

1.

(a)

Organism: *Homo sapiens*

Sequence length: 597 residues

Experimental method: Cryo-EM (3.00 Å resolution)

(b)

Chains present: 3 (A, B – protein; C – tRNA)

Ligands present: AMP, LYS, Na⁺

(c)

Secondary structure (A: 380, 381, 382, 382): **Loop / Coil**

(d)

Pseudo-torsion angle (Cα 380–381–382–383): **≈ -53°**