

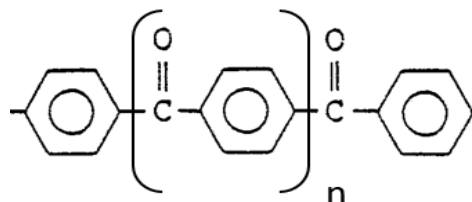
Macromolecular structure and interactions

Forces in Biomolecules

- The small molecule urea can form hydrogen bonds with good affinity to peptide bonds in proteins and peptides.
 - What is expected to happen to a folded protein if urea is added to the solution?
 - Explain the molecular origin of this effect.
- In an unfolded protein, the pK_A values of glutamate and lysine are 4.3 and 10.5, respectively. In folded lysozyme exists a ion-pair interaction between K_1 and E_8 which stabilizes the protein by 3 kJ/mol ($\Delta G^0 = 3$ kJ/mol)
 - Which are the pK_A values of K_1 and E_8 in native Lysozyme?
 - How would a substitution of E_8 to Q alter Lysozyme stability at both pH 7 and pH 2?

Conformation of macromolecules

- In the nuclear pore complexes, there exist unfolded protein domains of the sequence $(GLFG)_n$ which act as a filter. In average, what is the approximate size (end-to-end distance) of one of these proteins if n is in average $n = 45$?
- The radius of gyration of denatured and reduced Ribonuclease A measured by small angle X-ray scattering is 3.32 nm. From this result, estimate the molecular weight of the protein. Compare your result to literature values (search the protein sequence on <https://www.uniprot.org/>, then calculate the MW using <https://web.expasy.org/protparam/>) . Explain your findings.
- The human cell contains a diploid genome with approximately 6.4 billion base pairs. The helical rise (distance between adjacent bases) in DNA is $3.4 \text{ \AA}$ per base pair.
 - Calculate the radius of gyration of such a DNA molecule. Note that the persistence length l_p of DNA is 50 nm.
 - Compare the volume such a molecule would take up to the volume of a human cell nucleus. How many fold is the DNA compacted in our cells?
- Estimate the characteristic ratio and persistence length of the following polymer. Would you expect that your calculation comes close to an experimental value? Explain!



- You study the stability (ΔG) of a protein. A single amino-acid mutation, detected in a cancer patient, lowers the stability of the protein strongly such that it loses function. However, looking at the protein structure, this mutation localizes to a loop of the protein and the mutated amino acid does not seem to be involved in an interaction in the native state.

→ Propose a mechanism how this mutation could lead to protein destabilization. Use the protein stability energy landscape (ΔG vs. folding coordinate) for your answer.

8. You need to synthesize a very stable, helical peptide as an inhibitor of a particular receptor. The peptide is however not very strongly helical. You suspect that the helical dipole has an unfavorable interaction with the N- and C-terminus of the peptide.
 - a. Explain the reason for this unfavorable interaction.
 - b. Propose a strategy, e.g. via chemical modification of the peptide, how to mitigate this problem.

9. To generate circular polarized light, you use a plate made from magnesium fluoride (MgF_2), whose birefringent properties are given below.
 - a. How thick should the plate minimally be to provide either left or right-handed circular polarized light for green light at 532 nm?
 - b. How thick should the plate be if a minimal thickness of 1 mm is required for manufacturing purposes?

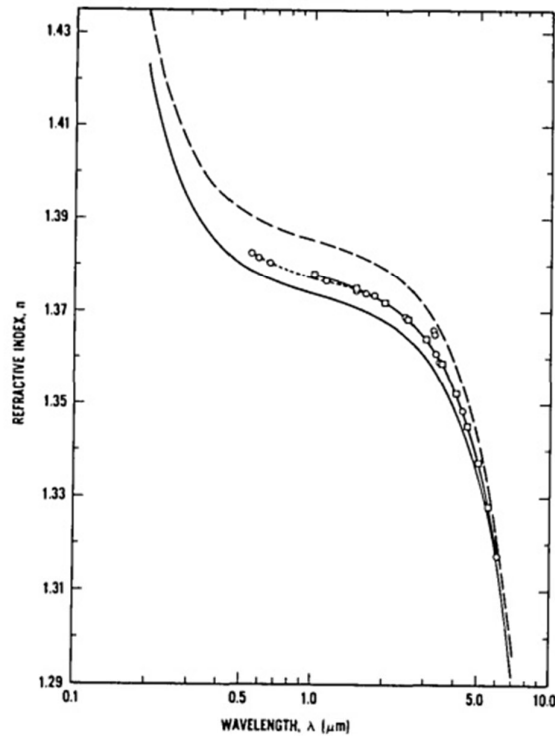


Fig. 2 Refractive index vs wavelength (μm) for the *O* and *E* rays of single-crystal MgF_2 as determined in the current study and for two specimens of hot-pressed MgF_2 . Single-crystal MgF_2 : *O* ray (—); *E* ray (---). Hot-pressed MgF_2 : Buckner *et al.*, ref. [19] ($\circ$); Herzberger and Salzberg, ref. [20] ($\square$).

<https://opg.optica.org/ao/fulltext.cfm?uri=ao-23-12-1980&id=27584>