SUPPLEMENTARY INFORMATION

How do immobilised cell-adhesive Arg-Gly-Asp-containing peptides behave at the PAA brush surface?

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ARTICLE HISTORY
Compiled July 5, 2018

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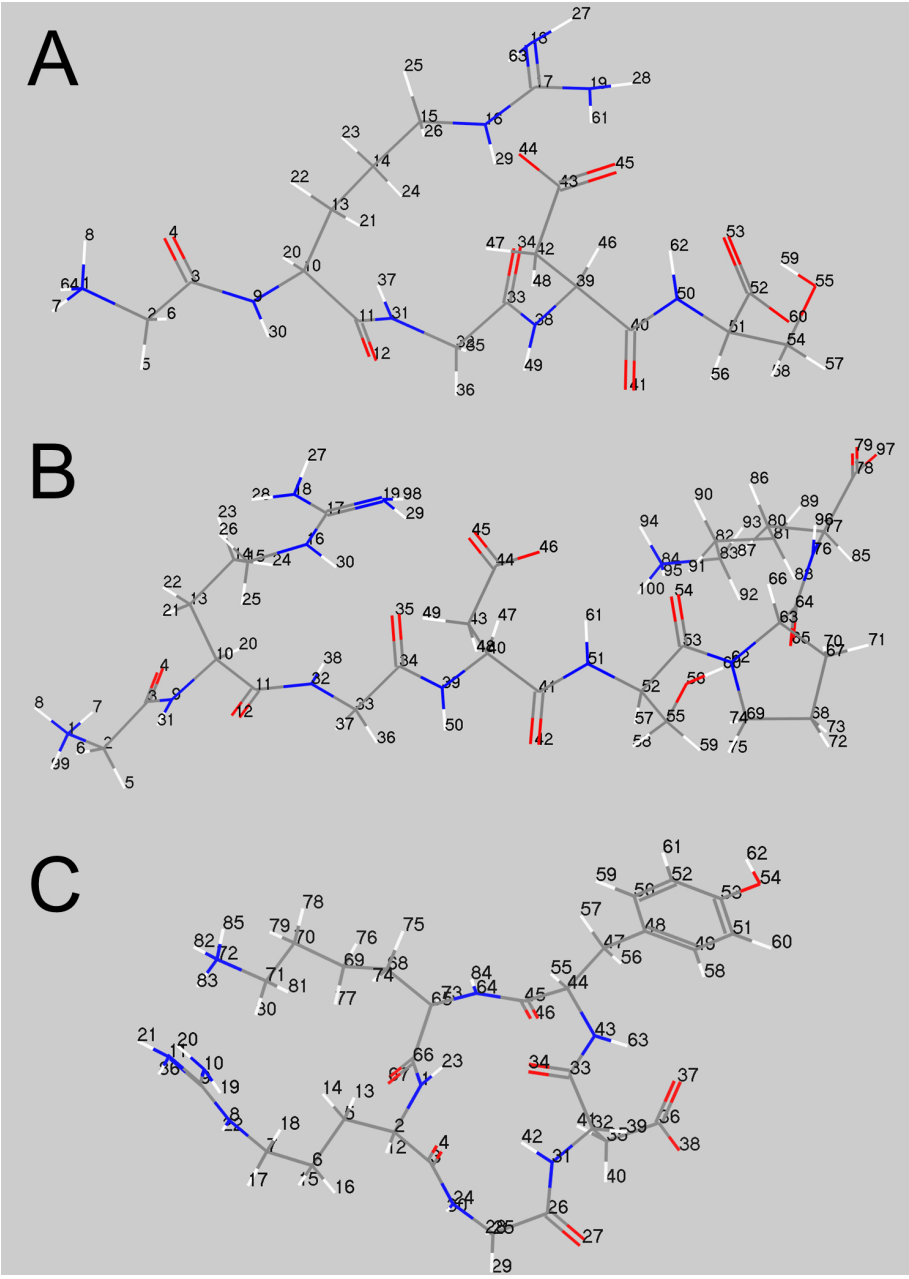

Figure S1 The atom numbers of the RGD peptides: GRGDS (a), GRGDSPK (b) and cRGDyK (c).

Table S1 Comparison of calculated bond lengths l, selected bond angles Θ and dihedrals Ω of the RGD sequences in GRGDS with experimental values [3]. The root-mean-square deviations (RMSD) are given for bonds and valence angles.

	RGD sequence of GRGDS					
Definition	l_{DFT} [Å]	$l_{\mathrm{exp.}}$ [Å]	Θ_{DFT}[°]	Θ_{exp}[°]	Ω_{DFT}[°]	Ω_{exp}[°]
N_9C_{10}	1.469	1.507				
$C_{10}C_{13}$	1.568	1.536				
$C_{14}C_{15}$	1.546	1.525				
$C_{15}N_{16}$	1.483	1.471				
$N_{16}C_{17}$	1.335	1.326				
$C_{17}N_{18}$	1.360	1.337				
$C_{17}N_{19}$	1.360	1.332				
$C_{10}C_{11}$	1.547	1.518				
$C_{11}O_{12}$	1.244	1.223				
$C_{11}N_{31}$	1.362	1.344				
$N_{31}C_{32}$	1.474	1.457				
$C_{32}C_{33}$	1.545	1.543				
$C_{33}O_{34}$	1.255	1.231				
$C_{33}N_{38}$	1.348	1.344				
$N_{38}C_{39}$	1.470	1.436				
$C_{39}C_{40}$	1.551	1.554				
$C_{39}C_{42}$	1.563	1.554				
$C_{42}C_{43}$	1.558	1.503				
$C_{43}O_{44}$	1.275	1.246				
$C_{43}O_{45}$	1.274	1.270				
RMSD (bonds)	0.025					
$C_9C_{10}C_{11}$			107.1	108.8		
$C_{15}N_{16}C_{17}$			125.5	124.3		
$N_{16}C_{17}N_{18}$			119.7	117.9		
$N_{16}C_{17}N_{19}$			120.4	121.4		
$C_9C_{10}C_{13}$			111.0	112.1		
$N_{38}C_{39}C_{40}$			108.7	108.9		
$C_{42}C_{43}O_{44}$			115.5	115.4		
$C_{42}C_{43}O_{45}$			118.3	120.5		
RMSD (angles)	1.4					
$C_3N_9C_{10}C_{11}$					-158.3	-
$N_9C_{10}C_{11}N_{31}$					147.6	160.3
$C_{11}N_{31}C_{32}C_{33}$					-77.8	-85.5
$N_{31}C_{32}C_{33}N_{38}$					-110.6	-129.7
$C_{33}N_{38}C_{39}C_{40}$					-144.4	-102.6
$N_{38}C_{39}C_{40}N_{50}$					172.0	-

Table S2 Comparison of calculated bond lengths l, selected bond angles Θ and dihedrals Ω of the RGD sequences in GRGDSPK with experimental values [3]. The root-mean-square deviations (RMSD) are given for bonds and valence angles.

	RGD sequence of GRGDSPK					
Definition	l_{DFT} [Å]	$l_{\mathrm{exp.}}$ [Å]	Θ_{DFT}[°]	Θ_{exp}[°]	Ω_{DFT}[°]	Ω_{exp}[°]
N_9C_{10}	1.473	1.507				
$C_{10}C_{13}$	1.559	1.536				
$C_{14}C_{15}$	1.553	1.525				
$C_{15}N_{16}$	1.475	1.471				
$N_{16}C_{17}$	1.339	1.326				
$C_{17}N_{18}$	1.348	1.337				
$C_{17}N_{19}$	1.364	1.332				
$C_{10}C_{11}$	1.546	1.518				
$C_{11}O_{12}$	1.245	1.223				
$C_{11}N_{32}$	1.361	1.344				
$N_{32}C_{33}$	1.458	1.457				
$C_{33}C_{34}$	1.544	1.543				
$C_{34}O_{35}$	1.253	1.231				
$C_{34}N_{39}$	1.348	1.344				
$N_{39}C_{40}$	1.468	1.436				
$C_{40}C_{41}$	1.548	1.554				
$C_{40}C_{43}$	1.564	1.554				
$C_{43}C_{44}$	1.557	1.503				
$C_{44}O_{45}$	1.274	1.246				
$C_{44}O_{46}$	1.277	1.270				
RMSD (bonds)	0.123					
$C_9C_{10}C_{11}$			106.8	108.8		
$C_{14}N_{16}C_{17}$			128.1	124.3		
$N_{18}C_{17}C_{19}$			118.5	117.9		
$N_{16}C_{17}C_{19}$			118.9	121.4		
$N_9C_{10}C_{13}$			110.5	112.1		
$N_{39}C_{44}O_{45}$			115.7	115.4		
$C_{43}C_{44}O_{46}$			118.4	120.5		
RMSD (angles)	2.1					
$C_3N_9C_{10}C_{11}$					-146.3	-
$N_9C_{10}C_{11}N_{32}$					133.7	160.3
$C_{11}N_{32}C_{33}C_{34}$					-78.2	-85.5
$N_{32}C_{33}C_{34}N_{39}$					-178.2	-129.7
$C_{34}N_{39}C_{40}C_{41}$					-156.6	-102.6
$N_{39}C_{40}C_{41}N_{51}$					163.9	-

Table S3 Comparison of calculated bond lengths l, selected bond angles Θ and dihedrals Ω of the RGD sequences in cRGDyK with experimental values [3]. The root-mean-square deviations (RMSD) are given for bonds and valence angles.

	RGD sequence of cRGDyK					
Definition	l_{DFT} [Å]	$l_{\mathrm{exp.}}$ [Å]	Θ_{DFT}[°]	Θ_{exp}[°]	Ω_{DFT}[°]	Ω_{exp}[°]
N_1C_2	1.481	1.507				
C_2C_5	1.549	1.536				
C_6C_7	1.538	1.525				
C_7N_8	1.483	1.471				
N_8C_9	1.334	1.326				
C_9N_{10}	1.343	1.337				
C_9N_{11}	1.377	1.332				
C_2C_3	1.549	1.518				
C_3O_4	1.247	1.223				
C_3N_{24}	1.360	1.344				
$N_{24}C_{25}$	1.471	1.457				
$C_{25}C_{26}$	1.557	1.543				
$C_{26}O_{27}$	1.246	1.231				
$C_{26}N_{31}$	1.356	1.344				
$N_{31}C_{32}$	1.476	1.436				
$C_{32}C_{33}$	1.562	1.554				
$C_{35}C_{36}$	1.559	1.554				
$C_{32}C_{35}$	1.551	1.503				
$C_{36}O_{37}$	1.286	1.246				
$C_{36}O_{38}$	1.265	1.270				
RMSD (bonds)	0.024					
$N_1C_2C_3$			107.5	108.8		
$C_7N_8C_9$			126.4	124.3		
$N_{10}C_9N_{11}$			118.3	117.9		
$N_{11}C_9N_8$			119.4	121.4		
$C_5C_2C_3$			111.3	112.1		
$N_{31}C_{32}C_{33}$			103.6	108.9		
$C_{39}C_{36}O_{37}$			116.2	115.4		
$C_{39}C_{36}O_{38}$			118.6	120.5		
RMSD (angles)	4.9					
$C_{66}N_1C_2C_3$					149.8	-
$N_1C_2C_3N_{24}$					105.32	160.3
$C_3N_{24}C_{25}C_{26}$					-88.2	-85.5
$N_{24}C_{25}C_{26}N_{31}$					-134.2	-129.7
$C_{26}N_{31}C_{32}C_{33}$					166.7	-102.6
$N_{31}C_{32}C_{33}N_{43}$					168.2	-

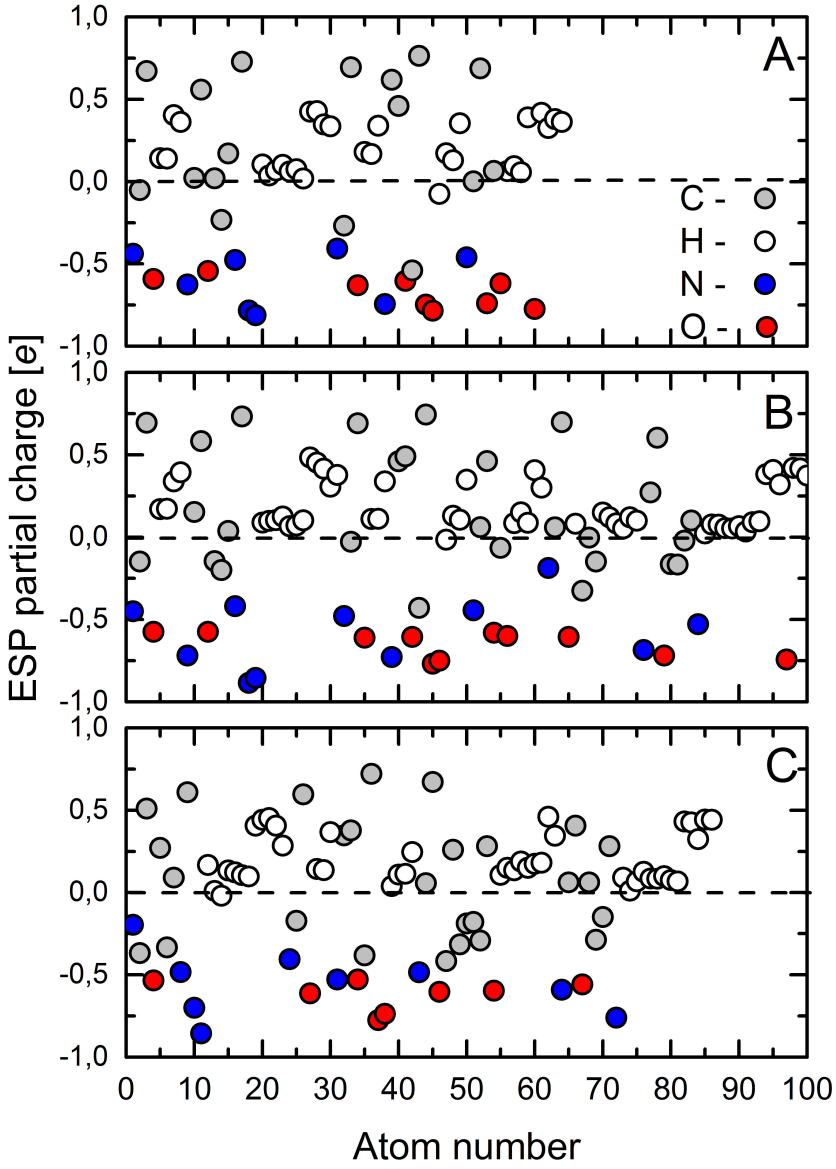

Figure S2 Calculated ESP partial charges *versus* atom number in GRGDS (a), GRGDSPK (b) and cRGDyK (c) at pH=8. For the atom numbers, See Figure S1.

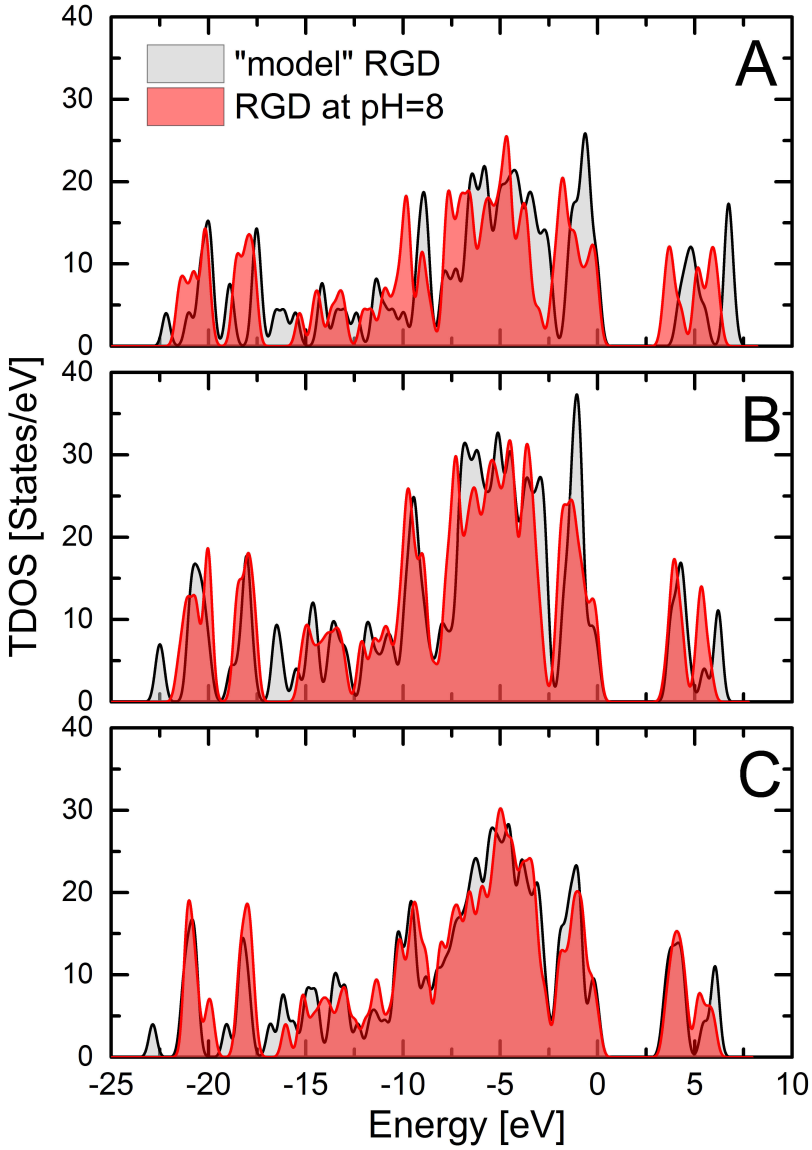

Figure S3 The calculated total density of states (TDOS) of GRGDS (a), GRGDSPK (b) and cRGDyK (c). The energy of HOMO state is set at 0 eV. The energy gap is 3.74/3.57 eV, 4.17/3.44 eV and 3.43/3.51 eV for the neutral/charged GRGDS, GRGDSPK and cRGDyK peptides, respectively.

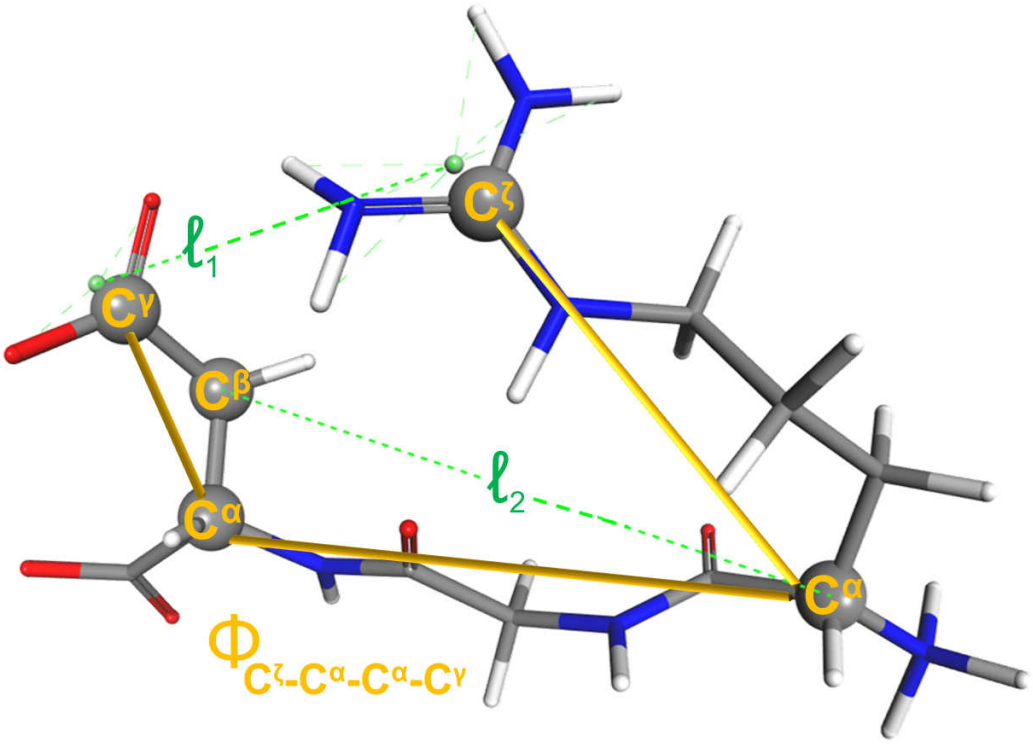

Figure S4 The definitions of three criteria for the evaluation of the structure-activity relationship of RGD-containing peptides [1,2]: ℓ_1 is a distance between the centroids of the charged side groups of Asp and Arg, shown as green beads; ℓ_2 is a distance between C^{α} of Arg and C^{β} of Asp; the pseudo-dihedral angle $\Phi_{C^{\zeta}-C^{\alpha}-C^{\alpha}-C^{\gamma}}$ describes the mutual orientation of the Arg and Asp side chains.

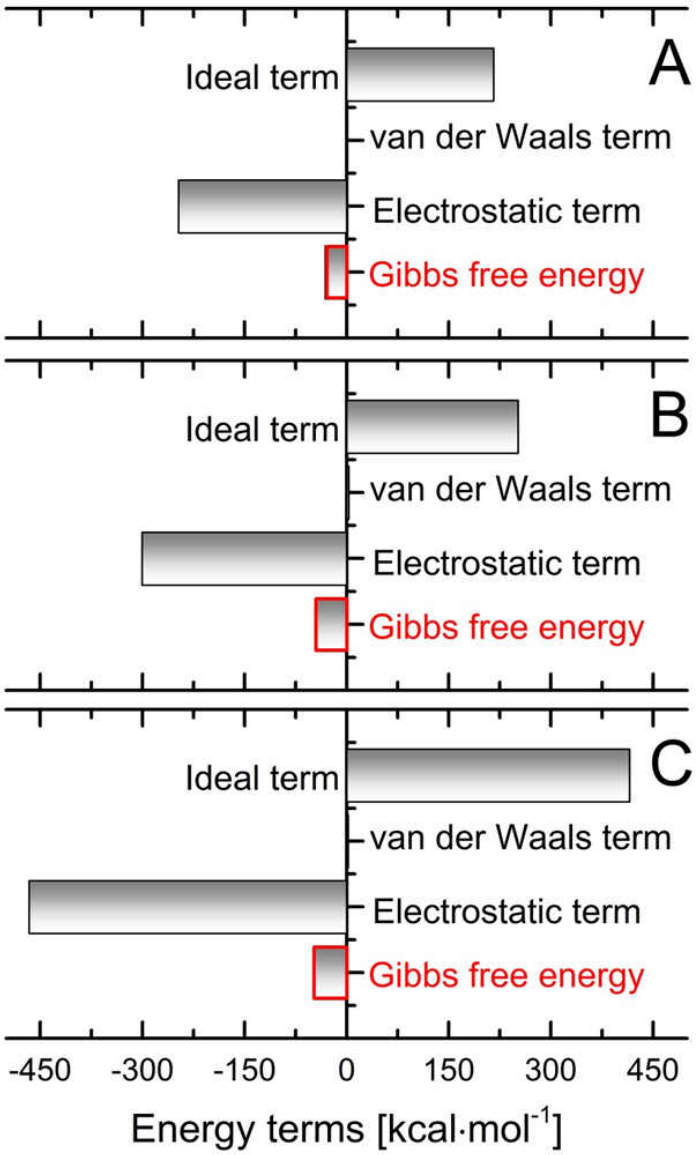

Figure S5 The contributions and the Gibbs free energy of hydration of "neutral" GRGDS (a), GRGDSPK (b) and cRGDyK (c) RGD peptides. $\Delta G_{solv,\mathrm{GRGDS}}$=-31.58 kcal·mol^{-1}, $\Delta G_{solv,\mathrm{GRGDSPK}}$=-45.58 kcal·mol^{-1} and $\Delta G_{solv,\mathrm{cRGDyK}}$=-48.87 kcal·mol^{-1}.

References

[1] Kostidis S, Stavrakoudis A, Biris T, Tsoukatos D, Sakarellos C, Tsikaris V. The relative orientation of the Arg and Asp side chains defined by a pseudodihedral angle as a key criterion for evaluating the structure-activity relationships of RGD peptides. J Peptide Sci. 2004;10:494–509.

[2] Poully J-C, Nieuwjaer N, Schermann JP. Structure and dynamics of molecules of pharmaceutical interest in gas phase and in aqueous phase. Phys Scr. 2008;78:058123(1–5).

[3] Eggleston DS, Feldman SH. Structure of the fibrinogen binding sequence: Arginylglycylaspartic acid (RGD). Int J Peptide Protein Res. 1990;36:161–166.