



TOPSIS-based ranking of alternative proteins based on their juiciness-related functional properties in meat analogues[☆]

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ABSTRACT

Population growth has intensified the demand for sustainable protein sources, driving the development of meat analogues. However, poor juiciness after cooking remains a key limitation, mainly driven by protein functional properties. In this study, thirteen alternative proteins were evaluated for juiciness-related characteristics. Yeast and rice proteins showed the highest water-holding capacity, followed by hemp, pumpkin, and carob bean. Pea, faba bean, and potato proteins exhibited superior emulsifying activity. Potato, almond, and sunflower proteins required the lowest concentration (8%) to form gels, with potato protein displaying the highest gel strength (4.67 N). Multivariate analysis clustered potato, faba bean, pea, and cowpea proteins, indicating similar functional behavior. Finally, TOPSIS ranking identified potato protein as the most promising ($C = 0.676$), followed by cowpea, while pea, faba bean, and wheat showed comparable performance. Overall, this study provides a structured basis for selecting alternative proteins to enhance juiciness and extend the approach to other food applications.

1. Introduction

In recent years, the consumption of plant-based products has increased worldwide due to several interconnected factors. Rapid population growth, with the global population projected to reach approximately 9.7 billion by 2050 (Boukid, 2021), has intensified the demand for sustainable and efficient protein sources (Smith et al., 2024). At the same time, ethical and religious considerations, particularly concerns about animal welfare, have encouraged more consumers to adopt vegetarian and vegan diets. Environmental sustainability further supports this shift, as plant-based products generally have a lower environmental impact than animal-derived foods. Additionally, the perceived health benefits associated with plant-based diets have enhanced their appeal among consumers (Boukid, 2021). Consequently, the food market has increasingly focused on meat alternatives, which serve as a primary protein source for many consumers.

Plant-based meat analogues (PBMA) are mainly formulated using

plant-derived proteins, which are processed and structured to replicate the sensory attributes of conventional meat. Ideally, these products are expected to closely mimic the texture, and flavor of meat in order to meet consumer expectations. Despite significant technological advances, the palatability of currently available PBMA remains inferior to that of meat products (Brouwer et al., 2025). Consumer acceptance for meat analogues in terms of texture is highly dependent on juiciness and tenderness (Godschalk-Broers et al., 2022). In particular, limitations related to the juiciness of meat analogues, which is the sensation of the liquid released in the mouth while masticating a food product, continue to pose major challenges, ultimately affecting products' palatability (Zhang, Brouwer, et al., 2024; Zhang, Sala, et al., 2024). Juiciness in PBMA is strongly influenced by the physicochemical properties of incorporated plant-based proteins and bolus properties of meat analogues (Zhang, Király, et al., 2025; Zhang et al., 2025).

Therefore, selecting appropriate plant-based proteins for juicier PBMA is challenging because of the wide variability in their functional

Abbreviations: Cb, Carob bean protein; Y, Yeast Protein; Pt, Potato protein; W, Wheat Gluten protein; Fb, Faba bean protein; P, Pea protein; Cp, Cow pea flour; L, Lentil protein; A, Almond protein; Sf, Sunflower protein; H, Hemp protein; Pm, Pumpkin protein; R, Rice protein; PBMA, Plant-based meat analogues; MCDM, Multi-Criteria Decision Making; TOPSIS, Technique for Order Preference by Similarity to Ideal Solution; WHC, Water holding capacity; OHC, Oil holding capacity; LGC, Least gelation concentration; EAI, Emulsifying activity index; ESI, Emulsion stability index; FTIR, Fourier Transform Infrared spectroscopy..

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properties, including water and fat retention, gelation behavior, and the ability to form fibrous-like meat textures. These properties are directly linked to juiciness perception, as they influence moisture and lipid retention within the product matrix and their release during oral processing. This challenge is further intensified by the rapidly growing diversity of plant proteins available for alternative protein applications. Plant protein selection based on traditional independent indicator comparison models presents several drawbacks. These models often rely on a single or a small set of functional indicators, which fail to capture the complexity of protein functionality. Because food-related indicators differ in scale and nature, and protein properties are interrelated rather than independent, such simplified approaches can lead to biased conclusions and limit the ability to accurately predict the optimal protein sources for a specific application or desired property. Moreover, although the functional properties of plant proteins have been previously evaluated and ranked using structured frameworks, these studies were not specifically aimed at optimizing juiciness (Shi et al., 2025).

Multi-Criteria Decision Making (MCDM) provides a systematic framework for evaluating and ranking alternatives based on multiple, often interrelated criteria (Celik et al., 2015). It can overcome the limitations of traditional single-criterion selection approaches by integrating diverse quantitative indicators into a structured decision-making process. In addition, MCDM enables comprehensive assessment and optimization of complex systems, significantly improving the scientific robustness of decision-making (Aruldoss et al., 2013). This method is well-suited to select plant proteins for functional targets, such as enhanced juiciness, where multiple protein properties, including water and oil holding capacity as well as gelation, must be considered simultaneously. Despite its successful application in fields such as engineering, technology, and economics, the use of MCDM in food science remains limited (Montella et al., 2025). Among available MCDM methods, the Technique for Order Preference by Similarity to Ideal Solution (TOPSIS) is especially attractive for food-related applications due to its conceptual clarity, computational simplicity, and ability to directly relate evaluation criteria to product performance. TOPSIS ranks alternatives by measuring their relative distances from positive and negative ideal solutions, allowing for an intuitive comparison of complex multi-dimensional data. Some studies have demonstrated that this method can effectively identify optimal types and concentrations of proteins based on combined physicochemical indicators, confirming its reliability and suitability for optimizing food formulation and processing strategies (Xie et al., 2024).

Unlike previous study that evaluated five plant proteins based on general functional properties and rank them generally only based on objective weights (Shi et al., 2025), this work introduces a more targeted, multi-criteria framework specifically designed to optimize expected juiciness applying both subjective and objective weights in plant-based meat analogues. By integrating a broad range of protein sources (13 in total, including less-studied options such as carob bean protein) with weighted functional indicators and multivariate analysis, this study offers a more application-oriented and mechanistic framework for protein selection. However, the TOPSIS-based ranking should not be considered definitive, rather, it serves as a practical tool to narrow down better protein candidates for subsequent stages of investigation.

However, while many studies have examined the physicochemical properties of plant proteins, few have systematically linked these properties to juiciness using a structured decision-making framework. To address this gap, the present study aims to differentiate thirteen commercially available alternative flours (ranging from protein concentrates to isolates) based on their measured functional properties. Importantly, these properties were evaluated for whole flours, encompassing both the protein fraction and non-protein components (e.g., fiber, ash, and carbohydrates), which collectively influence functionality. Subsequently, the TOPSIS method was applied to rank these ingredients according to their potential to enhance juiciness in PBMA.

2. Materials and methods

2.1. Materials

Thirteen alternative proteins including carob bean, cowpea, faba bean, lupin, pea, potato, yeast, almond, rice, pumpkin, hemp, sunflower, and wheat gluten were evaluated. The protein content flour composition, supplier/brand information and the source of each protein are provided in Table 1. Sunflower oil (100% food grade, coop Italia) was used for the oil-holding capacity and emulsifying properties measurements. Sodium dodecyl sulfate (SDS, ReagentPlus®, ≥98.5% (GC)), 8-Anilino-1-naphthalenesulfonic acid (ANS) and acetic acid 99.7% were purchased from Sigma-Aldrich (St. Louis, MO, USA).

2.2. Water holding capacity (WHC)

Water holding capacity was measured based on the previous method reported by (Webb et al. AL-Ansi et al., 2023). Approximately 2.5 g of each protein was dispersed in 30 mL of deionized water in pre-weighted 50 mL centrifuge tubes. Protein solutions were vortexed for 30s and left at room temperature for 30 min. Every ten minutes, solutions were vortexed again (3 times) to ensure complete hydration of the protein. They were then centrifuged at 3000×g for 30 min, after which the tubes were inverted for 2 min to completely remove the supernatant. The tube with the sediment inside was weighed, and WHC was calculated using Eq. (1). Three independent experiments were done for each protein.

$$WHC \text{ (g water/g protein)} = (W_{\text{precipitate}} - W_{\text{protein}}) / (W_{\text{protein}}) \quad (1)$$

2.3. Oil holding capacity (OHC)

Oil holding capacity was determined based on the method of (Webb et al. AL-Ansi et al., 2023). Approximately 2.5 g of each protein was vortexed with 30 mL of sunflower oil until completely dispersed. The 50 mL centrifuge tubes were then kept at room temperature for 30 min, with the contents shaken 3 times during this period. Samples were centrifuged at 3000×g for 30 min, inverted for 20 min to allow excess oil to decant, and then weighed. Eq. (2) was used to calculate OHC. Three independent experiments were done for each protein.

$$OHC \text{ (g oil/g protein)} = (W_{\text{precipitate}} - W_{\text{protein}}) / (W_{\text{protein}}) \quad (2)$$

2.4. Least gelation concentration (LGC)

The least gelation concentration was determined based on the common method (Ma et al., 2022). Different protein concentrations were prepared, ranging from 2 to 20% (w/v), in glass tubes, and stirred for 1 h. The tubes were then heated in a water bath at 100 °C for about 1 h to induce thermal denaturation of the proteins. After heating, the protein suspensions were rapidly cooled under running tap water and stored at 4 °C for 2 h. LGC is defined as the lowest protein concentration at which the protein dispersion remains in the test tube upon inversion.

2.5. Protein emulsifying activity index (EAI) and emulsion stability index

The emulsifying properties of proteins were measured according to previously described methods (Sun et al., 2022; Tang et al., 2023), with minor modifications. A 0.25% protein solution was made by dissolving the protein in sodium phosphate buffer (pH = 7). The emulsion was then prepared by adding 7.5 g of protein solution and 2.5 g sunflower oil in 15 mL tubes and was homogenized with Ultra-Turrax (IKA-Werke GmbH & Co. KG, Staufen, Germany) at 25,000 rpm for 2 min. A 200 µL aliquot of the fresh emulsion was diluted in 5 mL of 0.1% SDS solution and vortexed for 30 s. The absorbance of the emulsion at zero time was measured at 500 nm using a spectrophotometer (Cary 60 UV-Vis Spectrophotometer, Agilent, California, USA) with 0.1% SDS as the

Table 1

Protein sources used in the study including declared protein content, sources, suppliers, and brand information. ND stands for not declared.

Protein Source	Protein Content (%)	Carbohydrate (%)	Fiber (%)	Ash (%)	Fat (%)	Supplier/Company	Brand	Source
Carob bean	50	16–18	22	Less than 8	6	LBG Sicilia S.r.l.	–	Legume
Cowpea flour	51	32.7	ND	4.26	5.24	Afropulse Food and Ingredients Co.	–	Legume
Faba bean	60	5.8	18	ND	3.4	Union Française de Biologic Agriculture (UFAB)	–	Legume
Lupin	60	7.6	14.6	2.5–3.5	9.8	Inveja Netherlands B.V.	–	Legume
Pea	54	13	16	ND	4.7	Union Française de Biologic Agriculture (UFAB)	–	Legume
Potato	80	6	2–3	0.7	2–3	Nab Food, Italy	–	Tuber
Yeast	80	ND	ND	Less than 5	ND	Biospringer (Lesaffre)	–	Microbial
Almond	50	11.7	24.3	ND	4.65	Magellan Food Ingredients	–	Nut
Rice	80	4	3.4	ND	8.7	–	Buon Food	Cereal
Pumpkin	65	4.9	ND	ND	9.3	–	Gust Vivo	Oilseed
Hemp	50	7.8	ND	ND	9	–	Buon Food	Oilseed
Sunflower	53	4.1	23	ND	7.2	–	Cibo Crudo	Oilseed
Wheat gluten	85	4.6	1.2	ND	3.8	–	Instant Seitan Bio	Cereal

blank. After 10 min of storage at room temperature, a fresh aliquot of the emulsion was diluted in SDS solution as described above, and the absorbance at 500 nm was measured and recorded as A_{10} . EAI and ESI were calculated with the following equations:

$$EAI (m^2/g) = 2 \times \ln 10 \times (A_0 \times D) / (10000 \times \theta \times C) \quad (3)$$

$$ESI (\%) = A_0 / (A_0 - A_{10}) \times \Delta A \quad (4)$$

where $\ln 10$ is 2.303, D is the dilution factor (100), C is the initial concentration of the sample (0.0025 g/mL), θ is the oil volume fraction in emulsion (0.25), A_0 is the absorbance of the emulsion at zero time, A_{10} is the absorbance of the emulsion after 10 min, and ΔA is 10 min.

2.6. Protein secondary structure

The secondary structure of proteins was determined using a Fourier transform infrared spectrometer (FT-IR) (Bruker Corporation, Billerica, MA, USA). The absorbance of protein powder samples was measured at a spectral resolution of 4 cm^{-1} with 64 scans; the transmission spectrum was recorded from 400 to 4000 cm^{-1} . The amide I region (1600–1700 cm^{-1}) was used to analyze protein secondary structure with the help of Spectragryph (version 1.2.16.12022) and R (R version 4.4.2) to first extract the amide I region from FTIR spectrum, fit Gaussian model and compute the percentage of each peak area (Tang et al., 2021).

2.7. Protein gel strength

Protein gelation was measured based on the previously defined method in deionized water at the natural pH of each protein solution (Bengoechea et al., 2017). Protein dispersions (20%, w/v) and dispersions at their least gelation concentration (LGC) were prepared by stirring for 1 h at room temperature. The dispersions were transferred into glass tubes, heated to 95–100 °C in a water bath for 1 h, immediately cooled, and stored at 4 °C for 15 h to allow gel stabilization. At 20% concentration, most proteins formed self-supporting gels, which were analyzed by a puncture test. Gels formed in cylindrical glass tubes were tested using a Texture Analyzer (TA.XT Plus, Stable Micro Systems, UK) equipped with 5 kg loading cell and a 5 mm cylindrical stainless-steel probe. The probe penetrated the gel to 50% of its height at a speed of 1.0 mm/s. From the force–time curve, the maximum value of the force indicates the gel strength.

For LGC and proteins that did not form rigid gels at 20% concentration and instead exhibited a viscous, semi-gel-like structure, the texture was assessed using a spreadability test with a spreadability rig. Samples were placed between two conical plates, and the upper probe was lowered at 1.0 mm/s while the strain was held at 70%. The

force–distance curve provides measures of the first maximum force, which indicates gel strength, and the negative area, which determines gel adhesiveness (Florowska et al., 2020).

2.8. Protein surface hydrophobicity

The surface hydrophobicity (H_0) of all protein samples was measured using 1-anilino-8-naphthalene sulfonate fluorescence or ANS probe, based on the method stated by (AL-Ansi et al. AL-Ansi et al., 2023), with some modifications. ANS reagent (8 mM in acetic acid) and a 50 mM acetic acid solution were first prepared. Approximately 150 mg of each protein sample was dispersed in 20 mL of the prepared acetic acid solution, then shaken at room temperature for 2 h, followed by centrifugation at 10,000 g for 2 min. Supernatant from each protein was used to make five concentrations (0.2–0.4–0.6–0.8–1 mg/mL). Then 20 μ L of ANS solution was added to the samples. After being in a dark room 15 min, the fluorescence intensity was recorded by a fluorescence spectrophotometer (Tecan Sunrise Microplate Absorbance Reader, Männedorf, Switzerland) at an emission wavelength of 470 nm and an excitation wavelength of 390 nm. Fluorescence values were then corrected by subtracting the ANS fluorescence in buffer without protein. Finally, protein surface hydrophobicity was calculated from the initial slope of the regression line plotting the corrected fluorescence intensity signal against protein concentration.

2.9. Protein solubility

The solubility of the proteins was measured using the Bradford method (Bradford, 1976), with some modifications. The standard calibration curve was drawn using bovine serum albumin (BSA), which was chosen as the standard protein. For protein extraction, 100 mg of each protein was mixed with 10 mL of phosphate buffer (pH: 7) and stirred for 30 min. After being centrifuged at 10,000 g for 15 min, 20 μ L of the supernatant was collected and mixed with 200 μ L of Bradford reagent. The mixtures were kept in a microplate for 5 min, and the absorbance was measured at 595 nm using a microplate reader (Tecan Sunrise Microplate Absorbance Reader, Männedorf, Switzerland). Protein relative solubility was calculated as the percentage of soluble protein determined by the Bradford assay in the supernatant relative to the total protein content of the protein powder.

2.10. Proteins ranking

Multi-criteria-decision-making (MCDM) was adopted to identify plant-based proteins with the greatest potential to enhance juiciness in the final product. Additionally, the Technique for Order Preference by

Similarity to Ideal Solution (TOPSIS) was used to rank protein alternatives by measuring their distances from the best and worst possible solutions. After normalizing the criteria, weights are assigned to each criterion (using a hybrid weighting scheme for the protein properties), and the option closest to the ideal and farthest from the negative-ideal solution received the highest rank and was considered the best choice. Among different methods of MCDM, TOPSIS was selected because it provides a clearer measure of distance from the ideal protein and was more commonly used in food formulation studies (Giallanza et al., 2017; Shi et al., 2025).

Subjective weights were determined using the direct ranking (DR) method based on the judgments of four experts with expertise in food science and protein functionality. The experts assessed the relative importance of each criterion with respect to the final juiciness of plant-based meat alternatives (PBMA). Their evaluations were aggregated by calculating the arithmetic mean and subsequently normalized to derive the final subjective weights. To reduce potential bias associated with subjective judgment and enhance the robustness of the results, objective weighting was also incorporated. The entropy method was employed to calculate the objective weights. The integration of both subjective and objective weighting approaches improved the reliability of the final rankings and enhanced the consistency of the decision-making outcomes (Ponhan & Sureeyatanapas, 2022). A balancing factor (α) was applied in the hybrid weighting scheme and fixed at 0.6, since varying α within the range of 0.5–0.7 did not alter the ranking of the top five-performing proteins. A higher contribution was assigned to the subjective component to prioritize juiciness over variability in the measured data.

$$w^{Hybrid} = \alpha w^{subjective} + (1 - \alpha)w^{objective} \quad (5)$$

2.11. Statistical analysis

All measurements were performed in triplicate unless otherwise specified. Statistical analyses were conducted using *t*-tests and one-way analysis of variance (ANOVA) at the $\alpha < 0.05$ significance level, employing Jamovi (version 2.6.26) and R (version 4.4.2). Standard errors were calculated for selected parameters. Principal component analysis (PCA) and hierarchical clustering analysis (HCA) were performed in R to differentiate proteins by their functional and structural properties and to cluster them based on their similarities. Prior to PCA, the data were centered and scaled via Z-score normalization. A clustered heatmap was generated using the scaled averaged data, with Euclidean distance and Ward's linkage (Ward.D2) applied to both rows and columns.

3. Results and discussion

3.1. Water holding capacity and oil holding capacity

Water-holding capacity (WHC) and oil-holding capacity (OHC) of plant proteins play a crucial role in mimicking the juiciness and fattiness of meat in plant-based meat analogues (Sakai et al., 2023).

Juiciness is a dynamic sensory attribute that evolves during oral processing and, in PBMA, is largely governed by serum release during the early stages of mastication, while structural breakdown plays a more limited role in later chewing stages (Zhang, Brouwer, et al., 2024; Zhang, Király, et al., 2025; Zhang et al., 2025; Zhang, Sala, et al., 2024). This early-stage serum release is closely linked to the ability of the protein matrix to absorb, retain, and subsequently release water. In this context, proteins play a central role at the molecular level, as their water-holding capacity prior to extrusion determines how water is incorporated into their structure and bound with their groups. Proteins with higher pre-extrusion WHC tend to form a more porous, sponge-like internal network during extrusion, characterized by larger and/or more numerous air cells (Li, 2024). This porous structure enhances water retention within the matrix while also enabling efficient water release

under compressive forces during mastication, thereby directly contributing to perceived juiciness.

In particular, proteins with higher WHC tend to form a more porous, sponge-like internal structure with larger and/or more numerous air cells during extrusion processing. This structural characteristic enhances the ability of the final product to retain water, thereby contributing to improved juiciness and mouthfeel (Li, 2024). WHC can be influenced by several parameters, such as protein concentration, mixing time, temperature in the analytic method, and pH of the protein solution (Ma et al., 2022).

Both the WHC and OHC values shown in Fig. 1 are in the range indicated by previous studies, 0.9–6.8 g/g for WHC and 0.9–6.4 g/g for OHC (Li, 2024). In terms of WHC, rice and yeast exhibited the highest values, exceeding 5.5 g of water per g of protein. This may be related to rice and yeast's lower bulk density, which reflects higher porosity, and to the presence of exposed hydrophilic residues that can interact with water. However, as indicated by their low solubility (Table 2), much of the water was likely only physically entrapped between the protein particles rather than bound at the molecular level (Zhao et al., 2020). In contrast, most of the other proteins exhibited similar WHC values, with the exception of pea, lupin, and faba bean, which showed noticeably lower WHC, close to 3 g of water per g of protein. These results are consistent with those reported by (Webb et al., 2023) who found that pea and faba had the same WHC, both lower than wheat gluten. Moreover, potato protein showed no ability to absorb and hold water during centrifugation. This might be due to the high surface hydrophobicity of potato protein, as shown in Table 2, consistent with previous studies reporting that higher surface hydrophobicity can limit protein-water interactions and reduce WHC (Ma et al., 2022).

OHC is critical in replicating the mouthfeel of animal fat experienced in PBMA. Regarding OHC, values were higher than WHC for most proteins, except for faba bean, pea, and potato. This suggests that the majority of the proteins tested predominantly contain charged and polar amino acid residues, making them more hydrophilic rather than hydrophobic (Ma et al., 2022). OHC values ranged from 3 to 5.7 g oil/g protein, with potato (5.62 ± 0.56), rice (5.24 ± 0.14), faba (4.53 ± 0.12) and cowpea (4.35 ± 0.21) exhibiting the highest capacities and almond (3.06 ± 0.09) the lowest. As a correlation between OHC and protein content was represented in hierarchical clustering of variables in Fig. 4 showing a distinct cluster, more OHC in rice and potato (80%) may be due the high protein content they had. Wheat's OHC was comparable to that of sunflower, yeast, lupin, and carob bean, likely due to their lower content of non-polar amino acids. Pea and faba bean showed statistically similar OHC values, consistent with the findings of (Webb et al., 2023) who reported comparable OHC for these legumes.

3.2. Emulsifying activity index and emulsion stability index

Plant proteins are widely used as emulsion stabilizers due to their amphiphilic nature, as they contain both hydrophobic and hydrophilic groups. This property enables them to adsorb at the oil–water interface, reduce interfacial tension, and inhibit emulsion destabilization processes (Li, 2024). Emulsification plays a critical role in determining the sensory attributes and consumer perceptions of PBMA. Therefore, the characterization of the emulsifying properties of plant proteins is essential for effective product development. EAI is the maximum interfacial area (m^2) that is covered per gram of protein, and ESI measures how well the plant protein resists changes in stability of the emulsion in a defined period of time, which was 10 min.

As shown in Fig. 2, highest EAI is related to pea (150.32 ± 0.16) and faba bean (150.98 ± 0.75) which have the same values. In general legume proteins have good emulsifying properties and stability at pH 3. Therefore, in more acidic environments such as salad dressings proteins like pea, faba, lupin, carob and cowpea will be more suitable (Tiwari & Healy, 2023).

As stated by (Stone et al., 2015), a positive correlation is observed

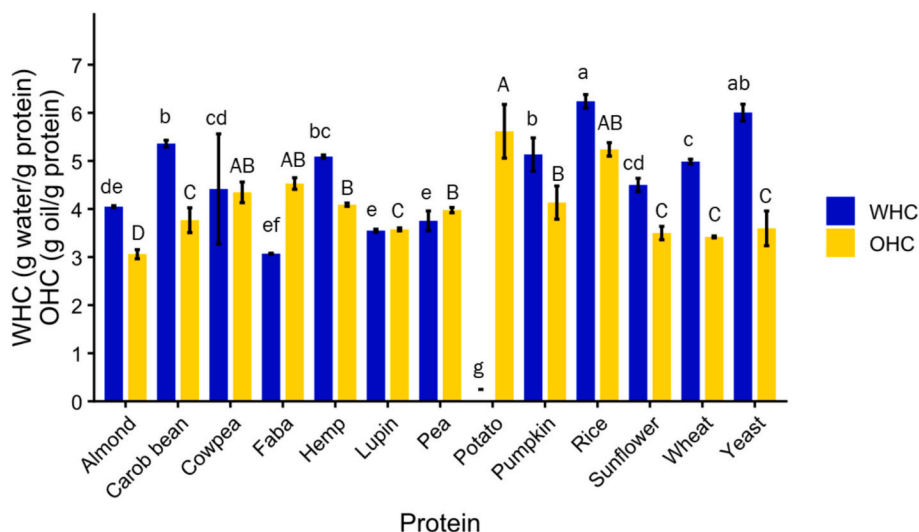


Fig. 1. Blue bars indicate water-holding capacity (WHC, g water/g protein) and yellow bars indicate oil-holding capacity (OHC, g oil/g protein). Bars represent mean values ± standard deviation in error bars ($n = 3$). Different lowercase and uppercase letters indicate significant differences ($p < 0.05$) for WHC and OHC, respectively. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

Table 2

Physical properties measured for the different protein-based samples. Means shown with the same letter within a column indicate no significant ($p > 0.05$) differences.

Protein	LGC (%)	Solubility (%)	Surface hydrophobicity H_0	β -sheet (%)	Random coil (%)	Gel strength (N)
Almond	8	16.06 ± 0.77 ^b	1471 ± 818 ^h	27.70 ± 0.44 ^{bc}	24.70 ± 0.10 ^d	0.47 ± 0.07 ^{cd}
Carob bean	16	6.20 ± 0.19 ^{de}	2235 ± 900 ^{gh}	28.40 ± 0.42 ^b	29.60 ± 0.06 ^{bc}	0.11 ± 0.07 ^c
Cowpea	10	32.26 ± 0.27 ^a	1477 ± 675 ^h	26.50 ± 0.23 ^c	31.90 ± 0.15 ^{ab}	0.69 ± 0.03 ^c
Faba	12	12.45 ± 0.19 ^c	2886 ± 341 ^{fg}	27.10 ± 0.56 ^{bc}	31.30 ± 0.29 ^{ab}	0.44 ± 0.14 ^{cd}
Hemp	16	2.29 ± 0.43 ^{fg}	676 ± 114 ⁱ	27.00 ± 0.25 ^{bc}	28.00 ± 0.47 ^c	0.15 ± 0.04 ^e
Lupin	16	12.90 ± 0.49 ^c	9354 ± 200 ^d	27.90 ± 0.35 ^b	30.50 ± 0.10 ^b	0.09 ± 0.03 ^e
Pea	10	14.31 ± 0.79 ^{bc}	2766 ± 242 ^{fg}	26.00 ± 0.25 ^c	31.50 ± 0.10 ^{ab}	0.65 ± 0.31 ^c
Potato	8	12.78 ± 0.49 ^c	13,347 ± 1260 ^c	28.00 ± 0.35 ^b	33.00 ± 0.12 ^a	4.67 ± 0.54 ^a
Pumpkin	18	4.04 ± 0.17 ^{ef}	12,863 ± 1576 ^c	28.30 ± 0.32 ^b	29.10 ± 0.91 ^{bc}	0.64 ± 0.09 ^c
Rice	20	0 ^h	71,527 ± 729 ^a	26.40 ± 0.12 ^c	28.90 ± 0.20 ^{bc}	0.60 ± 0.15 ^c
Sunflower	8	8.66 ± 1.75 ^d	23,461 ± 1024 ^b	26.60 ± 0.15 ^c	29.20 ± 0.95 ^{bc}	0.25 ± 0.01 ^{de}
Wheat	–	2.41 ± 0.66 ^{fg}	5379 ± 1774 ^e	27.60 ± 0.35 ^{bc}	30.70 ± 0.06 ^b	1.29 ± 0.68 ^b
Yeast	–	1.11 ± 0.09 ^{gh}	4516 ± 1052 ^{ef}	30.50 ± 0.21 ^a	28.70 ± 1.08 ^{bc}	–

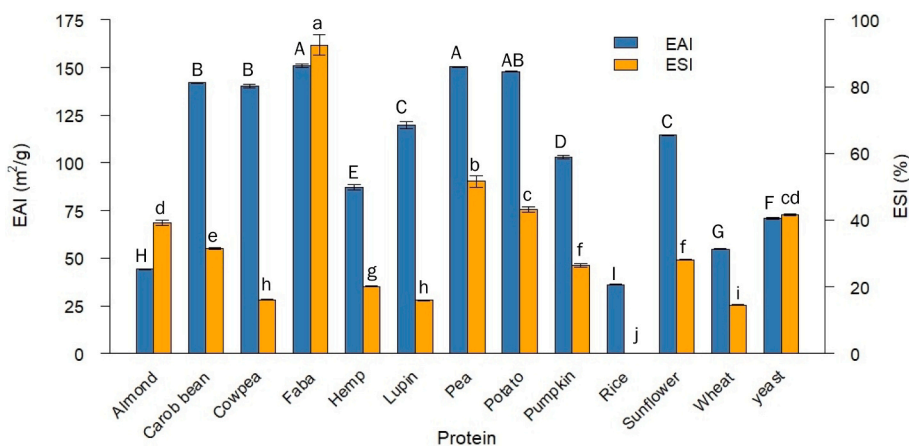


Fig. 2. Emulsifying activity index (EAI) and emulsion stability index (Khalessi et al., 2024) of different protein sources. Blue bars represent EAI (m²/g) and orange bars represent ESI (%). Bars show mean values ± standard deviation ($n = 3$). Different uppercase letters indicate significant differences in EAI, while different lowercase letters indicate significant differences in ESI among samples ($p < 0.05$). (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

between EAI and surface hydrophobicity due to the faster adsorption of the protein on the interfacial surface (Ding et al., 2026). On the other side, a negative correlation is measured between EAI and protein

solubility. The findings were confirmed in the present study with EAI measured in pea and faba protein having both not statistically different values of solubility and surface hydrophobicity (Table 2). However,

although rice and yeast, with the same protein concentration (80%), showed low equal solubility, their emulsifying properties were correspondingly poor, which is in contrast to the results mentioned before (Stone et al., 2015). Since poorly soluble proteins lead to the formation of coarse emulsions with large droplet sizes, they act only as Pickering stabilizers, and emulsion stability relies mainly on an increased viscosity of the continuous phase rather than effective interfacial adsorption, which increases the likelihood of phase separation (Ding et al., 2026). Moreover, potato protein reported high EAI mainly due to the patatin fraction in it, which has good emulsifying properties (Galves et al., 2023).

In terms of ESI, wheat, lupin, and cowpea proteins showed the lowest ability to stabilize emulsions over a 10-min period, while sunflower and pumpkin proteins exhibited similar ESI values of approximately 27% (Fig. 2). Although both wheat and rice exhibited low protein solubility, wheat showed a slightly significant higher EAI. This may be attributed to shear-induced partial denaturation of wheat proteins, which can expose hydrophobic groups and enhance interfacial activity, thereby improving emulsifying performance, consistent with the findings reported by (Zhao et al., 2020). In contrast, rice protein showed no ability to contribute to emulsion stability, mainly due to its low solubility value (Table 2).

3.3. Least gelation concentration (LGC)

There are two types of protein gels: one made from unfolding protein and random aggregation, which occurs in most of the proteins, and another with the association of proteins in more ordered strands (Hettiarachchy et al., 2013). LGC is the least concentrated form of a protein in which polypeptides crosslink and form a three-dimensional network, entrapping a large amount of water in it.

On the one hand, the ability of proteins to absorb water, reflected by their water-holding capacity, is a key factor that has been discussed previously. On the other hand, the ability of proteins to form a network that can entrap water, as indicated by the least gelation concentration, together with the strength of this network which is related to the water holding capacity of protein gel, plays a crucial role in determining both water retention and release. Specifically, LGC reflects the ability of a protein to form a continuous network capable of entrapping water. Gel strength describes the mechanical stability of this network and its resistance to deformation. This property is closely related to the WHC of the protein gel and is influenced by gel coarseness and stiffness under compressive forces during the initial stages of mastication, as well as by the gel's viscoelastic behavior (i.e., whether it behaves more viscously or elastically), ultimately affecting perceived juiciness (Hui et al., 2025; Kim et al., 2024; Urbonaite et al., 2014).

The types of interactions in gel formation are highly dependent on pH (Khalesi et al., 2024). In the present study, proteins were dissolved at their native pH without modification, which is the standard procedure for LGC determination; the pH of the dispersions ranged from 5.8 to 6.9.

The LGC of the heat-induced protein gels is shown in Table 2. Yeast protein has poor gelation ability due to its low sulfhydryl group and disulfide bond content and gelled when combined with another protein such as soy protein (Xia et al., 2023) or another polysaccharide such as alginate, xanthan gum or konjac glucomannan (Peleg-Evron et al., 2025; Xia et al., 2023). Wheat gluten proteins were excluded from testing because their hydrophobic nature leads to rapid aggregation and poor dispersion when hydrated prior to heating (Webb et al., 2023).

The lowest LGC was observed for almond, potato, and sunflower proteins, which formed gels at a concentration of 8%, indicating superior gelling ability. In general, a lower LGC reflects a stronger gelation capacity of plant proteins. Moreover, cowpea protein revealed superior gelling capacity (10%) due to the abundance of vicilins in it, forming a gel network through non-covalent interactions (Shevkani, 2025). In contrast, proteins exhibiting LGC values higher than 16% demonstrated poor gelling properties, which is consistent with their low solubility values reported in Table 2. Rice protein required the highest

concentration for gel formation, which can be attributed to its protein composition dominated by glutelins and the presence of prolamins. These fractions are rich in non-polar amino acids, resulting in high surface hydrophobicity and the lowest water solubility among other proteins (Table 2). Moreover, the observed 20% concentration may not represent true gel formation but rather reflects extensive intermolecular aggregation of rice proteins that hinders the structure's flow during the tube inversion test. However, some modifications, such as reduction-oxidation treatments or crosslinking, can significantly enhance their gelation properties (Hettiarachchy et al., 2013).

3.4. Protein solubility

Protein solubility is described as the amount of protein that can be dissolved in an aqueous solution and is dependent on the surface hydrophilicity and the presence of highly charged polar amino acids on the surface. Having the knowledge of protein solubility is essential, as it informs other properties, such as gelation, emulsification, and foaming (Khalesi et al., 2024). Various factors govern plant protein solubility, including intrinsic factors (e.g., amino acid composition and hydrophobicity) as well as extrinsic parameters such as pH, ionic strength, extraction, and drying processes (Gao et al., 2024).

Higher native protein solubility facilitates improved dispersion and hydration prior to extrusion, enabling more uniform unfolding and controlled aggregation. This is consistent with findings by (Flory et al., 2023), who reported that increased protein solubility enhances protein texturization during extrusion. Consequently, a more continuous protein network is formed through texturization, capable of effectively entrapping and releasing water during mastication, thereby enhancing the perceived juiciness of the final product.

Differences in solubility of different plant protein sources are mainly correlated with the prevalent protein classes presented in the raw material. For instance, solubility in proteins with high amounts of prolamin (wheat gluten 2.41%) and glutelin (rice protein 0% and pumpkin 4.04%) was lower than the samples reporting higher globulins (for almond 16.06%, pea 14.31%, sunflower 8.66%) and albumins (potato 12.78%) (Ebert et al., 2020; Tan et al., 2023). Cowpea protein also exhibited the highest solubility (32.26%), compared to the other pulse proteins, despite having only about 24% protein content. This higher solubility may be attributed to its high globulin content, which constitutes approximately 80% of the total protein fraction (Shevkani, 2025). Pretreatments done on raw proteins also affect the solubility of them, for instance defatting and solvent extraction of oil from protein powders result in protein denaturation and lower solubility of them. This may be the reason of low solubility in pumpkin powder (4.04 ± 0.17) (Tiwari & Healy, 2023).

The low water solubility of rice glutelin was mainly attributed to three factors: (1) extensive hydrogen bonding among glutamine and asparagine residues, which replaces hydrogen bonding with water molecules, (2) the formation of inter- and intra-molecular disulfide bonds between cysteine residues, leading to large protein aggregates; and (3) a high content of hydrophobic amino acids on its surface convinced by high surface hydrophobicity (71,527 au in Table 2) which promotes hydrophobic interactions and limits water penetration into the protein structure (Yang et al., 2023). Furthermore, potato protein, composed mainly of patatin and a smaller fraction of protease inhibitor, exhibits high solubility at its native pH (above 6), comparable to that of pea, faba bean, and lupin proteins (Grossmann & McClements, 2023).

3.5. Surface hydrophobicity

Surface hydrophobicity refers to the distribution of hydrophobic amino acid residues on the surface of plant protein, which is crucial for defining some functional properties, including emulsification and foaming stabilization (Li, 2024).

The highest surface hydrophobicity was observed in rice protein,

resulting in the lowest solubility among the proteins, followed by sunflower protein (23,461 au), and then potato and pumpkin, with equal H_0 . In contrast to the results gathered by da Silva et al., the values obtained in the present study were substantially higher for rice protein and lower for pea protein (da Silva et al., 2021; Galves et al., 2023). As surface hydrophobicity is correlated with protein content in heatmap clustering shown in Fig. 4, this may be attributed to the more protein content of rice protein we used (80% in comparison to 71% they used) and lower amount of protein proportion in pea we had (54% compared to 67% they measured).

Surface hydrophobicity is generally negatively correlated with protein solubility because aggregation is driven by exposed hydrophobic regions. However, as fluorescence-based measurements are reported in arbitrary, instrument-dependent units, comparisons across studies remain challenging (Xu et al., 2022). In this study, although a general inverse trend between solubility and surface hydrophobicity was observed, proteins with similar surface hydrophobicity, such as potato and pumpkin, exhibited markedly different solubility, while hemp protein, with the lowest H_0 , also reported low solubility, indicating that surface hydrophobicity alone does not fully govern solubility behavior in all the proteins.

3.6. Secondary structure

FTIR spectroscopy is used to examine conformational differences between soluble and insoluble protein fractions. The Amide I region (1600–1700 cm^{-1}) is particularly informative because it is highly dependent on protein secondary structure. This band mainly arises from C=O stretching vibrations with a minor contribution from out-of-phase C–N stretching vibrations, CCN deformation, and N–H bending. Because of the N–H bending contribution, this band is sensitive to changes in the protein backbone, such as N-deuteration (Barth & Zscherp, 2002). Amide I contains contributions from α -helices, β -sheets, random coils, and β -turns, each absorbing within specific wavenumber ranges: 1650–1660 cm^{-1} , 1615–1640 cm^{-1} , 1640–1650 cm^{-1} and 1660–1690 cm^{-1} , respectively (Badjona et al., 2025). β -sheet and α -helix structures are highly ordered and stabilized by intramolecular hydrogen bonding, whereas β -turns are less ordered, and random coil structures are primarily stabilized by hydrogen bonding between C=O groups and water molecules (Xiao et al., 2023). The secondary structure of proteins is crucial as it can affect their functional properties. For example, higher β -sheet content increases protein thermal stability, thereby reducing the ability of proteins to unfold under heat during extrusion and limiting intermolecular aggregation required for gel network formation (Shevkani, 2025).

The content of each secondary structure in proteins is summarized in Table 2. β -sheet content ranged from 26% to 30.5%, with yeast having the highest proportion of β -sheet, confirming its high thermal stability and tolerance to being gelled and denatured by heat (Khetan Shevkani et al., 2019). As regards to the pulse proteins (pea, faba and cowpea), they are known to have more proportions of β structures (β -sheets and β -turns), thus they are more heat stable having higher denaturation temperature (Tiwari & Healy, 2023).

α -helix ranged from 23.5% to 25.4%, and the β -turn content ranged from 14.9% to 23.8%, with almond protein exhibiting the highest proportion. This suggests a more compact and stable molecular structure, as higher β -turn content reflects increased folding and reduced peptide chain mobility due to constrained conformational entropy (Sun et al., 2023). The proportion of random coil structures ranged from 23.7% to 33.0% and was highest in potato protein, suggesting a more unfolded structure potentially favorable for gel formation.

Protein secondary structure is mainly governed by hydrogen bonding and plays an important role in protein folding and food structure. When proteins contain a high proportion of highly ordered structures (β -sheets and α -helices), they are generally less flexible and less soluble, and tend to bury functional groups within their structure, resulting in fewer

exposed reactive sites. Consequently, higher temperatures or longer heating times are required to induce unfolding and expose side chains necessary for protein–protein interactions. If unfolding is limited under given conditions, network formation may be incomplete, leading to weaker gel structures and lower gel strength. Therefore, an appropriate balance between ordered structures and random coils in proteins prior to gelation facilitates sufficient unfolding and controlled aggregation, promoting the formation of a continuous three-dimensional network and resulting in stronger gels. This also explains why plant proteins are often modified prior to application, in order to optimize their secondary structure and improve functional properties (Kim et al., 2024).

This behavior is consistent with our observations as native potato protein, characterized by a relatively high random coil content and moderate β -sheet proportion, exhibits good solubility and strong gelation properties. In contrast, yeast proteins with higher β -sheet content displayed lower solubility and limited gel-forming ability. Furthermore, after gel formation, stronger gels are often associated with increased β -sheet content, as β -sheet structures contribute to intermolecular interactions and the stabilization of a dense and rigid protein network (Wang et al., 2022).

3.7. Gel strength

Gel texture is also a major parameter for describing the gelling properties of plant proteins (Li, 2024). The strength of a gel is described by the stress at which the gel structure breaks and is strongly affected by the protein extraction method, which may cause protein denaturation and some degree of aggregation (Nicolai & Chassenieux, 2019).

Potato protein exhibited significantly higher gel strength than all other proteins (4.67 N), while wheat gluten formed an intermediate group (1.29 N). Cowpea, pea, pumpkin, and rice showed comparable gel strengths, with no significant differences among them. The high gel strength of the potato protein isolate can be attributed to high temperature-induced aggregation of high-molecular-weight protein fractions (~250 kDa), which actively formed a gel network, while patatin remained largely soluble (Katzav et al., 2020).

As reported by (Guldiken et al., 2021), surface hydrophobicity plays a significant role in the gel strength of pulse proteins (cowpea, carob bean, pea, faba bean, and lupin), where higher surface hydrophobicity is generally associated with the formation of denser and firmer protein gel networks. However, the results of the present study did not fully align with these findings. Although lupin exhibited the highest surface hydrophobicity (H_0), it showed the weakest gel strength among the pulse proteins, comparable to that of carob bean. This discrepancy may be attributed to excessive exposure of hydrophobic amino acid residues, which can promote protein aggregation rather than the formation of a well-connected gel network, ultimately weakening gel structure.

Pea and faba protein showed the same gel strength mainly due to the same storage proteins they contain (7S-globulins named as vicilins and 11S-globulins named as legumins) (Kimura et al., 2008). Despite similar protein contents in pea and lupin (55% vs 60%), lupin reported substantially lower gel strength (0.09 ± 0.03 N) than pea (0.65 ± 0.31 N), likely due to its higher thermal stability, which limits protein unfolding and favors intramolecular aggregation during heating (Nicolai & Chassenieux, 2019), confirmed by the higher β -sheet content (27.9%) compared to pea protein (26%).

3.8. Correlation and multivariate analysis

Principal component analysis (PCA) was applied to reduce the multidimensional dataset of protein techno-functional properties into fewer dimensions while preserving most of the original information. The analysis, described PC1 and PC2, which together explained 46.8% of the total variability. PCA biplot (Fig. 3) revealed clear functional differentiation among the proteins studied and captured the correlation between their functional properties.

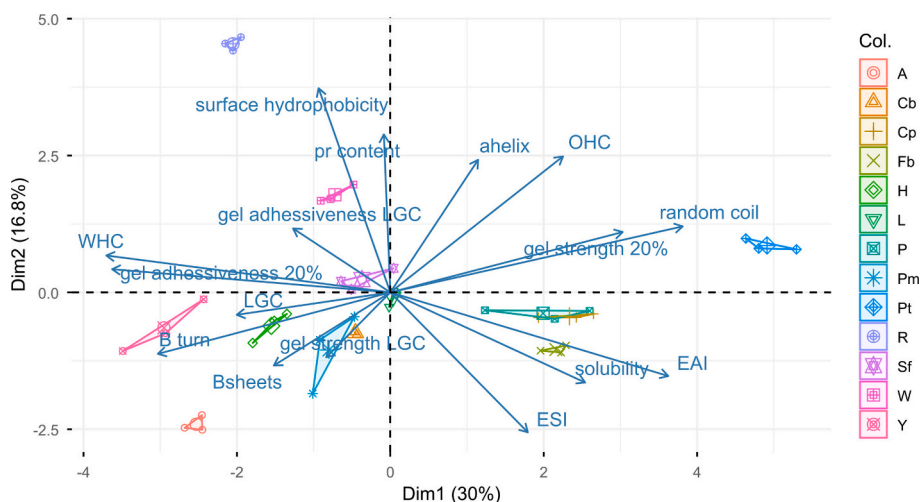


Fig. 3. Principal component analysis biplot showing the first two principal components of the data (PC1 and PC2: 46.8% of the total variance). Proteins are colored and arrows represent the contribution of variables to the principal components. The length of these arrows indicates how well the variables affect the PCs.

The first principal component (PC1) was positively associated with gel strength (at 20% concentration), EAI, OHC, random coil content, and solubility, and to a lesser extent with ESI. Potato protein exhibited one of the highest positive scores on PC1, reflecting higher values of gel strength, random coil, and EAI. In contrast, PC1 was negatively associated with WHC, β -turn, β -sheet, LGC, and protein content, indicating that yeast proteins were highly positioned on the negative side. PC2 separated proteins with higher rigidity and gelation concentration (β -sheet and LGC) on the positive side from those exhibiting greater conformational flexibility and surface activity (α -helix and surface hydrophobicity) on the negative side.

Moreover, hierarchical cluster analysis (HCA) (Fig. 4) was applied to both variables and samples to further explore correlations among functional parameters and to discriminate proteins according to their overall property profiles.

Regarding the correlation between the variables, consistent trends were observed in both PCA and HCA. β -sheet content was strongly correlated with LGC, with a correlation coefficient of 0.730, indicating

that higher β -sheet content is associated with lower gelling ability, requiring more protein concentrations to form a gel. This agrees with the secondary structure analysis, where increased β -sheet content limited protein unfolding during heating, thereby reducing network formation. In contrast, β -turn structures appeared to contribute positively to gel strength at the LGC, likely due to their role in forming more compact and stable protein conformations. Surface hydrophobicity showed a strong positive correlation with OHC, supporting that increased exposure of hydrophobic amino acid residues enhances oil absorption by proteins. This is in agreement with the findings of Varayil et al., who reported a strong correlation between OHC and non-polar amino acids in legume proteins (Varayil & Mitra, 2026).

Gel strength was also closely associated with protein concentration, as higher protein levels promote the formation of denser and more rigid gel networks. This was also approved by Tiong et al., who see that increasing protein concentration directly affects protein gel strength and make higher G' in rheological tests for soy and pea proteins (Tiong et al., 2024).

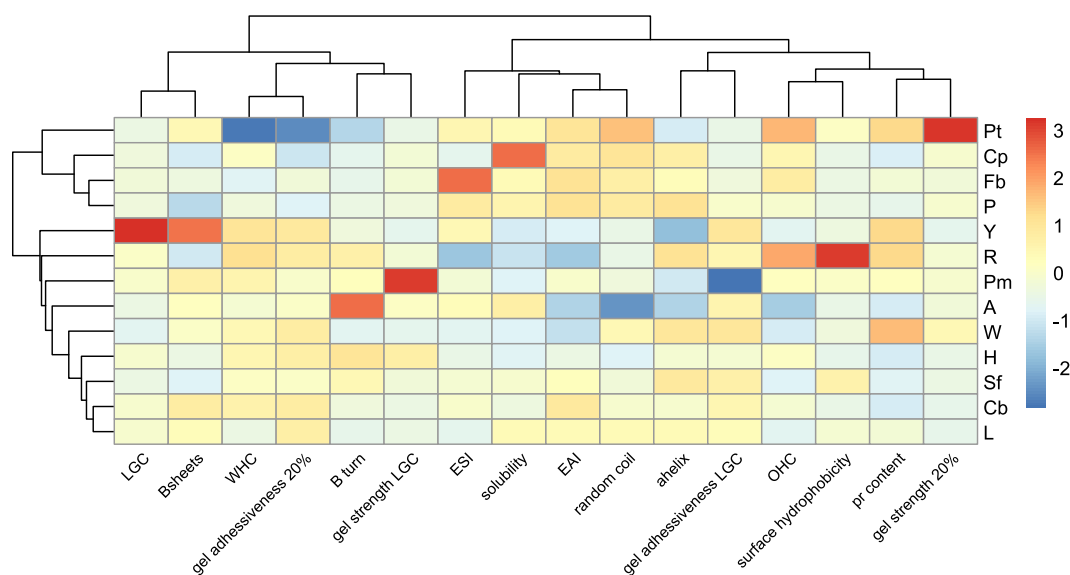


Fig. 4. Clustered heatmap of proteins across the clustered functional properties measured. Rows correspond to proteins, Columns correspond to the measured properties, and colour intensity represents scaled protein abundance, with reddish shades indicating higher abundance for a given property. Hierarchical clustering from HCA of both rows and columns was performed using Ward's method with Euclidean distance, grouping proteins with similar abundance patterns across properties.

Emulsifying properties were primarily linked to protein solubility, with both EAI and ESI index showing positive correlations with solubility. Notably, EAI was strongly associated with random coil content (0.704 correlation coefficient), suggesting that more disordered protein structures facilitate adsorption and rearrangement at the oil–water interface.

Regarding the PCA biplot and the dendrogram of protein samples, two main clusters were observed, in which cowpea, pea, and faba bean generally occupied similar positions in the PCA space, indicating comparable functional and structural profiles and partial overlap with potato protein. In contrast, the remaining proteins formed a clearly distinct cluster. In particular, a second cluster on the left side of the PCA plot comprised carob, lupin, sunflower, hemp, and wheat proteins, which were positioned closer to one another than to the other samples, suggesting shared property patterns within this group. Yeast and rice proteins exhibited markedly different characteristics compared to all other samples and formed isolated clusters, indicating unique functional behaviors and distinguishing them from other protein groups.

3.9. MCDM, TOPSIS

Selection of optimal alternative proteins for improving juiciness in plant-based meat alternatives cannot be reliably based on a single or two individual functional properties, as protein functionalities differ substantially and may interact in complex ways. Therefore, a multivariate decision-making approach, such as TOPSIS, enables simultaneous evaluation of multiple parameters. In TOPSIS, the positive (D^+) and negative (D^-) distances represent the Euclidean distances of each alternative from the ideal best and ideal worst solutions, respectively. The closeness coefficient (C^*) is then calculated based on these distances, and proteins with higher coefficients are considered more similar to the ideal solution and are ranked accordingly (Shi et al., 2025).

In Table 3 all the parameters used for the TOPSIS analysis are reported. Information entropy (E_n) and the degree of diversification (d_n) were calculated to determine the objective weights of the evaluated criteria. The entropy method for giving the objective weights assigns higher weights to criteria with greater variability among samples, as these provide stronger discriminatory power. To complement the objective weights, subjective weights based on direct ranking method were incorporated using a balancing factor of 0.6, which was our expert judgment regarding the relative importance of functional properties having the potential of influencing juiciness in plant-based proteins.

Water-holding capacity was assigned the highest subjective weight, as it is considered the primary factor affecting juiciness in protein matrices.

Oil-holding capacity is a second critical parameter influencing juiciness due to its role in lipid retention and lubrication within the protein matrix. Lipids contribute not only to flavor but also to mouthfeel by acting as lubricants during mastication, thereby enhancing the perception of juiciness. Higher fat retention has been associated with reduced product hardness and improved tenderness, both of which are closely

linked to increased juiciness perception in meat analogues. Conversely, products with higher instrumental hardness are often perceived as less juicy, particularly in burger-type systems (Godschalk-Broers et al., 2022).

In addition, the microstructural distribution of lipids plays a key role. A fine and homogeneous dispersion of small fat globules within the protein network promotes uniform lubrication and facilitates controlled release during chewing, enhancing both juiciness and overall sensory acceptability. Therefore, OHC, together with lipid distribution within the matrix (which is defined by proteins emulsifying properties), is essential for achieving a softer, more meat-like texture and improved juiciness in plant-based products. (Godschalk-Broers et al., 2022).

In terms of secondary structure, a higher β -sheet content and lower α -helix content after extrusion or heat-induced gelation are generally associated with stronger gel networks and improved textural properties, as intermolecular β -sheet formation promotes protein aggregation and water entrapment (Zhuang et al., 2018).

However, in the protein native state, high β -sheet content indicates a compact, rigid structure that may hinder protein unfolding during processing. Therefore, lower native β -sheet content and more random coil which allows greater structural flexibility, can be advantageous for facilitating denaturation and subsequent gel network formation which can promote better water release during mastication.

Native protein surface hydrophobicity is closely related to solubility and plays a key role in determining protein behavior prior to extrusion. Lower surface hydrophobicity generally enhances protein solubility, improving dispersion and hydration, which in turn promotes more uniform unfolding and controlled aggregation during processing. As higher solubility supports more effective protein texturization, it can lead to the formation of a continuous network structure (Flory et al., 2023).

At the same time, an optimal balance in surface hydrophobicity is necessary to enable sufficient protein–protein hydrophobic non-covalent interactions for stable network formation. This structured network is more capable of entrapping and releasing water during mastication, thereby improving water retention and enhancing the perceived juiciness of the final product (Kim et al., 2024; Urbonaite et al., 2014).

The remaining properties were weighted according to their functional relevance as discussed above. Based on the final TOPSIS ranking (Table 4), potato protein achieved the highest closeness coefficient ($C^* = 0.676$), followed by cowpea, faba bean, wheat, and pea proteins, with only minor differences between wheat and pea. These findings suggest that the evaluated properties are most favorable in potato protein, followed by legumes, for enhancing juiciness in the final product. However, yeast and rice, which ranked lowest, may require structural or functional modifications to improve gel formation and enhance water entrapment without exudation.

Although potato protein did not exhibit high intrinsic WHC, it ranked first, which can be explained by its superior gelation properties, OHC and surface characteristics. Potato protein exhibits the highest OHC,

Table 3

Parameters used for the TOPSIS analysis. Criteria and their corresponding entropy-based objective weights, assigned subjective weights based on direct ranking, and combined hybrid weights used in the TOPSIS analysis. Hybrid weights were calculated using a balancing factor (α) of 0.6 for subjective weights.

Criteria	Information entropy	Information utility	Objective weight coefficient	Subjective weight coefficient	Hybrid weight coefficient
Water holding capacity	0.962	0.038	0.045	0.23	0.156
Oil holding capacity	0.914	0.086	0.102	0.18	0.149
Least gelation concentration	0.968	0.032	0.038	0.08	0.063
Emulsifying Activity Index	0.910	0.090	0.106	0.09	0.096
Emulsion Stability Index	0.930	0.070	0.083	0.09	0.087
Protein solubility	0.854	0.146	0.172	0.09	0.123
Protein surface hydrophobicity	0.967	0.033	0.039	0.05	0.046
β -sheet	0.957	0.043	0.051	0.07	0.062
Random coil	0.968	0.032	0.038	0.05	0.045
Gel strength 20%	0.725	0.275	0.325	0.07	0.172

Table 4

Distances from the positive ideal protein (D⁺) and from the negative ideal protein (D⁻), Closeness coefficient (C*) and corresponding ranking of protein samples based on the TOPSIS analysis. Higher C* values represent closer proximity to the ideal solution.

Protein	D ⁺	D ⁻	C*	Rank
Carob bean (50%)	0.175	0.092	0.346	8
Yeast (80%)	0.192	0.079	0.292	13
Potato (80%)	0.087	0.181	0.676	1
Wheat (85%)	0.151	0.098	0.394	5
Faba bean (60%)	0.156	0.107	0.408	3
Pea (55%)	0.149	0.100	0.402	4
Cowpea (51%)	0.145	0.124	0.463	2
Lupin (60%)	0.174	0.084	0.325	11
Almond (50%)	0.157	0.096	0.379	6
Sunflower (53%)	0.170	0.084	0.331	9
Hemp (50%)	0.180	0.086	0.323	10
Pumpkin (65%)	0.163	0.087	0.349	7
Rice (80%)	0.181	0.084	0.316	12

which enhances juiciness by improving lipid retention and lubrication within the protein matrix. This increases perceived fattiness and tenderness, reduces hardness, and ultimately leads to a juicier product. Moreover, as previously reported, the WHC of plant protein gels is largely governed by gel network microstructure and intermolecular interactions, rather than solely by intrinsic water-binding capacity (Ge et al., 2023). In this context, the higher surface hydrophobicity of potato protein likely promotes stronger protein–protein interactions and hydrophobic bonds, facilitating the formation of a well-connected and self-supporting gel network. Same as previous study which showed a positive correlation between WHC of protein gels and hydrophobic interactions of legume proteins (Ge et al., 2023).

However, as this study focused on commercially available flours with varying protein contents rather than purified protein isolates, it is important to recognize that some measured properties may not be solely attributed to protein characteristics. In particular, parameters such as gel strength (20%), surface hydrophobicity, and oil-holding capacity (OHC, as reflected in the HCA) can be significantly influenced by non-protein components present in the flours. For instance, starch presented in the carbohydrate section of flours can contribute to gel formation and increase apparent gel strength through gelatinization and water immobilization. Dietary fiber may enhance water- and oil-holding capacities by providing additional binding sites and a porous structure. Additionally, ash and associated minerals can affect protein solubility and intermolecular interactions by altering ionic strength. Consequently, the TOPSIS ranking obtained in this study reflects the overall functional performance of the flours as complex matrices, rather than the intrinsic properties of the proteins alone.

4. Conclusion

Understanding techno-functional properties of alternative proteins such as WHC, OHC, gelation, and emulsifying behavior is essential for the rational selection of plant proteins for specific applications in meat analogue systems. In this study, thirteen commercial and emerging protein sources, including yeast and carob bean, were systematically evaluated and compared. Regarding WHC, considered a key contributor to juiciness, yeast, rice, hemp, and carob bean exhibited the highest values. Multivariate analysis revealed clear differences in functional profiles among the proteins. PCA and HCA showed that cowpea, pea, and faba bean shared similar techno-functional characteristics, partially overlapping with potato protein, whereas carob, lupin, sunflower, hemp, and wheat formed a separate cluster. Yeast and rice displayed distinctly different behavior from others. Multi-criteria ranking using TOPSIS identified potato protein as the best overall performer (C* = 0.676), followed by cowpea, faba bean, pea, and wheat, with only minor differences among them, in agreement with the clustering results.

Although these findings provide a useful comparative framework, validation in finished products is still required to confirm how the measured properties translate into sensory and instrumental juiciness. This is particularly important because extrusion, one of the main texturization techniques used in meat analogue production, can substantially alter protein functionality through heat- and shear-induced unfolding, aggregation, and structural reorganization. As a result, the current ranking primarily reflects the behavior of native ingredients prior to extrusion, and caution is needed when extrapolating these results to final extruded systems. Future work will therefore focus on extruded and final product matrices, where processing-induced structural changes are expected to further influence moisture retention and texture. Beyond identifying proteins with higher juiciness potential, this study proposes a transferable multi-criteria methodology that links structural and techno-functional properties to targeted product performance. By adjusting the weighting of the evaluation criteria, the same approach can be extended to other food applications. For example, in plant-based beverages, protein solubility and emulsion stability may become more relevant than gel strength or WHC. Therefore, the framework presented can support the rational and application-oriented selection of alternative proteins across a wide range of food systems.

AI declaration

During the preparation of this work the authors used ChatGPT in order to improve the readability and linguistic quality. After using this tool/service, the authors reviewed and edited the content as needed and take the full responsibility for the content of the published article.

CRedit authorship contribution statement

Faezeh Khoobbakht: Writing – original draft, Investigation, Formal analysis. **Waleed AL-Ansi:** Validation, Data curation. **Giovanna Ferrentino:** Writing – review & editing. **Eugenio Aprea:** Supervision, Project administration, Conceptualization.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.foodchem.2026.149732>.

Data availability

Data will be made available on request.

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