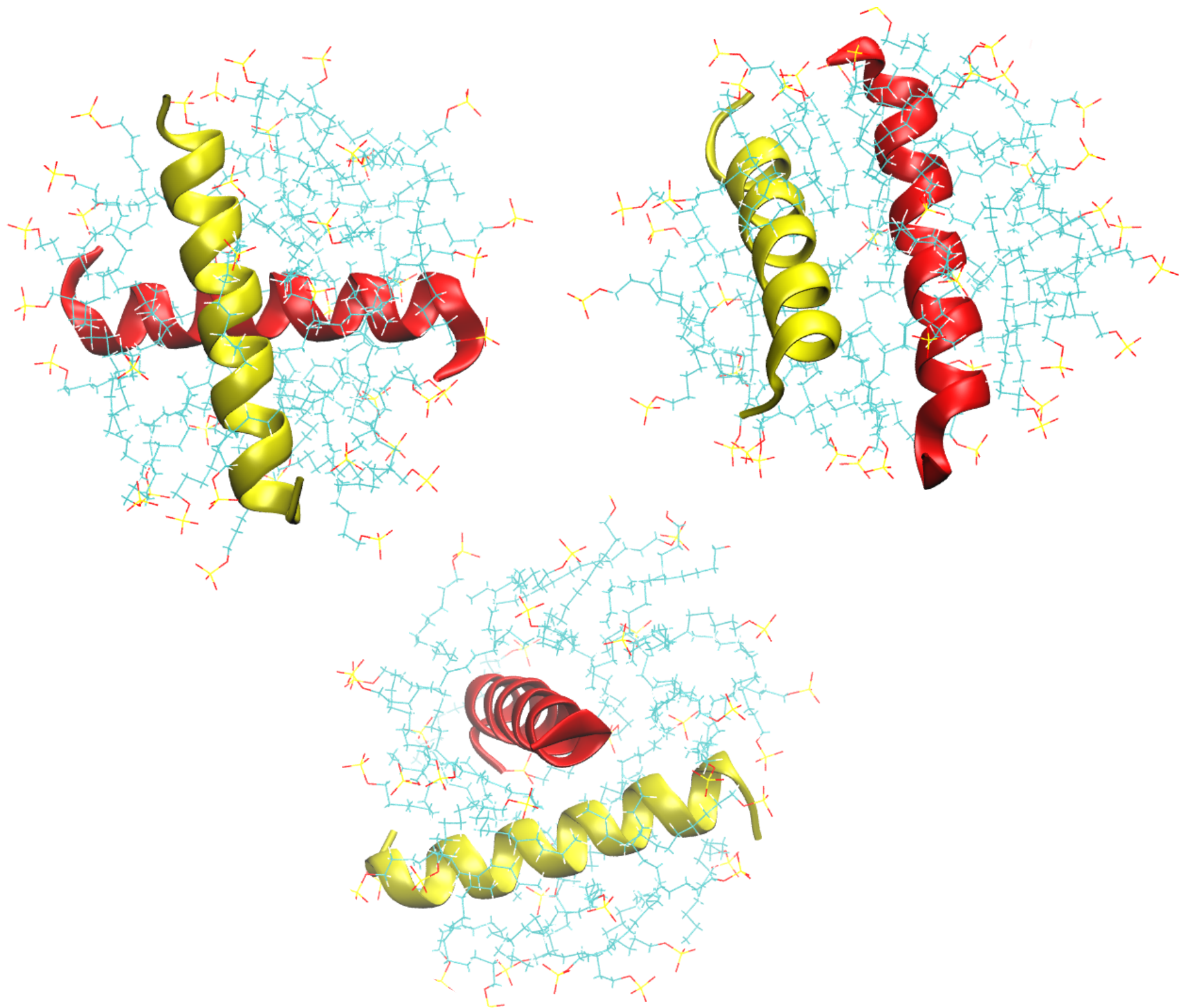
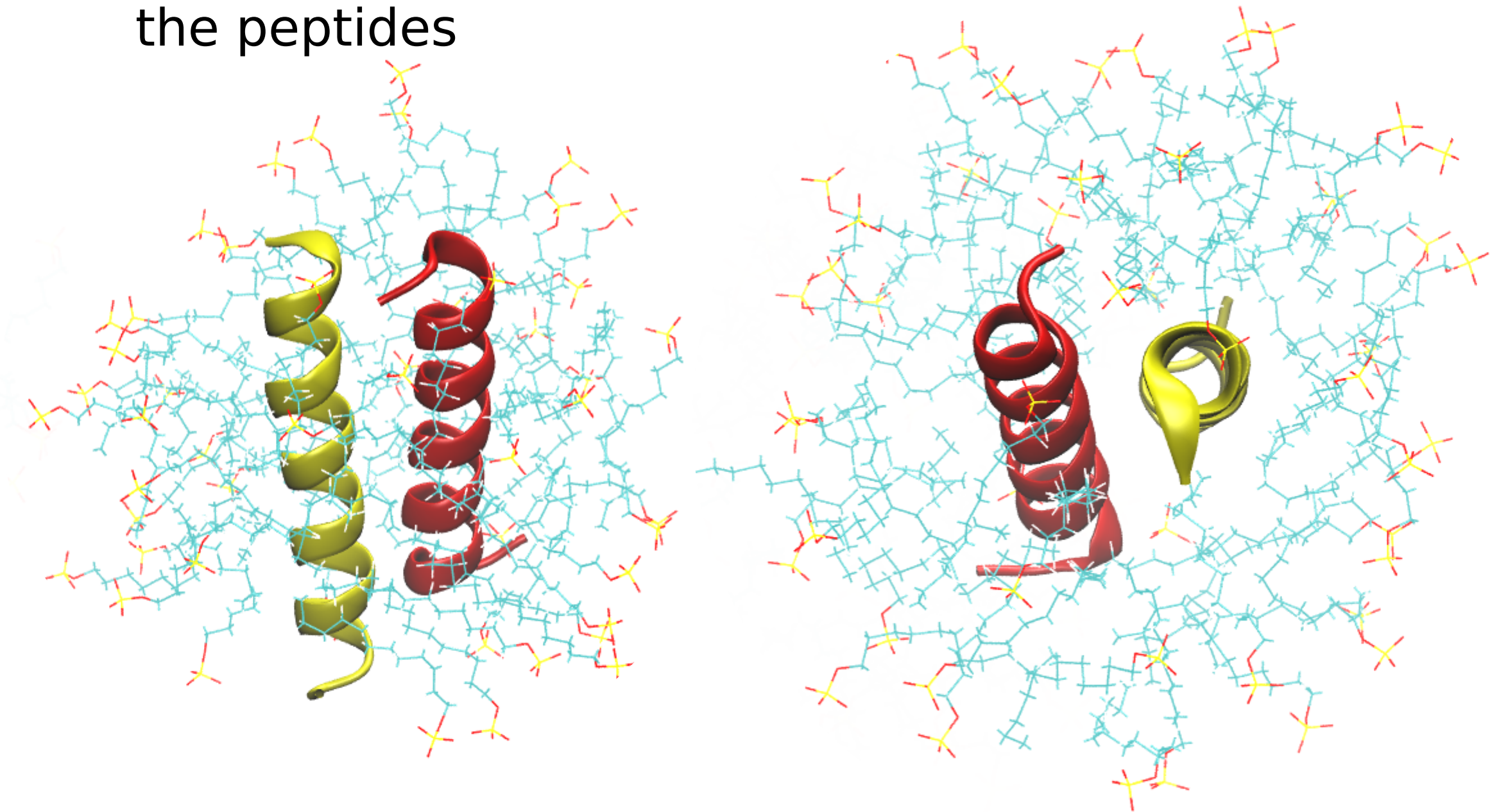


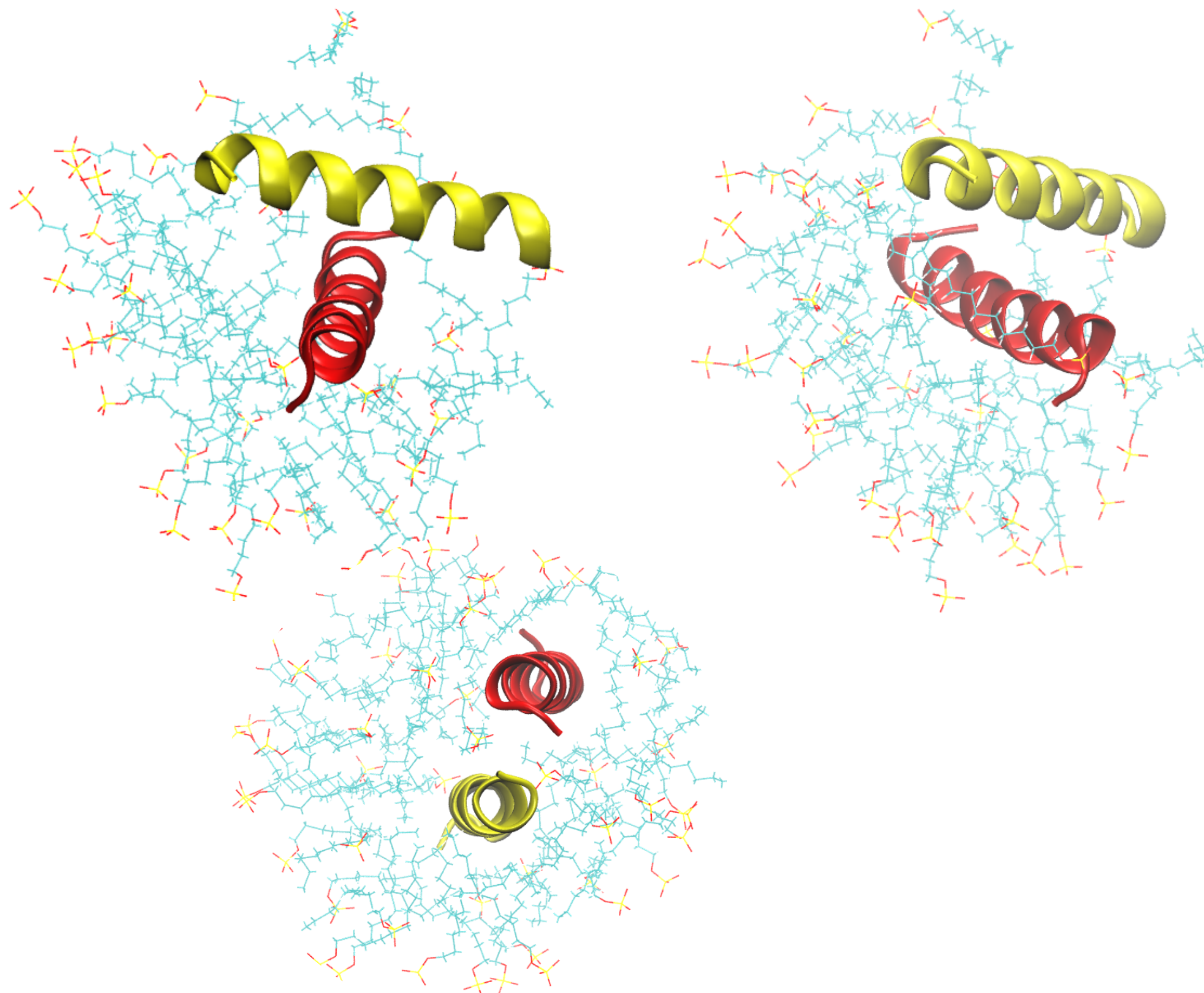
40 SDS - both helical during the simulation; orientation changes possibly direct contact between the peptides in the middle



50 SDS - both helical during the simulation; orientation stays roughly the same; no lipids between the peptides



60 SDS - both helical during the simulation; orientation changes possibly direct contact between the peptides in the middle



70 SDS - the peptide 1 is significantly less helical throughout the full simulation compared to all the other cases; peptide seems not to interact; there are always lipids between them

