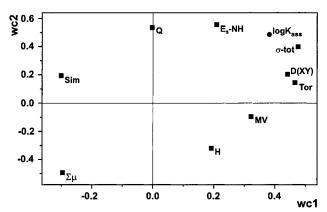


Figure 7. Loading plot of first two components from PLS analysis applied to descriptors fixed in MODEL III.

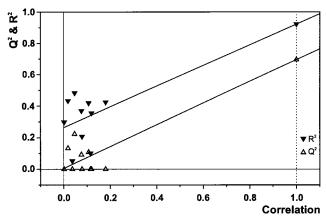


Figure 8. Validation plot of **MODEL III**. Ten fixed permutations were used for validation. See Figure 5 for explanation of plot interpretation.

On the basis of previous theoretical studies, 6,22 and also supported by X-ray analysis of hydrogen bonding of anions in amides,²¹ we propose that the conformational behavior of the amide molecule is one of the most important parameters influencing the stability of the complexes. A planar conformation is not a global minimum on the conformational energy hypersurface, and the total π -electron system conjugation is slightly disrupted by repulsion between substituents in *ortho* positions of the aromatic rings on one side and atoms of the amidic group on the other side. On the other hand, this repulsion opens the space around the amidic hydrogen and allows the anion to interact with the amide molecule. The steric "opening" effect predominates over the activation of the amidic hydrogen by electronacceptor properties of substituents on aromatic moieties. which are the most significant for the compounds with fluorine atoms in *ortho* positions on the CO ring. The above observation is expressed by the **Tor** and **D(XY)** descriptors. The former includes information about conformation around the bond between the amidic carbonyl and the aromatic ring. The latter one gives information about the conformational behavior of both the aromatic moieties simultaneously.

The substituents in *ortho* positions of both aromatic units may also influence the interaction with the anion by electrostatic forces. This is confirmed by the fact that the sum of partial charges \mathbf{Q} on the atoms around the binding site is one of the significant electronic descriptors. The amidic hydrogen creates a hydrogen bond with the anion and the atoms in X and Y positions (Figure 1) have a complementary

effect on the interaction with the anion. When the fluorine atom is bonded in position X or Y, the intramolecular hydrogen bond between this atom and the amidic hydrogen is preferred to the intermolecular hydrogen bond with the bromide anion. On the other hand, the fluorine atom in either ortho position of both the aromatic moieties may interact with the carbonyl oxygen and this repulsion leads to a conformational movement between the planes of the amidic group and the aromatic rings. The acidity of the amidic hydrogen and its ability to interact with the anion is expressed by the partial charge qH.

The aromatic amides contain a large conjugated π -electron system. Both the aromatic moieties of the studied amides were substituted in various positions of the rings. The empirical descriptors based on the Hammett (σ) and Taft $(E_{\rm S})$ constants were used for the characterization of the electronic and steric effects of these substituents. The ability of the amidic hydrogen to interact with the anion may be influenced by the electron-acceptor properties of substituents on aromatic rings through out the π -electron conjugation. While substituents in *meta* and *para* positions only interact with the amidic hydrogen through the π -electron system, substituents in ortho positions also interact by steric and Coulombic effects. The influence of meta and para substituents is expressed by the σ -tot descriptor. The properties of substituents in ortho positions on both aromatic rings are described by the Taft E_S constants. The descriptor E_S -NH represents the sum of Taft E_S constants on NH connected ring. The E_S descriptors of ortho substituents in combination with the conformational behavior of the molecule on the amidic group partially include the steric and Coulombic properties of the anion binding site. The E_s-NH descriptor is an indikator variable only for compounds 1 and 8, but its elimination from the data set results in worse statistics for both the final models (MODEL II: $R^2 = 0.82$, $Q^2 = 0.50$, 20 compounds, seven descriptors; MODEL III: $R^2 = 0.80$, $Q^2 = 0.52$, 22 compounds, eight descriptors). There is no other descriptor in the data set that can describe the substituents in ortho positions on NH connected aromatic ring. An additional descriptor $\Sigma \mu$ was incorporated in MODEL III for a better description of the electronic properties of the amide molecule. This descriptor quantifies the sum of bond orders on the central amidic group. Such parameters complement information about the distribution of electronic density in the molecule provided by the empirical descriptor σ -tot and partially by the descriptors E_S-NH. Global steric descriptors, the molecular volume MV and the similarity index Sim, complement the set of steric and electronic descriptors.

The quality of QSPR models could be compared with our previous results from the DFT quantum chemical calculations of the interaction energies applied to the identical system.⁶ The predictions based on the interaction energies are substantially worse than the predictions generated by the QSPR models. Moreover, the QSPR modeling required significantly less computational resources compared to the DFT and ab initio quantum chemical calculations. Developed

QSPR models will be used for predictions of association constants of other complexes, which are not included in the tested set.

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