X-ray images and map them to the corresponding osteoporosis classes.
Results: The study demonstrated a high performance of the developed algorithm in classifying osteoporosis based on X-ray images. The developed algorithm exhibited a strong performance, achieving an impressive accuracy rate of up to 0.86, with a precision of 0.83 and specificity of 0.82. This accuracy metric indicates the proportion of correctly classified X-ray images compared to the total number of images in the dataset.
Conclusion: The application of AI and deep learning techniques to osteoporosis classification based on X-ray scans carries substantial implications for patient care. By accurately identifying individuals with osteoporosis through AI-based classification, healthcare professionals can intervene at earlier stages of the disease, implement tailored treatment plans, and potentially mitigate the potential complications associated with osteoporosis.

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INNOVATIVE WORKFLOW FOR THE IDENTIFICATION OF CATHEPSIN K CLEAVAGE SITES IN TYPE I COLLAGEN

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Objective: In this work, we propose a degradomics mass spectrometry-based workflow that combines protein digestion, Nano-LC-UDMS^E, and several software tools to identify cathepsin K cleavage sites.
Methods: Type I collagen standards were subjected to digestion by cathepsin K at various protein/enzyme ratios for different incubation times. The digested proteins were subsequently injected into the nanoAQUITY UPLC-system Nano-LC (Waters). Chromatographic separation was accomplished using a nanoEaseTM M/Z HSS T3, 100Å, 1.8µm, 300µm x 150mm Column (Waters). The identification of peptides was conducted using PEAKS X, employing a combination of database searching and de novo sequencing.
Results: This workflow not only identified previously known cleavage sites, but also discovered new ones. Multiple cleavage hotspots were found and described in type I α1 and type I α2 collagen, many of which coincided with pyridinoline crosslinks, known to stabilize the triple helix. Our results allowed us to establish a chronology of digestion and conclude that cathepsin K preferentially cleaves the extremities of type I collagen before the helical part. We also found that cathepsin K preferentially cleaves amino acid residues with long and hydrophobic lateral chains at the beginning of digestion, whereas no preferred amino acid residues were identified later in the digestion.
Conclusion: Our workflow successfully identified new cleavage sites and can be easily applied to other proteins or proteases.

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CONFOUNDING FACTORS OF THE EXPRESSION OF MTBI BIOMARKERS, S100B, GFAP AND UCH-L1, IN AN AGING POPULATION

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Objective: Mild traumatic brain injury (mTBI) is one of the most common conditions seen in emergency departments. Recently, guidelines have proposed the combined use of the measurement of biomarkers, namely S100b and the "GFAP-UCH-L1" mTBI test to rule out mTBI. As older adults are the most at risk for mTBI, this study evaluates confounding factors that influence the concentration of S100 Calcium Binding protein B (S100B), Glial Fibrillary Acidic Protein (GFAP), and Ubiquitin carboxyl-Terminal Hydrolase L-1 (UCH-L1) in older individuals.
Methods: The protein S100B and the "GFAP and UCH-L1" mTBI test were measured using Liaison XL (Diasorin) and Alinity I (Abbott), in 330 and 341 individuals with non-suspected mTBI from the SarcoPhAge cohort, respectively.
Results: S100B, GFAP and UCH-L1 were all significantly correlated with renal function while alcohol consumption, geriatric depression score (GDS), smoking habits and anticoagulant intake were not associated with any of those 3 biomarkers. BMI and age were associated with GFAP and UCH-L1 expression while sex and mini-mental state examination (MMSE) were only associated with GFAP. Additionally, according to the manufacturers' cut-offs for mTBI rule-out, only 5.5% of the subjects were positive for S100B whereas 66.9% were positive for the "GFAP-UCH-L1" mTBI test. All "GFAP-UCH-L1" mTBI positive tests were GFAP+/UCH-L1-. Among individuals with cystatin C >1.55 mg/L, 25% were positive for S100b whereas 90% were positive for the mTBI test.
Conclusion: Our data show that confounding factors have a different impact on the positivity rate of the "GFAP-UCH-L1" mTBI test compared to S100B.