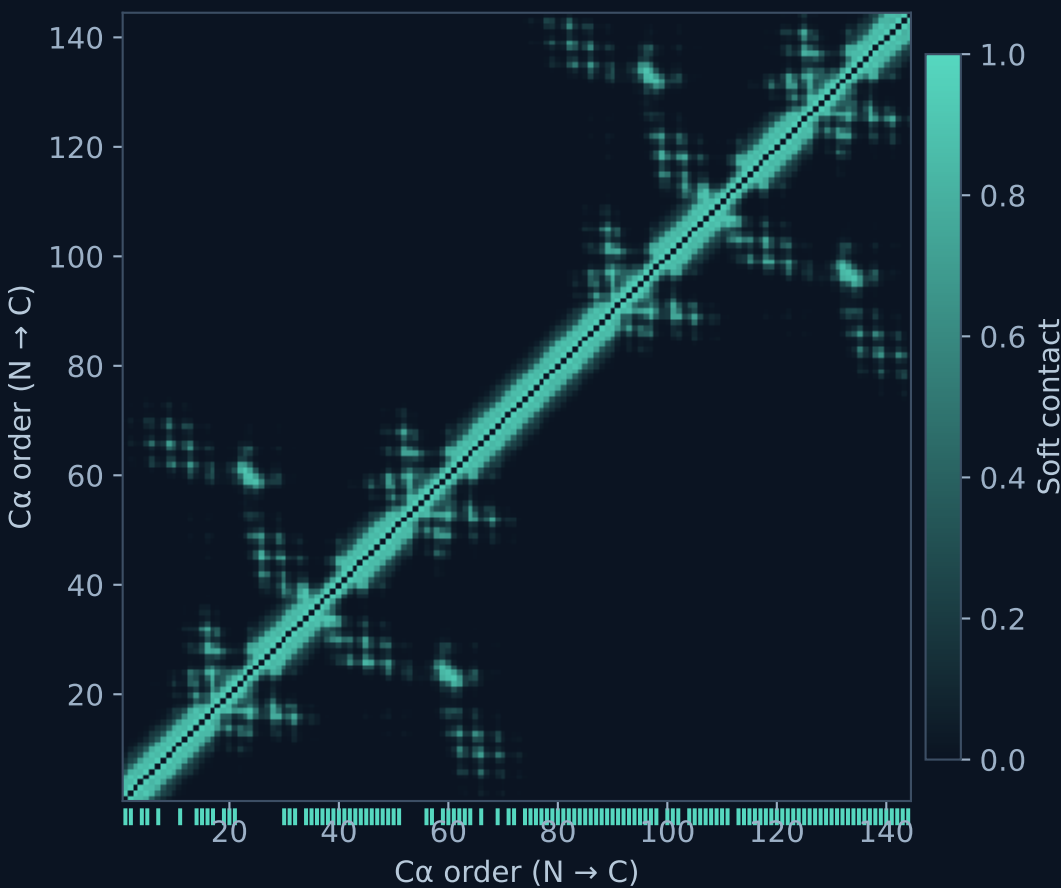
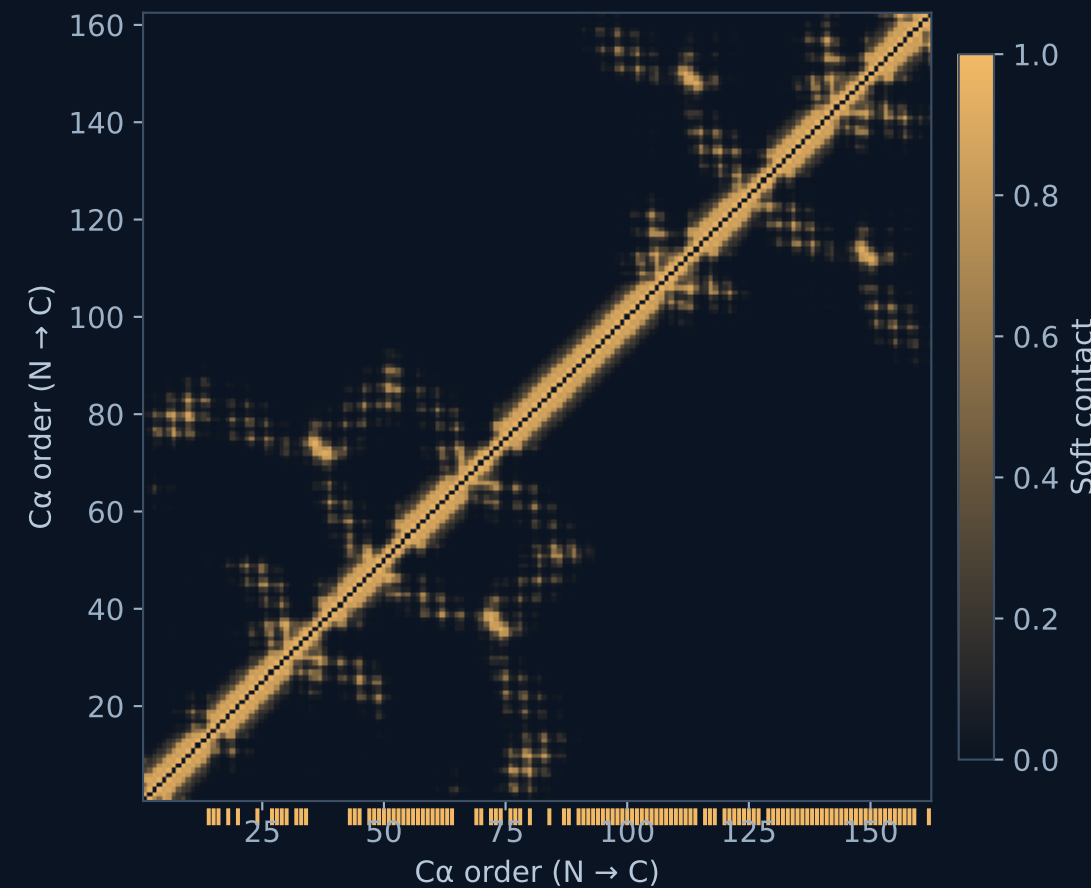


Contact-guided backbone morph / 114 matched residue pairs

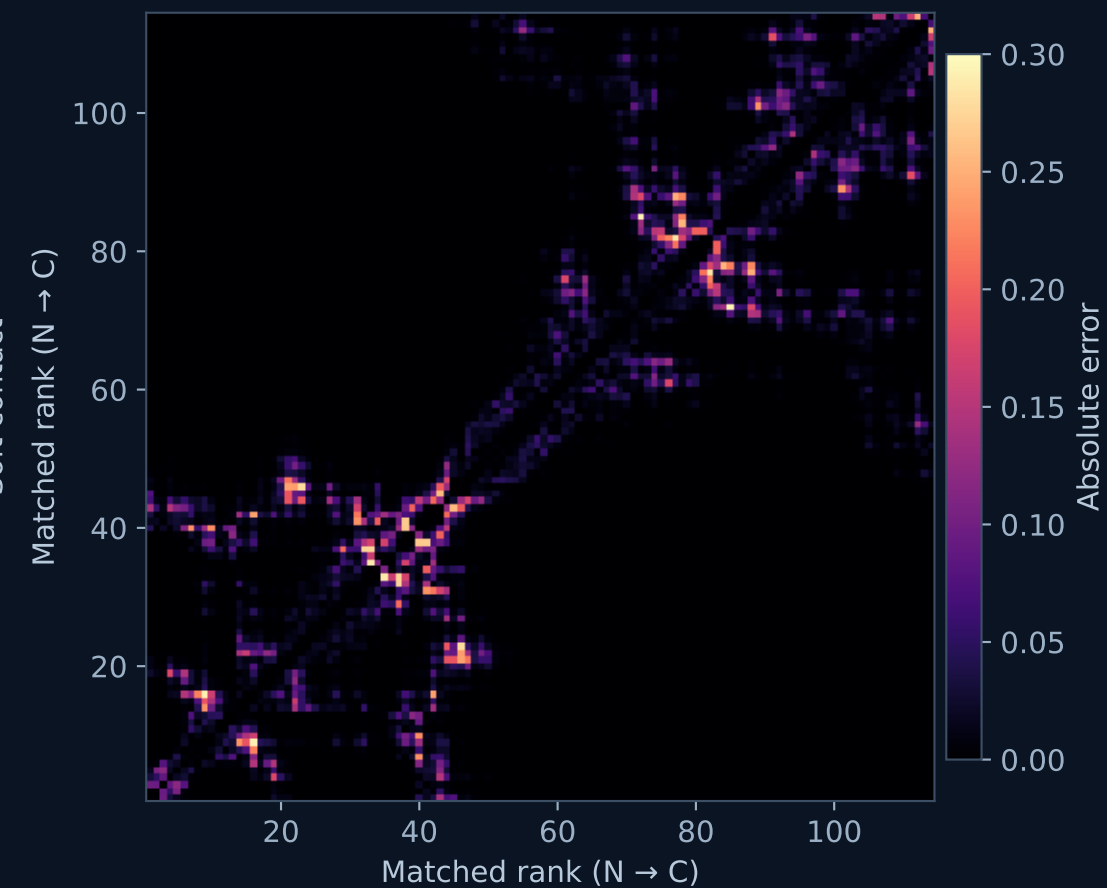
Calmodulin · 1CLL
114/144 Cα residues selected



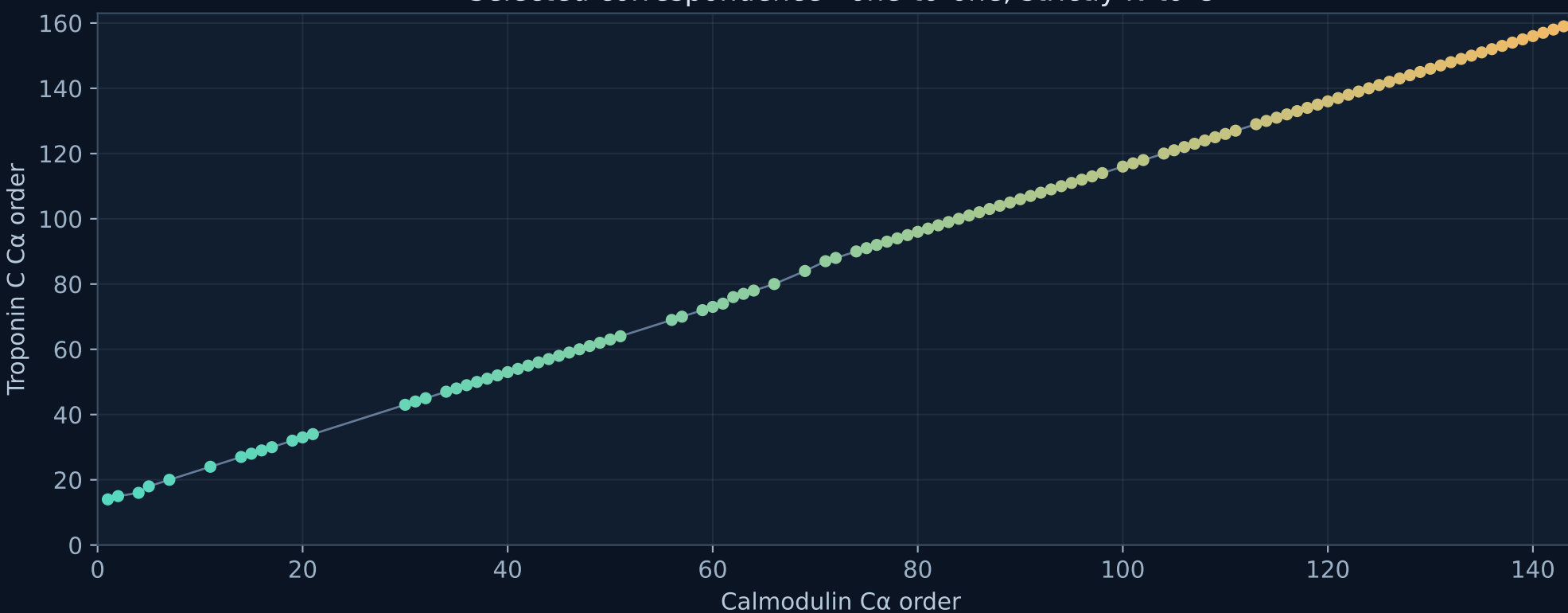
Troponin C · 1NCX
114/162 Cα residues selected



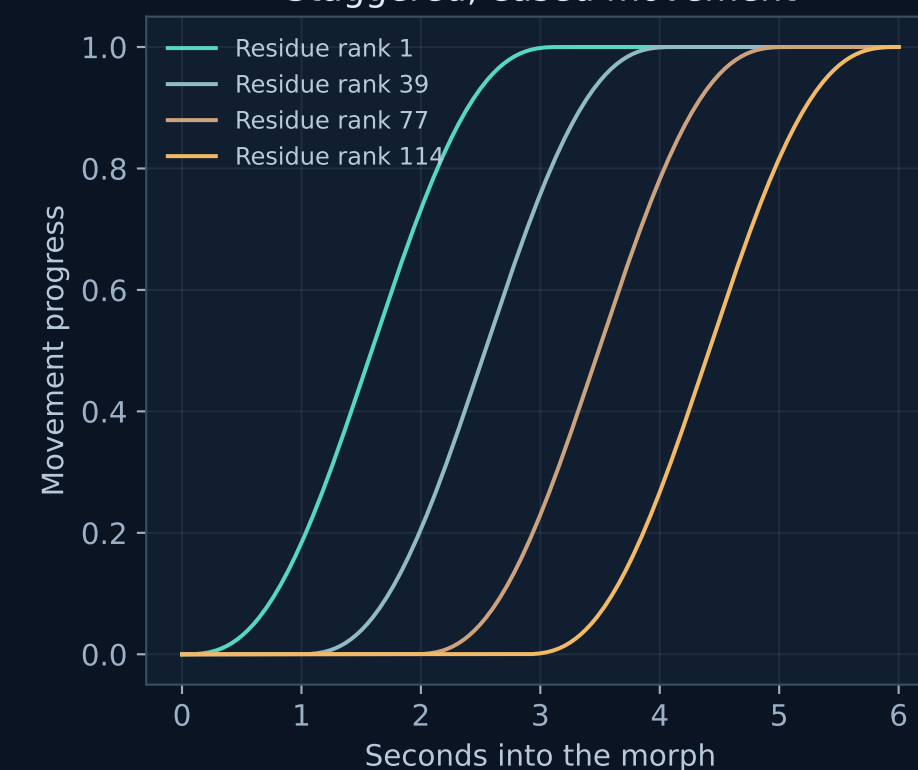
Matched contact disagreement
RMS 0.0275 · max 0.2936



Selected correspondence · one-to-one, strictly N-to-C



Staggered, eased movement



Soft contacts: $\text{sigmoid}((8 \text{ \AA} - \text{distance})/1.5 \text{ \AA})$. Pairwise error ≤ 0.30 . Delay = 25 ms/residue.
Bounded search found this feasible mapping; global optimality was not proved. This is a visual morph, not a simulated transition.