Electronic Supplementary Material (ESI) for Physical Chemistry Chemical Physics.

On the Coupling between the Dynamics of Protein and Water

Supporting Information

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Table S1. Average water residence time constants (τ_1, τ_2, τ_3), amplitude-weighted average residence times (τ_{avg}) and amplitudes (a, b, c) of water molecules within 3.5 Å from the flexible peptides' surface.

residue[1]	a	b	c	τ_1, ps	τ_2, ps	τ_3, ps	τ_{avg}, ps
I	0.29	0.22	0.49	0.66	3.58	13.50	7.58
V	0.31	0.43	0.26	0.77	6.75	15.87	7.25
L	0.34	0.44	0.21	0.80	7.38	17.17	7.21
F	0.37	0.37	0.26	0.93	6.43	17.39	7.23
C	0.27	0.44	0.29	0.70	4.32	13.53	6.05
M	0.40	0.28	0.33	0.86	5.69	13.51	6.33
A	0.26	0.49	0.25	0.84	5.30	14.19	6.35
T	0.26	0.57	0.17	0.93	7.59	16.21	7.32
S	0.23	0.39	0.38	0.91	4.98	11.96	6.73
W	0.35	0.36	0.29	0.95	5.29	17.75	7.36
Y	0.31	0.41	0.28	0.87	5.66	17.47	7.47
H	0.30	0.42	0.28	0.98	5.42	15.84	6.98
N	0.21	0.35	0.44	0.88	4.05	12.83	7.28
Q	0.23	0.43	0.34	0.97	4.67	13.75	6.90
D	0.17	0.28	0.54	1.10	7.69	25.47	16.19
E	0.17	0.31	0.52	0.98	8.17	21.74	14.02
K	0.27	0.62	0.11	1.01	6.79	19.71	6.66
R	0.33	0.48	0.19	1.06	6.52	17.59	6.76
Bulk[b]	0.001	0.28	0.72	5.06	5.12	4.76	4.84

[1]Residue X in $(XXGG)_5$ peptides; [b]Residence time of water in the bulk.

Table S2. Average water residence time constants (τ_1, τ_2, τ_3), amplitude-weighted average residence times (τ_{avg}) and amplitudes (a, b, c) of water molecules within 3.5 Å from the constrained peptides' surface.

residue	a	b	c	τ_1, ps	τ_2, ps	τ_2, ps	τ_{avg}, ps
I	0.34	0.33	0.34	0.79	7.04	19.76	9.20
V	0.29	0.40	0.32	0.79	5.66	15.90	7.55
L	0.36	0.46	0.18	0.85	8.71	21.84	8.22
F	0.37	0.32	0.30	0.95	6.32	18.87	8.12
C	0.33	0.37	0.30	0.95	4.66	14.52	6.45
M	0.42	0.41	0.16	0.97	6.82	18.83	6.30
A	0.25	0.42	0.33	0.81	4.73	13.66	6.71
T	0.25	0.55	0.20	0.99	7.72	19.54	8.35
S	0.23	0.48	0.29	0.89	6.08	14.76	7.37
W	0.36	0.37	0.27	0.94	5.98	20.90	8.22
Y	0.33	0.45	0.22	0.99	6.57	21.79	8.01
H	0.27	0.39	0.35	0.82	4.65	16.62	7.79
N	0.24	0.40	0.36	0.93	5.06	16.11	8.04
Q	0.26	0.48	0.26	1.10	5.98	14.47	6.90
D	0.19	0.33	0.48	1.32	9.66	33.01	19.34
E	0.16	0.30	0.54	1.11	7.62	24.30	15.64
K	0.27	0.48	0.25	1.00	5.99	17.69	7.64
R	0.35	0.53	0.12	1.13	8.37	25.19	7.84

Table S3. Average water residence time constants (τ_1, τ_2, τ_3), amplitude-weighted average residence times (τ_{avg}) and amplitudes (a, b, c) of water molecules within 3.5 Å from the flexible peptides' surface.

residue	a	b	c	τ_1, ps	τ_2, ps	τ_3, ps	τ_{avg}, ps
W	0.35	0.36	0.29	0.95	5.29	17.75	7.36
R	0.33	0.48	0.19	1.06	6.52	17.59	6.76
R TIP5P[1]	0.33	0.50	0.17	1.32	11.30	33.82	11.89
Bulk TIP5P[1]	~0	0.14	0.86	0.05	0.97	8.54	7.51

[1]An alternative water model was used (TIP5P). In other cases SPC/E water model was used.

Table S4. Average water residence time constants (τ_1, τ_2, τ_3), amplitude-weighted average residence times (τ_{avg}) and amplitudes (a, b, c) of water molecules within 3.5 Å from the constrained peptides' surface.

residue	a	b	c	τ_1, ps	τ_2, ps	τ_3, ps	τ_{avg}, ps
W	0.36	0.37	0.27	0.94	5.98	20.90	8.22
W#2[1]	0.39	0.38	0.23	1.08	6.74	24.09	8.60
R	0.35	0.53	0.12	1.13	8.37	25.19	7.84
R TIP5P	0.30	0.49	0.21	1.15	11.69	41.35	14.62

[1]An alternative conformation of constrained $(WWGG)_5$

Table S5. Values of average water residence time (%) within different cutoff distances $(\tau_{avg}^{Constrained} - \tau_{avg}^{Flexible})$.

residue	3.5 Å	5 Å	8 Å	12Å
T	1.02	1.21	3.48	4.17
W	0.87	1.33	4.49	8.00
E	1.61	2.56	2.71	4.40
R	1.07	1.74	3.33	6.33

Table S6. Amplitude-weighted average residence times (τ_{avg}, ps) of water molecules within the distances 8-12 Å from the flexible / constrained peptides' surface.

residue	8-12 Å	Δ
T	7.30 / 8.13	0.83
W	7.34 / 7.70	0.36
E	7.40 / 7.88	0.48
R	7.32 / 7.91	0.59

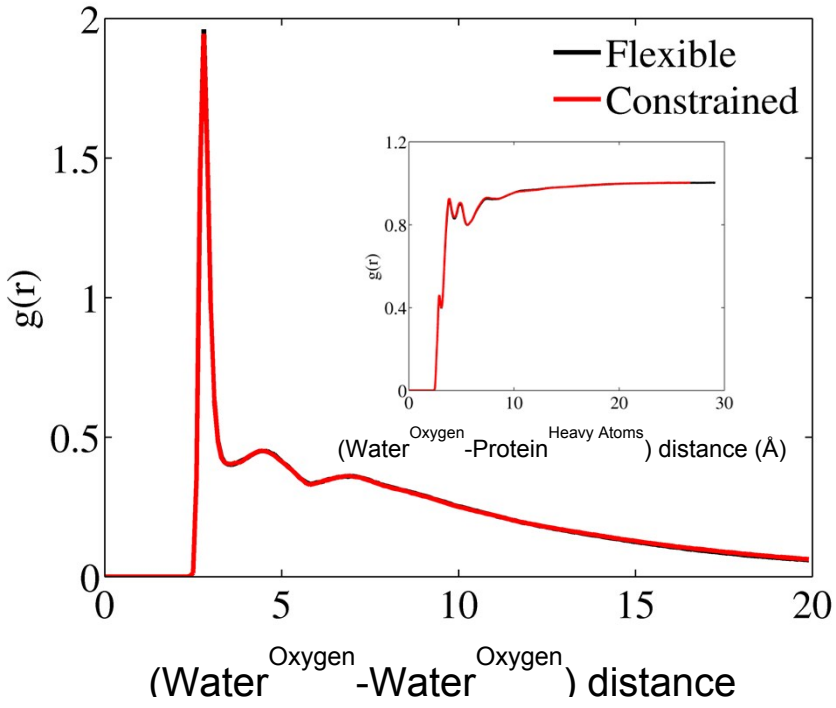


Figure S1. Radial distribution function (RDF) $Water^{Oxygen}$ -$Water^{Oxygen}$ of water molecules close to flexible (black) and constrained (red) version of peptide RRGG. Main panel: oxygen–oxygen RDF of water molecules within 3.5 Å of the peptide surface; insertion: RDF function for $Water^{Oxygen}$ -$Protein^{Heavy\ atoms}$, including all simulated water molecules.

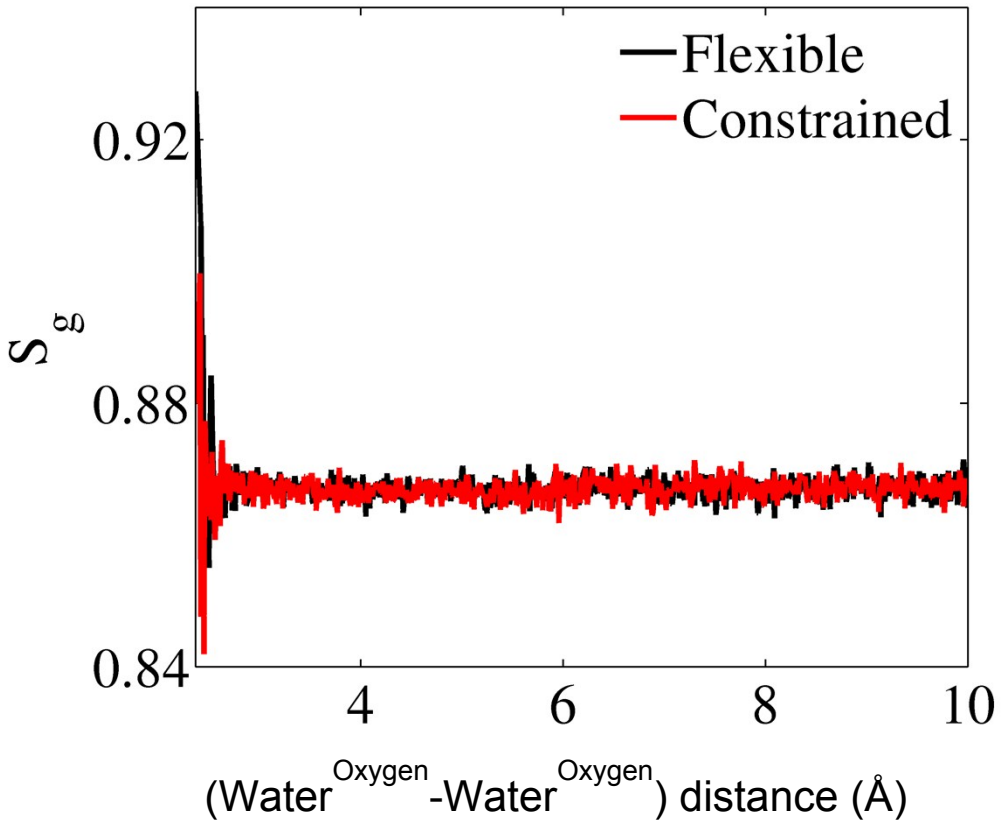
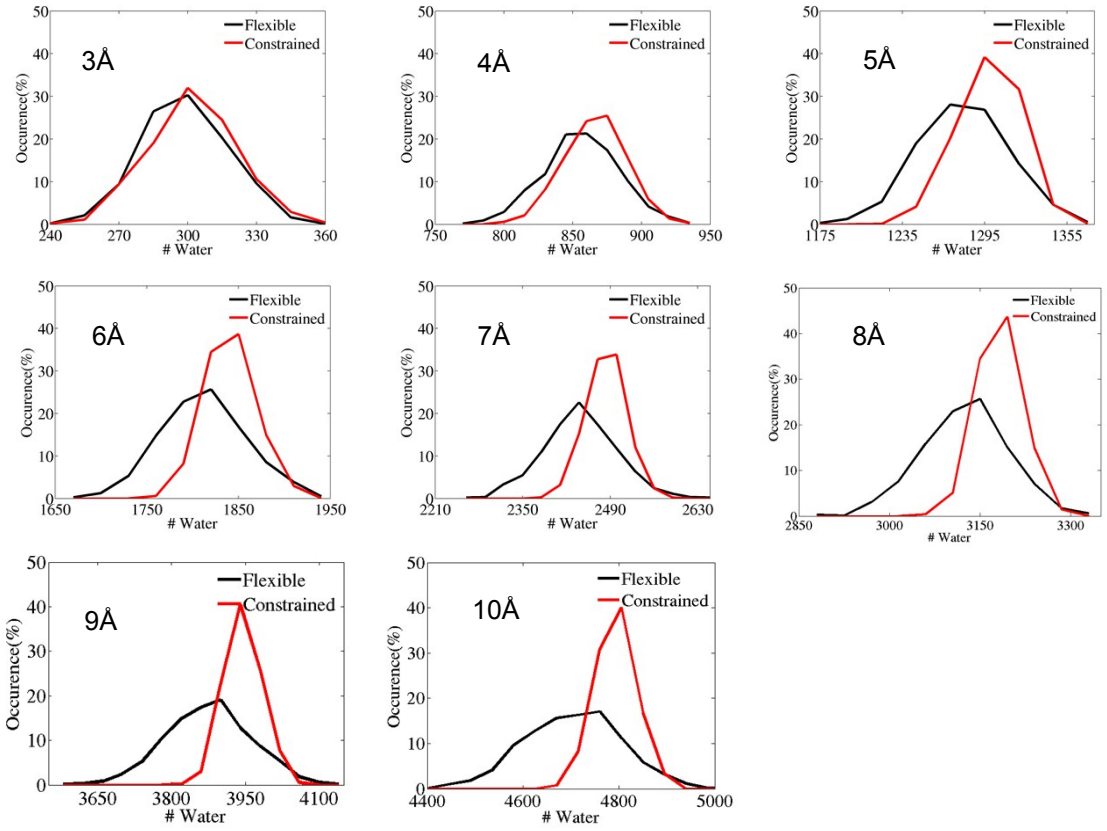
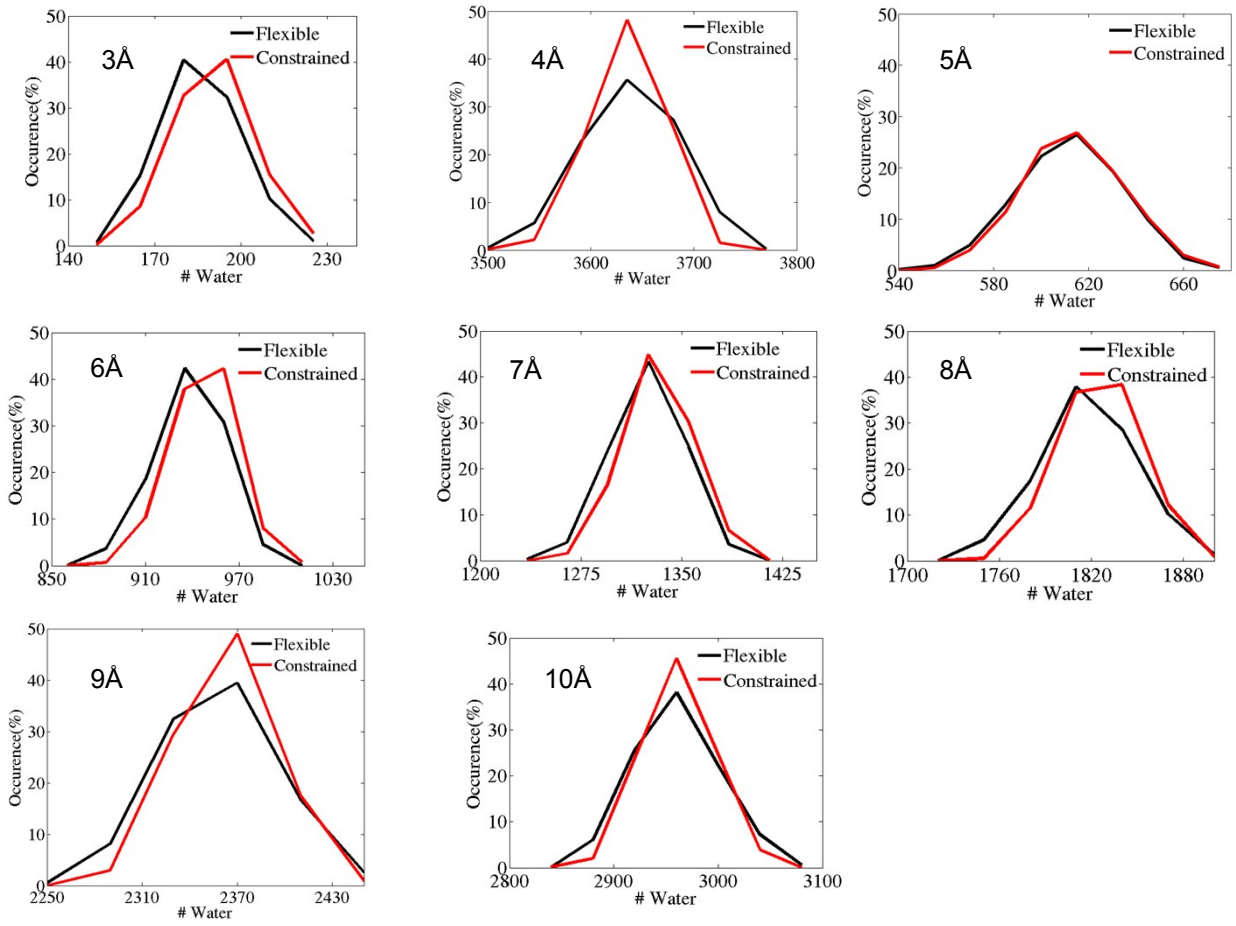


Figure S2. Tetrahedral order parameter of water molecules around flexible (black) and constrained (red) versions of the RRGG peptide versions.



Figures S3. Distribution of water molecules number within the certain cutoff distance from the RRGG peptide surface. Black – flexible peptide version; red – constrained peptide version. Cutoff distances: 3, 4, 5, 6, 7, 8, 9, 10 Å.



Figures S4. Distribution of water molecules number within the certain cutoff distance from the VVGG peptide surface. Black – flexible peptide version; red – constrained peptide version. Cutoff distances: 3, 4, 5, 6, 7, 8, 9, 10 Å.

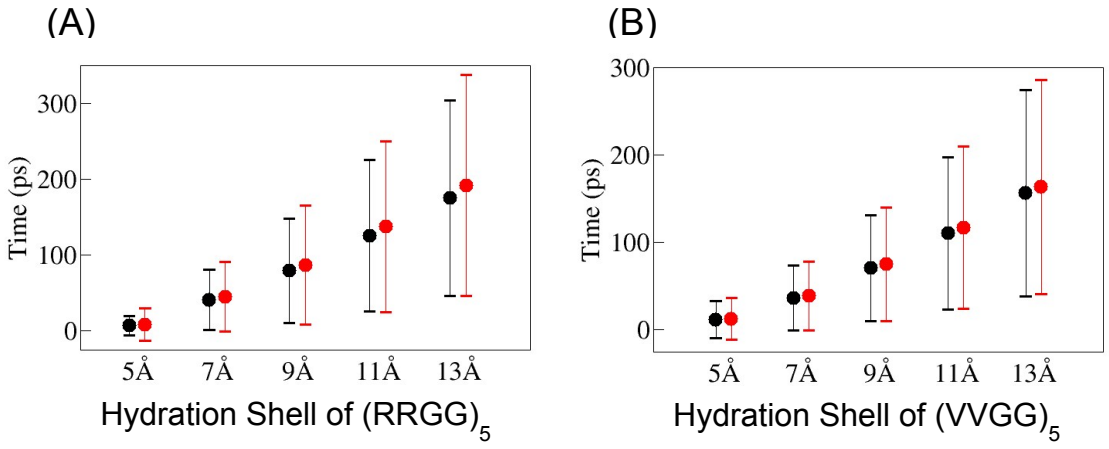


Figure S5. Average time (ps) it takes a water molecule to reach a distance of 5, 7, 9, 11, 13 Å from the peptide surface. Black – flexible peptide version; red – constrained peptide version. (A) Water close to RRGG peptide; (B) Water close to VVGG peptide.

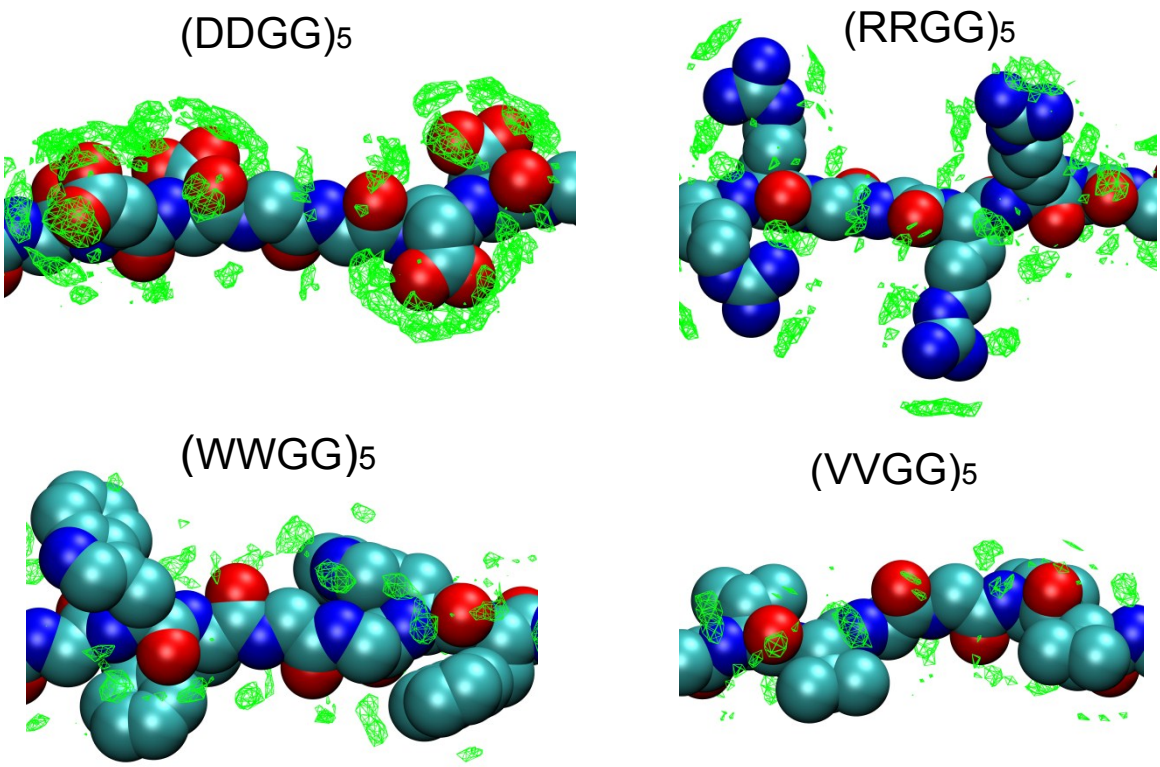


Figure S6. Thermodynamically favorable hydration sites ($\Delta A \leq -2$ kcal/mol) on the surface of different peptides (constrained versions of DDGG, RRGG, WWGG, and VVGG). The sites are marked with the green wireframe; peptides are represented as vdW spheres. In the peptides: oxygens are red, nitrogens are blue, and carbons are cyan.