Supporting information

Feasibility of Non-Invasive Measurement of Cardiac Biomarkers Using Mid-Infrared Spectroscopy: Finite Element Analysis and Experimental Validation

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Table S1. Spectral characteristics of common interfering molecules in the mid-infrared region

Interfering Molecule	Amide I Band (~1650 cm^{-1})	Amide II Band (~1550 cm^{-1})	Other Characteristic Absorptions	Dominant Secondary Structure
Human Serum Albumin	1652 cm^{-1} (α-helix)	1545 cm^{-1} (N-H bending and C-N stretch)	1235 cm^{-1} (Amide III) and ~3300 cm^{-1} (N-H stretching)	Predominantly α-helix
Immunoglobulin G	1640 cm^{-1} (β-sheet dominant)	1538 cm^{-1} (strong β-sheet feature)	1230-1240 cm^{-1} (Amide III) and ~3070 cm^{-1} (aromatic C-H)	Predominantly β-sheet
Cathepsins (e.g., Cathepsin D)	1635-1650 cm^{-1} (mixed α/β)	1520-1550 cm^{-1}	1210 cm^{-1} (proline C-N vibration) and 1315 cm^{-1} (tyrosine)	Mixed α/β with notable tertiary structure

Table S2 Comparison of MIR spectral features of cTnI, NT-proBNP, and CRP

Biomarker	Main Absorption Peaks (cm^{-1})	Origin of Peaks
cTnI	1650 (Amide I)	β-sheet structure
	1545 (Amide II)	Proline side chain vibration
	1210 (Proline vibration)	
NT-proBNP	1650 (Amide I)	Dominantly α-helical structure
	1550 (Amide II)	Protein backbone modes
	1450 (CH_2 bending)	
CRP	1645 (Amide I)	Rich in β-sheets and β-turns
	1538 (Amide II)	Carboxylic acid side chains
	1390 (COO^- symmetric stretch)	