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Supporting Material

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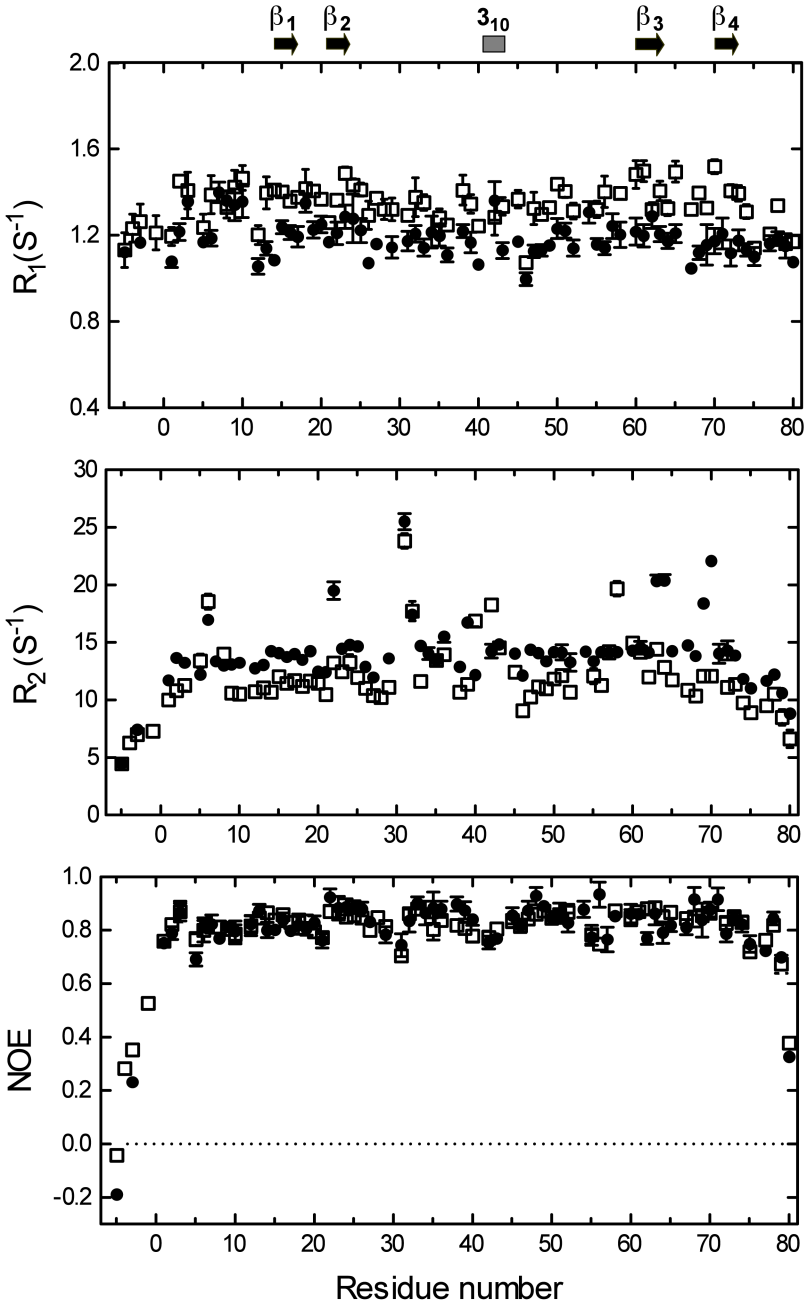

FIGURE S1 Backbone ^{15}N relaxation data of $K2_{Pg}$ both in the absence (open squares) and presence (filled circles) of VEK-30 plotted according to the amino acid sequence of $K2_{Pg}$. Elements of secondary structure (top) are marked at the top of the diagrams (PDB entry 2KJ4).

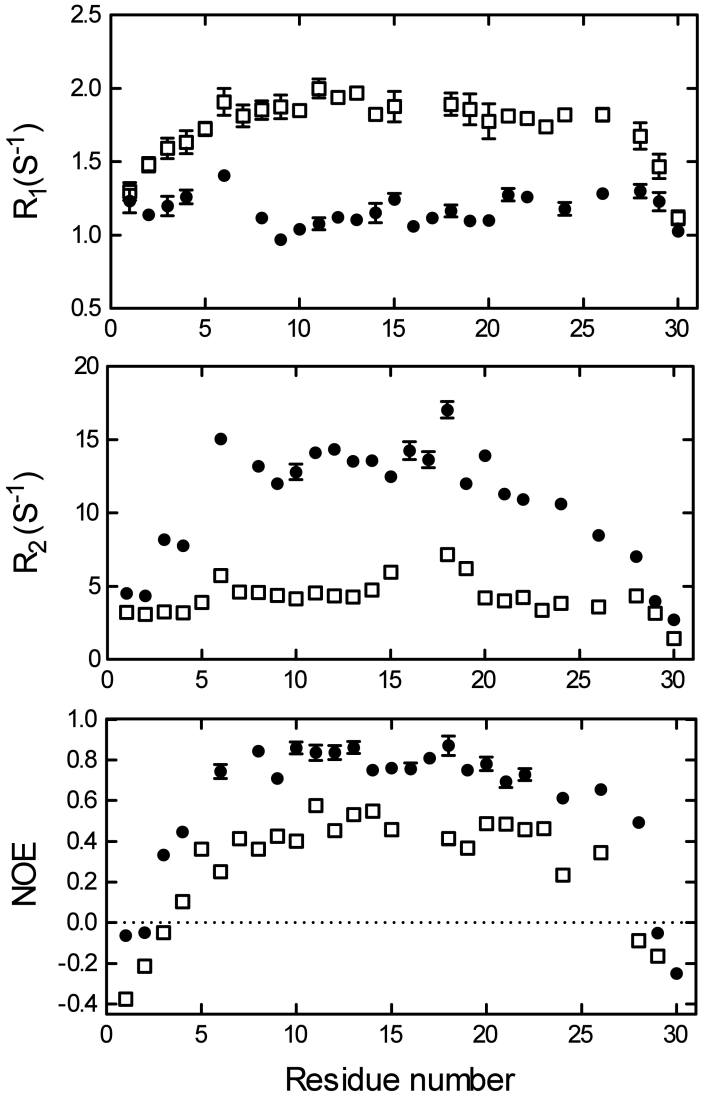

FIGURE S2 Backbone ^{15}N relaxation data of VEK-30 both in the absence (open squares) and presence (filled circles) of $K2_{Pg}$ plotted according to the amino acid sequence of VEK-30.

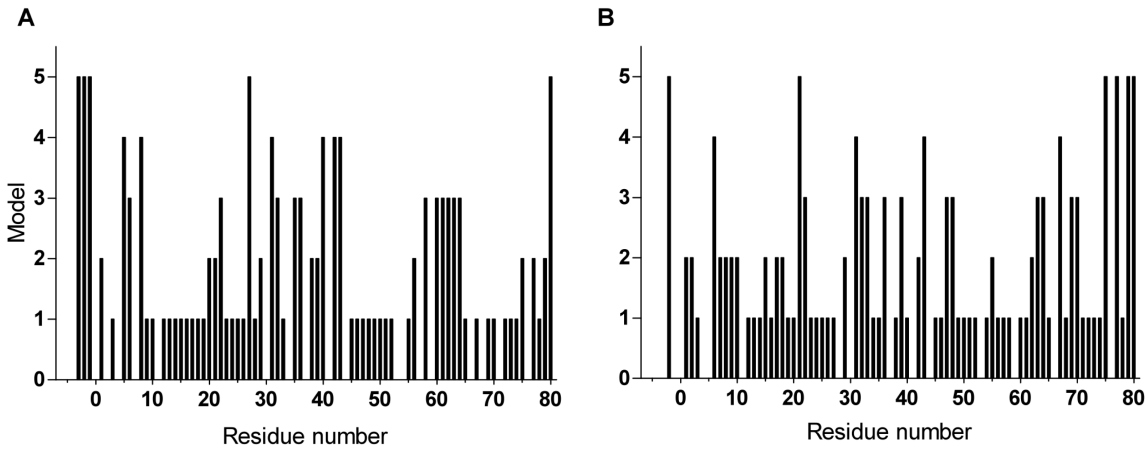

FIGURE S3 Motional models used in the model-free analysis are plotted as a function of the residue numbers of $K2_{Pg}$, depicting the dynamics in the absence (A) and presence (B) of VEK-30.

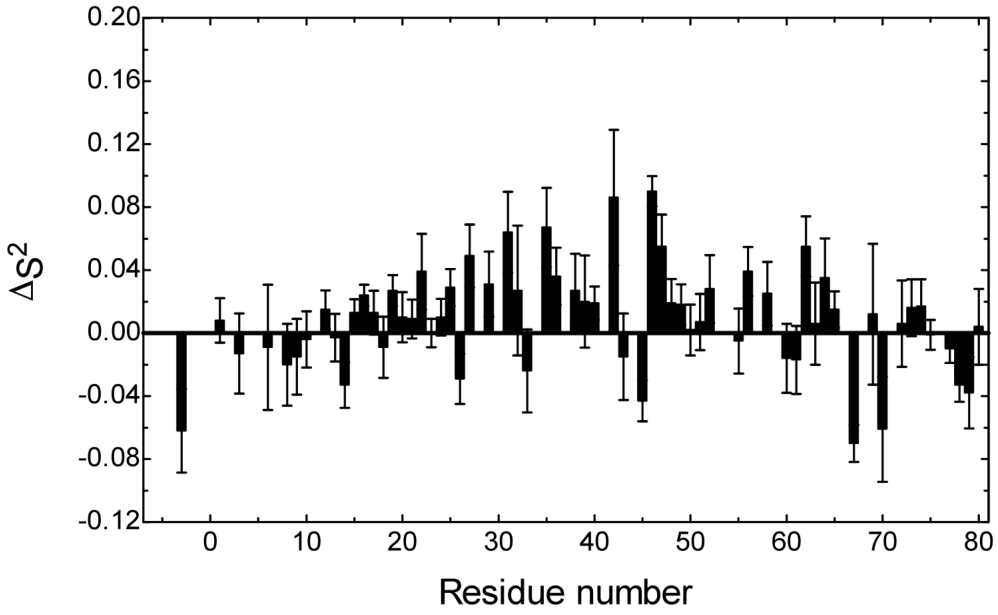

FIGURE S4 Differences of the generalized order parameter (S^2) between apo-$K2_{Pg}$ and VEK-30-complexed $K2_{Pg}$. A positive ΔS^2 denotes enhanced rigidity of the protein backbone upon binding.