

Problem on Sedimentation.

Analytical ultracentrifuge data is shown for two protein samples.

The proteins are a hen egg white lysozyme sample, and a sample of a fragment of the bacterial translation initiation factor IF2 known as "IF2 domain-1".

The hen egg white lysozyme contains 129 amino acids, and the IF2 domain-1 contains 156 amino acids. The hen egg white lysozyme sample is known to be a monomer in solution.

The hen egg white lysozyme has the amino acid sequence:

KVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGS
TDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDG
NGMNAWVAWRNRCKGTDVQAWIRGCRL

In each centrifugation experiment, the rotation rate of the rotor is 45 000 rpm, and the temperature is 20 C.

(a) Use the centrifugation data to calculate the sedimentation coefficient for each of the two proteins.

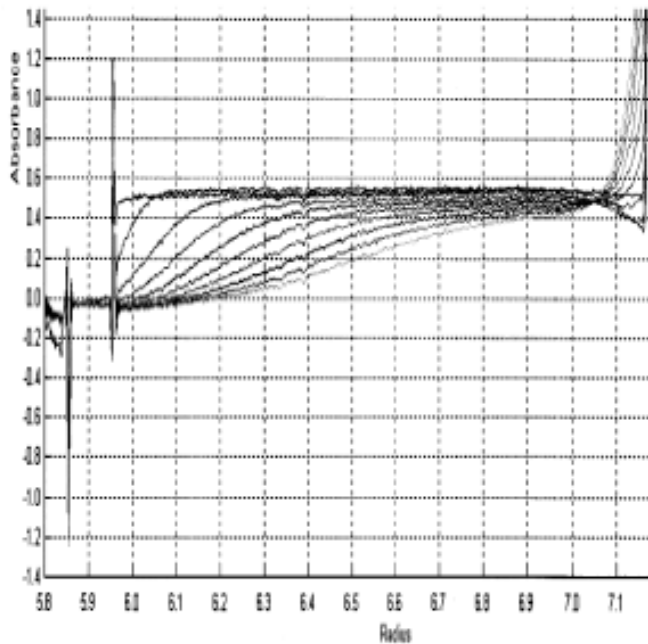
(b) What are the approximate dimensions of the hen egg white lysozyme molecule, in Å? What are the approximate lengths of the longest and shortest axis of the protein molecule?

(c) Use the centrifugation data to draw conclusions regarding the likely shape of the IF2 domain-1. Is it more or less elongated than the lysozyme?

Lysozyme – 129 amino acids.

UV scans at intervals of 5, 35, 65, 95, 125, 155, 185, 215, 245, 275 minutes.

Absorption at 230nm. Buffer = water at pH 7



IF2 N-terminal domain (2-157) - 156 aa

UV scans at intervals of 15, 75, 135, 195, 255, 315, 375, 435 minutes.

Absorption at 230nm. Buffer = water at pH 7

