## Electronic Supplementary Information

## Do zwitterion species exist in the non-enzymatic peptide bond formation?

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Electronic Supplementary Material (ESI) for Chemical Communications This journal is The Royal Society of Chemistry 2012



**Figure S1.** Time evolution of some geometrical parameters obtained in the QM/MM MD simulations carried out on the zwitterionic intermediate state. The different conformers appeared at different times on the trajectory are indicated.



Figure S2. Zwitterion intermediates located at M06-2X/MM level of theory.



**Figure S3**. PES for the non-catalyzed peptide bond formation mechanism obtained at AM1/MM level. Distances are in Å and energies in kJ·mol<sup>-1</sup>

		RC	ZWa	ZWb	ZWc	ZWd
water	01	-0.68	-1.11	-1.03	-1.03	-1.00
	NH <sub>2</sub>	-0.40	+0.50	+0.40	+0.25	+0.24
	μ	3.92	8.87	4.61	9.40	5.79
no water	01	-0.55	-0.85	-0.78	-0.74	-0.72
	NH <sub>2</sub>	-0.29	+0.27	+0.26	+0.21	+0.16
	μ	2.70	6.36	3.50	6.68	4.13

**Table S1**. Dipole moments (in Debyes) and NPA charges (in a.u) on  $NH_2$  and O1 moieties in reactant and zwitterion structures in solution. Results of single point calculations in gas phase are also reported to evaluate the polarization effect.

**Table S2.** Key distances (in Å) of final optimized structures obtained at M06-2X level with the standard 6-31+G(d,p) basis set and including the effect of the aqueous solution by means of the CPCM<sup>1</sup> and SMD<sup>2</sup> continuum models, as implemented in Gaussian 09 program.<sup>3</sup> First column correspond to the initial structure employed in the calculations while column 4<sup>th</sup> and 7<sup>th</sup> indicates the character of the optimized structure within the CPCM and SMD models.

starting structure	Optimized structure with CPCM model			Optimized structure with SMD model		
	d(N-C)	d(C-O)	character	d(N-C)	d(C-O)	character
ZWa	1.64	1.43	ZWa	1.59	1.43	ZWa
ZWb	1.64	1.43	ZWb	1.65	1.43	ZWb
ZWc	2.85	1.34	Reactant Complex	1.62	1.44	ZWc
ZWd	3.14	1.34	Reactant Complex	3.14	1.34	Reactant Complex

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