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

Modeling of minimal systems based on ATP-Zn coordination for chemically fueled self-assembly

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Supporting Information

S1. Hysteresis assessment

Table 1: Free energy (FE) from WT-MTD simulations of MTP-[$ZnCH_3TACN]^{2+}$ in water, starting from ion-contact (i.c.) and from water-mediated (w.m.) coordination. All quantities are expressed in kcal/mol and the ground state is taken as a reference. The uncertainty ΔFE is calculated as the semi-difference between the two simulations.

Configuration	FE (i.c.)	FE (w.m.)	Average FE	ΔFE
$\alpha\gamma$	0	0	0	0
$\alpha\gamma\gamma$	5.37	6.35	5.86	0.49
$\beta\gamma$	7.47	8.75	8.11	0.64
γ	8.39	8.14	8.27	0.13
β	8.93	10.14	9.54	0.61
$\alpha\alpha\gamma$	9.96	10.27	10.12	0.16
α	10.72	10.56	10.64	0.08
$\gamma\gamma$	10.76	11.40	11.08	0.32
$\alpha\beta$	14.87	14.40	14.64	0.24
$\beta\gamma\gamma$	14.58	15.73	15.16	0.58
$\alpha\alpha$	18.31	17.60	17.96	0.36
no contacts	18.72	16.37	17.55	1.18
$\alpha\beta\gamma$	19.55	20.02	19.79	0.24
$\beta\beta$	24.50	24.99	24.75	0.25
$\alpha\beta\beta$	28.68	32.21	30.45	1.77
$\beta\beta\gamma$	33.91	33.26	33.59	0.33
$\alpha\alpha\beta$	36.42	38.67	37.55	1.13

S2. Simulations details

Table 2: Settings of standard MD simulation of ATP in water.

Total number of atoms	2258
ATP	1
Na^+	4
H_2O	737
Ensemble	NPT
Temperature	300K
Pressure	1 atm
Timestep	1 fs
Length	100 ns

Table 3: Settings of standard MD simulation of $[ZnCH_3TACN]^{2+}$ in water.

Total number of atoms	4872
$[ZnCH_3TACN]^{2+}$	1
Cl^-	2
H_2O	1614
Ensemble	NPT
Temperature	300 K
Pressure	1 atm
Timestep	1 fs
Length	160 ns

Table 4: General settings for WT-MTD simulations.

Equilibration	
Ensemble	NPT
Temperature	300K
Pressure	1 atm
Timestep	1 fs
Length	20 ns
WT-MTD	
Ensemble	NVT
Temperature	300K
Pressure	1 atm
Timestep	1 fs
Hill width	2.0
Initial hill height	0.2 kcal/mol
Grid width	0.1
Bias factor	15
Hill deposition frequency	500 fs
Parameters of coordination number (c.n) function (for the definition of the function see Equation 1 of the main text)	
Cutoff d_0	2.7 Å
n	6
m	12
Half-harmonic wall on c.n.s	
Upper walls position	2.4
Rescaled force constant	15 kcal/mol
Half-harmonic wall on distance between Zn^{2+} and the center of mass of phosphorus	
Upper walls position	10.2 Å
Rescaled force constant	15 kcal/mol
Harmonic constraints on $[ZnCH_3TACN]^{2+}$	
Secondary N-Zn equilibrium distance	2.05 Å
Tertiary N-Zn equilibrium distance	2.15 Å
Force constant	200 kcal/mol Å^2

Table 5: Settings of WT-MTD simulation of ATP-Zn^{2+} in water.

Total number of atoms	997
ATP	1
Zn^{2+}	1
Na^+	2
H_2O	317
Box size	(21.40 Å)^3
Length	1.4 μs

Table 6: Settings of WT-MTD simulation of MTP-Zn^{2+} in water.

Total number of atoms	386
MTP	1
Zn^{2+}	1
Na^{+}	2
H_2O	122
Box size	$(15.68\ \text{Å})^3$
Length	1.4 μs

Table 7: Settings of WT-MTD simulation of ATP-$[ZnCH_3TACN]^{2+}$ in water.

Total number of atoms	1405
ATP	1
$[ZnCH_3TACN]^{2+}$	1
Na^{+}	2
H_2O	444
Box size	$(24.16\ \text{Å})^3$
Length	2.2 μs

Table 8: Settings of WT-MTD simulations of MTP-$[ZnCH_3TACN]^{2+}$ in water, either from ion-contact or from water-mediated initial configuration.

Total number of atoms	383
MTP	1
$[Zn\ CH_3TACN]^{2+}$	1
Na^{+}	2
H_2O	112
Box size	$(15.55\ \text{Å})^3$
Length	1.7 μs

S3. Characterization of $[ZnCH_3TACN]^{2+}$

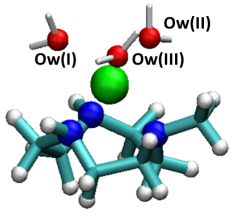

Figure 1: Structure of $[ZnCH_3TACN]^{2+}$ with coordinated water molecules, as obtained from standard MD simulation.

Table 9: Zn-N and Zn-Ow distances in $[ZnCH_3TACN]^{2+}$ from standard MD simulation. Ow indicates water oxygens and NS, NT refer to secondary and tertiary nitrogens of TACN, respectively.

Atoms	Distance (Å)
Zn-NS	2.09 ± 0.06
Zn-NT	2.16 ± 0.07
Zn-Ow (I)	2.05 ± 0.06
Zn-Ow (II)	2.05 ± 0.05
Zn-Ow (III)	2.05 ± 0.06

S4. Conformational analysis

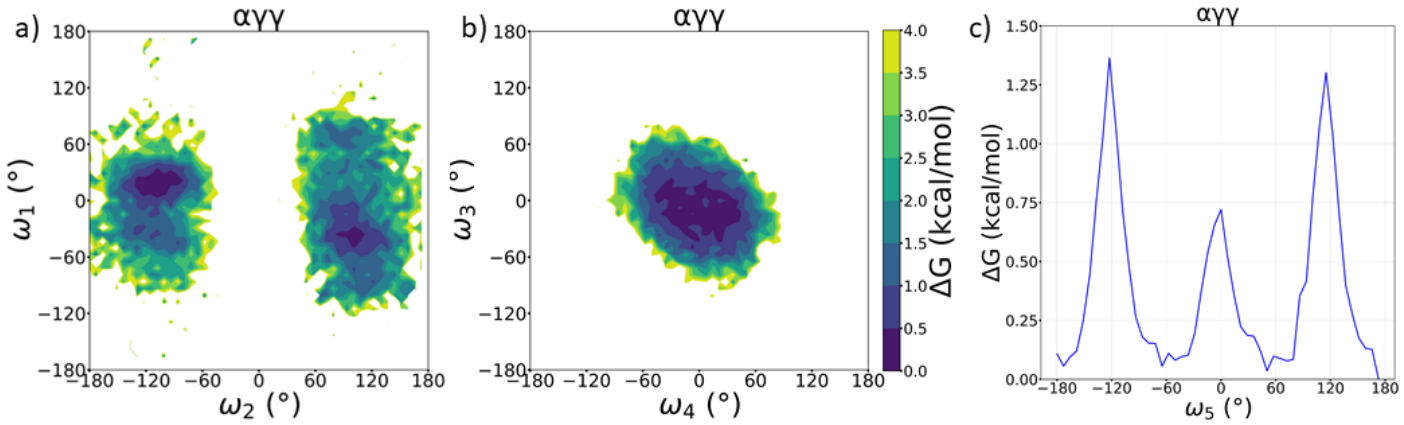

Figure 2: Free energy as a function of the dihedrals a) ω_2/ω_1, b) ω_4/ω_3 and c) ω_5 of the triphosphate chain (definition of angles in Fig. 5 of the main text), obtained by reweighting of WT-MTD run for the $\alpha\gamma\gamma$ coordination mode of ATP-Zn^{2+} in water.

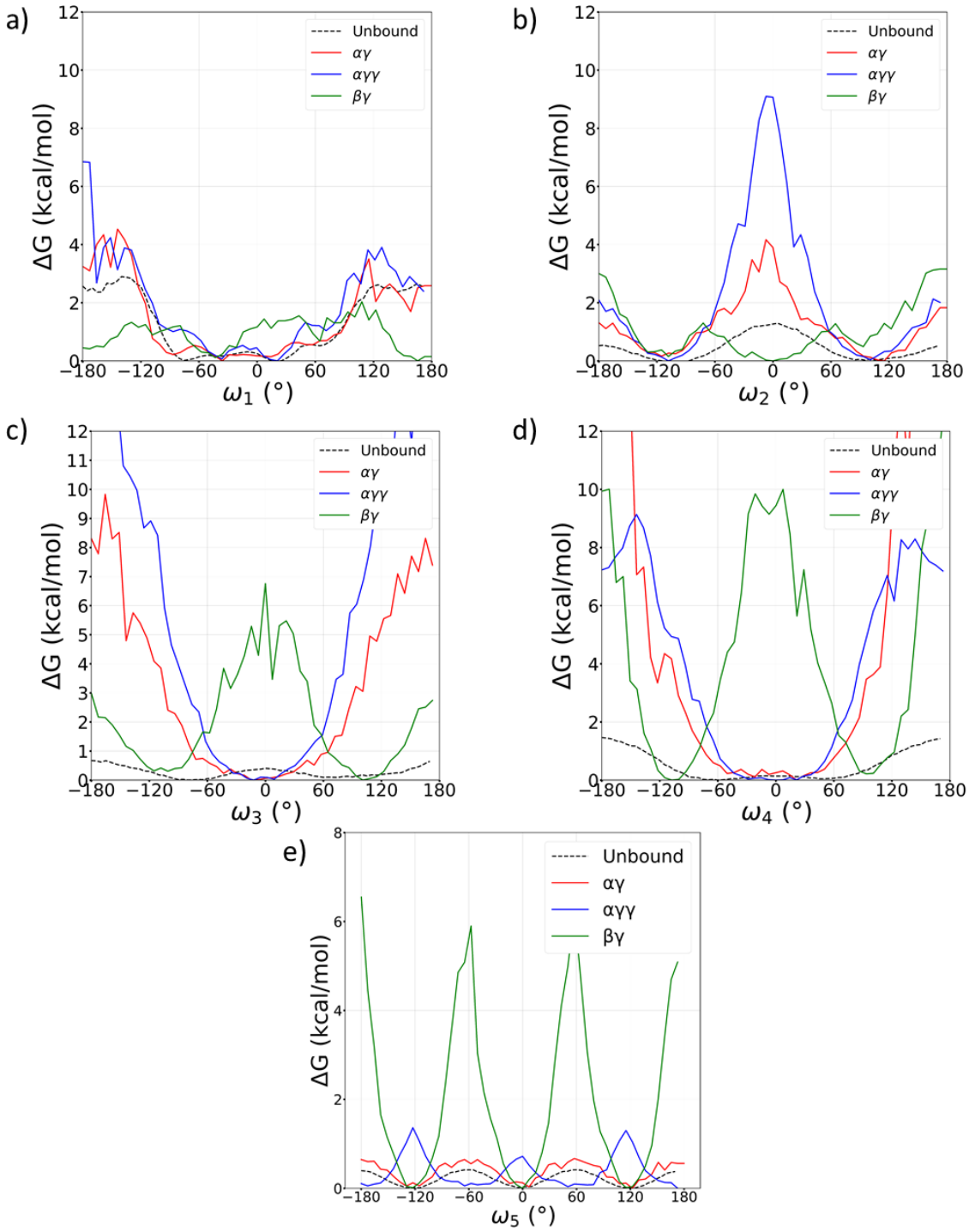

Figure 3: Free energy profiles as a function of the dihedral angles a) ω_1, b) ω_2, c) ω_3, d) ω_4, e) ω_5 of the triphosphate chain (definition of angles in Fig. 5 of the main text), obtained for free ATP in water (black dashed) by standard MD simulations and for $\alpha\gamma$ (red solid), $\alpha\gamma\gamma$ (blue solid) and $\beta\gamma$ (green solid) coordination modes of ATP-Zn^{2+} in water by reweighting of WT-MTD run.

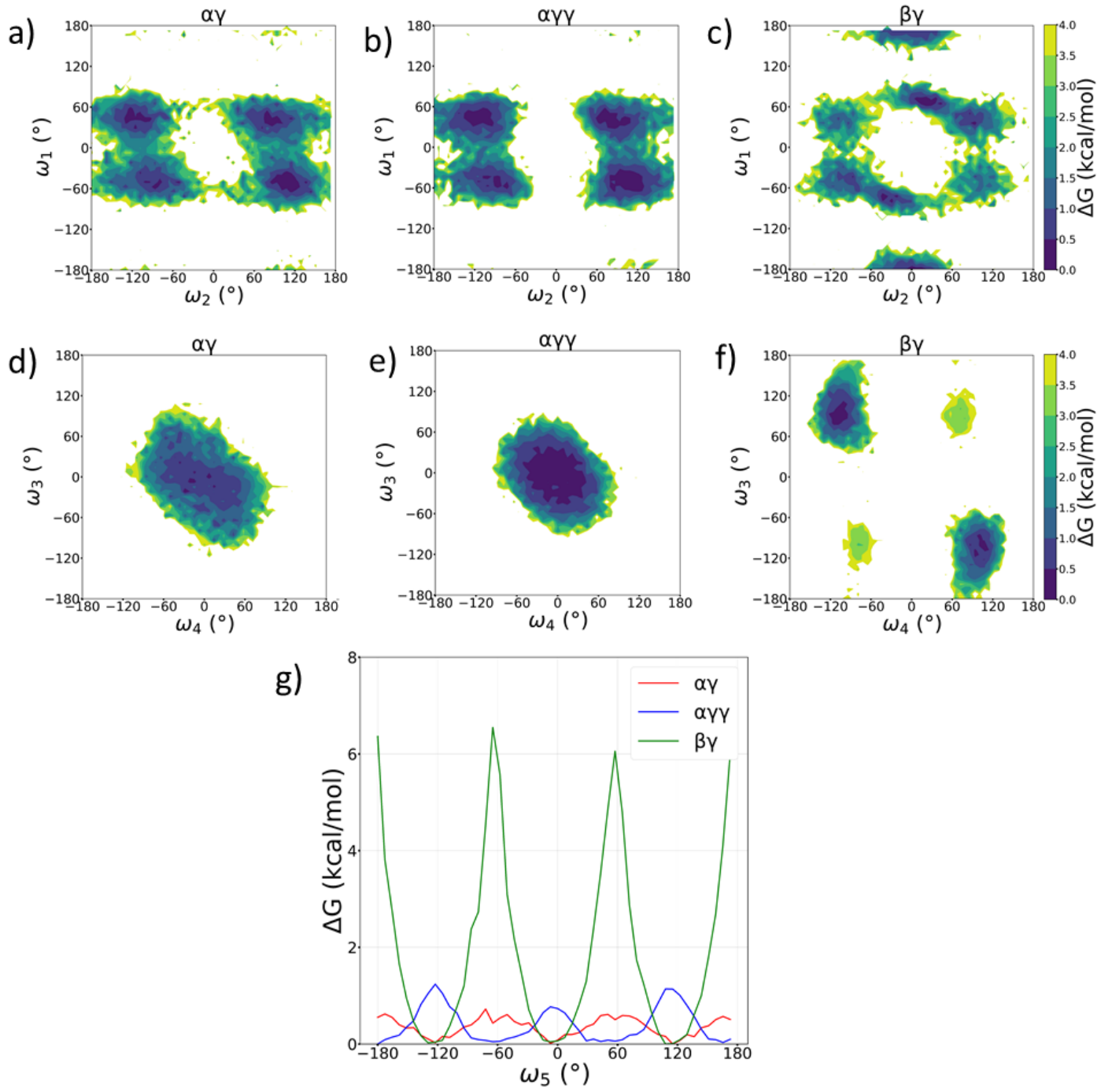

Figure 4: Free energy as a function of the dihedrals a-c) ω_2/ω_1, d-f) ω_4/ω_3 and g) ω_5 of the triphosphate chain (definition of angles in Fig. 5 of the main text), obtained by reweighting of WT-MTD run for the $\alpha\gamma$, $\alpha\gamma\gamma$ and $\beta\gamma$ coordination modes of MTP-Zn^{2+} in water.

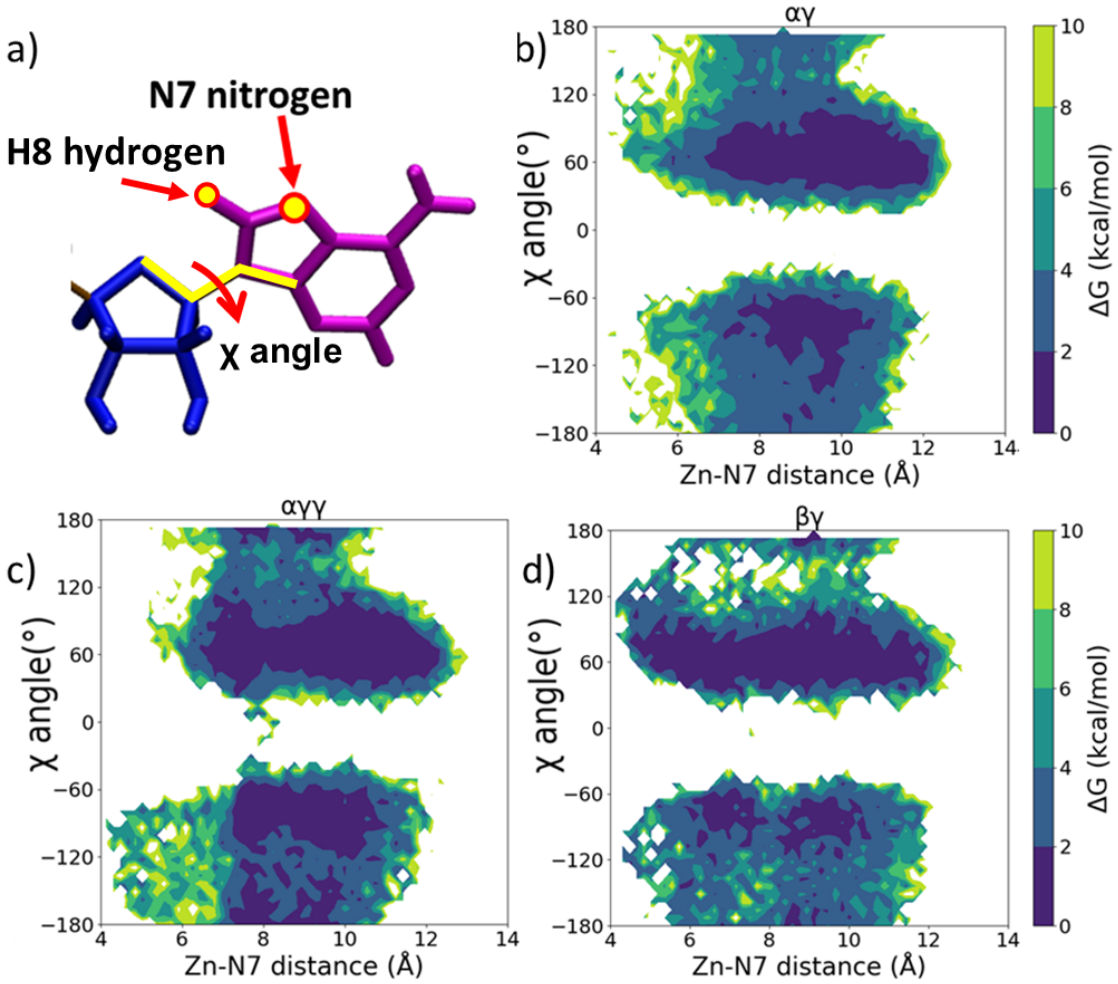

Figure 5: a) Structure of adenosine, highlighting the position of the N7 and the H8 atoms and the glycosidic angle, χ. FES as a function of χ and of the Zn-N7 distance, for the b) $\alpha\gamma$, c) $\alpha\gamma\gamma$, d) $\beta\gamma$ binding modes of ATP-Zn^{2+}, reconstructed from WT-MTD run.

S5. Free energy surfaces as a function of coordination numbers

MTP-Zn^{2+}

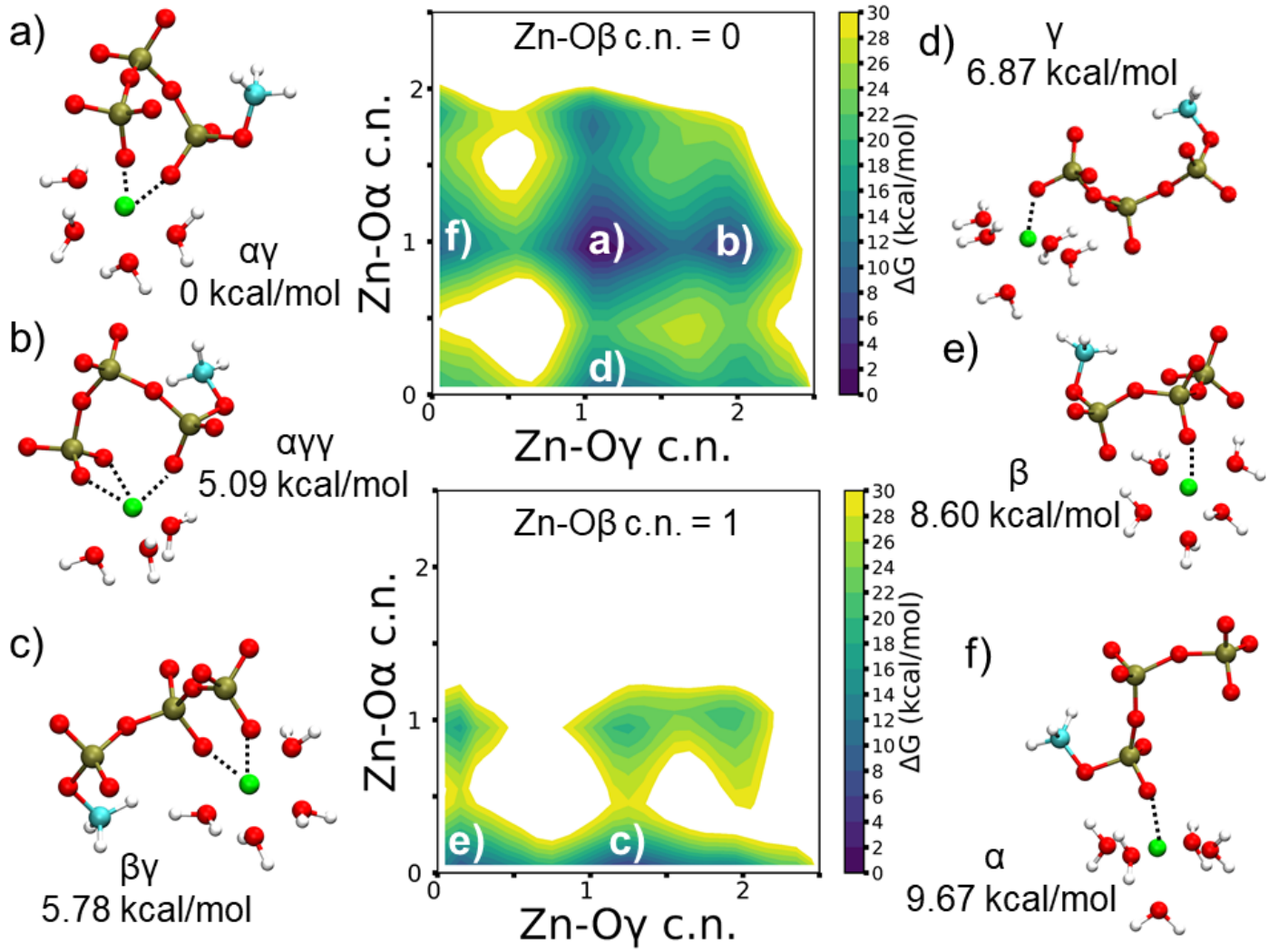

Figure 6: FESs from WT-MTD simulations of MTP-Zn^{2+} in water. States with two Zn-Oβ contacts are disregarded as higher in energy. a-f) Representative configurations for minima lying within ∼10 kcal/mol from the global minimum.

ATP-[$ZnCH_3TACN$]$^{2+}$

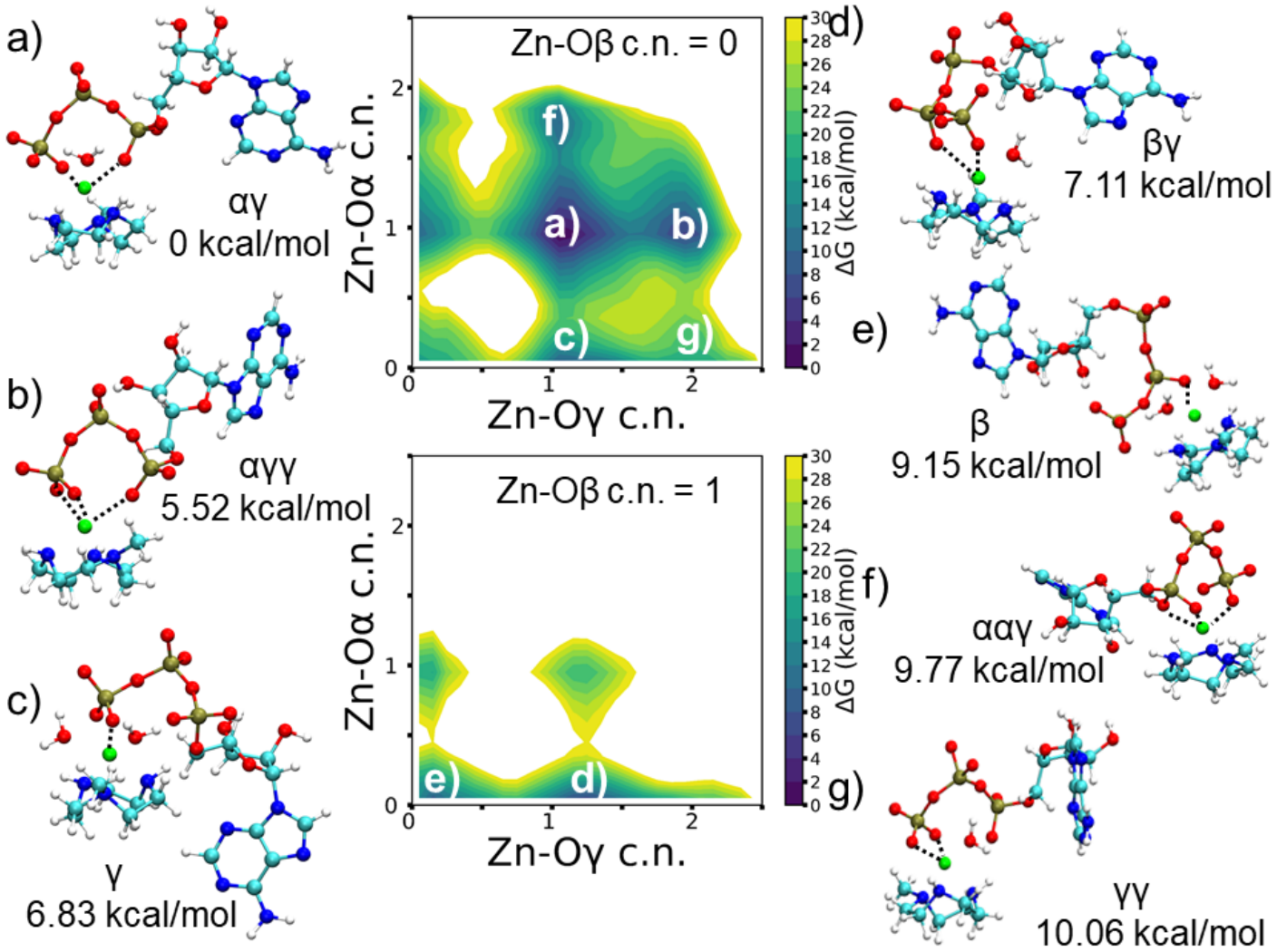

Figure 7: FESs from WT-MTD simulation of ATP-[$ZnCH_3TACN$]$^{2+}$ in water. States with two Zn-Oβ contacts are disregarded as higher in energy. a-g) Representative configurations for minima lying within ∼10 kcal/mol from the global minimum.

MTP-[ZnCH$_3$TACN]$^{2+}$

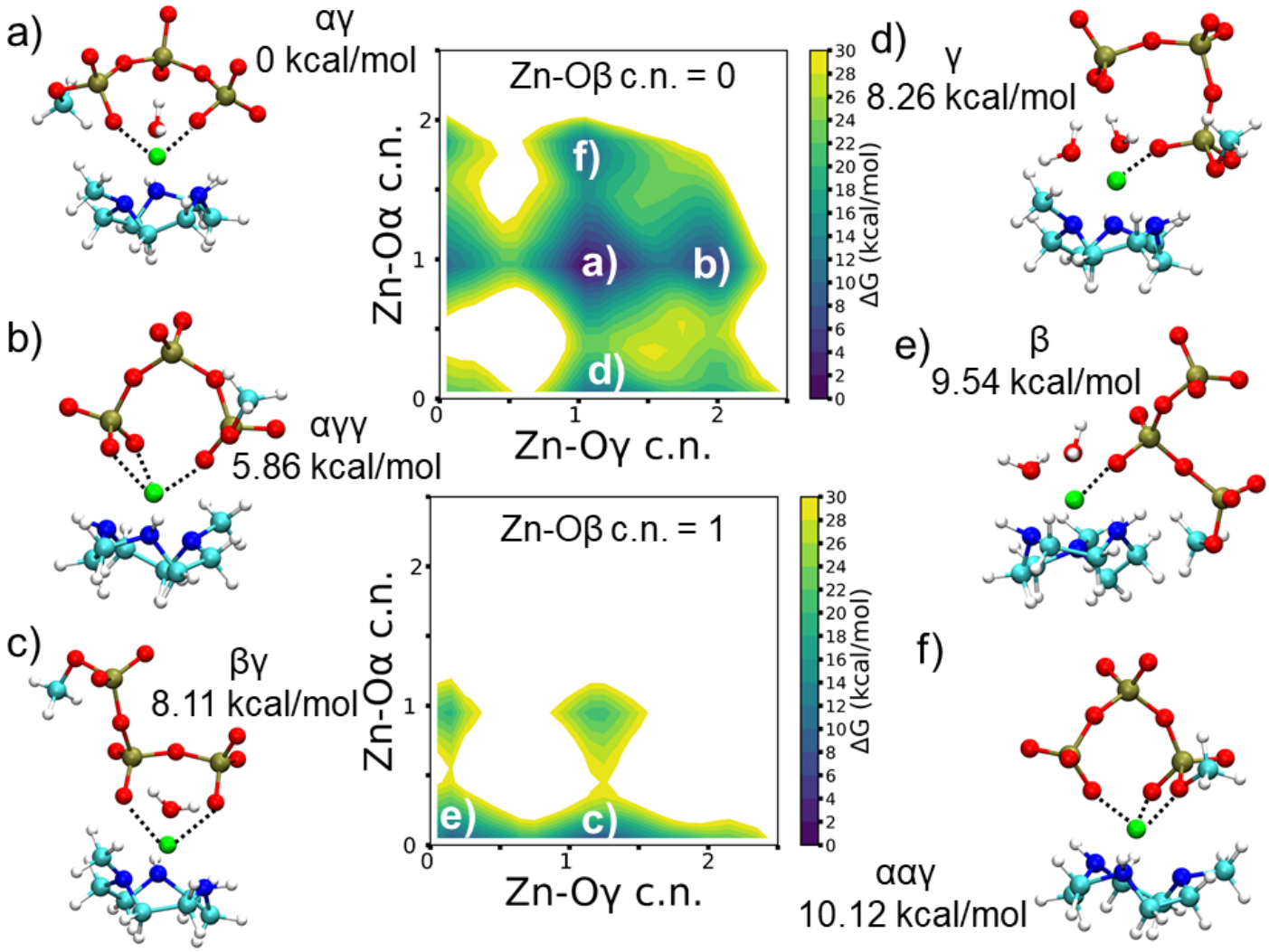

Figure 8: Average FESs from WT-MTD simulations of MTP-[ZnCH$_3$TACN]$^{2+}$ in water starting from ion-contact and from water-mediated coordination. States with two Zn-Oβ contacts are disregarded as higher in energy. a-f) Representative configurations for minima lying within ∼10 kcal/mol from the global minimum.

S6. Convergence assessment

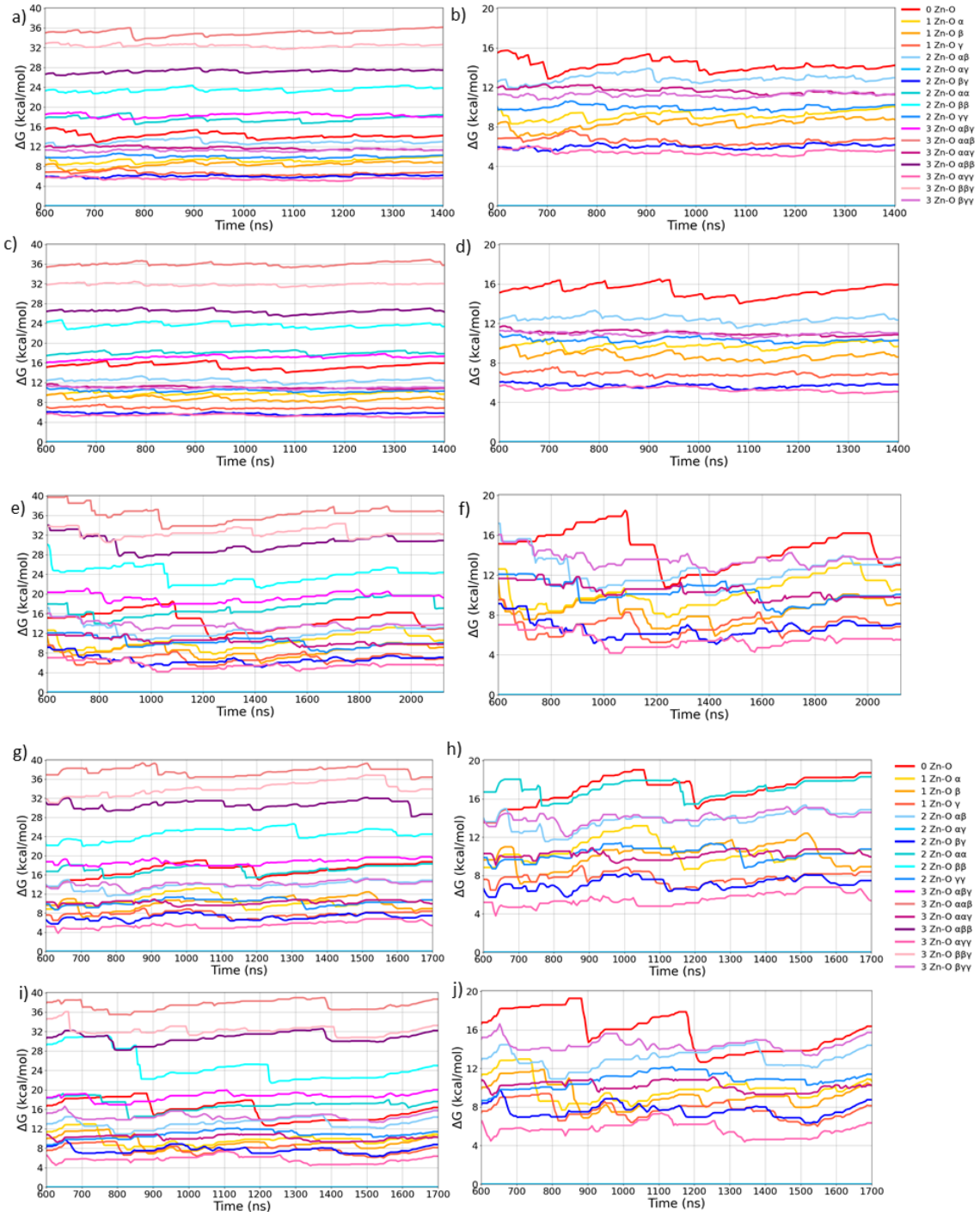

Figure 9: Time evolution of the free energy along WT-MTD trajectories, for a,b) ATP-Zn^{2+}, c,d) MTP-Zn^{2+}, e,f)ATP-$[ZnCH_3TACN]^{2+}$, MTP-$[ZnCH_3TACN]^{2+}$ in water, starting from g,h) ion contact and from i,j) water-mediated coordination. For each system the global minimum is taken as a reference. On the left all coordination modes are shown, whereas on the right only the modes lower in energy than the unbound state are retained.

S7. Zn^{2+}-ATP WT-MTD simulation with Zn^{2+} dummy model

Table 10: Settings of WT-MTD simulation of ATP-Zn^{2+} in water with the dummy model by Duarte *et al.*.

Total number of atoms	997
ATP	1
Zn^{2+}	1
Dummies	6
Na^+	2
H_2O	315
Box size	$(21.19\ \text{Å})^3$
Length	1.1 μs

The settings of the WT-MTD simulation are the same reported in Tab.4.

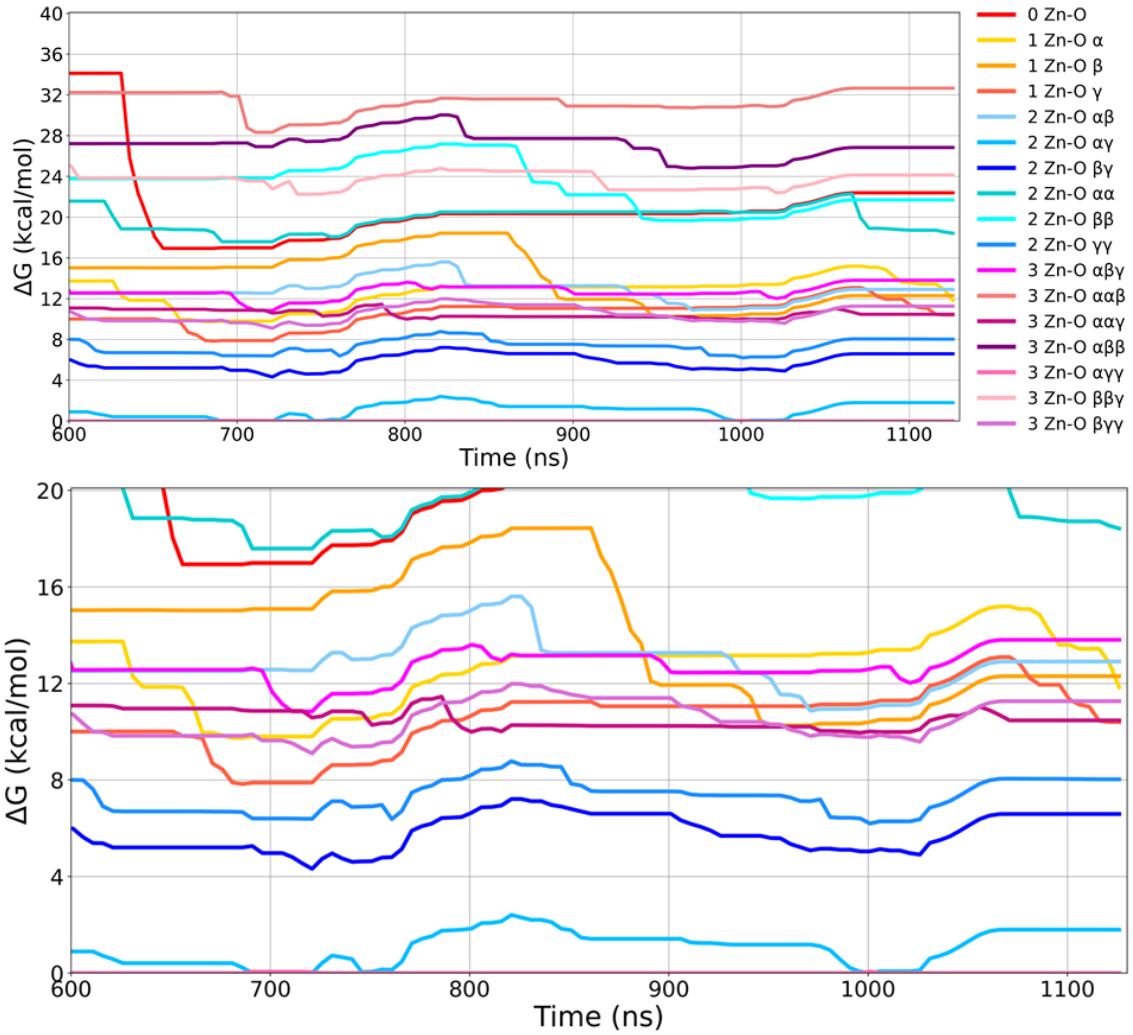

Figure 10: Time evolution of the free energy along WT-MTD trajectories, for ATP-Zn^{2+} with the dummy model by Duarte *et al.* starting from water-mediated coordination. The global minimum is taken as a reference. In the upper panel all coordination modes are shown, whereas in the lower panel only the modes lower in energy than the unbound state are retained.

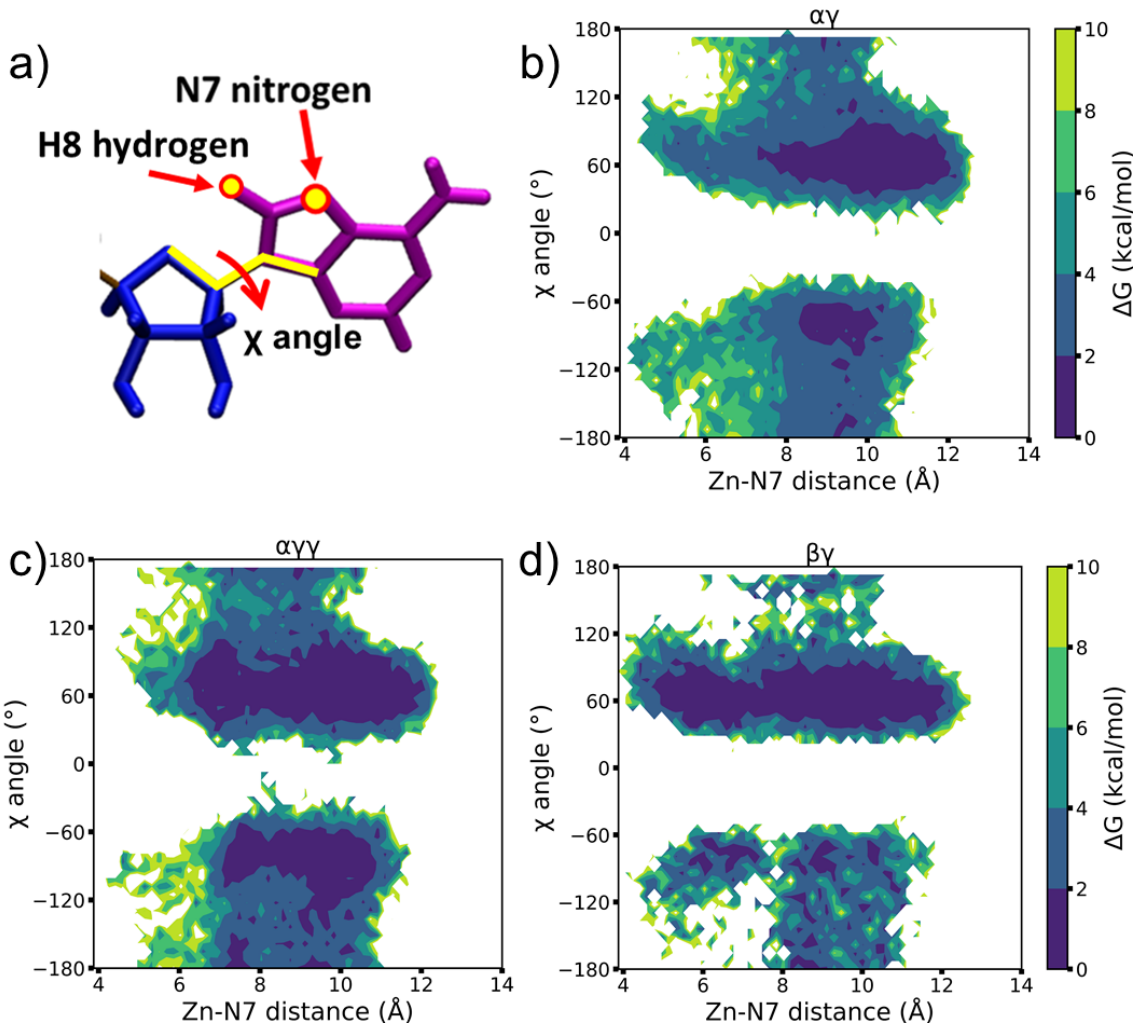

Figure 11: a) Structure of adenosine, highlighting the position of the N7 and the H8 atoms and the glycosidic angle, χ. FES as a function of χ and of the Zn-N7 distance, for the b) $\alpha\gamma$, c) $\alpha\gamma\gamma$, d) $\beta\gamma$ binding modes of ATP-Zn^{2+}, reconstructed from WT-MTD run with the dummy model by Duarte *et al.*.

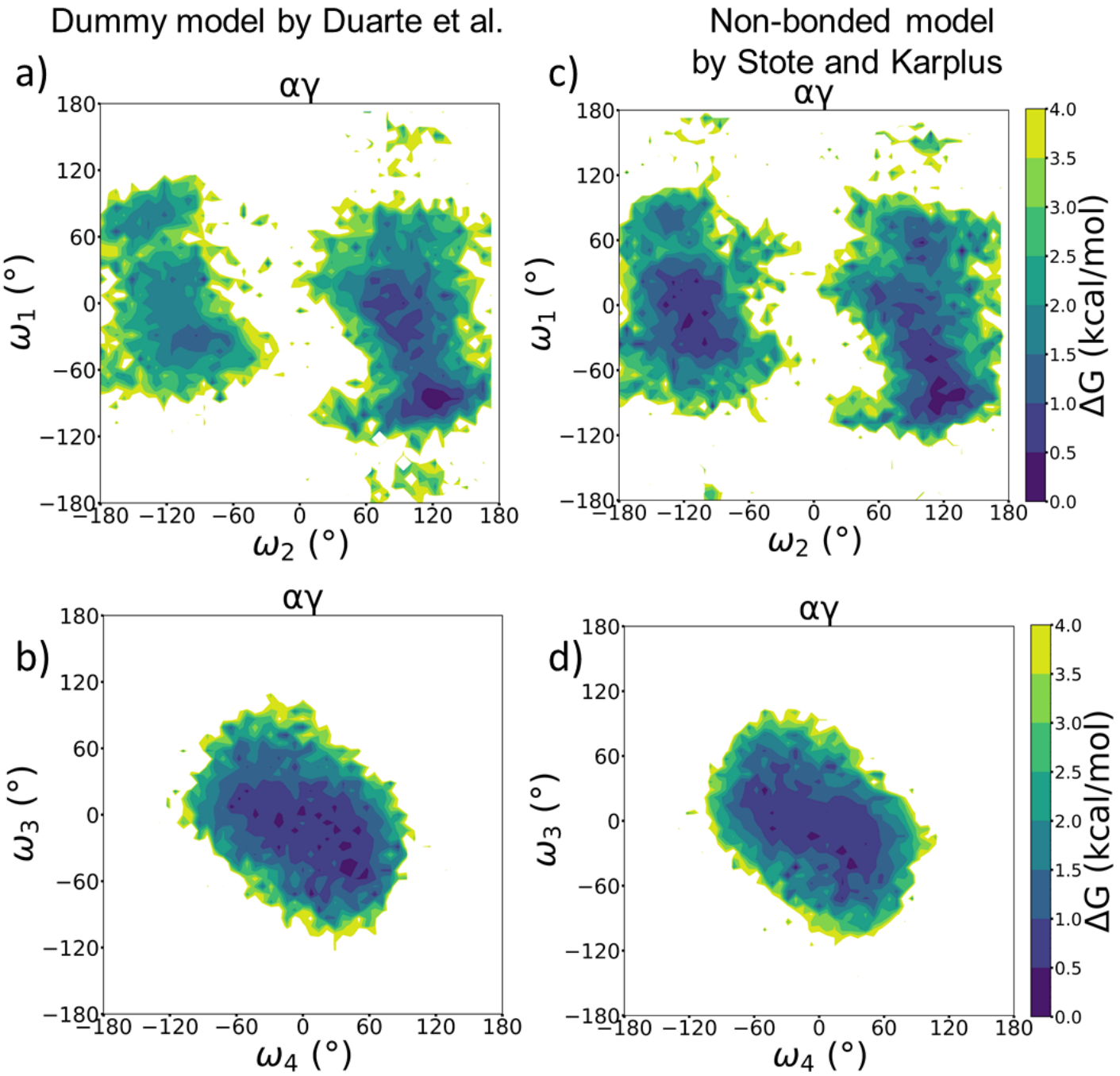

Figure 12: Comparison of free energy as a function of the dihedrals ω_2/ω_1, ω_4/ω_3 of the triphosphate chain (definition of angles in Fig. 5 of the main text), obtained by reweighting of WT-MTD run for the $\alpha\gamma$ coordination modes of ATP-Zn^{2+} in water for the dummy model by Duarte *et al.* (a-b) and for the non-bonded model by Stote and Karplus (c-d).

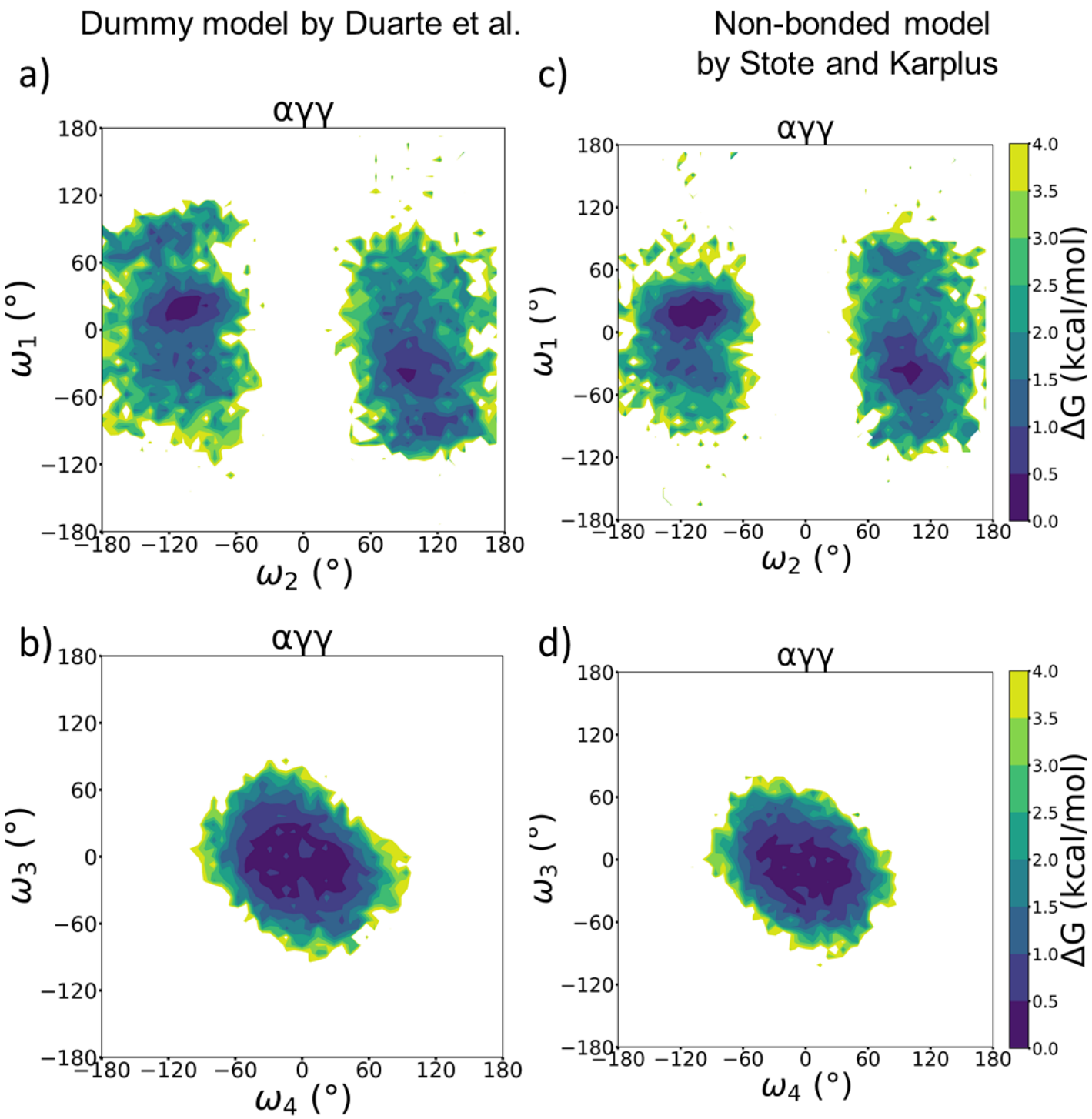

Figure 13: Comparison of free energy as a function of the dihedrals ω_2/ω_1, ω_4/ω_3 of the triphosphate chain (definition of angles in Fig. 5 of the main text), obtained by reweighting of WT-MTD run for the $\alpha\gamma\gamma$ coordination modes of ATP-Zn^{2+} in water for the dummy model by Duarte *et al.* (a-b) and for the non-bonded model by Stote and Karplus (c-d).

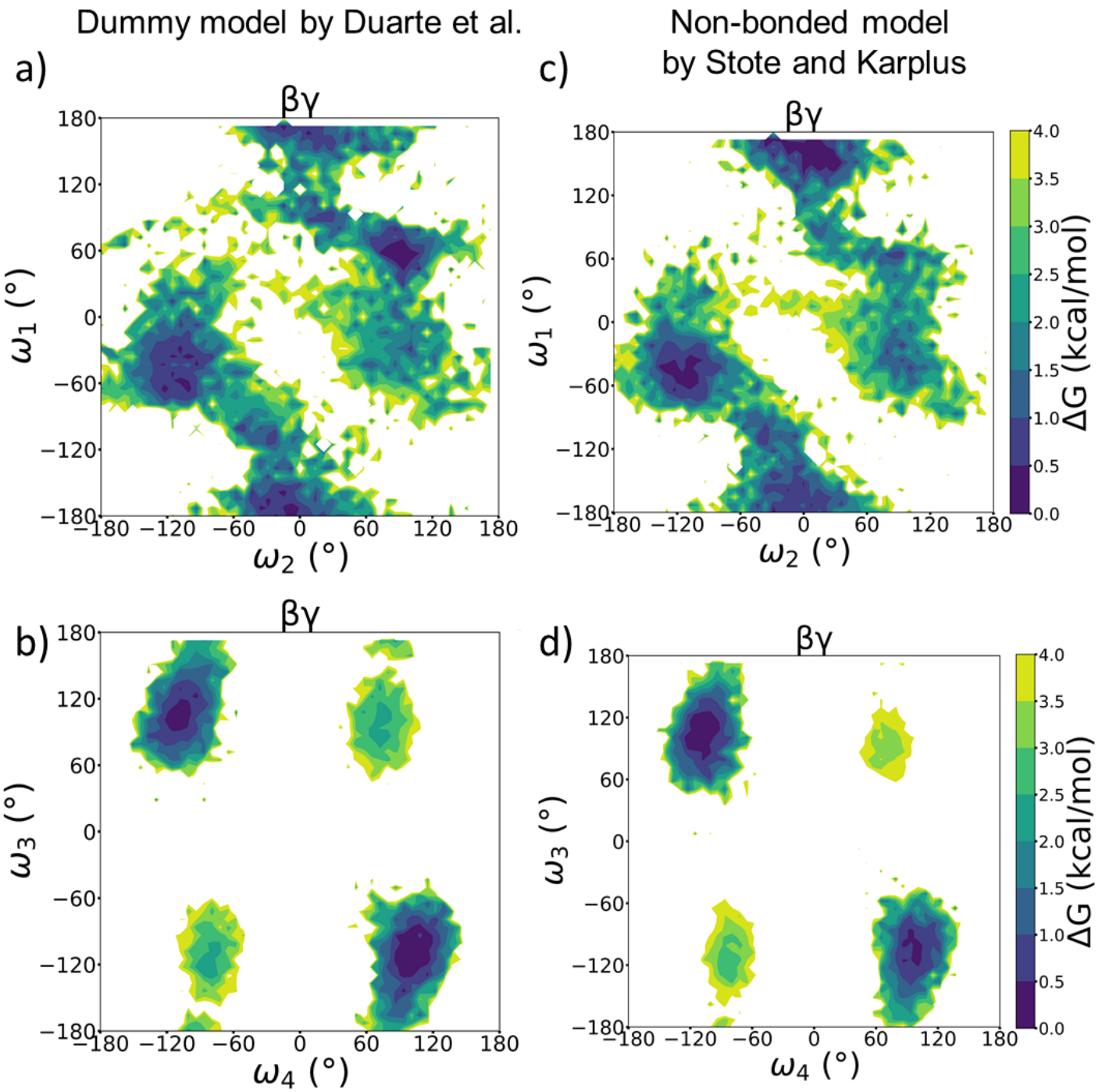

Figure 14: Comparison of free energy as a function of the dihedrals ω_2/ω_1, ω_4/ω_3 of the triphosphate chain (definition of angles in Fig. 5 of the main text), obtained by reweighting of WT-MTD run for the $\beta\gamma$ coordination modes of ATP-Zn^{2+} in water for the dummy model by Duarte *et al.* (a-b) and for the non-bonded model by Stote and Karplus (c-d).

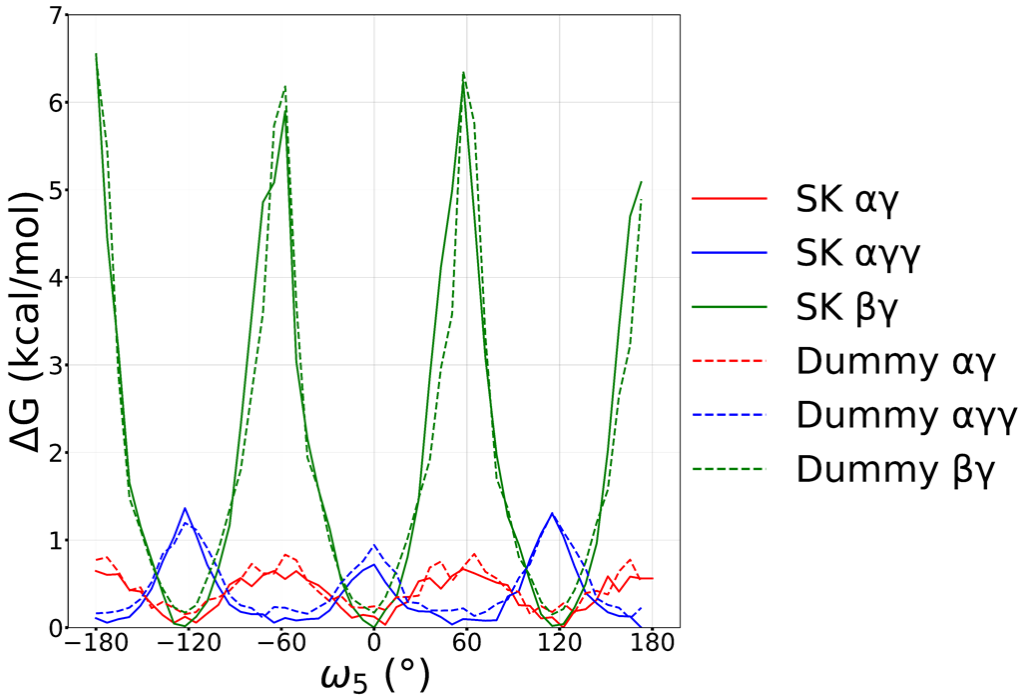

Figure 15: Comparison of free energy as a function of the dihedral ω_5 of the triphosphate chain (definition of the angle in Fig. 5 of the main text), obtained by reweighting of WT-MTD run for the $\alpha\gamma$, $\alpha\gamma\gamma$ and for $\beta\gamma$ coordination modes of ATP-Zn^{2+} in water for the dummy model by Duarte *et al.* (Dummy) and for the non-bonded model by Stote and Karplus (SK).

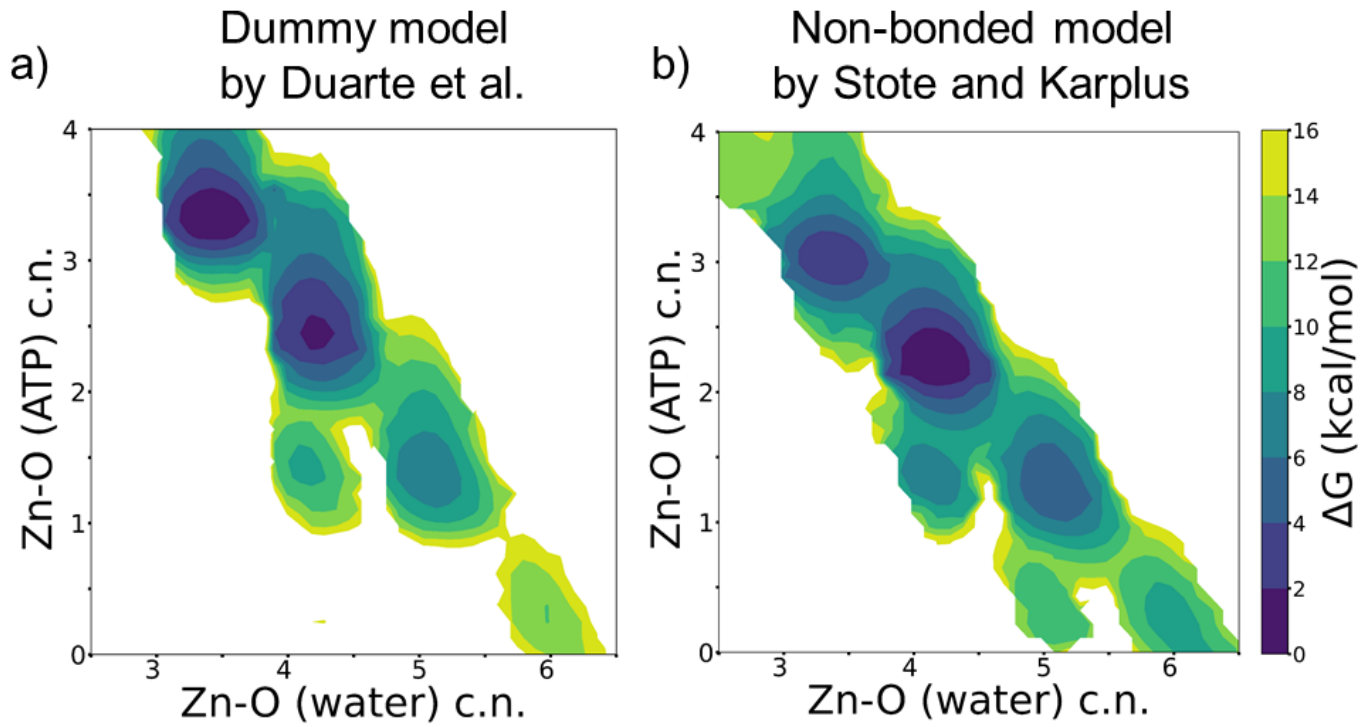

Figure 16: FES of ATP-Zn^{2+} as a function of c.n. of Zn^{2+} to water and triphosphate oxygens, reconstructed from WT-MTD run using a) the model by Duarte *et al.* and b) the model by Stote and Karplus for the metal.