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Supplemental Figures

A)

Protein Standard	Kav	MW (daltons)	LogMW	Ve (ml)
Thyroglobulin	0.088932	669000	5.825426	9.76
Ferritin	0.208573	440000	5.643453	11.63
Catalase	0.316059	232000	5.365488	13.31
Aldolase	0.330774	158000	5.198657	13.54
Albumin	0.415227	67000	4.826075	14.86
Ovalbumin	0.477287	43000	4.633468	15.83
Chymotrypsinogen A	0.575816	25000	4.39794	17.37
Ribonuclease A	0.611644	13700	4.136721	17.93

Vo = 8.37 ml
Vt = 24.0 ml
Kav = (Ve - Vo)/(Vt - Vo)

B)

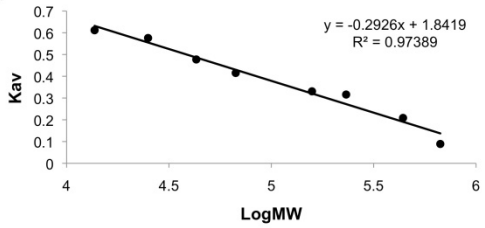

Figure S1: Calibration of S200 gel filtration column. Data for protein standards used in calibration are given in panel A. The standard curve generated from this data is shown in panel B. Apparent molecular weight of pleckstrin samples were calculated from the equation of the best-fit line.

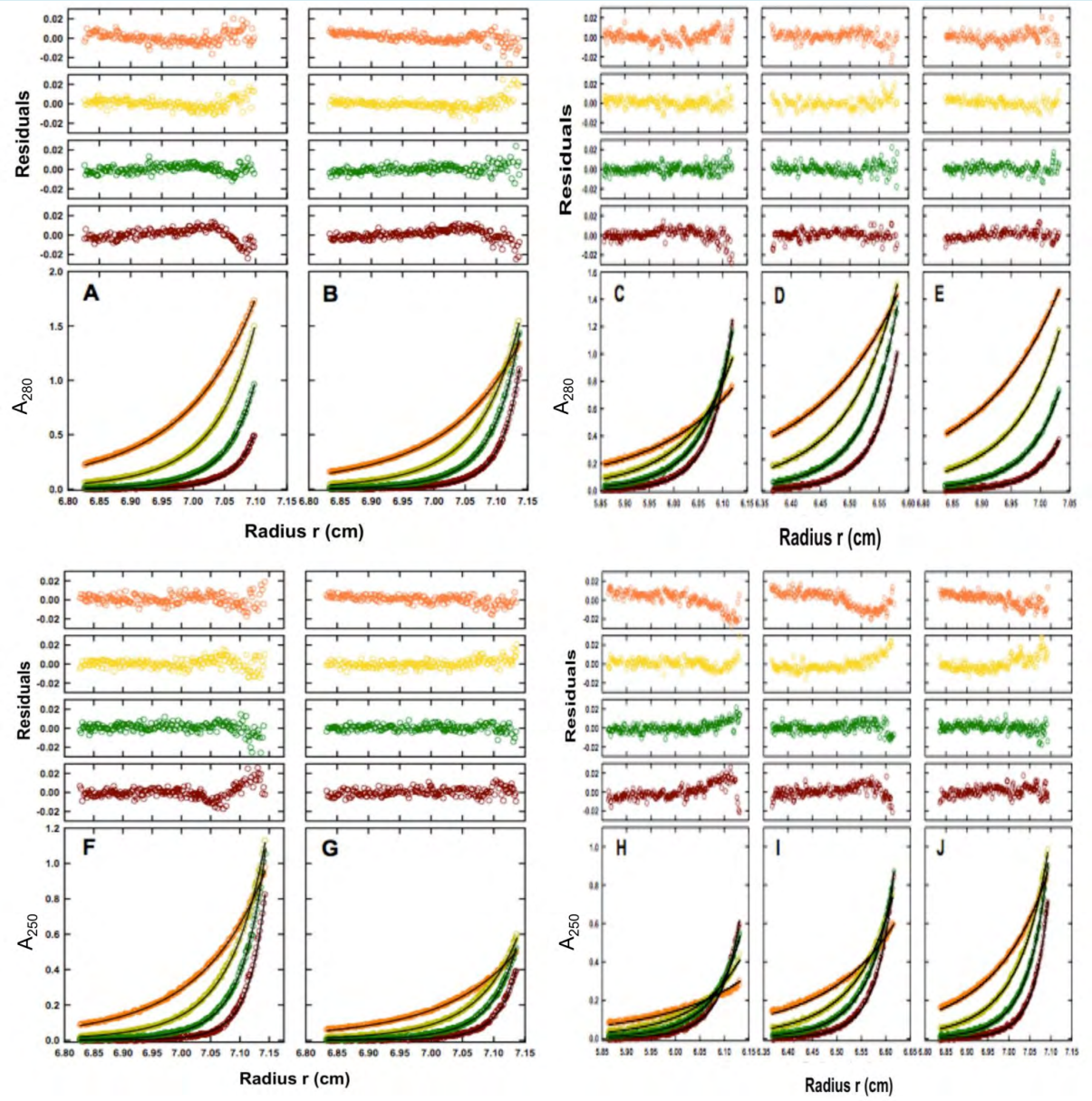

Figure S2: Native pleckstrin self-associates to form dimers. Sedimentation equilibrium profiles obtained for pleckstrin shown in terms of the A280 (A – E) or A250 (F – J) versus the radius r for data collected at loading concentrations of (A, F) 86, (B, G) 48, (C, H) 7.6, (D, I) 15.5 and (E, J) 24.1 μM. Data were collected at 4.0°C and rotor speeds of 12 (orange), 16 (yellow), 20 (green) and 24 (brown) krpm and analyzed globally in terms of a monomer-dimer reversible association using mass conservation. Best fits are shown as black lines through the experimental points; the corresponding distributions of the residuals are shown stacked above the plot. Note that data for the 86 and 48 μM solutions were collected using 3 mm path length cells.

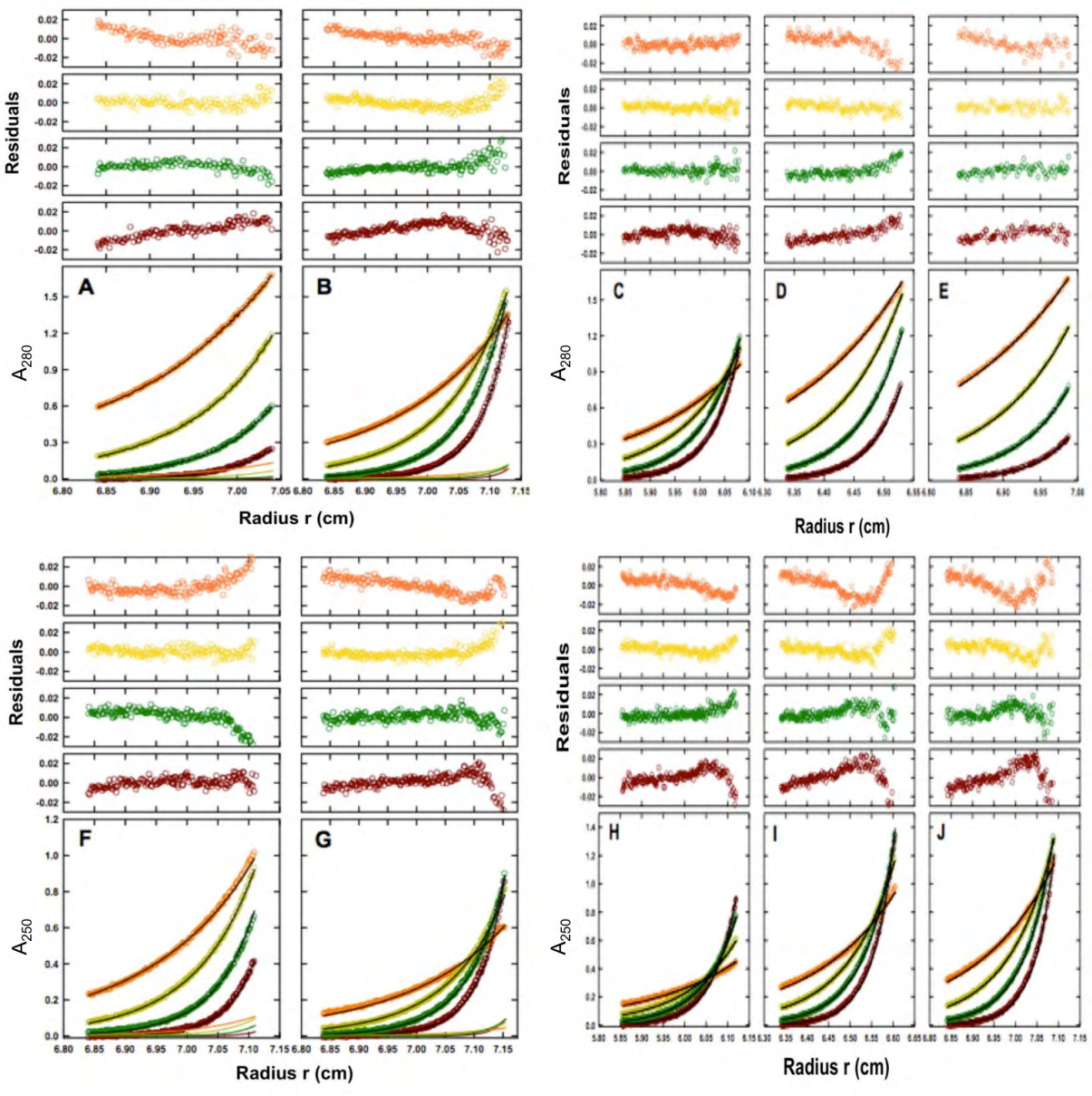

Figure S3: Pseudophosphorylated pleckstrin self-associates to form dimers with lower affinity. Sedimentation equilibrium profiles obtained for pseudophosphorylated pleckstrin shown in terms of the A280 (A – E) or A250 (F – J) versus the radius r for data collected at a loading concentrations of (A, F) 150, (B, G) 68, (C, H) 13.5, (D, I) 28.9 and (E, J) 37.8 μM. Data were collected at 4.0°C and rotor speeds of 12 (orange), 16 (yellow), 20 (green) and 24 (brown) krpm and analyzed globally in terms of a monomer- dimer reversible association using mass conservation. Best fits are shown as black lines through the experimental points; the corresponding distributions of the residuals are shown stacked above the plot. Note that data for the 133 and 61 μM solutions were collected using 3 mm path length cells, in these cases the contribution of the dimer to the overall signal is shown in solid-colored lines (A, B, F, G).