

# Evaluation and Refinement of Sample Preparation Methods for Extracellular Matrix Proteome Coverage

## Authors

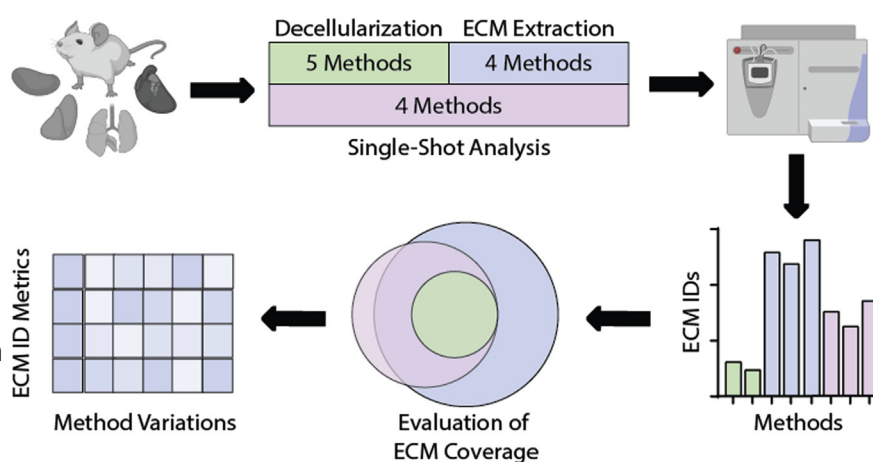
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Due to their insolubility, many extracellular matrix (ECM) proteins are resistant to typical extraction and require optimized extraction methods for proteomic analysis. A wide variety of decellularization and ECM extraction methods have been published, but it remains unclear how these methods perform compared with one another on a complex, ECM-rich sample. A direct comparison of both cell and ECM extraction methods on a whole organism sample and four additional organs serves as a reference for future ECM proteomics.

## Graphical Abstract



## Highlights

- Decellularization drastically improves ECM coverage.
- ECM coverage is the highest with a dual chemical/enzymatic digestion method.
- SPEED is the best tested single-shot method for ECM identification.
- A fourfold improvement in ECM peptide IDs was achieved compared with standard methods.



# Evaluation and Refinement of Sample Preparation Methods for Extracellular Matrix Proteome Coverage

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**The extracellular matrix is a key component of tissues, yet it is underrepresented in proteomic datasets. Identification and evaluation of proteins in the extracellular matrix (ECM) has proved challenging due to the insolubility of many ECM proteins in traditional protein extraction buffers. Here we separate the decellularization and ECM extraction steps of several prominent methods for evaluation under real-world conditions. The results are used to optimize a two-fraction ECM extraction method. Approximately one dozen additional parameters are tested, and recommendations for analysis based on overall ECM coverage or specific ECM classes are given. Compared with a standard in-solution digest, the optimized method yielded a fourfold improvement in unique ECM peptide identifications.**

The extracellular matrix (ECM) is a noncellular component of tissues, which provides structural scaffolding and mediates signaling in the extracellular space to govern a wide range of biological processes including cell differentiation, wound healing, and fibrosis (1). Knowledge of ECM composition is critical to fields ranging from biomedical to food science, yet data regarding the ECM proteome is relatively sparse. In general, proteins of the ECM assemble into, or interact with, extended noncovalent polymers (2). Several core structural proteins undergo posttranslational modifications including cross-link generation to further stabilize the assembled structures (3), rendering this sizable covalent fraction resistant to extraction in the strongest detergents and chaotropic agents (4). Often, collagen-containing ECM structural fibers are quantified using assays measuring hydroxyproline as a surrogate for collagen after total protein hydrolysis (5). The results are a crude measurement of total collagen and provide

no information about collagen subtype distribution or solubility. Additionally, hydroxyproline residues are present in other cellular and extracellular proteins such as HIF-1 $\alpha$  (6) and elastin (7), which hinders the specificity of the assay. In other studies, second harmonic generation (SHG) and two-photon autofluorescence (TPAF) imaging have been successfully used to characterize ECM fibers by taking advantage of the intrinsic properties of collagen fibers and elastin autofluorescence to allow for analysis of ECM architecture (8, 9). SHG and TPAF along with other imaging approaches can be used to determine the properties of ECM fibers and their degree of alignment and branching, yet they fail to provide specific qualitative and quantitative information about matrix protein abundance and subtype.

Proteomics is an attractive approach to complement these methods due to its ability to provide both compositional and quantitative readouts. Preliminary draft proteomes have been reported in recent years with deep proteome coverage of tissues obtained from protein extraction in a strong chaotrope and extended LC-MS acquisition (10–13). However, ECM proteins that were expected to be highly abundant (e.g., collagens I, III, V, elastin, etc) were not found at high abundance in these datasets. This is likely a result of approximately 75–85% of the fibrillar ECM residing in a chaotrope-resistant insoluble fraction that has eluded analysis by these and other standard proteomic methods (14).

Protein extraction protocols have been developed, which specifically target enrichment of the ECM. These methods typically consist of a decellularization step followed by chaotrope extraction, either alone (15–18) or followed by dilution and digestion with LysC and/or Trypsin in preparation for LC-MS/MS analysis (19–25). Without the decellularization step,

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lower-abundance ECM proteins would not be identified. Biochemical methods have also been developed, which use chemical digestion to solubilize and access highly insoluble ECM proteins of interest (4, 26). We have previously developed methods that utilize chemical digestion with cyanogen bromide (CNBr) (14) and hydroxylamine (HA) hydrochloride (4). While both methods efficiently extract insoluble proteins, HA digestion has been the method of choice due to its safety, low cost, and lack of additional transfer steps during processing (4). However, nonspecific Asn-X cleavages should be considered during database searching, and the digestion process can induce oxidative modifications that, if extended beyond methionine single oxidation, can convolute data analysis, leaving room for improvement of the method (4).

A wide variety of decellularization and ECM extraction methods have been published, but it remains unclear how these methods perform compared with one another on a complex, ECM-rich sample. Previous matrisome enrichment method comparisons have been performed (27) revealing the strength of chemical digestion in identifying core matrisome (structural ECM) proteins. However, significant advancements and new methods have since been developed. A direct comparison of both cell and ECM extraction methods on a whole organism sample and four additional organs serves as an important reference for future ECM proteomics. Putative proteins that compose the ECM have been previously defined using *in silico* and proteomic approaches, generating the MatrisomeDB, which is divided into core matrisome and matrisome-associated proteins (28). Here, we utilize core matrisome annotations of collagens, ECM glycoproteins, and proteoglycans for comparison of ECM protein characterization. For this comparison, five widely used decellularization methods (4, 19, 29) and four methods for single-shot extraction and analysis (21, 30, 31) (Table 1) have been used for evaluation. In addition, four ECM extraction methods: a two-step extraction with guanidine hydrochloride (Gnd-HCl) followed by HA hydrochloride (Gnd-HCl/HA) digestion (4), chaotrope-assisted in-solution digest with ultrasonication (CAISU) (19), chaotrope-assisted in-solution digest (CAIS) (20), and surfactant and chaotropic agent-assisted sequential extraction/on-pellet digestion (SCAD) (21) were evaluated. The findings are used to make recommendations for tissue analysis based on factors including matrisome protein sequence coverage, the number of matrisome proteins identified, and variability of results.

### EXPERIMENTAL PROCEDURES

#### *Tissue Preparation*

**Whole Mouse Powder (WMP) Production:** Whole male C67BL/6J mouse was frozen in liquid nitrogen and fractured into approximately 1 cm<sup>3</sup> pieces. Fur and blood were not removed from the mouse before milling. The resulting pieces were kept frozen in liquid nitrogen before milling to a fine powder under liquid nitrogen using a SPEX 6870

freezer/mill. The milled powder was kept frozen and lyophilized for 24 h. Approximately 100 mg aliquots of lyophilized powder were then delipidated by four successive extractions with 2 ml 100% ice-cold acetone and briefly dried at room temperature in a fume hood. Isolated mouse organs (heart, liver, kidney, and lung) were prepared using the same method.

#### *Decellularization Methods*

**1-Fraction A**—Approximately 5 mg of WMP was homogenized (Bullet Blender, Model BBX24, Next Advance, Inc) for 3 min on power 8 in 200  $\mu$ l/mg of high salt buffer (50 mM Tris-HCl, 0.25% CHAPS, 25 mM EDTA, 3 M NaCl, pH 7.4) supplemented with 10  $\mu$ l/ml fresh protease inhibitor (Halt Protease Inhibitor Cocktail, Thermo Scientific #78429) with the addition of approximately 50 1 mm glass beads (4). Homogenate was vortexed at 4 °C for 20 min. Homogenized tissue was spun at 18,000  $\times$  g (4 °C) for 15 min. The resulting supernatant was removed and saved, and the pellet was further extracted with 1 ml high salt buffer two times with homogenization after each buffer addition. Cellular extracts were pooled into a single soluble fraction.

**1-Fraction B**—Approximately 5 mg of WMP was placed in 200  $\mu$ l/mg 10 mM Tris-HCl (pH 8.0) with 0.1% ethylenediamine tetraacetic acid (EDTA) and 1X protease inhibitors (Halt Protease Inhibitor Cocktail, Thermo Scientific #78429) at 4 °C for 48 h (29). Triton X-100 (Sigma-Aldrich #T9284) was added to a final concentration of 3%, and samples were vortexed at medium power at 4 °C for 72 h. The solution was changed every 24 h by spinning at 18,000  $\times$  g (4 °C) for 15 min, and samples were resuspended by vortexing. The resulting supernatant from each buffer exchange was pooled into a single cellular fraction. Samples were then incubated in 50 mM Tris-HCl pH 7.4, 10 mM MgCl<sub>2</sub>, 1% benzonase (Millipore #70746) at 37 °C for 24 h, spun at 18,000  $\times$  g (4 °C) for 15 min, and the supernatant was discarded. Decellularized WMP was then washed with PBS with 1X protease inhibitors for 24 h to remove residual reagents. All steps were conducted under continuous shaking.

**2-Fraction**—Approximately 5 mg of lyophilized WMP was homogenized (Bullet Blender, Model BBX24, Next Advance, Inc) in 200  $\mu$ l/mg buffer 1 (150 mM NaCl, 50 mM Tris-HCl (pH 7.5), 5% glycerol, 1% NP-40 (US Biological #N3500), 1 mM MgCl<sub>2</sub>, 1X protease inhibitors (Halt Protease Inhibitor Cocktail, Thermo Scientific #78429)) at power 8 for 3 min with the addition of approximately 50 1 mm glass beads and vortexed at 4 °C for 20 min. Homogenized tissue was spun at 18,000  $\times$  g (4 °C) for 15 min, and the supernatant was collected (fraction 1). After the addition of each extraction buffer, samples were resuspended for 1 min at power 8 using the Bullet Blender. Sample was then homogenized in 200  $\mu$ l/mg (of starting tissue dry weight) buffer 2 (50 mM Tris-HCl (pH 7.4), 2% CHAPS, 2 mM EDTA, 3M NaCl, 1X protease inhibitors) at power 8 for 3 min and vortexed at 4 °C for 15 min. Homogenized tissue was spun at 18,000  $\times$  g (4 °C) for 15 min, and the supernatant was collected (fraction 2).

**3-Fraction**—Approximately 5 mg of lyophilized WMP was homogenized (Bullet Blender, Model BBX24, Next Advance, Inc) in 500  $\mu$ l PBS containing protease inhibitors (Halt Protease Inhibitor Cocktail, Thermo Scientific #78429) at power 8 for 3 min with the addition of approximately 50 1 mm glass beads (19). Homogenate was centrifuged at 16,000  $\times$  g for 20 min at 4 °C, and the supernatant was collected. After the addition of each extraction buffer, samples were resuspended for 1 min at power 8 using the Bullet Blender. Sample was then homogenized in 500  $\mu$ l buffer 1 (150 mM NaCl, 50 mM Tris-HCl (pH 7.5), 5% glycerol, 1% NP-40 (US Biological #N3500), 1 mM MgCl<sub>2</sub>, 1X protease inhibitors, 1% benzonase (Millipore #70746)) at power 8 for 15 s before incubating 20 min on ice. Homogenate was centrifuged at 16,000  $\times$  g for 20 min at 4 °C, and the supernatant was collected and pooled with the first wash to make fraction 1. Sample was then homogenized in 500  $\mu$ l buffer 2 (150 mM NaCl, 50 mM

TABLE 1

Descriptions of tested decellularization, ECM extraction, and single-shot methods with required time and composition of each extraction buffer

Method	Steps involving buffer exchange	Time	Buffer composition
1-Fraction A (4)	3	3 h	1. 50 mM Tris-HCl, 0.25% CHAPS, 25 mM EDTA 3M NaCl, 10 µl/ml PI, pH 7.4
1-Fraction B (28)	5	7 days	1. 10 mM Tris-HCl, 0.1% EDTA, 1× PI, pH 8.0 2. 50 mM Tris-HCl pH 7.4, 10 mM MgCl <sub>2</sub> , 1% benzoylase, 1× PI
2-Fraction	2	2 h	1. 150 mM NaCl, 50 mM Tris-HCl, 5% glycerol, 1% NP-40, 1 mM MgCl <sub>2</sub> , 1× PI 2. 50 mM Tris-HCl pH 7.4, 2% CHAPS, 2 mM EDTA, 3M NaCl, 1× PI
3-Fraction (18)	4	3 h	1. 150 mM NaCl, 50 mM Tris-HCl pH 7.5, 5% glycerol, 1% NP-40, 1 mM MgCl <sub>2</sub> , 1× PI, 1% benzoylase 2. 150 mM NaCl, 50 mM Tris-HCl pH 7.5, 5% glycerol, 1% NP-40, 0.5% DOC, 0.1% SDS, 1× PI, 1% benzoylase 3. 500 mM NaCl, 50 mM Tris-HCl pH 7.5, 5% glycerol, 1% NP-40, 2% DOC, 1% SDS, 1× PI, 1% benzoylase
4-Fraction	10	8.5 h	1. Buffer C (HEPES pH7.9, MgCl <sub>2</sub> , KCl, EDTA, sucrose, glycerol, NaOV), 1× PI 2. Buffer W (HEPES pH7.9, MgCl <sub>2</sub> , KCl, EDTA, sucrose, glycerol, NaOV), 1× PI 3. Buffer N (HEPES pH7.9, MgCl <sub>2</sub> , KCl, EDTA, glycerol, DOC, NP-40, NaOV), 1× PI, 1% benzoylase 5. Buffer M (HEPES pH7.9, MgCl <sub>2</sub> , KCl, EDTA, sucrose, glycerol, DOC, NP-40, NaOV), 1× PI 6. Buffer CS (Pipes pH6.8, MgCl <sub>2</sub> , NaCl, EDTA, sucrose, SDS, NaOV), 1× PI
Gnd-HCl/HA (4)	3	2.5 days	1. 6M Gnd-HCl, 100 mM ABC pH8.0 2. 1M HA, 4.5M Gnd-HCl, 0.2M K <sub>2</sub> CO <sub>3</sub> , pH 9.0
CAISU (17)	1	19 h	1. 6M Gnd-HCl 2. 10 mM Tris-HCl pH8.5, 2M Gnd-HCl, 2.7M Urea, 3% ACN 3. 10 mM Tris-HCl pH8.5, 600 mM Gnd-HCl, 800 mM Urea, 3% ACN
CAIS (18)	1	1 day	1. 8M Urea, 100 mM ABC pH8.0 2. 2M Urea, 100 mM ABC pH8.0, 1000U PNGaseF
SCAD (20)	3	1.7 days	1. 4% SDS, 50 mM Tris 2. 8M Urea, 100 mM ABC, pH 8.0
In-Gel (30)	11	21 h	1. 25 mM ABC, 50% ACN 4. 25 mM/50 mM ABC
In-Solution	1	17 h	1. 25 mM ABC
SPEED (29)	1	17 h	1. TFA 2. 2M Tris Base

Green—decellularization methods, Blue—ECM extraction methods, Purple—Single-shot analysis methods.

Tris-HCl (pH 7.5), 5% glycerol, 1% NP-40, 0.5% sodium deoxycholate (DOC), 0.1% SDS, 1X protease inhibitors, 1% benzoylase) at power 8 for 15 s before incubating 20 min on ice. Homogenate was centrifuged at 16,000 × g for 20 min at 4 °C, and the supernatant was collected (fraction 2). Sample was then homogenized in 500 µl buffer 3 (500 mM NaCl, 50 mM Tris-HCl (pH 7.5), 5% glycerol, 1% NP-40, 2% DOC, 1% SDS, 1X protease inhibitors, 1% benzoylase) at power 8 for 15 s before incubating 20 min at room temperature. Homogenate was centrifuged at 16,000 × g for 20 min at 4 °C, and the supernatant was collected (fraction 3). Soluble fractions were precipitated with 80% acetone and resuspended in 8M urea for subsequent digestion.

**4-Fraction (Millipore Compartment Protein Extraction Kit, #2145)**—In total, 5 mg of lyophilized WMP was homogenized (Bullet Blender, Model BBX24, Next Advance, Inc) in 500 µl of Buffer C containing protease inhibitors (Halt Protease Inhibitor Cocktail, Thermo Scientific #78429) for 3 min on power 8 with the addition of approximately 50 1 mm glass beads. Homogenate was vortexed at power 4 for 20 min at 4 °C. Homogenate was then centrifuged at 16,000 × g for 20 min at 4 °C, and the supernatant was collected (fraction 1) and flash frozen.

After the addition of each extraction buffer, samples were resuspended for 1 min at power 8 using the Bullet Blender. The pellet was resuspended in 400 µl of Buffer W containing protease inhibitors and vortexed at power 4 for 20 min at 4 °C. Sample was centrifuged at 16,000 × g for 20 min at 4 °C, and the supernatant was discarded. The pellet was then resuspended in 150 µl of Buffer N containing protease inhibitors, 1% benzoylase (Millipore #70746) and vortexed at power 4 for 20 min at 4 °C. Homogenate was centrifuged at 16,000 × g for 20 min at 4 °C, and the supernatant was collected (fraction 2) and flash frozen. Centrifugation was repeated and the remaining supernatant was added to the N fraction. The pellet was resuspended in 400 µl of Buffer W containing protease inhibitors and vortexed at power 4 for 20 min at 4 °C. Sample was centrifuged at 16,000 × g for 20 min at 4 °C, and the supernatant was discarded. The pellet was then resuspended in 100 µl of Buffer M containing protease inhibitors and vortexed at power 4 for 20 min at 4 °C. Homogenate was centrifuged at 16,000 × g for 20 min at 4 °C, and the supernatant was collected (fraction 3) and flash frozen. The pellet was then resuspended in 200 µl of Buffer CS containing protease inhibitors and



vortexed at power 4 for 20 min at 4 °C. 9. Homogenate was centrifuged at 16,000 × *g* for 20 min at 4 °C, and the supernatant was collected (fraction 4). The pellet was resuspended in 150 µl of Buffer C containing protease inhibitors and vortexed at power 4 for 20 min at 4 °C. Homogenate was then centrifuged at 16,000 × *g* for 20 min at 4 °C, and the supernatant was pooled with fraction CS before flash-freezing the CS fraction. Additional washes were performed by resuspending the pellet in 500 µl of PBS containing protease inhibitors and vortexing at power 4 for 5 min at 4 °C. Homogenate was centrifuged at 16,000 × *g* for 20 min at 4 °C, and the supernatant was discarded. Washes were repeated three times.

**Digestion and Preparation of Extracts from Decellularization for MS**—All fractions from decellularization were digested using the filter-aided sample preparation (FASP) protocol as previously described (32) using 10 kDa molecular weight cutoff filters (Sartorius, Vivacon #VN01H02). Digests were performed for 16 h in 25 mM ABC pH 8.0 using trypsin at a 1:100 enzyme:protein ratio at 37 °C in an oven. Aliquots of digested samples containing 10 µg of protein were desalted using Pierce C18 Spin Tips (Thermo Scientific #84850) according to the manufacturer's protocol.

### Single-Shot Methods

**Surfactant and Chaotropic Agent-Assisted Sequential Extraction/ on-Pellet Digestion (SCAD) (21)**—Approximately 5 mg of WMP was solubilized in 300 µl of buffer (4% SDS, 50 mM Tris buffer) and incubated at 95 °C for 10 min. After allowing the solution to return to room temperature, protein extract was reduced with 10 mM dithiothreitol (DTT) for 30 min at room temperature and alkylated with 50 mM iodoacetamide (IAM) for an additional 15 min in the dark. The reaction was then quenched with an additional 2 mM DTT. SDS was removed by two rounds of precipitation. For the first precipitation, cold acetone (−20 °C) was added to a final concentration of 80% (v/v), and the protein was precipitated overnight at −20 °C. For the second round, 80% acetone/water (v/v) was added, followed by incubation at −20 °C for 2 h. The samples were centrifuged at 18,000 × *g* for 15 min, and the pellet was briefly air-dried in a fume hood. Pellet was dissolved in 125 µl of 8M urea, and on-pellet digestion was performed with Lys-C (1:100, Wako #121-05063) for 4 h at 37 °C. Samples were diluted with 875 µl of 50 mM Tris buffer along with Trypsin (1:100, Promega #V511 C) for overnight digestion. The reaction was quenched with 1% FA. Aliquots of digested samples containing 10 µg of protein were desalted using Pierce C18 Spin Tips (Thermo Scientific #84850) according to the manufacturer's protocol.

**In-Gel Digest**—Approximately 1 mg of WMP was suspended in SDS-PAGE loading buffer (5% SDS, 250 mM Tris-HCl pH 7.0, 50% glycerol) and heated to 95 °C for 5 min (31). The protein homogenate was then loaded onto a 3–8% TAE (Tris-acetate-EDTA) gel and run 1 cm into 8 cm × 8 cm, 1 mm gel. The gel was stained with Brilliant Blue R (Sigma-Aldrich #B7920), and the entire protein-containing band was excised. In-gel digestion was performed as previously described (31). Aliquots of digested samples containing 10 µg of protein were desalted using Pierce C18 Spin Tips (Thermo Scientific #84850) according to the manufacturer's protocol.

**In-Solution Digest**—Approximately 1 mg of WMP was suspended in 20 µl of 50 mM ABC, 0.2% ProteaseMax. Sample was vortexed for 60 min. Sample was diluted with 100 µl 50 mM ABC. DTT was added to the sample to reach a final concentration of 10 mM and incubated at 37 °C for 15 min. Sample was removed from heat and allowed to cool for 5 min to condense and then spun down to collect condensate. IAM was added to sample at 2.5 M excess DTT and incubated in the dark at room temperature for 30 min. Alkylation was quenched with 10% excess DTT. Digestion was performed using 3 µg Trypsin in 0.03% ProteaseMax overnight at 37 °C. Samples were then acidified to 0.1% FA to stop digestion. Aliquots of digested samples containing

10 µg of protein were desalted using Pierce C18 Spin Tips (Thermo Scientific #84850) according to the manufacturer's protocol.

**Sample Preparation by Easy Extraction and Digestion (SPEED)**—Approximately 5 mg of WMP was suspended in 100 µl trifluoroacetic acid (TFA) and incubated at room temperature for 10 min (30). Samples were further irradiated for 10 s at 800 W using a microwave oven. Samples were neutralized with 2M TrisBase using 10× volume relative to TFA before adding DTT to 10 mM and reducing for 30 min at 37 °C. Iodoacetamide was added to a 2.5× molar excess over DTT, and samples were incubated in the dark for 15 min. Digestion was carried out for 20 h at 37 °C using trypsin at an enzyme:protein ratio of 1:50. Aliquots of digested samples containing 10 µg of protein were desalted using Pierce C18 Spin Tips (Thermo Scientific #84850) according to the manufacturer's protocol.

### ECM Extraction Methods

**Hydroxylamine Chemical Digest (Gnd-HCl/HA)**—ECM-enriched pellets were homogenized in 6M Gnd-HCl, 100 mM ammonium bicarbonate (ABC) at power 8 for 1 min (Bullet Blender, Model BBX24, Next Advance, Inc) and vortexed (power 5) at room temperature overnight (4). Homogenate was spun at 18,000 × *g* (4 °C) for 15 min, and the supernatant was collected as the Gnd-HCl fraction. Remaining pellets were reduced and alkylated by incubating in 10 mM DTT, 100 mM ABC pH 8.0 for 30 min at 37 °C before adding 2.5× molar excess of IAM (over DTT) and incubating in the dark for 15 min. Samples were spun at 18,000 × *g* (4 °C) for 15 min, and the supernatant was discarded. Pellets were then treated with freshly prepared HA buffer (1 M NH<sub>2</sub>OH-HCl, 4.5 M Gnd-HCl, 0.2 M K<sub>2</sub>CO<sub>3</sub>, pH adjusted to 9.0 with NaOH) at 200 µl/mg of the starting tissue dry weight. Each tube was placed under a stream of nitrogen gas and sealed before being homogenized at power 8 for 1 min and incubated at 45 °C with shaking (1000 rpm) for 4 h. Following incubation, the samples were spun for 15 min at 18,000 × *g*, and the supernatant was removed and stored as the HA fraction at −80 °C until further proteolytic digestion with trypsin. All Gnd-HCl and HA fractions were subsequently subjected to enzymatic digestion with trypsin using a FASP approach (32) and aliquots of digested samples containing 10 µg of protein desalted using Pierce C18 Spin Tips (Thermo Scientific #84850) according to the manufacturer's protocol.

**Chaotrope-Assisted In-solution Digest with Ultrasonication (CAISU)**—Digestion of ECM-enriched pellets was performed in two steps (19). Samples were resuspended in 6M guanidinium hydrochloride (Gnd-HCl). Samples were reduced with 10 mM DTT for 30 min at room temperature and alkylated with 50 mM IAM for 15 min in the dark, and the reaction was quenched with additional DTT. The first digestion was done at 37 °C for 2 h with LysC (1:50 enzyme to protein ratio) in 10 mM Tris-HCl (pH 8.5) containing 2M Gnd-HCl, 2.7 M urea, and 3% acetonitrile. Prior to the 2-h incubation, samples were sonicated for 15 min (37 °C) using a Bioruptor plus ultrasonicator (Diagenode). The second digestion step was done using fresh LysC (1:50 enzyme to protein ratio) and trypsin (1:20 enzyme to protein ratio) in 600 mM Gnd-HCl, 800 mM urea, and 3% acetonitrile at 37 °C overnight. An additional sonication step was also performed prior to the overnight digest. Aliquots of digested samples containing 10 µg of protein were desalted using Pierce C18 Spin Tips (Thermo Scientific #84850) according to the manufacturer's protocol.

**Chaotrope-Assisted In-solution Digest (CAIS)**—ECM-enriched pellets were resuspended in 50 µl of 8M urea, 100 mM ABC, 10 mM DTT and incubated with continuous agitation at 1400 rpm for 2 h at 37 °C (20). Samples were cooled to RT, and 500 mM IAM in water was added to a final concentration of 25 mM. Samples were then incubated in the dark for 30 min at RT. Sample buffer was diluted to 2M urea with 100 mM ABC pH 8.0, and 1000U PNGaseF was added before incubating with continuous agitation at 1400 rpm for 2 h at

37 °C. Lys-C (1 µg) was added, and samples were incubated with continuous agitation at 1400 rpm for 2 h at 37 °C. Trypsin (3 µg) was added, and samples were incubated with continuous agitation at 1400 rpm O/N at 37 °C. A second aliquot of trypsin (1.5 µg) was added, and samples were incubated with continuous agitation at 1400 rpm for an additional 2 h at 37 °C. Trypsin was then inactivated by acidifying the sample with 10% formic acid. Acidified samples were centrifuged at 16,000 × g for 5 min at RT, and the supernatant was collected. Aliquots of digested samples containing 10 µg of protein were desalted using Pierce C18 Spin Tips (Thermo Scientific #84850) according to the manufacturer's protocol.

SCAD—Protocol was performed as described above using except an ECM-enriched pellet generated with the 1-fraction A method was used rather than WMP (21).

*Sample Preparation of Isolated Organs for Instrument Comparison*—Samples of the isolated heart, kidney, and liver from C57BL/6J mice were dissected and flash frozen by the Jackson Lab. Each organ was cryo-milled into a fine, homogenous powder using a mortar and pestle under liquid nitrogen and lyophilized for future processing. Organ samples from three individual mice were pooled and mixed thoroughly before weighing. Samples were decellularized using the 1-fraction A method, as described above, followed by the Gnd-HCl/HA, CAISU, CAIS, and SCAD ECM extraction methods. All ECM extraction methods were performed as previously described for WMP comparisons.

#### ECM Extraction Method Optimization

*Gnd-HCl/HA Digest Optimization*—For antioxidant testing, hydroxylamine digest was performed as described above with the addition of 50 mM methionine, 100 µM/500 µM caffeic acid, 100 µM/500 µM gallic acid, or 2 mM ascorbic acid (vitamin C) to the HA digest buffer immediately before pellet treatment. Acid pretreatment testing was performed by incubating the insoluble pellet in 0.2% formic acid (FA) for 10 min before spinning at 18,000 × g (4 °C) for 15 min and discarding the supernatant. For each condition, HA buffer at the stated HA concentration was pH-adjusted prior to pellet treatment, and the digest was carried out for the stated time under vortexing.

*PNGase F Digestion*—PNGase F digestion was performed on a 10 kDa cutoff filter (Sartorius #VN01H02) prior to FASP digestion. Filters were first equilibrated with successive washes of 0.1% FA followed by 8M urea, 100 mM ABC pH 8.0. All washes were spun through at 14,000 × g for 15 min. Samples were then loaded onto filters and spun at 14,000 × g for 20 min before washing with 200 µl of 8M urea, 100 mM ABC. Filters were then washed with three aliquots of 100 µl 50 mM ABC pH 8.0 before adding 1000U PNGase F (NEB #P0704) in 2M urea, 100 mM ABC pH 8.0 directly to the top of the filter membrane. PNGase F digestion was allowed to proceed for 2 h at 37 °C before spinning at 14,000 × g for 15 min to remove digest volume, retaining deglycosylated protein on the membrane. Filters were then washed with 100 µl 50 mM ABC pH 8.0 to remove residual buffer. Trypsin digest was performed in 20 mM ABC pH 8.0 with 0.02% ProteaseMax (Promega #V207 A) for 16 h using a 1:100 enzyme:protein ratio. Samples were eluted and acidified in 150 µl 0.2% FA. Aliquots of digested samples containing 10 µg of protein were desalted using Pierce C18 Spin Tips (Thermo Scientific #84850) according to the manufacturer's protocol.

*PNGase F Digestion with GAG Removal*—Removal of N-linked glycans and glycosaminoglycans (GAGs) using PNGaseF (NEB #P0704), heparinase II (NEB #P0736), and chondroitinase ABC (Sigma-Aldrich #C3667) was performed across multiple digestion steps. Filter equilibration, sample loading, and predigest washes were performed as described above for the PNGase F digestion. After performing three washes with 50 mM ABC, 1000U PNGase F and 0.5U heparinase II in 100 µl 100 mM NaCl, 20 mM Tris-HCl, 1.5 mM

CaCl<sub>2</sub> were added directly to each filter membrane. Digests were carried out for 16 h at 37 °C before spinning for 15 min at 14,000 × g to remove digest volume, retaining deglycosylated protein on the membrane. The filter was then washed with 100 µl 50 mM Tris-HCl pH 7.5 before adding 100 µl of 50 mM Tris-HCl pH 7.5, 60 mM sodium acetate, 0.02% BSA containing 0.5U chondroitinase ABC. Chondroitinase ABC digestion was performed for 8 h at 37 °C before spinning filters for 15 min at 14,000 × g to remove digest volume. Filters were then washed with 100 µl 50 mM ABC pH 8.0. Trypsin digest was performed by adding trypsin at a 1:100 enzyme:protein ratio in 100 µl 25 mM ABC pH 8.0, 0.02% ProteaseMax (Promega #V2071) and allowing the digest to proceed for 16 h at 37 °C. Samples were eluted and acidified in 150 µl 0.2% FA. Aliquots of digested samples containing 10 µg of protein were desalted using Pierce C18 Spin Tips (Thermo Scientific #84850) according to the manufacturer's protocol.

#### Data Acquisition and Processing

*Sample Quantification and Normalization*—Samples from all methods were quantified after trypsin digest using a Micro BCA protein assay kit (Thermo Fisher Scientific #23235) according to the manufacturer's protocol. Aliquots containing 10 µg of protein from each digest were loaded onto Pierce™ C18 Spin Tips (Thermo Scientific #84850) and desalted using the manufacturer's protocol. Each sample was dried to approximately 2 µl under vacuum and was brought up in 16 µl 0.1% FA.

*MS/MS Acquisition*—Global proteomics for all comparative method testing was carried out (n = 3 per group) on an LTQ Orbitrap Velos mass spectrometer (Thermo Fisher Scientific) coupled to an Eksigent nanoLC-2D system through a nanoelectrospray LC-MS interface. Eight microliter of each sample was injected into a 20 µl loop using the autosampler. The analytical column was then switched on-line at 600 nl/min over an in house-made 100 µm i.d. × 150 mm fused silica capillary packed with 2.7 µm CORTECS C18 resin (Waters; Milford, MA). After 10 min of sample loading at 600 nl/min, each sample was separated on a 120-min gradient consisting of a linear gradient from 2 to 8% ACN with 0.1% FA at a flow rate of 600 nl/min from 3 min to 20 min, followed by a linear gradient from 8 to 22% ACN with 0.1% FA at a flow rate of 350 nl/min from 20 min to 90 min. Gradient elution was followed by a linear increase to 60% ACN at 350 nl/min from 90 min to 98 min and further to 90% ACN from 98 min to 104 min to remove remaining peptides. The column was then re-equilibrated with 2% ACN in 0.1% FA at 350 nl/min from minutes 104 to 120. LC mobile-phase solvents consisted of 0.1% FA in water (Buffer A) and 0.1% FA in acetonitrile (Buffer B, Optima LC/MS, Fisher Scientific, Pittsburgh, PA). Data acquisition was performed using the instrument supplied Xcalibur (version 4.1) software. The mass spectrometer was operated in the positive ion mode. Each survey scan of m/z 300–2000 was followed by collision-induced dissociation (CID) MS/MS of the 20 most intense precursor ions with an isolation width of 2.5 m/z. Dynamic exclusion was performed after fragmenting a precursor two times within 15 s for a duration of 30 s. Singly charged ions were excluded from CID selection. Normalized collision energies of 35 eV were employed using helium as the collision gas.

tsiMS Pro data acquisition for isolated organs was carried out (n = 3 per group) using a Bruker NanoElute LC system through a nanoelectrospray LC-MS interface. One microliter of each sample was injected into a 20 µl loop using the autosampler. The analytical column was then switched on-line at 600 nl/min over a 15 cm NanoElute column (Bruker Daltonics) using ReproSil 1.9 µm C18 resin (Dr Maisch GmbH, Germany). After 4 min of sample loading at 800.0 bar, each sample was separated on a 120-min gradient. For cellular and Gnd-HCl fractions, the LC method consisting of a linear gradient from 2 to 24% ACN with 0.1% FA at a flow rate of 500 nl/min from 2 min to

112 min, followed by a linear increase to 95% ACN at 500 nl/min from 112 min to 115 min. Column washing at 95% ACN was performed from minutes 115 to 120. For HA fractions, the same LC method was followed but with a linear gradient from 2 to 20% ACN from 2 min to 112 min. LC mobile-phase solvents consisted of 0.1% FA in water (Buffer A) and 0.1% FA in acetonitrile (Buffer B, Optima LC/MS, Fisher Scientific, Pittsburgh, PA). Data acquisition was performed using the manufacturer-supplied tofControl (version 6.0) software with the instrument default data-dependent acquisition (DDA) parallel accumulation–serial fragmentation (PASEF) method with a cycle time of 1.1s. The mass spectrometer was operated in the positive ion mode. In brief, each survey scan of  $m/z$  100–1700 was followed by ten PASEF MS/MS scans employing CID. Active exclusion was performed with an intensity threshold of 2500 cts/s and releasing after 0.2 min, reconsidering precursors if the current intensity is fourfold greater than the previous intensity.

**Data Processing**—All Orbitrap-acquired raw MS files were converted to .mgf format using Proteome Discoverer version 2.4 (Thermo Fisher Scientific) using the default parameters. Converted files were then searched using an in-house Mascot server (Version 2.5, Matrix Science). For Orbitrap-acquired data mass tolerances were  $\pm 15$  ppm for MS peaks and  $\pm 0.6$  Da for MS/MS fragment ions. Protein probability thresholds were set at 99.9% with a minimum of two peptides and peptide thresholds were set at 95% using local false discovery rate (LFDR) scoring implemented in Scaffold (version 4.9.0, Proteome Software Inc), resulting in a protein FDR of 0.0% and a peptide FDR of 0.5%. For timsTOF Pro acquired raw files, searching was performed using Peaks Studio (Version 10.5, Bioinformatics Solutions Inc). Data refinement was performed by correcting precursor mass only, associating features with chimera scans, and filtering features for charge between 2 and 8. PeaksDB search was performed using  $\pm 15$  ppm for MS peaks and  $\pm 0.1$  Da for MS/MS fragment ions. Data was filtered to 1% FDR at the peptide level, and protein probability threshold was set to  $p \leq 0.01$  using PEAKS.

For all searches, data was searched against SwissProt (Downloaded 5/27/2019, 17,029 sequences) restricted to *Mus musculus* using version 1.1 of the CRAPome for common contaminants (33). Trypsin-specific cleavage was used in searches for cellular and enzyme-extracted ECM fractions, while HA/Trypsin specificity was used for HA digested fractions, both allowing for two missed cleavages. HA/Trypsin specificity was defined as cleaving C-terminal of K and R but not before P, as well as C-terminal of N but not before C, F, H, I, M, N, Q, S, W, or Y based on previous HA cleavage data (4). Fixed modifications were set as carbamidomethyl (C). Variable modifications were set as oxidation (M), oxidation (P) (hydroxyproline), Gln->pyro-Glu (N-term), deamidated (NQ), and acetyl (Protein N-term).

To identify additional experimentally induced modifications, Mascot searches were performed as described above with additional variable modifications (Search 1: Oxidation (D), Oxidation (HW), Oxidation (K), Oxidation (R); Search 2: Carbamyl (K), Carbamyl (R), Carbamyl (N-term)). Search 1 was used to assess the oxidative effects of HA compared with other ECM extraction buffers.

**Data Analysis—Protein Classification.**Core matrisome annotations, including collagens, proteoglycans, and ECM glycoproteins, were mapped using the mouse matrisome database (MatrisomeDB, <http://matrisomeproject.mit.edu/>) (28). Cellular proteins are defined as all proteins not annotated within the MarisomeDB as core matrisome or matrisome-associated.

**Normalization to Equal Run Time.**To compare methods generating different numbers of fractions, PSMs were normalized to total run time by dividing the sum of PSMs in all fractions of a single method by the number of fractions analyzed.

**Weighted Average Sequence Coverage.**Sequence coverage was determined using an in-house Mascot server (Version 2.5, Matrix

Science) and Scaffold (version 4.9.0, Proteome Software Inc). For each round of sample runs, fractional abundance of a given protein was calculated by dividing peptide spectral matches (PSMs) for that protein by the total number of PSMs for proteins in that category (*i.e.*, collagens) across all compared samples. The sequence coverage for an individual protein was then multiplied by the fractional abundance. The weighted sequence coverage for proteins in that category was summed to provide the weighted average sequence coverage for that category.

**Statistical Significance.**Standard one-way ANOVA was performed on all comparison groups to determine significance. In all comparisons where significance between any groups is reported, ANOVA resulted in  $p < 0.05$  for the comparison group. For pairwise comparisons,  $p$ -values were calculated using a two-tailed equal variance Student's  $t$ -test.  $p$ -values in text are reported as the least significant relevant comparison. In figures, “\*” denotes  $p < 0.05$ , “\*\*” denotes  $p < 0.01$ , and “\*\*\*\*” denotes  $p < 0.001$ .

**Overall Method Scoring.**Method scores were determined by scoring each method based on a variety of relevant criteria and calculating a weighted average of these scores. These weighted averages were translated to a 1–10 scale, with 1 representing the lowest possible score and 10 representing the highest. For example, for the “MS Compatibility” category, a 1 would represent a sample that requires extensive cleaning and has high potential to contaminate the mass spectrometer while a 10 would represent a sample that can easily be injected onto the mass spectrometer with little or no cleaning. Scores for “Time” were derived based on total method duration. Scores for “Ease” were given based on required number of processing steps and subjective experimenter difficulty ratings, with points deducted for use of potentially hazardous reagents. Scores for “MS Compatibility” were derived based on concentrations of MS-incompatible reagents in extraction buffers. Scores for “Precision” were derived based on total variance and CV of measurements for proteins of interest. Scores for “ECM in Cell Fraction” were derived based on PSM, protein, and EUP identifications of core matrisome proteins in decellularization fraction. Scores for “Total Protein IDs,” “Collagens,” and “Glycoproteins and Proteoglycans” were determined based on identification of these protein categories by each method. For categories “Time” and “ECM in Cellular Fraction,” higher scores are given to methods with lower actual values because lower processing time and fewer ECM IDs in the cellular fraction are positives for a method. Decellularization was scored based on time (10%), ease (10%), MS compatibility of buffers (10%), total protein identification (30%), precision (20%), and ECM in the cellular fraction (20%). For comparison to decellularization methods, single-shot methods were compared on all metrics except ECM in the cell fraction, dividing the weight for this metric evenly among the other categories. ECM extraction methods were scored based on time (10%), ease (10%), collagen identification (30%), glycoprotein and proteoglycan identification (30%), and precision (20%). Identical scoring and weighting were applied to single-shot methods for comparison to ECM extraction methods.

## RESULTS

### Evaluation of Cellular Protein Extraction Methods for ECM Enrichment

To compare the various decellularization methods, we evaluated extraction of cellular proteins and preservation of ECM proteins for subsequent ECM analysis. WMP was chosen for method development as it is a complex mixture that includes a representative sampling of all tissues and covers



matrix components across a wide dynamic range. The single-shot methods were also compared for extraction of cellular proteins (Fig. 1A). For decellularization methods with multiple fractions, each fraction was analyzed separately, and data is presented as both fraction sums and per-fraction averages. When normalized to equal MS run time, the 1-fraction A method generates more cellular PSMs than other methods, with 15% more PSMs than the next-highest 4-fraction method ( $p = 0.014$ ), while in-solution digest yields the least (Fig. 1B). No significant differences in cellular spectral matches were observed between 2-fraction, 3-fraction, and 4-fraction extractions when comparing per-fraction averages. Of note, the 4-fraction method displayed significantly higher variability than other methods, attributed to one outlier sample. All tested ECM extraction protocols were repeated in triplicate with new starting material, and the results were consistent based on performance comparisons against the 1-fraction A method (supplemental Fig. S1). Therefore, the observed

variability is likely attributed to the method rather than an error in sample preparation. The 1-fraction B method resulted in significantly fewer cellular PSMs than any other decellularization method ( $p = 0.0052$ ). With increased decellularization fractions, there is roughly a linear increase in total cellular PSMs (Fig. 1B). In comparison of single-shot methods, in-gel and SPEED digestion result in the most cellular PSMs ( $p = 0.0043$  and  $0.0027$  respectively), although all single-shot extractions generate fewer cellular PSMs than the 1-fraction, 2-fraction, and 4-fraction decellularization methods when normalized to equal run time (Fig. 1B).

As stated, decellularization methods prior to ECM analysis should efficiently extract high-abundance cellular proteins while minimizing ECM extraction for subsequent analysis. Therefore, any ECM proteins removed by decellularization would be considered adverse for accuracy of subsequent ECM protein analysis. The 1-fraction B method results in the lowest number of core matrisome PSMs identified in the

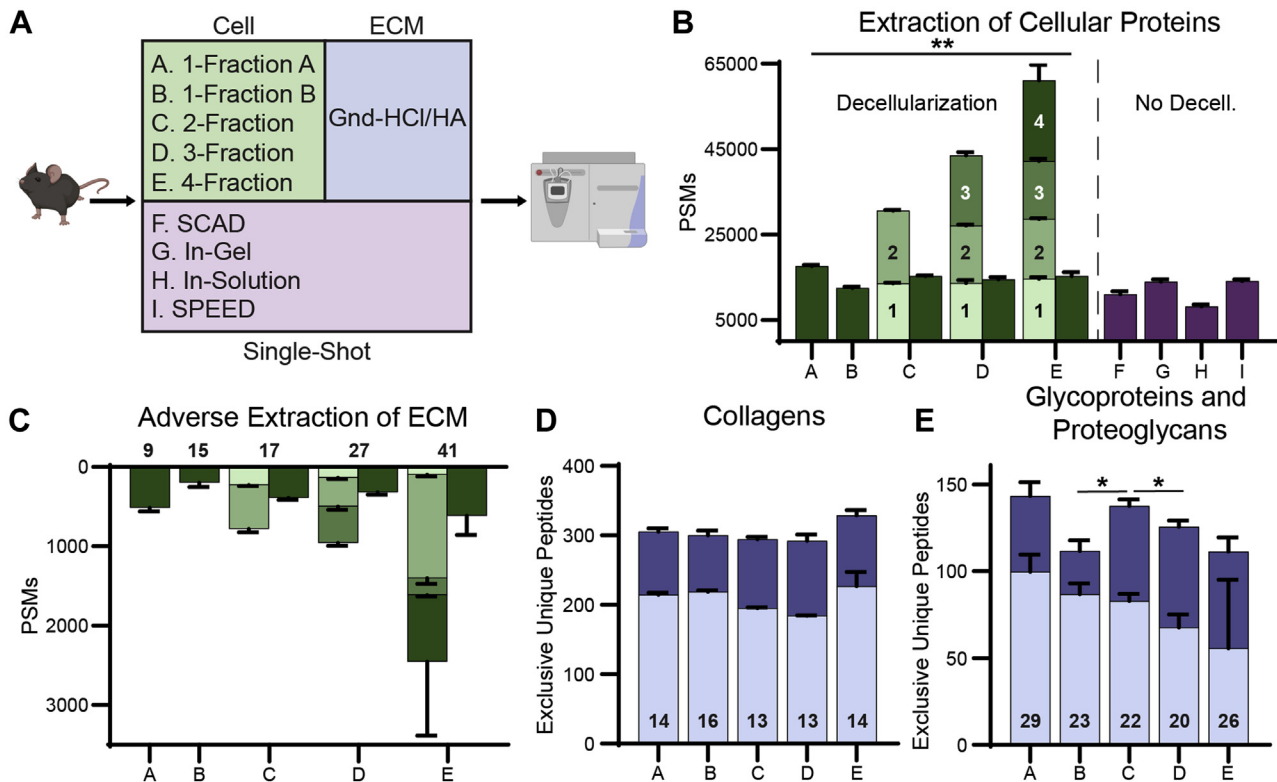


FIG. 1. Effects of soluble protein extraction methods on extracellular matrix identification. A, workflow of decellularization and single-shot methods used. All decellularization methods were followed by a single ECM analysis method (Gnd-HCl/HA extraction). B, total cellular PSMs identified by each decellularization (green) and single-shot (purple) method. Multistep methods are shown as both a sum of all fractions and the average PSMs per fraction. Increasing shade of green represents increasing fraction number and darkest green represents group average. C, total ECM PSMs lost during decellularization. Multistep methods are shown as both a sum of all fractions and the average PSMs per fraction. Numbers above bars indicate the number of core matrisome proteins identified with a minimum of two peptides. D, total exclusive unique collagen peptides identified in the subsequent Gnd-HCl/HA ECM extraction following each decellularization method. Light blue indicates Gnd-HCl fraction, dark blue indicates new unique peptides from HA fraction. Numbers on bars indicate the number of distinct collagen chains identified with a minimum of two peptides. E, total exclusive unique peptides for proteoglycans and glycoproteins identified in the subsequent ECM extraction following each decellularization method. Numbers on bars indicate the number of ECM glycoproteins and proteoglycans identified with a minimum of two peptides. All bar plots present group averages with standard deviation (SD).



cellular fraction ( $p = 0.026$ ) (Fig. 1C). This finding, in addition to the low number of cellular PSMs identified using the 1-fraction B method, indicates that this method provides the mildest decellularization conditions of all the tested methods. In contrast, the 1-fraction A and 4-fraction methods extract the largest amount of core matrisome PSMs per fraction in their cellular fractions, although increased variability in the 4-fraction method prevents significance from being reached (Fig. 1C). Significantly more core matrisome PSMs were identified in the second fraction of the 4-fraction decellularization method than in any individual cellular fraction from another method (136% greater,  $p = 8.5 \times 10^{-5}$ ), confirming that this method extracts the largest amount of ECM proteins during decellularization. For all decellularization methods, greater than 75% of PSMs for proteins classified as matrisome-associated (28) were identified in the cellular fractions (supplemental Fig. S2). The solubility of matrisome-associated proteins in all tested decellularization buffers supports the decision to focus on the core matrisome when evaluating ECM extraction and analysis.

### *Evaluation of Resulting ECM Fractions Following Various Decellularization Approaches*

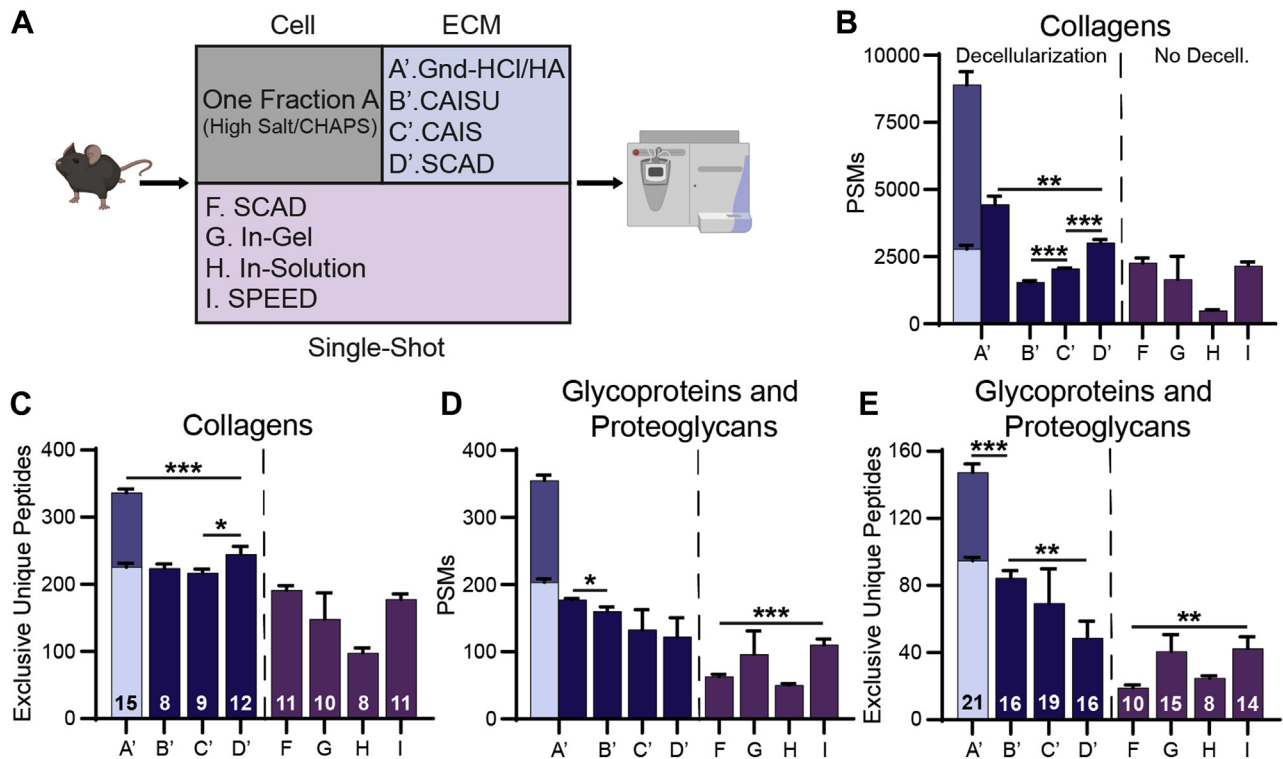
To facilitate comparison of the remaining ECM pellets from each decellularization method, the protein composition was assessed *via* a single approach (the Gnd-HCl extraction followed by HA digestion (Gnd-HCl/HA) method) for ECM analysis (Fig. 1A, Table 1). The most effective decellularization method should result in high sequence coverage for core ECM components such as collagen, proteoglycans, and glycoproteins within the ECM fractions. The 4-fraction decellularization method resulted in 45% higher collagen PSMs within the subsequent ECM fractions than other methods ( $p = 0.0029$ ) (supplemental Fig. S3A). However, it did not produce significantly more unique collagen peptides than other methods (Fig. 1D). No significant difference in unique collagen peptides within the ECM fractions was identified between any tested methods (Fig. 1D). By pairwise comparison, the 1-fraction A (14% greater,  $p = 0.011$ ) and 2-fraction (9% greater,  $p = 0.022$ ) methods provide more unique peptides for proteoglycans and ECM glycoproteins, while the 1-fraction B and 4-fraction methods generate 12% fewer unique peptides than other methods (Fig. 1E). However, differences in ECM glycoprotein and proteoglycan unique peptides and PSMs were not significant by ANOVA (Fig. 1E, supplemental Fig. S3B).

### *Evaluation of ECM Extraction and Digestion Methods*

To assess ECM extraction methods on uniform starting material, a single decellularization method (1-fraction A) was performed on all samples prior to the four ECM extraction methods under evaluation (Fig. 2A). Comparing all methods, the Gnd-HCl/HA method was found to result in the greatest

number of identified collagen proteins, unique peptides, and PSMs even when normalized to equal run time, providing 37% more unique collagen peptides than the next best method: SCAD postdecellularization ( $p = 0.0002$ ) (Fig. 2, B and C). Additionally, Gnd-HCl/HA ( $p = 0.0008$ ) and SCAD postdecellularization ( $p = 0.045$ ) extractions generate significantly more sequence coverage of collagen proteins than the CAISU extraction method (supplemental Fig. S4A). The CAISU and CAISU extractions resulted in similar numbers of unique collagen peptide identifications (Fig. 2C). However, the CAISU method produced the lowest number of spectral matches for collagen peptides of the tested postdecellularization ECM extractions ( $p = 0.0002$ ) and also produced fewer collagen PSMs than the SCAD ( $p = 0.0032$ ) and SPEED ( $p = 0.0029$ ) single-shot methods despite their lack of cellular protein removal (Fig. 2B). Single-shot protocols SCAD and SPEED performed similarly in all assessed metrics for collagen extraction (Fig. 2, B and C). Decellularization prior to the SCAD protocol offered significant improvement in identification of collagen spectral matches ( $p = 0.0039$ ) and unique collagen peptides ( $p = 0.0024$ ) (Fig. 2, B and C). Single-shot in-solution digestion resulted in the lowest number of collagen PSMs and unique peptides (Fig. 2B). When comparing individual fractions, the HA fraction from the Gnd-HCl/HA extraction yielded the most collagen PSMs ( $p = 0.0042$ ) (Fig. 2B).

Identification of glycoproteins and proteoglycans was also assessed to determine the best method for comprehensive core ECM analysis. The two-fraction Gnd-HCl/HA method resulted in the identification of more glycoproteins and proteoglycans (21) than any other method with 74% more unique peptides than the next best method, CAISU ( $p = 0.0001$ ) (Fig. 2E). Additionally, the Gnd-HCl/HA extraction generated a 25% increase in glycoprotein and proteoglycan sequence coverage ( $p = 0.024$ ) (supplemental Fig. S4B) and 10% more PSMs ( $p = 0.011$ ) than the next best method, even when normalized to equal run time (Fig. 2D). SCAD extraction postdecellularization, on the other hand, produced significantly fewer unique peptides for glycoproteins and proteoglycans than both the Gnd-HCl/HA ( $p = 0.00015$ ) and CAISU ( $p = 0.0051$ ) methods (Fig. 2E). SPEED extraction produced 14.5% higher glycoprotein and proteoglycan PSMs than other single-shot methods (Fig. 2D), although this method identified significantly fewer unique peptides in these categories than either the Gnd-HCl/HA ( $p = 0.00005$ ) or CAISU ( $p = 0.00096$ ) extractions (Fig. 2E) and fewer glycoproteins and proteoglycans than any postdecellularization method (Fig. 2E). When comparing individual fractions, the first fraction generated by the Gnd-HCl/HA method generates the greatest number of unique glycoprotein and proteoglycan peptides ( $p = 0.023$ ) (Fig. 2E). Overall, utilizing a two-fraction Gnd-HCl/HA extraction provides significantly greater identification of collagen, proteoglycan, and glycoprotein peptides than all other tested methods.

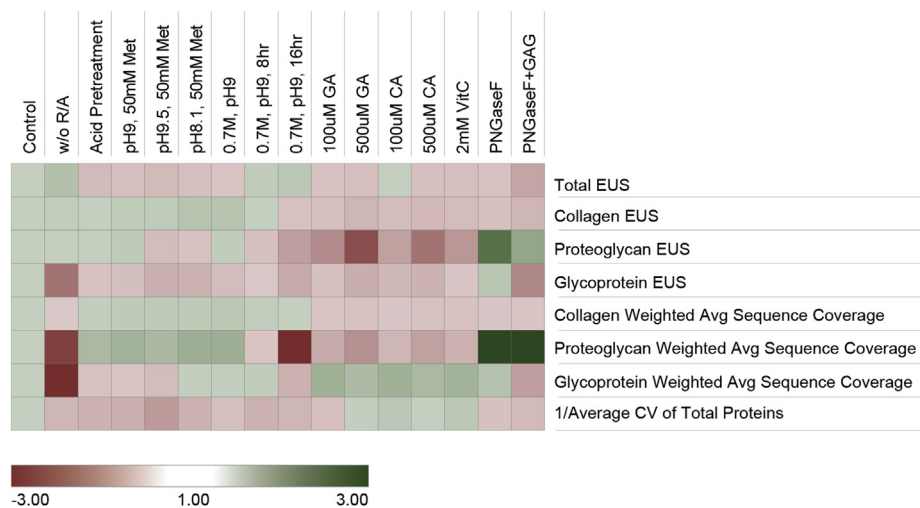


**FIG. 2. Effects of differing extracellular matrix extraction methods on uniform decellularized protein pellet.** A, workflow of ECM extraction (blue) and single-shot (purple) methods used. All ECM methods were preceded by the same decellularization. B, total collagen PSMs identified by each method. Multistep extraction (1') is shown as both a sum of the two fractions and the average PSMs per fraction. Plotted as average values with SD. For Gnd-HCl/HA method, light blue indicates Gnd-HCl fraction, darker blue indicates HA fraction. C, exclusive unique collagen peptides identified by each method. Numbers on bars represent the number of distinct collagen chains identified with a minimum of two peptides. D, Bar graph of glycoprotein and proteoglycan PSMs by each method. Multistep extraction (1') shown as both a sum of two fractions and the average PSMs per fraction. E, exclusive unique peptides identified for glycoproteins and proteoglycans by each method. Numbers on bars represent the number of glycoproteins and proteoglycans identified with a minimum of two peptides.

ECM extraction methods that utilize urea have the potential to induce carbamylation at lysine and arginine residues, as well as peptide N-termini. This modification can inhibit trypsin digestion and increase sample heterogeneity, convoluting data analysis, and subsequent quantification (34). In our analysis, we identify averages of 763, 641, and 1523 carbamylated peptides per run in the CAISU, CAIS, and SCAD methods, respectively, compared with an average of 34 carbamylated peptides identified across the two fractions of the Gnd-HCl/HA method (supplemental Fig. S5A). While the SCAD method induces more carbamylation than the other enzymatic extractions, all methods that utilize urea in an extraction buffer induce this modification extensively, likely contributing to deficits in ECM identification. On the other hand, hydroxylamine digest induces oxidation (15.9949) over other methods, where an average of 5954 oxidized peptides per run were identified in the HA fraction of the Gnd-HCl/HA method, compared with averages of 1702, 2290, and 3286 oxidized peptides in the CAISU, CAIS, and SCAD extracts, respectively (supplemental Fig. S5B). While oxidation does not inhibit peptide cleavage, it can convolute analysis and protein quantification.

#### ECM Extraction and Digestion Method Optimization

The 2-fraction Gnd-HCl/HA extraction method was used for further optimization of ECM coverage, based on the above findings. Oxidative modifications observed with the use of hydroxylamine digestion (4) can convolute data analysis and have the potential to reduce both the quantity and quality of protein identifications. On the other hand, if oxidation of Met residues is pushed toward completion without inducing other significant oxidations, this would have an advantageous effect on these metrics. In order to optimize this step, iterative changes to the HA digestion protocol were explored with the goal of reducing unwanted modifications and ultimately increasing ECM protein identification. A reference protocol, as used in the previous section, was analyzed in parallel with each group of optimization conditions. Briefly, the reference protocol involves digestion with 1M HA, pH 9.0 for 4 h at 37 °C with reduction and alkylation (R/A) prior to digestion. The previously published Gnd-HCl/HA method (4) did not include R/A due to the lack of reducible disulfide bonds in collagen. However, R/A provided a 60% improvement in unique glycoprotein peptide identifications ( $p = 0.0088$ ), including a



**FIG. 3. Optimization of hydroxylamine (HA) digestion conditions.** Hydroxylamine digest optimization was tested over several rounds of sample processing. Results were aggregated by comparing each digestion method with the reference sample run in parallel with treatment conditions (all  $n = 3$ ). Results are presented and colored as fold change in relation to reference. Reference HA digest was performed in 1M HA-HCl pH 9.0 at 37 °C for 4 h with reduction and alkylation prior to digestion. A detailed reference protocol can be found in the [Experimental Procedures](#) section. In the final column, GAG refers to the addition of GAG-digesting enzymes. Samples with fold change  $< 1$  are shown as negative reciprocal values.

tenfold increase in PSMs for fibrillin-1 ([supplemental Fig. S6](#)) and improved overall CVs ([Fig. 3](#)). Therefore, R/A prior to HA digest was used as the reference method for the subsequent method optimization experiments. The second variable tested was pretreatment of the pellet with 0.2% FA, as suggested by Bornstein and Bailan ([35](#)), which showed no significant benefit and increased the overall CV of ECM measurements ([Fig. 3](#)).

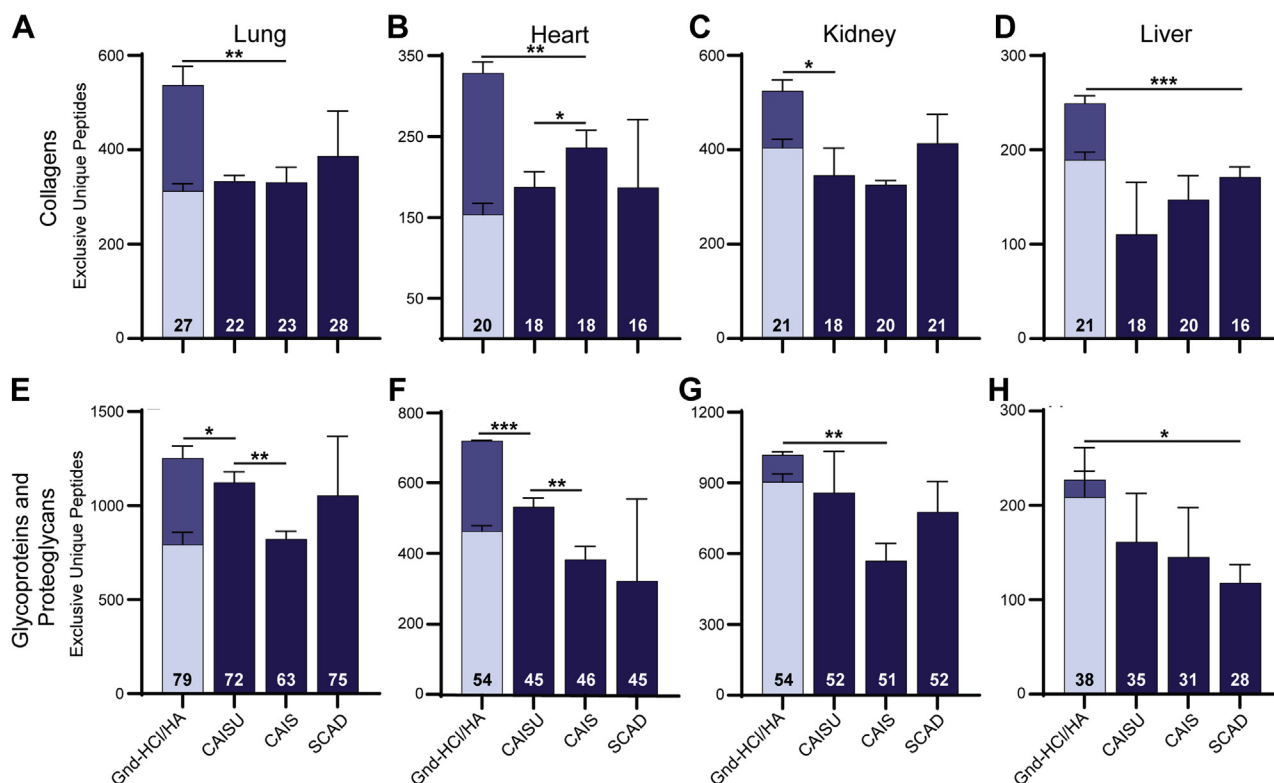
We also evaluated the effects of changes in pH, HA concentration, digestion time, and addition of an antioxidant (50 mM methionine) on identification of ECM components. Most tested variations led to slight improvements in collagen PSMs but higher CVs and fewer total PSMs ([Fig. 3](#)). Of note, pH 8.1 with 50 mM methionine improved the number of identified collagen PSMs. However, decreases in total and glycoprotein PSMs, as well as increased CV, make the method less suitable than the reference method unless maximizing total collagen PSMs is an objective of the analysis. In addition, 0.7 M HA digestion for 16 h performed significantly worse for all scoring metrics ([Fig. 3](#)). This was consistent with previous findings where extended digestion times result in extensive peptide modification ([4](#)).

In total, 50 mM methionine showed potential improvements in collagen PSMs and coverage over conditions without antioxidant. Therefore, the effects of more potent antioxidants including caffeic acid (CA), gallic acid (GA), and ascorbic acid (VitC) at varying concentrations on HA digestion were tested. All antioxidants showed significant improvement in sequence coverage of glycoproteins but not of proteoglycans or collagens ([Fig. 3](#)). This is coupled with a significant drop in proteoglycan PSMs in comparison to the reference method. A final variable explored was deglycosylation, as improved

identification of ECM glycoproteins and proteoglycans has been reported using PNGase F to remove N-linked glycans ([20, 36](#)), as well as GAG-digesting enzymes chondroitinase ABC and heparinase II ([36–38](#)). The addition of PNGaseF slightly improved proteoglycan PSMs and sequence coverage over the reference method but also generated slight decreases in collagen PSMs and sequence coverage. PNGase F digestion significantly improved glycoprotein coverage ( $p = 0.017$ ) but did not improve glycoprotein PSMs ([Fig. 3](#)). The addition of GAG removal enzymes (chondroitinase ABC and heparinase II) offered a significant improvement in proteoglycan coverage ( $p = 0.012$ ) but not PSMs. Improvement in proteoglycan identification was coupled with decreases in collagen ( $p = 0.0044$ ) and glycoprotein ( $p = 0.0002$ ) PSMs, causing GAG removal to result in overall worse ECM characterization than the reference method ([Fig. 3](#)). When comparing deglycosylation (PNGase F) of both the Gnd-HCl and HA fractions, in general similar trends were observed when compared with the reference method for PSMs and sequence coverage of proteoglycans ([supplemental Fig. S7](#)). However, improvement of proteoglycan coverage with the addition of PNGase F was highly significant ( $p = 0.00082$ ) when the Gnd-HCl fraction was taken into account.

#### *Evaluation of ECM Extraction and Digestion Methods on Isolated Organs*

All previous comparisons of ECM extraction methods were performed on an early generation Orbitrap mass spectrometer (MS) due to the widespread use of this analytical platform and accessibility in core facilities. In order to perform more in-depth comparisons of ECM extraction methods and to



**FIG. 4. Effects of ECM extraction methods on uniformly decellularized mouse lung, heart, kidney, and liver.** A–D, total exclusive unique collagen peptides for each ECM extraction method. Numbers on bars represent the number of distinct collagen chains identified. For Gnd-HCl/HA method, *light blue* indicates Gnd-HCl fraction, *dark blue* indicates new unique peptides from HA fraction. E–H, total glycoprotein and proteoglycan exclusive unique peptides identified by each ECM extraction method. Numbers on bars represent the number of glycoproteins and proteoglycans identified. Bars represent the average of three replicates with error bars showing standard deviation (SD).

determine if conclusions drawn from WMP hold true for organ specific analysis, extractions of the lung, heart, kidney, and liver were analyzed on a modern, trapped ion mobility spectroscopy time-of-flight (timsTOF) MS system (Fig. 4). Acquisition performed using parallel accumulation–serial fragmentation on a timsTOF instrument has been shown to provide tenfold faster sequencing speeds over conventional shotgun proteomics methods without sacrificing sensitivity, resulting in more peptide fragmentations per second and greater proteome coverage in complex samples (39, 40). WMP analysis on the timsTOF MS system resulted in 2.5× more core matrisome PSMs and 74 additional core matrisome protein IDs (supplemental Fig. S8). Organs were chosen based on their widespread study in biomedical research and their varying ECM compositions. Organ samples were prepared using the 1-fraction A decellularization followed by the four tested ECM extraction methods.

Consistent with our findings from WMP analysis, the Gnd-HCl/HA method provides more exclusive unique peptides for collagens in the lung (39% greater), heart (38% greater), kidney (26% greater), and liver (46% greater) than any other method (Fig. 4, A–D). Additionally, the Gnd-HCl/HA method performs similarly to, or better than, other methods in terms of

glycoprotein and proteoglycan identification. The Gnd-HCl/HA method provided significantly more collagen exclusive unique peptides than the next best method in the lung (11% greater,  $p = 0.026$ ) and heart (32% greater,  $p = 0.0004$ ) samples, but statistical significance was not reached in other organ comparisons largely due to the variability of the SCAD method (Fig. 4, E–H). Also consistent with results from WMP, the CAISU method performs better for identification of glycoproteins and proteoglycans across all organs than either the CAIS or SCAD extraction method (Fig. 4, E–H).

#### DISCUSSION

Based on the significant role that the structural matrix plays in shaping cellular phenotype (41, 42) and, likewise, the influence of cell phenotype on stromal and matrix composition (43), optimized proteomic methods for ECM characterization are needed. In general, accurate tissue characterization requires analysis of the extracellular matrix, yet this class of proteins is underrepresented in tissue proteomic datasets. Several proteomic methods have been developed to improve characterization of the ECM over the last two decades. Key elements of these protocols involve 1) removal of cellular material to create an ECM enriched fraction, primarily using



differential detergent extraction, and 2) solubilization and efficient digestion of the resulting ECM.

Various published decellularization methods were assessed for their ability to extract cellular proteins while leaving ECM proteins behind for analysis in subsequent fractions. The 1-fraction A and 4-fraction methods were found to remove more cellular proteins from the starting material than other tested methods. If cellular characterization and solubility profiling of cellular components are desired alongside ECM characterization, multifraction methods provide more cellular protein coverage when all fractions are analyzed. Also, of no surprise, single-shot methods result in fewer cellular PSMs than nearly all decellularization methods, with lower identifications due to the increased complexity and dynamic range of the extracted proteins, in part due to partial ECM extraction.

The largest amount of ECM proteins was extracted during decellularization using the 4-fraction method, evidenced by the high number of core matrisome protein and PSM identifications in the cellular fractions. Extraction of ECM proteins in the cellular fraction is undesirable due to difficulty detecting ECM proteins of interest against the background of abundant cellular protein. Additionally, when the 4-fraction method is used for decellularization prior to ECM extraction, the cellular fractions are often not analyzed *via* MS (20, 44), causing all ECM proteins present in these fractions to be lost and ultimately resulting in quantitative error and potentially fewer identified core matrisome proteins within the ECM fractions. In our experience, to analyze these cellular fractions *via* LC-MS/MS, additional detergent removal steps must be performed to avoid instrument contamination. Although the 1-fraction B method removes the least amount of ECM during decellularization, it does not efficiently extract cellular proteins, thus limiting subsequent ECM characterization.

After decellularization, the resulting pellets were processed using a single method for direct comparison of the resulting ECM fractions. Similar collagen PSMs were identified in the 1-fraction A, 2-fraction, and 3-fraction methods, while the 4-fraction method resulted in significantly more collagen PSMs but fewer collagens and similar collagen sequence coverage to other methods. This is due to the high stringency of the 4-fraction decellularization method, extracting most noncollagen proteins in earlier fractions and allowing more sequencing time to be devoted to a subset of collagen peptides in the final ECM fraction. If optimal collagen signal is desired, performing 4-fraction decellularization before ECM extraction can provide greater collagen spectral matches but not necessarily higher sequence coverage of collagen proteins. Additionally, the 1-fraction A and 2-fraction methods performed significantly better peptide identification for glycoproteins and proteoglycans by pairwise *t*-test but not by ANOVA, making these the methods of choice when these protein classes are a priority.

Total PSMs, ECM PSMs, and method precision have been discussed above. These evaluation metrics along with time,

ease, and MS compatibility are shown in Table 2. Each category was ranked on a scale of 1–10 with 1 being the lowest possible score and 10 being optimal (ranking criteria are further defined in methods). MS compatibility was ranked based on the use of MS-incompatible detergents throughout the course of the method. Acetone precipitation or a detergent removal column can be utilized within any protocol to reduce risk of MS contamination, but these steps can generate additional cost, variability, and protein loss. Methods that utilize SDS and NP-40, such as the 3-fraction method, can cause residual contamination during MS analysis of subsequent ECM fractions and require additional pellet washing or acetone precipitation of the ECM fractions. The ease criterion is a ranking of the relative ease of each method in comparison to the other protocols, considering the number of processing steps and potential for increased analytical CV. The 4-fraction method displayed higher variability than other methods across two triplicate rounds, likely due to the large number of buffer exchanges required during processing (10) compared with other methods. As this table shows, there is not one method that is superior in all categories. Instead, a method should be selected specifically based on project aims, constraints, and proteins of interest.

The second key element of an effective ECM proteomic approach is efficient digestion of matrix proteins. This task is hampered by the relative protease resistance of the ECM. Four published ECM extraction methods were evaluated on both WMP and isolated organ samples following uniform decellularization. While it is impractical to test all published methods and extensively test all variables, these four methods cover the major ECM-based methods that are currently used. As stated above, the two-step Gnd-HCl/HA method identified the greatest number of proteins, PSMs, and unique peptides from all core matrisome categories in analysis of both WMP and isolated organs. While the Gnd-HCl fraction of the Gnd-HCl/HA extraction alone performs similarly to other tested methods, the following HA digest provides 355 additional unique core matrisome peptides on average across analyzed organs, leading the 2-fraction HA digest method to provide improved core matrisome characterization over other tested methods. This, combined with the higher sequence coverage of collagens, glycoproteins, and proteoglycans, makes the Gnd-HCl/HA extraction the recommended method for obtaining more in-depth coverage of the ECM, despite the additional time it requires. The proportion of ECM peptides, which are uniquely identified by the HA digest in the Gnd-HCl/HA method, varies greatly between tested organs, with 40% of ECM peptides uniquely identified in the HA fraction of the heart samples but only 15% in the HA fraction of the kidney. These differences reflect varying relative ECM protein abundance, association, and cross-linking—attributes that are often altered during development and disease progression.

Of the enzymatic ECM extractions, SCAD after decellularization provides a greater number of identified collagens and

TABLE 2  
Comparison of decellularization methods for ECM enrichment

Method	Time	Ease	MS Compatability	Total protein IDs	Precision	ECM in cell fraction	Total score
1-Fraction A	8	9	7	8	9	8	82
1-Fraction B	3	9	6	7	8	9	74
2-Fraction	9	8	6	8	9	7	79
3-Fraction	8	7	6	9	8	7	77
4-Fraction	6	6	6	9	6	6	68
SCAD	6	8	8	6	8	N/A	71
In-Gel	7	7	8	7	6	N/A	69
In-Solution	9	9	9	5	9	N/A	78
SPEED	9	7	9	7	9	N/A	81

Decellularization (green) and single-shot (purple) methods are ranked in each category from 1 to 10— with 1 being totally insufficient and 10 being optimal. Total score is calculated as a weighted average of all assessed categories (described in [Experimental Procedures](#)).

more unique collagen peptides than the CAIS or CAISU method in WMP analysis. The CAISU method, on the other hand, yielded more unique glycoprotein and proteoglycan peptide identifications and greater sequence coverage than other enzymatic methods in all samples. Therefore, enzymatic methods should be chosen depending on the ECM protein categories of interest when only one ECM fraction is analyzed.

When comparing faster, single-shot methods, SCAD and SPEED generated significantly higher PSMs for collagens than the CAISU method, even though these methods lack decellularization steps to remove cellular contaminants. SPEED also provides the greatest number of unique peptides from glycoproteins and proteoglycans of the tested single-shot methods. SCAD performs poorly in this matrixome category, revealing that SPEED is the best-performing single-shot method for overall ECM coverage. SPEED is a favorable alternative to longer ECM extractions that provides good ECM coverage and unique peptide IDs when higher-throughput ECM analysis is desired, and multiplexing is not available or otherwise used. However, the SPEED method requires heating concentrated TFA *via* microwave radiation in a glass vessel. The SCAD method provides a viable single-shot alternative, which does not require the use of glass reaction vessels or hazardous reagents.

A condensed evaluation of all ECM extraction and single-shot methods can be found in [Table 3](#). Some of the criteria for evaluation have already been discussed above. This table also addresses the time needed to perform each extraction and the relative ease of each protocol. There is no one perfect choice for an ECM extraction method, but these evaluation metrics should help guide researchers to a method of choice for a given set of objectives.

Based on the favorable results obtained using the two-step Gnd-HCl/HA method, we performed comparisons aimed to improve upon this method. Reduction and alkylation prior to HA digestion were the first change tested. Based on superior initial results, HA digestion with prior reduction and alkylation became the reference method for subsequent optimization. Most tested variables resulted in both improved and reduced

individual ECM category performance. Given the fact that most alterations added an additional cost or step, which increases potential variability, for most projects the published HA digestion method (4) with added reduction and alkylation prior to HA digestion is recommended. The one exception is the addition of PNGaseF for proteoglycan coverage. Somewhat surprisingly, there is a clear increase in proteoglycan PSMs upon addition of PNGaseF but no improvement in identification of collagens or ECM glycoproteins. It is important to note that the use of PNGaseF adds extra cost to each sample preparation. In addition, the improvement in proteoglycan coverage but not PSMs suggests that some extracted glycopeptides remained unidentified by database searching until deglycosylated by PNGaseF. The addition of PNGaseF could be a worthwhile investment if optimizing proteoglycan coverage is a priority.

The first set of analysis was performed using an older-generation orbitrap instrument that is likely to be encountered by many groups interested in the analysis of ECM through collaboration or core facilities. While this analytical platform offers high mass accuracy and resolution, which are valuable for reducing false positives, the sensitivity and scan speed do not match more modern instrumentation. Additionally, WMP was used for initial testing due to the high complexity of the sample, allowing for comparison of methods without biasing results toward a specific application. However, proteomics studies are generally performed using isolated tissue samples, their substructures, or micro-dissected regions. As a result, we also evaluated the chosen ECM extraction methods on isolated organs using a modern timsTOF mass spectrometer to assess method performance on real-world samples using a state-of-the-art instrument. In general, comparisons between methods revealed during WMP testing were consistent with those observed in analysis of individual organs. While method comparisons are mostly consistent across the tested organs, further method optimization may be required to obtain high-quality ECM characterization for organs with very unique compositional profiles (e.g., bone). Here, we evaluated extraction and digestion of tissues in a nonlimiting sample regime (1–5 mg dry weight).

TABLE 3  
Comparison of ECM extraction/digestion methods

Method	Time	Ease	Collagens	Glycoproteins and proteoglycans	Precision	Total score
Gnd-HCl/HA	5	6	9	9	8	81
CAISU	8	7	6	8	9	75
CAIS	6	8	7	7	7	70
SCAD + Decell.	5	8	8	6	7	69
SCAD	5	8	6	3	8	56
In-Gel	7	7	5	5	5	54
In-Solution	9	9	4	4	8	58
SPEED	9	7	6	6	7	66

ECM extraction (blue) and single-shot (purple) methods are ranked in each category from 1 to 10—with 1 being totally insufficient and 10 being optimal. Total score is calculated as a weighted average of all assessed categories (described in [Experimental Procedures](#)).

However, we have also had success applying our ECM extraction method to human tissue samples (<10 µg) from laser-capture microdissection (LCM) extraction ([supplemental Fig. S9](#)) with good ECM coverage, extending these techniques for spatial analysis of the ECM.

Of the over 200 proteins defined as “core matrisome” within the MatrisomeDB (28), 138 were identified across the four analyzed organs. Within the ECM, collagen is both highly abundant and highly modified. Increased fractionation of ECM samples may reveal differences in identification of low-abundance ECM proteins between methods that were not addressed in this study. All data was acquired using data-dependent acquisition because it is the most accessible acquisition method and does not require generation of a spectral library to achieve high-quality results. However, this allows for stochastic sampling of low-abundance precursor species and generates more missing values. This limitation could be diminished by using data-independent acquisition, as has been previously demonstrated for ECM analysis (45). However, the high complexity of posttranslational modifications commonly encountered on ECM peptides (more than five modifications per peptide with various positional isomers) presents a significant, largely unresolved issue with search routines. This also presents unique opportunities for the use of ion mobility for further resolution and characterization of these complex peptide species.

The choice of decellularization method should be based on the objectives of a given project. If minimizing sample processing time and ECM extraction are priorities, the 1-fraction A method is recommended. However, if deeper proteome coverage or solubility profiling of cellular components is desired, the 2-fraction or 3-fraction decellularization methods with analysis of all produced fractions are recommended. Deeper cellular coverage could also be provided by performing the 1-fraction A decellularization followed by offline fractionation prior to MS analysis with less potential for variability compared with these methods. For optimal ECM coverage, the Gnd-HCl/HA extraction protocol is recommended as it produces the greatest number of PSMs and highest sequence coverage of core matrisome proteins. Disease progression

and aging have been shown to increase the resistance of the insoluble ECM to extraction (46), increasing the necessity of effectively extracting the insoluble ECM via chemical digestion. Additionally, the Gnd-HCl/HA extraction produces two separate ECM fractions, which can be analyzed independently, further increasing ECM identifications and allowing for assessment of ECM solubility. Alterations in protein solubility can provide important information regarding disease progression (47, 48), which cannot be derived from single-fraction abundance measurements alone. Therefore, the Gnd-HCl/HA method is the method of choice for optimized ECM analysis. For a single-shot method, the SPEED method is the method of choice due to its ability to provide moderately high coverage of both core matrisome and cellular components using a single MS run. However, throughput can also be increased using multiplexing reagents and faster acquisition times available on modern MS instrumentation.

Mass spectrometry has increasingly played a central role in biomolecular characterization of tissues for the study of development, health, and disease. While the instrumentation, data acquisition routines, and bioinformatic tools facilitating proteomics workflows are consistently improving, less attention has been given to improving sample preparation methods and ensuring that all relevant material from a sample is analyzed. Without optimized sample preparation methods, a significant portion of the tissue proteome will be missed. ECM proteins will remain insoluble, and studies will not achieve characterization of a protein fraction that is largely responsible for the underlying cell phenotype and biomechanics of a tissue. The methods evaluated and optimized here should help facilitate studies of tissue microenvironments in development, disease progression, and aging.

#### DATA AVAILABILITY

The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the MassIVE partner repository with the dataset identifier PXD021778.

**Supplemental data**—This article contains [supplemental data](#).

**Acknowledgments**—This work was supported by the NIH (Grant No. R33CA183685, RM1GM131968, P01HL152961, R01HL146519) and the University of Colorado Cancer Center Support Grant (P30CA046934) and the Lung Foundation Netherlands (Longfonds, 6.1.15.017).

We would like to thank the numerous students, technicians, and collaborators that have evaluated, utilized, and provided feedback on these methods throughout the years. Workflow figures throughout the publication were created with [BioRender.com](#).

**Author contributions**—M. C. M.: Conceptualization, Methodology, Formal Analysis, Investigation, Data Curation, Writing—Original Draft, Writing—Review and Editing, Visualization. L. R. S.: Conceptualization, Methodology, Formal Analysis, Investigation, Validation, Writing—Original Draft, Writing—Review and Editing, Visualization. R. C. H.: Methodology, Validation, Writing—Review and Editing. M. D.: Methodology, Resources. M. M.: Investigation, Writing—Review and Editing. W. F. D.: Resources, Writing—Review and Editing. T. H. v. K.: Resources, Writing—Review and Editing. D. J. H.: Resources, Writing—Review and Editing. K. C. H.: Conceptualization, Methodology, Writing—Original Draft, Writing—Review and Editing, Visualization, Supervision, Project Administration, Funding Acquisition

**Conflict of interest**—The authors declare no competing interests.

**Abbreviations**—The abbreviations used are: ABC, ammonium bicarbonate; ACN, acetonitrile; CA, caffeic acid; CAIS, chaotrope-assisted in-solution digest; CAISU, chaotrope-assisted in-solution digest with ultrasonication; CHAPS, 3-[(3-cholamidopropyl)dimethylammonio]-1-propanesulfonate; CV, coefficient of variance; DOC, sodium deoxycholate; DTT, dithiothreitol; ECM, extracellular matrix; EDTA, ethylenediaminetetraacetic acid; EUP, exclusive unique peptides; FA, formic acid; FDR, false discovery rate; GA, gallic acid; GAG, glycosaminoglycan; Gnd-HCl, guanidine hydrochloride; HA, hydroxylamine hydrochloride; HEPES, 4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid; IAM, iodoacetamide; K<sub>2</sub>CO<sub>3</sub>, potassium carbonate; KCl, potassium chloride; LC-MS/MS, liquid chromatography tandem mass spectrometry; MgCl<sub>2</sub>, magnesium chloride; MS, mass spectrometry; NaCl, sodium chloride; NaOV, sodium orthovanadate; NP-40, Nonidet-P40; PI, protease inhibitor; Pipes, piperazine-N,N'-bis(2-ethanesulfonic acid); PSM, peptide spectral match; R/A, reduction and alkylation; SCAD, surfactant and chaotropic agent-assisted sequential extraction/on-pellet digestion; SDS, sodium dodecyl sulfate; SPEED, sample preparation by easy extraction and digestion; TFA, trifluoroacetic acid; timsTOF, trapped ion mobility spectroscopy time-of-flight; Tris-HCl,

Tris(hydroxymethyl)aminomethane hydrochloride; VitC, ascorbic acid; WMP, whole mouse powder.

Received January 13, 2021, and in revised form, March 31, 2021  
Published, MCPRO Papers in Press, , <https://doi.org/10.1016/j.mcpro.2021.100079>

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