

## **Legends to supplementary figures**

### **Supplementary figure 1**

Comparison of  $^1\text{H}$ - $^{15}\text{N}$  HSQC spectra of the  $^{15}\text{N}$ -labeled AP-1 $\gamma$ -ear domain in the absence (blue) or presence (red) of Gadkin ( $\Delta 51$ ) (1:1 ratio) including assignments. Changes in chemical shifts indicate changes in conformation induced by complex formation. Residues are numbered.

### **Supplementary figure 2**

Overview of the chemical shifts for the  $^{15}\text{N}$ -labeled AP-1 $\gamma$ -ear domain in the absence or presence of Gadkin ( $\Delta 51$ ).

### **Supplementary figure 3**

c(S)-distributions for mixtures of Gadkin ( $\Delta 51$ ) and AP-1 $\gamma$ -ear. The distributions are normalized to have a total area of unity. The formation of a new species is indicated by the progressive shift to larger s-values of the new peak and the disappearance of the peak for free Gadkin ( $\Delta 51$ ).



## Supplementary Figure 2

### Chemical shifts for the AP-1 $\gamma$ -ear domain with and without Gadkin

	$\gamma$ -ear		$\gamma$ -ear (with Gadkin 1:1)	
	$^1\text{H}^{\text{N}}$	$^{15}\text{N}$	$^1\text{H}^{\text{N}}$	$^{15}\text{N}$
706Ser	8.02	114.2	8.02	114.2
707Ile	8.44	111.0	8.45	111.1
708Thr	8.91	119.9	8.92	119.9
709Ala	8.49	131.7	8.50	131.7
710Tyr	7.46	116.7	7.48	116.8
711Ser	8.35	122.9	8.36	122.9
712Lys	8.41	128.5	8.42	128.6
714Gly	8.45	105.5	8.45	105.5
715Leu	7.97	124.2	7.97	124.1
716Lys	8.89	128.7	8.89	128.7
717Ile	9.28	123.4	9.30	123.4
718Glu	8.98	129.1	8.98	129.1
719Phe	9.34	122.1	9.36	122.2
720Thr	8.23	113.1	8.19	113.1
721Phe	9.11	118.3		
722Glu	9.07	121.2	9.08	121.2
723Arg	8.86	124.7	8.86	124.7
724Ser	8.94	118.6	8.89	118.5
729Ser	8.11	113.0	8.10	113.0
730Val	7.75	122.9	7.78	122.9
731Thr	9.15	125.7	9.14	125.8
732Val	9.20	129.1	9.18	128.9
733Ile	9.69	132.1	9.73	132.2
734Thr	8.69	123.8	8.69	123.8
735Ile	9.23	126.5	9.24	126.5
737Ala	9.36	131.0	9.38	131.0
738Ser	9.23	115.1	9.24	115.1
739Asn	9.33	121.4	9.33	121.4
740Ser	9.03	117.8	9.03	117.8
742Glu	9.11	114.2	9.10	114.2
743Leu	7.80	120.6	7.80	120.6
744Asp	8.96	123.3	8.96	123.3
745Met	7.88	122.0	7.87	122.0
746Thr	9.24	113.4	9.24	113.3
747Asp	8.95	118.8	8.94	118.9
748Phe	9.10	118.3		
749Val	8.96	131.8	8.95	131.8
750Phe	8.63	129.2	8.61	129.3
751Gln	7.99	125.3	8.00	124.3
752Ala	7.86	120.5		
753Ala	8.83	121.9		
754Val	8.53	114.5	8.51	113.3
756Lys	8.45	118.4	8.40	117.7
758Phe	8.20	121.3	8.23	121.2
759Gln	8.32	116.5	8.37	116.3
760Leu	8.85	124.0	8.80	123.8
761Gln	9.04	124.5		
762Leu	9.01	127.8	9.05	128.2
763Leu	8.74	127.9		

764Ser	8.22	114.1	8.28	114.0
766Ser	9.13	115.2	9.14	115.0
767Ser	7.45	112.7	7.43	112.4
769Val	7.96	121.7	7.97	121.7
770Val	9.21	128.0	9.21	128.0
772Ala	8.40	120.7	8.40	120.7
773Phe	8.69	113.5	8.68	113.5
774Asn	9.50	113.5	9.50	113.5
775Thr	7.36	107.0	7.36	107.0
776Gly	7.23	107.4	7.23	107.4
777Thr	8.40	111.2	8.40	111.2
778Ile	8.22	118.9	8.22	118.9
779Thr	8.71	118.4	8.71	118.4
780Gln	8.00	124.1	8.00	124.1
781Val	8.51	128.8	8.50	128.9
782Ile	9.39	124.3	9.38	124.6
783Lys	9.28	124.4	9.35	124.6
784Val	9.10	123.9	9.09	123.9
785Leu	9.19	129.7	9.16	129.6
788Gln	8.74	114.2	8.70	114.0
789Lys	7.64	119.1	7.61	118.9
790Gln	8.14	116.7	8.13	116.8
791Gln	7.86	119.6	7.84	119.6
793Arg	6.26	119.4	6.18	119.4
794Met	8.45	117.5	8.56	117.8
795Arg	8.83	126.1		
796Ile	9.36	119.4	9.42	117.4
797Lys	8.33	124.0	8.23	123.6
798Leu	8.69	126.3	8.63	126.5
799Thr	8.06	113.2	8.01	113.4
800Tyr	8.04	114.9	8.02	115.0
801Asn	9.58	118.1	9.56	118.1
802His	9.16	123.2	9.16	123.2
803Lys	9.40	126.6	9.39	126.6
804Gly	8.70	105.8	8.70	105.8
805Ser	7.84	116.3	7.82	116.2
806Ala	8.39	127.4	8.38	127.4
807Met	9.07	123.7	9.02	123.2
808Gln	8.23	119.5	8.19	119.9
809Asp	8.94	121.7	8.92	122.2
811Ala	8.93	124.7	8.95	124.2
812Glu	8.77	121.1	8.79	121.1
813Val	9.04	125.3		
814Asn	8.74	123.8		
815Asn	8.65	118.6	8.66	118.3
816Phe	8.10	118.2	8.10	118.1
819Gln	9.02	114.4	9.00	114.4
820Ser	8.21	111.9	8.19	111.9
821Trp	7.15	118.5	7.14	118.5
822Gln	7.16	126.0	7.13	125.9

Suppl. Fig. 3

