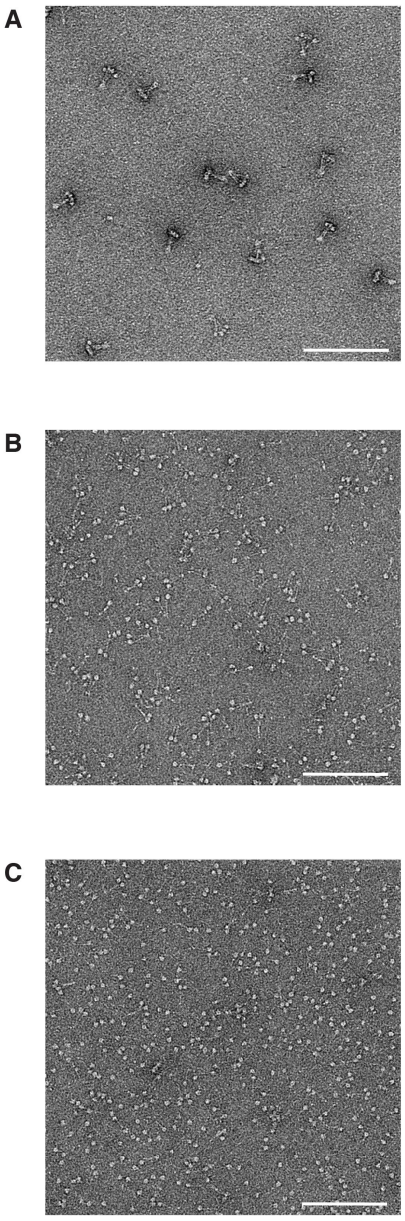

Figure S1: (A) Representative negative stain micrograph for the adiponectin HMW oligomer, corresponding to peak 1 two-dimensional class averages from Figure 1C. The scale bar is 100 nm. (B) Representative negative stain micrograph for the adiponectin hexamer, corresponding to peak 2 two-dimensional class averages from Figure 1C. The scale bar is 100 nm. (C) Representative negative stain micrograph for the adiponectin trimer, corresponding to peak 3 two-dimensional class averages from Figure 1C. The scale bar is 100 nm.

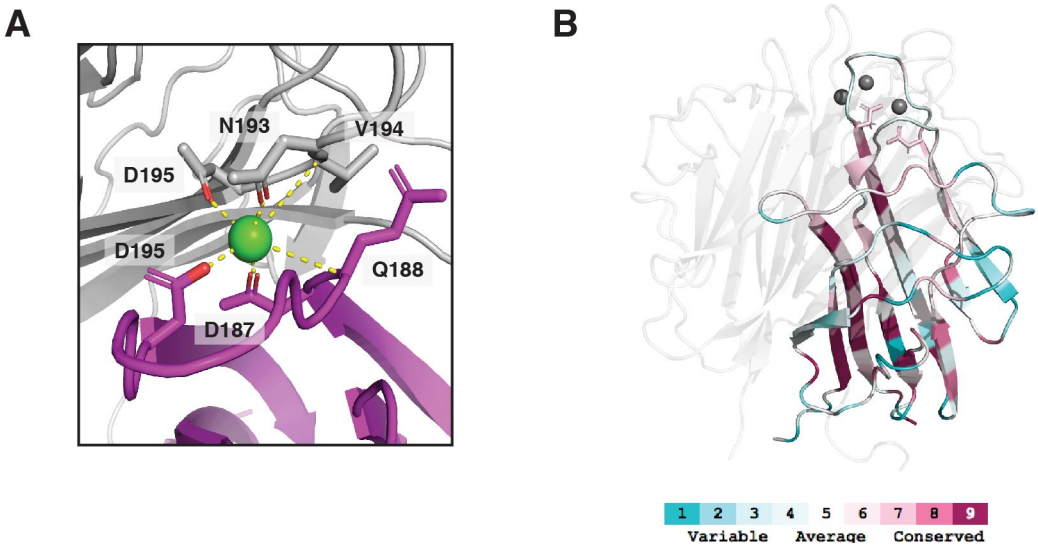

Figure S2: Calcium coordination. (A) Each calcium ion shows an octahedral coordination by Asp195, Asp187 and Gln188 from one chain and by Asn193, Val194 and Asp195 from a second chain. (B) Evolutionary conservation analysis of the globular domain of adiponectin performed through ConSurf. Most of the residues in the metal coordination pocket are highly conserved, with Asp187 and Asp195 showing the highest conservation value.

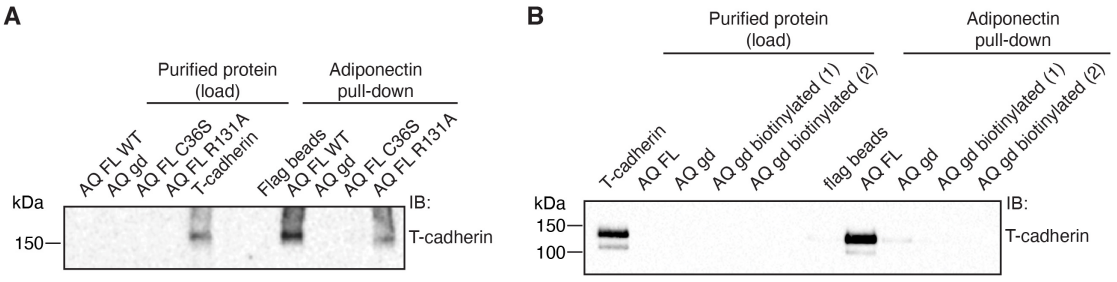

Figure S3: The globular domain of adiponectin does not bind T-cadherin. (A) FLAG pull-down assay. Purified FLAG-adiponectin proteins were immobilized on the anti-FLAG resin and then incubated with T-cadherin. The binding of T-cadherin was assessed by Western Blot. (B) FLAG pull-down assay. Purified FLAG-adiponectin proteins were immobilized on FLAG resin and then incubated with T-cadherin. The binding of T-cadherin was assessed by Western Blot. In samples numbered (1), biotinylated adiponectin globular domain or FLAG-adiponectin were incubated in a 10:1 molar ratio to streptavidin; in the samples labeled (2), biotinylated adiponectin globular domain or FLAG-adiponectin was incubated in a 1:10 ratio with streptavidin.

Table S1: Data collection and refinement statistics.

	AQ WT	AQ D187A/Q188A
Data collection *		
Number of crystals	1	1
Space group	P1	R3
Cell dimensions		
a, b, c (Å)	47.9, 49.7, 50.3	75.7, 75.7, 48.9
α, β, γ (°)	116.8, 100.9, 104.9	90, 90, 120
Resolution (Å)	50 – 1 (1.05 – 1)	50 – 2.15 (2.28 – 2.15)
$CC_{1/2}$ (%)	99.7 (24.8)	99.9 (71)
<I/σ(I)>	5.01 (0.32)	12.42 (1.59)
Completeness (%)	95.6 (92.9)	99.1 (94.4)
Multiplicity	3.95 (3.9)	5.3 (3.04)
Refinement		
Resolution (Å)	40.77 – 0.99 (1.02 – 0.99)	39.18 – 2.15 (2.27 – 2.15)
No. reflections	198521	5634
R_{work}/R_{free} (%)	17.57 / 19.78	20.96 / 25.56
No. atoms		
Protein	3541	992
Ligands	4	1
Solvent	506	11
B-factors (Å^2)		
Protein	12.82	68.2
Ligands	7.76	96.15
Solvent	25.73	58.79
RMS deviations		
Bond angles (°)	1.47	0.45
Bond lengths (Å)	0.016	0.002
Ramachandran		
Favored (%)	95.12	94.21
Allowed (%)	4.88	5.79
Outliers (%)	0	0

* Highest shell values in parenthesis