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1	Appendix A. Supplementary data for "3D-QSAR
2	predictions for bovine serum albumin-water
3	partitioning coefficients of organic anions using
4	quantum mechanically based descriptors"
5	
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## 26 S-1 Local sigma profiles

27 The number of local sigma profiles depends on the default  $\sigma$ -interval (delsig parameter in

- 28 COSMOsar3D) and the range of sigma values of all training set chemicals. We chose a *delsig* value of
- 29 0.006  $\sigma$  [e/Å<sup>2</sup>] as it was proposed as sufficient by Klamt *et al.* (Klamt, A. *et al.*; Journal of Chemical
- 30 Information and Modeling, 2012, **52** (8), 2157-2164). For the derivation of the LSPs a grid size of 2 Å
- 31 was chosen because this grid size was also proposed by Klamt *et al.* and it is a common setting for
- 32 3D-QSAR models (Verma, J. et al.; Current Topics in Medicinal Chemistry, 2010, 10 (1), 95-115).



33

34 Figure SI 1 Generation of the sigma profile (top) and the local sigma profiles (LSPs) (bottom). The 35 LSPs are shown for two exemplary grid points indicated with a black plus sign. The lattice is moved

36 through the whole molecule in steps of 2 Å and the MIFs are derived at each grid point. The figure

37 is designed following Linden et al. [CD paper model] and omitting LSP 1, LSP 2, and LSP 10 for the 38 sake of clarity.

# 40 S-2 Alignment Results

41 The alignment of the five template chemicals is illustrated in Figures SI2.

naphthalene-2-sulfonate



naphthalene-2-sulfonate 2-naphthaleneacetate pyrene benzo[*g*,*h*,*i*]perylene



naphthalene-2-sulfonate 2-naphthaleneacetate



naphthalene-2-sulfonate 2-naphthaleneacetate pyrene benzo[*g*,*h*,*i*]perylene chrysene

naphthalene-2-sulfonate 2-naphthaleneacetate pyrene



gure SI 2 R

43 Figure SI 2 Result of the COSMOsim3D alignment for the template chemicals. Note that the order of the chemicals is

44 arbitrary.



45 Comparison of the alignment of 2,4,6-trimethylbenzene sulfonate and 2,4,6-trimethylbenzoate:

48 Figure SI 3 Alignment of 2,4,6-trimethylbenzene sulfonate and 2,4,6-trimethylbenzoate. The green lines in the pictures

49 show the template chemicals while the blue sticks show 2,4,6-trimethylbenzene sulfonate and the red sticks show 2,4,6-

50 trimethylbenzoate. The teal area indicates the area where LSP7 is positively correlated to log  $K_{\text{BSA/water}}$  and the violet area 51 indicates the area where LSP8 is positively correlated to log K<sub>BSA/water</sub>. The alignment figures were generated using

52 Pymol38.

#### S-3 Results of the random test set predictions 53

#### 54 Table SI 1 Statistical results for the random test set predictions

test set	q <sup>2</sup> training set	RMSE <sub>test set</sub>	R <sup>2</sup> test set
random1	0.57	0.52	0.69
random2	0.60	0.59	0.60
random3	0.62	0.74	0.39
random4	0.60	0.72	0.40
random5	0.54	0.58	0.60

444		experimental	predicted log
lest set	name	$\log K_{\rm BSA/water}$	K <sub>BSA/water</sub>
random1	1,2-dichlorobenzene	3.03	3.17
	1-heptyne	2.49	2.7
	1-hexanol	1.64	2.65
	1-nitrooctane	3.38	3.39
	2,4,5-T (anion)	3.83	3.41
	2,4,6-trimethylbenzoic acid (anion)	2.26	1.95
	2,6-dichlorobenzoic acid (anion)	1.65	2.3
	2-naphthaleneacetic acid (anion)	4.77	4.06
	3-chlorophenol	2.35	1.91
	4-bromobenzoic acid (anion)	3.48	3.68
	4-ethylbenzoic acid (anion)	3.03	2.86
	4-fluorobenzoic acid (anion)	2.84	2.86
	4-fluorophenol	1.57	2.35
	4-iodoaniline	2.95	2.65
	4-methylbenzoic acid (anion)	2.67	3.48
	4-nitroaniline	1.69	2.45
	4-nitroanisole	2.48	2.42
	anisole	2.16	2.01
	benzophenone	2.62	3.18
	bisphenol A	2.88	2.57
	chlorobenzene	2.32	2.58
	chrysene	4.46	4.52
	dibenzofuran	3.79	3.95
	dibenzothiophene	4.16	4.13
	di-n-butyl ether	2.01	3.34
	ethylbenzene	2.7	2.42
	fenoprofen (anion)	3.92	3.68
	ketoprofen (anion)	3.35	3.28
	mefenamic acid (anion)	4.36	3.59
	methoxyflurane	1.77	2.18
	naphthalene	3.56	3.34
	n-nonane	4.45	3.55
random2	1.2.4-trimethylbenzene	3.35	2.33
	1-chlorooctane	3.85	3.31
	1-heptyne	2.49	2.83
	2,4,5-T (anion)	3.83	3.21
	2.4.6-trimethylbenzoic acid (anion)	2.26	1.84
	2-chlorobenzoic acid (anion)	1.84	1.69
	2-cvclohexvlbenzoic acid (anion)	3.59	3.45
	2-naphthaleneacetic acid (anion)	4.77	4.41
	2-nitrotoluene	2.12	1.76

56 Table SI 2 Chemicals, experimental and predicted log K<sub>BSA/water</sub> values of the random test sets

	2-nonanone	2.48	2
	2-phenylphenol	2.62	3.2
	3-chlorobenzoic acid (anion)	3.22	2.52
	4-iodophenol	3.41	2.92
	4-methylbenzoic acid (anion)	2.67	3.47
	a,4-dimethylphenylacetic acid (anion)	2.96	3.57
	di-n-butyl ether	2.01	3.7
	di-n-pentyl ether	3.00	3.78
	di-n-propyl phthalate	2.84	3.2
	fenoprofen (anion)	3.92	3.73
	fluoranthene	4.28	3.77
	hexafluorobenzene	1.55	2.47
	isoflurane	1.58	1.8
	ketoprofen (anion)	3.35	2.67
	mefenamic acid (anion)	4.36	4.27
	methoxyflurane	1.77	1.61
	methylpentafluorobenzene	2.32	2.67
	metolachlor	1.74	2.72
	n-propylbenzene	2.95	3.12
	phenanthrene	4.15	4.35
	pyrene	4.76	4.4
	styrene	2.76	2.67
	toluene	2.26	2.19
random3	1,2,4-trichlorobenzene	3.60	3.49
	1-naphthoic acid (anion)	2.81	3.41
	1-nitronaphthalene	3.17	2.85
	2,4,5-T (anion)	3.83	2.98
	2,4-dinitrotoluene	1.73	1.22
	2,6-dichlorobenzoic acid (anion)	1.65	2.07
	2-chloroaniline	1.95	2.69
	2-cyclohexylbenzoic acid (anion)	3.59	3.66
	2-decanone	2.88	3.97
	2-octanone	2.09	2.21
	3,4-dichlorobenzoic acid (anion)	4.06	2.83
	3-chlorobenzoic acid (anion)	3.22	3.14
	4-aminobiphenyl	2.55	3.74
	4-chlorobenzyl alcohol	2.10	3.27
	4-iodophenol	3.41	3.73
	4-methylbenzoic acid (anion)	2.67	3.49
	benzene	1.58	2.55
	benzo[ <i>b</i> ]fluoranthene	4.42	4.88
	benzoic acid (anion)	2.16	3.02
	diazepam	2.68	2.11
	flufenamic acid (anion)	4.83	2.93
	halothane	1.62	2.44
	indene	2.92	2.81
	indole	2.25	3.03

	ketoprofen (anion)	3.35	2.49
	mefenamic acid (anion)	4.36	3.61
	n-hexane	3.09	2.92
	n-octane	4.01	3.52
	pyrene	4.76	4.6
	styrene	2.76	2.93
	tetrachloroethene	2.40	2.73
	tri-n-butyl phosphate	2.47	2.69
random4	1-nitrooctane	3.38	2.83
	1-octanol	2.74	2.77
	2,4,5-T (anion)	3.83	2.99
	2,4-DB (anion)	4.12	2.96
	2-chloroaniline	1.95	2.72
	2-cvclohexvlbenzoic acid (anion)	3.59	3.3
	2-naphthaleneacetic acid (anion)	4.77	4.64
	2-nitrotoluene	2.12	1.77
	3-chlorobenzoic acid (anion)	3.22	2.3
	3-methoxy-2-naphthoic acid (anion)	2.86	3.88
	4-aminohinhenyl	2.55	3.86
	4-iodophenol	3.41	2.99
	4-methylbenzoic acid (anion)	2 67	3 59
	4-nitroanisole	2.07	2 34
	henzene	1 58	2.54
	chlorobenzene	2 32	2.51
	coumachlor (anion)	3 37	2.02
	cyclohevane	2 01	2.74
	dibenzofuran	3 79	2.20 4 10
	di-n-nronyl nhthalate	2.84	3 29
	estrone	2.64	3.23
	fluoranthene	1.28	3.75
	indene	4.20	2.00
	isoflurane	2.52	2.75
	metenamic acid (anion)	1.56	4.00
	meterianic acid (anon)	4.30	2.05
	metalachlor	1 7/	2.05
	n boxano	2.00	2.59
	n ostano	3.09	2.00
	n-octaile	4.01	5.50 2.14
		2.57	3.14
	pyrelle	4.70	4.49
	succtrione (anion)	1.72	3.70
random5	1,2,4-trimetnyibenzene	3.35	2.39
	1,4-upromobenzene	3.97	3.31
	1-naphthoic acid (anion)	2.81	3.01
	1-nonene	4.22	3.20
	2,4,5-1 (anion)	3.83	3.20
	2,4-DB (anion)	4.12	3.05
	2-chloroaniline	1.95	2.76

2-chlorobenzoic acid (anion)	1.84	1.67
2-octanone	2.09	2.48
4-aminobiphenyl	2.55	3.58
4-bromobenzoic acid (anion)	3.48	3.87
4-chlorobenzoic acid (anion)	3.21	3.75
4-fluorophenol	1.57	2.34
4-n-octylbenzenesulfonate (anion)	5.03	4.33
anisole	2.16	2.11
bisphenol A	2.88	2.98
coumachlor (anion)	3.37	2.80
coumafuryl (anion)	2.79	2.67
diazepam	2.68	1.94
dibenzothiophene	4.16	4.20
enflurane	1.59	2.28
indole	2.25	2.90
mesitylenesulfonate (anion)	4.23	3.82
metolachlor	1.74	2.44
n-heptane	3.59	3.26
n-hexane	3.09	2.87
n-propylbenzene	2.95	3.35
phenoxyacetic acid (anion)	2.57	3.29
pyrene	4.76	4.44
styrene	2.76	2.82
tetrachloroethene	2.4	2.65
tri-n-butyl phosphate	2.47	2.55









62 Figure SI 5 Prediction of the test set random2. The solid line indicates the 1:1 line and the dashed lines indicate a 63 deviation of 1 log unit from the 1:1 line



65 Figure SI 6 Prediction of the test set random3. The solid line indicates the 1:1 line and the dashed lines indicate a 66 deviation of 1 log unit from the 1:1 line



Figure SI 7 Prediction of the test set random4. The solid line indicates the 1:1 line and the dashed lines indicate a
 deviation of 1 log unit from the 1:1 line



71 Figure SI 8 Prediction of the test set random5. The solid line indicates the 1:1 line and the dashed lines indicate a

<sup>72</sup> deviation of 1 log unit from the 1:1 line

# 73 S-4 Conformers of isomer pairs



74

75 Figure SI 9 Side and top view of the used conformer of 2-methylbenzoate and 4-methylbenzoate





77 Figure SI 10 Side and top view of the used conformer of 2-chlorobenzoate and 4-chlorobenzoate



79 Figure SI 11 Side and top view of the used conformer of 2,6-dichlorobenzoate and 3,4-dichlorobenzoate

# 80 S-5 Comparison of 2,4,6-trimethylbenzene sulfonate and 2,4,6-

- 81 trimethylbenzoate
- 82 The COSMOfiles of 2,4,6-trimethylbenzene sulfonate and 2,4,6-trimethylbenzoate show the surface
- 83 polarisation, i.e., the distribution of the partial charges. The benzoic ring of 2,4,6-trimethylbenzene
- 84 sulfonate (Fig. SI 12) is less polarized than the benzoic ring of 2,4,6-trimethylbenzoate (Fig. SI 13),
- 85 which is indicated by the greenish patches of 2,4,6-trimethylbenzene sulfonate compared to the
- 86 yellow patches of 2,4,6-trimethylbenzoate.





Figure SI 12 COSMOfile of 2,4,6-trimethylbenzene sulfonate. The red colour indicates a negative partial charge, the green
 colour indicates a neutral surface segment, and yellow patches indicate a partial charge in between.



- 90
- Figure SI 13 COSMOfile of 2,4,6-trimethylbenzoate. The red colour indicates a negative partial charge, the green colour
  indicates a neutral surface segment, yellow patches indicate a partial charge in between.
- 93

# 94 S-6 Results of Tanimoto Index

		Brown–Forsythe	Mann-Whitney U
Tanimoto	mean group	variance analysis	median analysis
reference group	Test group	p-value	p-value
0.60-0.70 (n=30)	0.10-0.20 (n= 10)	0.09	0.35
0.60-0.70 (n=30)	0.20-0.30 (n= 24)	0.84	0.35
0.60-0.70 (n=30)	0.30-0.40 (n= 42)	0.28	0.04
0.60-0.70 (n=30)	0.40-0.50 (n= 26)	0.24	0.12
0.60-0.70 (n=30)	0.50-0.60 (n= 24)	0.67	0.70
0.60-0.70 (n=30)	0.70-0.80 (n= 4)	0.20	0.21

95 Table SI 3 Statistical results for the comparison of the different Tanimoto mean groups using the five random test sets

96

97 For the analysis of the domain of applicability, the standard test set selection procedure was 98 also modified to represent all chemicals in the test set once: the numbers one to four were 99 randomly assigned to the four chemicals of each bin and then all chemicals with an identical 100 number formed a test set while the rest of the chemicals formed the respective training set. 101 This is necessary to get the highest possible number of individual test cases and thus an 102 extended statistical evaluation of the domain of applicability.



104 Table SI 4 Statistical results for the comparison of the different Tanimoto mean groups using the four constructed test 105 sets

	Brown–Forsythe	Mann-Whitney U
Tanimoto mean group	variance analysis	median analysis
reference group	p-value	p-value

0.70-0.80 (n= 8)	0.10-0.20 (n= 9)	0.36	0.01
0.70-0.80 (n= 8)	0.20-0.30 (n= 21)	0.03	0.01
0.70-0.80 (n= 8)	0.30-0.40 (n= 29)	0.51	0.03
0.70-0.80 (n= 8)	0.40-0.50 (n= 19)	0.17	0.02
0.70-0.80 (n= 8)	0.50-0.60 (n= 27)	0.21	0.28
0.70-0.80 (n= 8)	0.60-0.70 (n=13)	0.64	0.21

106

## 107 S-7 COSMOconf template

- 108 COSMOconf was used to create more conformers than in common applications by increasing
- 109 the total number of possible conformers, reducing the energetic distance between
- 110 conformers, and loosening the clustering steps.
- 111 <?xml version="1.0" encoding="UTF-8" standalone="no"?>
- 112 <job>
- 113 <clean\_up>1</clean\_up>
- 114 <info>BP-TZVPD-FINE-COSMO+GAS\_new</info>
- 115 <molecule\_set\_in>input\_set.xml</molecule\_set\_in>
- 116 <molecule\_set\_out extractable="join">output\_set.xml</molecule\_set\_out>
- 117 <job\_schedule>
- 118 <step>
- 119 <number>1</number>
- 120 <info>conf. creation using balloon</info>
- 121 <method>BALLOON\_CONF\_GEN</method>
- 122 <status>ready</status>
- 123 </step>
- 124 <step>
- 125 <number>2</number>
- 126 <info>consistency check (using UNIQUECODE)</info>
- 127 <method>REDUCE\_TO\_UNIQUECODE</method>
- 128 <status>ready</status>
- 129 <reference>input\_set.xml</reference>

- 130 </step>
- 131 <step>
- 132 <number>3</number>
- 133 <info>sort w.r.t. energy</info>
- 134 <method>SORT\_BY\_E</method>
- 135 <status>ready</status>
- 136 </step>
- 137 <step>
- 138 <number>4</number>
- 139 <info>geodis clustering (thr1=1)</info>
- 140 <method>CLUSTER\_GEODIS</method>
- 141 <status>ready</status>
- 142 <geodis\_threshold1>1</geodis\_threshold1>
- 143 <geodis\_threshold2>1</geodis\_threshold2>
- 144 </step>
- 145 <step>
- 146 <number>5</number>
- 147 <info>reduce to 150 structures</info>
- 148 <method>REDUCE\_BY\_E\_MAX</method>
- 149 <status>ready</status>
- 150 <energy\_window>2000</energy\_window>
- 151 <n\_max>150</n\_max>
- 152 </step>
- 153 <step>
- 154 <number>6</number>
- 155 <info>BP/SV(P) cosmo single points</info>

- 156 <method>BP-SV\_P-COSMO-SP</method>
- 157 <status>ready</status>
- 158 </step>
- 159 <step>
- 160 <number>7</number>
- 161 <info>reduce to 50 structures or 25 kcal/mol energy window</info>
- 162 <method>REDUCE\_BY\_E\_MAX</method>
- 163 <status>ready</status>
- 164 <energy\_window>25</energy\_window>
- 165 <n\_max>50</n\_max>
- 166 </step>
- 167 <step>
- 168 <number>8</number>
- 169 <info>BP/SV(P) opt. with loose settings</info>
- 170 <method>BP-SV\_P-COSMO-LOOSE</method>
- 171 <status>ready</status>
- 172 </step>
- 173 <step>
- 174 <number>9</number>
- 175 <info>sort w.r.t. energy</info>
- 176 <method>SORT\_BY\_E</method>
- 177 <status>ready</status>
- 178 </step>
- 179 <step>
- 180 <number>10</number>
- 181 <info>standard geodis clustering (thr1=1)</info>

- 182 <method>CLUSTER\_GEODIS</method>
- 183 <status>ready</status>
- 184 <geodis\_threshold1>1</geodis\_threshold1>
- 185 <geodis\_threshold2>1</geodis\_threshold2>
- 186 </step>
- 187 <step>
- 188 <number>11</number>
- 189 <info>reduce to 25.0 kcal/mol window or max. 50 structures</info>
- 190 <method>REDUCE\_BY\_E\_MAX</method>
- 191 <status>ready</status>
- 192 <energy\_window>25</energy\_window>
- 193 <n\_max>12</n\_max>
- 194 </step>
- 195 <step>
- 196 <number>12</number>
- 197 <info>BP/TZVP COSMO optimization</info>
- 198 <method>BP-TZVP-COSMO</method>
- 199 <status>ready</status>
- 200 </step>
- 201 <step>
- 202 <number>13</number>
- 203 <info>sort w.r.t. energy</info>
- 204 <method>SORT\_BY\_E</method>
- 205 <status>ready</status>
- 206 </step>
- 207 <step>

- 208 <number>14</number>
- 209 <info>standard geodis clustering (thr=1)</info>
- 210 <method>CLUSTER\_GEODIS</method>
- 211 <status>ready</status>
- 212 <geodis\_threshold1>1</geodis\_threshold1>
- 213 <geodis\_threshold2>1</geodis\_threshold2>
- 214 </step>
- 215 <step>
- 216 <number>15</number>
- 217 <info>reduce to 50 conformers or 25 kcal/mol energy window</info>
- 218 <method>REDUCE\_BY\_E\_MAX</method>
- 219 <status>ready</status>
- 220 <energy\_window>25</energy\_window>
- 221 <n\_max>50</n\_max>
- 222 </step>
- 223 <step>
- 224 <number>16</number>
- 225 <info>BP-TZVP-COSMO conformer(s) info</info>
- 226 <method>PRINT\_CONF\_INFO</method>
- 227 <status>ready</status>
- 228 </step>
- 229 <step>
- 230 <number>17</number>
- 231 <molecule\_set\_out directory="BP-TZVP" extractable="separate">BP-TZVP-
- 232 COSMO.xml</molecule\_set\_out>
- 233 <info/>
- 234 <method>COPY\_COSMO\_FILE</method>

- 235 <status>ready</status>
- 236 <path>Results\_of\_BP-TZVP-COSMO</path>
- 237 </step>
- 238 <step>
- 239 <number>18</number>
- 240 <info>BP-TZVPD-FINE COSMO single point</info>
- 241 <method>BP-TZVPD-FINE-COSMO-SP</method>
- 242 <status>ready</status>
- 243 </step>
- 244 <step>
- 245 <number>19</number>
- 246 <info>sort w.r.t. energy</info>
- 247 <method>SORT\_BY\_E</method>
- 248 <status>ready</status>
- 249 </step>
- 250 <step>
- 251 <number>20</number>
- 252 <info>BP-TZVPD-FINE-COSMO conformer(s) info</info>
- 253 <method>PRINT\_CONF\_INFO</method>
- 254 <status>ready</status>
- 255 </step>
- 256 <step>
- 257 <number>21</number>
- 258 <molecule\_set\_out extractable="join">BP-TZVPD-FINE-
- 259 COSMO.xml</molecule\_set\_out>
- 260 <info/>
- 261 <method>COPY\_COSMO\_FILE</method>

- 262 <status>ready</status>
- 263 <path>Results\_of\_BP-TZVPD-FINE-COSMO</path>
- 264 </step>
- 265 <step>
- 266 <number>22</number>
- 267 <info>BP/TZVP GAS optimization</info>
- 268 <method>BP-TZVP-GAS</method>
- 269 <status>ready</status>
- 270 </step>
- 271 <step>
- 272 <number>23</number>
- 273 <info>sort w.r.t. energy</info>
- 274 <method>SORT\_BY\_E</method>
- 275 <status>ready</status>
- 276 </step>
- 277 <step>
- 278 <number>24</number>
- 279 <info>standard geodis clustering (thr=1)</info>
- 280 <method>CLUSTER\_GEODIS</method>
- 281 <status>ready</status>
- 282 <geodis\_threshold1>1</geodis\_threshold1>
- 283 <geodis\_threshold2>1</geodis\_threshold2>
- 284 </step>
- 285 <step>
- 286 <number>25</number>
- 287 <info/>

- 288 <method>PRINT\_CONF\_INFO</method>
- 289 <status>ready</status>
- 290 </step>
- 291 <step>
- 292 <number>26</number>
- 293 <molecule\_set\_out directory="BP-TZVP" extractable="separate">BP-TZVP-
- 294 GAS.xml</molecule\_set\_out>
- 295 <info/>
- 296 <method>WRITE\_ENERGY\_FILE</method>
- 297 <status>ready</status>
- 298 <path>Results\_of\_BP-TZVP-COSMO</path>
- 299 <add\_comment>METHOD=b-p;BASIS=def-TZVP;</add\_comment>
- 300 </step>
- 301 <step>
- 302 <number>27</number>
- 303 <info>BP-TZVPD-FINE single point</info>
- 304 <method>BP-TZVPD-GAS-SP</method>
- 305 <status>ready</status>
- 306 </step>
- 307 <step>
- 308 <number>28</number>
- 309 <info>sort w.r.t. energy</info>
- 310 <method>SORT\_BY\_E</method>
- 311 <status>ready</status>
- 312 </step>
- 313 <step>
- 314 <number>29</number>

- 315 <info>BP-TZVPD-FINE conformer(s) info</info>
- 316 <method>PRINT\_CONF\_INFO</method>
- 317 <status>ready</status>
- 318 </step>
- 319 <step>
- 320 <number>30</number>
- 321 <info/>
- 322 <method>WRITE\_ENERGY\_FILE</method>
- 323 <status>ready</status>
- 324 <path>Results\_of\_BP-TZVPD-FINE-COSMO</path>
- 325 <add\_comment>METHOD=b-p;BASIS=def2-TZVPD;</add\_comment>
- 326 </step>
- 327 </job\_schedule>
- 328 </job>
- 329