Association pathways in apoferritin-based nanovaccines: structural effects of pH-driven and direct assembly

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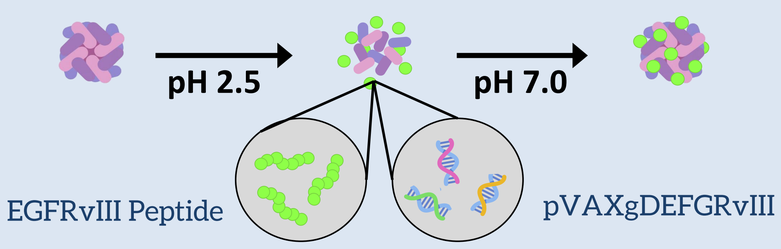
INTRODUCTION

Apoferritin (ApFt) is a self-assembling globular protein widely investigated as a versatile biotechnological platform for immunotherapeutic delivery (1). This study evaluates the conformational and intermolecular effects arising from distinct assembly protocols for peptide (PPT) (2) and plasmid DNA (pDNA)-based nanovaccines (3).

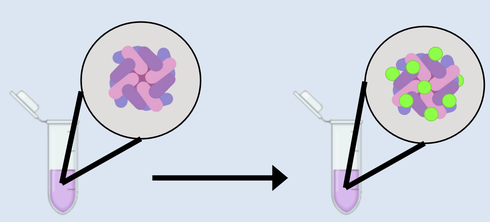
The goal is to elucidate the structural dynamics of ApFt association with these biomolecules to optimize the development of protein-based nanocarriers.

METHODOLOGY

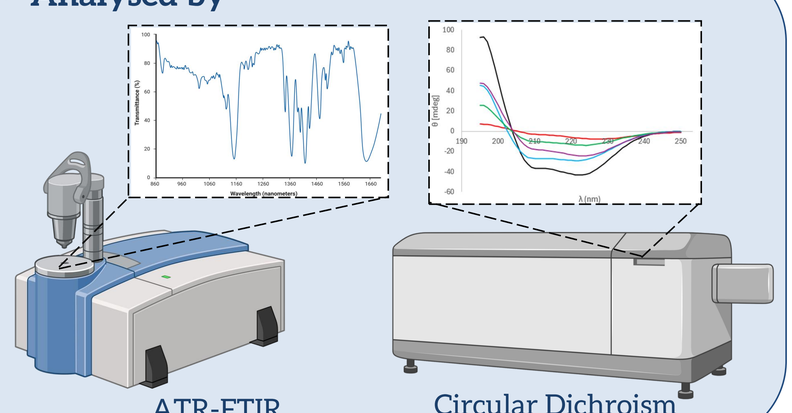
- **1st Association Pathways: pH- induced structural disassembly/reassembly**



- **2nd Association Pathways: direct association**



- **Analysed by**



RESULTS

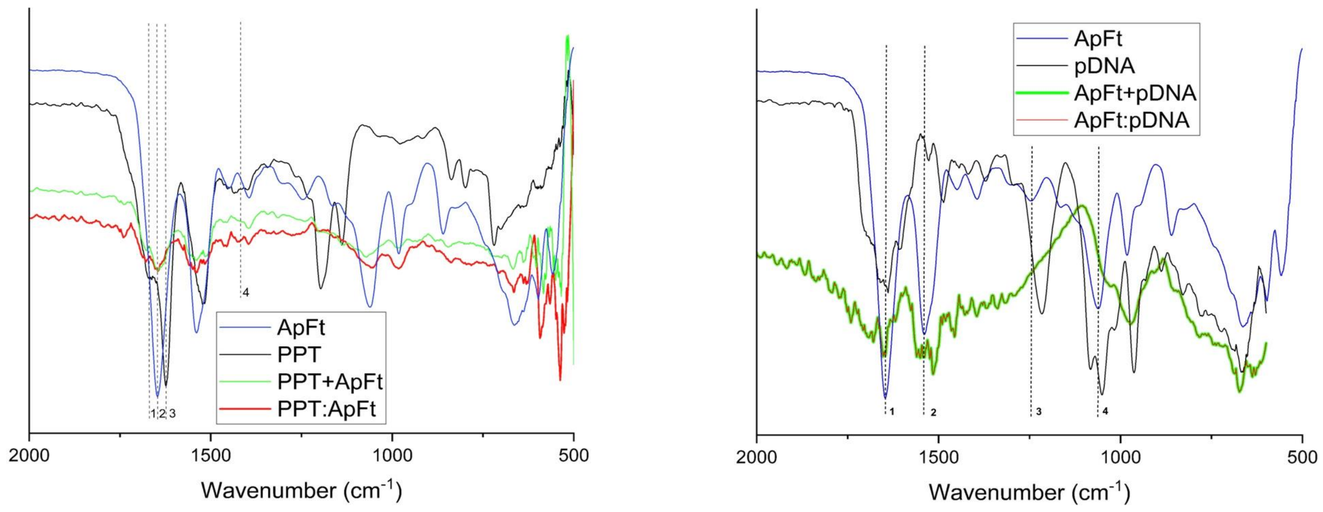
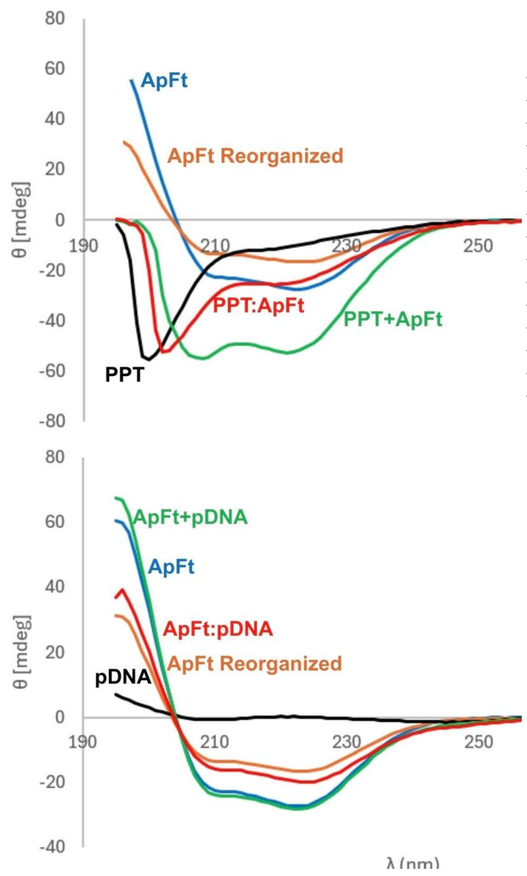


Figure 1- ATR-FTIR spectra of apoferritin-based nanovaccines systems containing EGFRvIII peptide (left) and pDNA (right)



Secondary Structure	ApFt	ApFt reorg	PPT	PPT+ApFt	PPT:ApFt
			%		
Helix1 (regular)	38.7	65.9	7.7	99.5	91.6
Helix2 (distorted)	58.0	18.9	0.0	0.0	0.0
Anti1 (left-twisted)	3.3	15.2	0.0	0.0	0.0
Anti2 (relaxed)	0.0	0.0	0.0	0.0	0.0
Anti3 (right-twisted)	0.0	0.0	88.6	0.5	8.4
Parallel	0.0	0.0	0.0	0.0	0.0
Turn	0.0	0.0	0.0	0.0	0.0
Others	0.0	0.0	0.0	0.0	0.0
Helix	96.7	84.8	7.7	99.5	91.6
Antiparallel	3.3	15.2	88.6	0.5	8.4
Parallel	0.0	0.0	0.0	0.0	0.0
Turn	0.0	0.0	0.0	0.0	0.0
Others	0.0	0.0	3.7	0.0	0.0

Secondary Structure	ApFt	ApFt reorg	pDNA	ApFt+pDNA	ApFt:pDNA
			%		
Helix1 (regular)	38.7	65.9	0.0	36.4	59.4
Helix2 (distorted)	58.0	18.9	5.0	63.6	22.2
Anti1 (left-twisted)	3.3	15.2	3.1	0.0	18.4
Anti2 (relaxed)	0.0	0.0	24.9	0.0	0.0
Anti3 (right-twisted)	0.0	0.0	11.3	0.0	0.0
Parallel	0.0	0.0	0.0	0.0	0.0
Turn	0.0	0.0	9.4	0.0	0.0
Others	0.0	0.0	46.4	0.0	0.0
Helix	96.7	84.8	5.0	100.0	81.6
Antiparallel	3.3	15.2	39.3	0.0	18.4
Parallel	0.0	0.0	0.0	0.0	0.0
Turn	0.0	0.0	9.4	0.0	0.0
Others	0.0	0.0	46.4	0.0	0.0

Figure 2- Circular dichroism (CD) spectra of apoferritin-based nanovaccines systems (left) and the relative content (%) of secondary structure obtained from spectral deconvolution (right).

CONCLUSION

CD/FTIR show ApFt preserves its α-helical fold with ligand-specific surface rearrangements. The assembly route significantly influenced ApFt–PPT interactions, while ApFt–pDNA showed method-independent stability. These results underscore ApFt's structural robustness and adaptability, reinforcing its potential as a nanovaccine platform for rational formulation design.

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References:

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