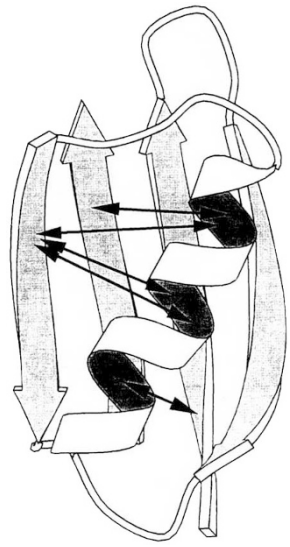
FIG. 4 Diagram of tertiary NOEs observed between the helix and sheet in both Chm-α and Chm-β. Tertiary NOEs represented by the arrows include: $H^{\beta}_{34} - H^{\beta}_{54}$, $H^{\beta}_{34} - H^{\gamma 1}_{54}$, $H^{\beta}_{34} - H^{\gamma 2}_{54}$, $H^{\gamma 1}_{26} - H^{\beta}_{3}$, $H^{\gamma 1}_{26} - H^{\beta}_{3}$, $H^{\gamma 2}_{26} - H^{\alpha}_{3}$, $H^{\rho 2}_{43} - H^{N}_{31}$, $H^{\rho 2}_{43} - H^{\alpha}_{31}$, $H^{\eta 2}_{43} - H^{N}_{30}$, $H^{\beta}_{34} - H^{\eta 2}_{43}$, $H^{\beta}_{34} - H^{\rho 2}_{43}$, for Chm-α; $H^{\rho 2}_{43} - H^{N}_{31}$, $H^{\eta 2}_{43} - H^{N}_{30}$, $H^{\beta}_{34} - H^{\gamma}_{54}$, $H^{\beta}_{34} - H^{\eta 2}_{43}$, $H^{\beta 1}_{3} - H^{\beta}_{26}$, $H^{\beta 2}_{3} - H^{\beta}_{26}$ for Chm-β. Competitive Fc binding experiments with GB1* indicate that both proteins bind Fc. Chm-α and Chm-β have relative dissociation constants (K_d/K_d^{GB1}) for Fc binding of 12.0 and 36.0, respectively; K_d for wild-type GB1 is 7.1 nM[28]. Binding was assayed at 4 °C as described[22]. Sedimentation equilibrium give values for relative molecular masses (M_rs) of 6,800 (calculated, 6,366) and 6,500 (calculated, 6,246) for Chm-α and Chm-β, respectively with random residuals, indicating that both are monomeric. The observed M_rs were independent of protein concentration (10–100 μM). A peptide, Ac-AWTVEKAFKTF-NH_2, corresponding to the Chm sequence with blocked ends, was examined. Its CD spectrum at 0 °C had features typical of unfolded polypeptides[29], was independent of concentration (10–200 μM) and the temperature dependence of the signal at 222 nm was linear from 0–70 °C (data not shown). NMR spectra showed chemical shift dispersion typical of unstructured peptides[25]. Chou–Fasman[30] values for the Chm sequence ($\langle P_\alpha \rangle = 1.15$ and $\langle P_\beta \rangle = 1.05$) indicate that this sequence has no strong statistical preference for α-helix or β-sheet formation.

METHODS. Sedimentation equilibrium measurements were made as described[9] at rotor speeds of 35,000 and 42,000 r.p.m. at 4 °C in 150 mM NaCl, 50 mM sodium acetate, pH 5.4. Dilutions were made into dialysate to obtain 10–100 μm protein samples. Apparent M_rs were calculated by fitting data sets from each sector to a single ideal species model. Partial specific volumes of 0.7323 and 0.7406 ml g^{-1} were used for Chm-α and Chm-β, respectively, and corrected for temperature[31]. The Chm peptide was synthesized by solid-phase Fmoc methods (Applied Biosystems peptide synthesizer 431A) and purified by Sephadex G-25 size-exclusion chromatography in 5% acetic acid and reverse-phase HPLC purification (on a Vydac C18 column using linear H_2O-acetonitrile gradients and 0.1% trifluoroacetic acid). Chm peptide identity was confirmed by MALDI mass spectrometry, measured as 1,367 (expected, 1,368) daltons. CD spectra of Chm peptide were run in 150 mM NaCl, 50 mM sodium acetate, pH 5.4; NMR spectra were obtained in 10% D_2O, pH 5.4.



that the information specifying α-helix or β-sheet secondary structures can be entirely non-local. Taken together, these results underscore the importance of context-dependent effects in protein folding. □

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RETRACTION

Long-term correction of rat model of Parkinson's disease by gene therapy

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J.A.W. writes — In my laboratory we have been attempting to extend the findings reported in this paper. During these efforts, it has come to my attention that the pertinent laboratory notebooks were replaced with edited text and data. An independent analysis of the remaining original data revealed that the published Fig. 2*b* and *c* contains errors that exaggerate both the reductions in the number of rotations after transplantation and the increments in the numbers of rotations following graft removal. Review of the protocol reported in the legend to Fig. 2 indicates that control transfections were done using TransfectACE (Promega) instead of Lipofectin (BRL), which may have affected the outcome of the experiments. Subsequent experiments have failed to replicate the original observations. Regrettably, therefore, I am unable to verify that the conclusions of this paper are correct. □