Supporting Information

Thermodynamic Study of Interactions between ZnO and ZnO Binding Peptides using Isothermal Titration Calorimetry

Marion J. Limo and Carole C. Perry*

Biomolecular and Materials Interface Research Group, Interdisciplinary Biomedical Research Centre, School of Science and Technology, Nottingham Trent University, Clifton Lane, Nottingham, NG1 8NS, U.K.

S1. Support for the choice of aqueous media for ITC experiments.

The ideal ITC experiment to probe interfacial changes would include all ionic species and solid phases present in solution during synthesis of ZnO, test their interaction with peptide simultaneously and be able to identify individual events that contribute to the global heat change measured. However, this is not always feasible, in most cases ITC experiments require a simplification of the actual event being studied to be able to interpret data and enable separation of individual events. Interactions were studied using aqueous media like in the synthesis studies but this meant that there was a decrease in the pH in the sample cell with continued titration of peptide into the sample cell. At a concentration of 3.1 mM, the pH of the peptides was pH $_{3.08 \pm 0.35}$ and the pH of the water was pH $_{5.77 \pm 0.23}$ without and with the ZnO particles. However the same decrease in pH occurred in the control dilution experiment (titration of peptide into water) and the interaction experiment (titration of peptide into water containing ZnO particles). At the end of the titration of the controls and interaction experiments the pH in the sample cell had been decreased to pH $_{3.92 \pm 0.35}$. In ITC experiments, matching the composition of the components in the sample cell and syringe such as concentration of salts used, pH and buffers helps to minimize dilution heat changes that may plausibly override binding signals. The heat changes measured from control dilution experiments were small in comparison to heat changes of interaction with ZnO therefore there was no interference.

S2. DLS size measurements of ZnO binding peptides 1 mg/ml (GT-16 = 0.62 mM, G-12 = 0.75 mM, G-12A6 = 0.78 mM) in water, close to the concentration of peptide in the ITC cell at the end of each experiment (0.52 mM). DLS data in volume percentage distribution shows that there were aggregates of different sizes in solution but the number percentage distribution shows that the average hydrodynamic diameter of the majority of aggregates was ~60 nm in size.







S4. (a-c) ITC isothermal profiles (replicates) showing titrations of 3.1 mM G-12 into a suspension of 0.1 mM ZnO platelets (bulk concentration). Isotherms have been fit using two sets of independent sites model. This demonstrates the practical difficulties in modelling where inconsistencies in values can be obtained even where isothermal profiles have very similar shapes. The shapes of the isothermal profiles in (a) and (b) appear to be very similar showing reproducibility of the experiment. The profile of the third repeat (c) looks slight less similar to the first two yet the values of thermodynamic parameters obtained after fitting data using two sets of independent sites model give more similar values for (b) and (c).



G-12 and ZnO	Dp	KA (M-1)	ΔH (Kcal mol-1)	T∆S (Kcal mol-1)	∆G (Kcal mol-1)
Experiment a	+ve	5.50 x 105 ± 1.11 x 105	58.78 ± 191 *	66.45 *	-7.67
	- ve	1.85 x 105 ± 4.56 x 104	-7.33 ± 0.64	-0.15	-7.19
Experiment b	+ve	9.94 x 105 ± 2.98 x 105	5.82 ± 2.4	14.01	-8.19
	-ve	1.30 x 105 ± 1.10 x 104	-6.30 ± 0.35	0.68	-6.98
Experiment c	+ve	2.15 x 106 ± 9.05 x 105	-0.97± 1.2 *	7.66	-8.63
	-ve	1.60 x 105 ± 1.40 x 104	-6.06 ± 0.16	1.03	-7.10

(+ve) endothermic, (-ve) exothermic, (*) unreasonable data for the rapidly completed endothermic process

S5. (a-d) ITC isothermal profile showing titrations of 3.1 mM G-12 into a suspension of 0.1 mM ZnO platelets (bulk concentration) fit using sequential binding sites model (to consider dependent binding). This is the same isotherm from Figure S4 b which was fit using two sets of independent binding sites model. Using sequential binding sites model, fitting improved with increase in number of binding sites but this generates more thermodynamic parameters with no meaningful interpretation.

