Effect of mechanical denaturation on surface free energy of protein powders

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ABSTRACT

Globular proteins are important both as therapeutic agents and excipients. However, their fragile native conformations can be denatured during pharmaceutical processing, which leads to modification of the surface energy of their powders and hence their performance. Lyophilized powders of hen egg-white lysozyme and β-galactosidase from *Aspergillus oryzae* were used as models to study the effects of mechanical denaturation on the surface energies of basic and acidic protein powders, respectively. Their mechanical denaturation upon milling was confirmed by the absence of their thermal unfolding transition phases and by the changes in their secondary and tertiary structures. Inverse gas chromatography detected differences between both unprocessed protein powders and the changes induced by their mechanical denaturation. The surfaces of the acidic and basic protein powders were relatively basic, however the surface acidity of β-galactosidase was higher than that of lysozyme. Also the surface of β-galactosidase powder had a higher dispersive energy compared to lysozyme. The mechanical denaturation decreased the dispersive energy and the basicity of the surfaces of both protein powders. The amino acid composition and molecular conformation of the proteins explained the surface energy data measured by inverse gas chromatography. The biological activity of mechanically denatured protein powders can either be reversible (lysozyme) or irreversible (β-galactosidase) upon hydration. Our surface data can be exploited to understand and predict the performance of protein powders within pharmaceutical dosage forms.

Keywords:

Protein denaturation; β-Galactosidase; Lysozyme; Conformational change; Inverse gas chromatography; Surface free energy.

1. Introduction

In the pharmaceutical field, there is considerable interest in the use of globular proteins for their therapeutic effects. During pharmaceutical processes, protein powders are often subjected to mechanical stresses. For example, milling has been used to prepare protein particles suitable for pulmonary delivery and protein-loaded microparticles in industrial quantities [1,2]. The mechanical stresses applied during the milling can partially or completely denature the proteins and change their bulk properties [3]. In recent years, denatured globular proteins have found extensive applications as excipients in pharmaceutical formulations [4,5]. Denatured globular proteins have been used to prepare emulsion systems designed to enhance the absorption of insoluble drugs and to form nanoparticles for drug delivery and targeting [4]. Globular proteins have also been successfully used to formulate controlled drug delivery tablets, which delay drug release in gastric conditions by forming a gel-layer stabilized by intermolecular–beta sheets of denatured globular proteins [5].

Surface energies of powders are critical properties to be considered during formulation and development of dosage forms in the pharmaceutical industry. Surface energy has significant effects on pharmaceutical processes such as granulation, tableting, disintegration, dissolution, dispersibility, immiscibility, wettability, adhesion, flowability, packing etc. Resultant data from recent determination of surface energies have been used to reduce the time of formulation development and enhance the quality of the final product [6-8].

The effect of the protein denaturation on their surface chemistry has been determined using time-of-flight secondary ion mass spectrometry [9]. However, the effect of mechanical denaturation on the surface energies of globular proteins has not been reported and these effects

must be understood to exploit the full potential of globular proteins in pharmaceutical industry both as therapeutic agents and excipients. Inverse gas chromatography (IGC) is a useful verified tool for surface energy measurements [10]. IGC has been used to measure the surface free energy of lyophilized protein particles, detecting lot-to-lot variations in the amorphous microstructure of lyophilized protein formulations [11].

This paper aims to evaluate the effects of mechanical denaturation on the surface energies of globular protein powders using IGC. β-Galactosidase is a hydrolytic enzyme that has been widely investigated for potential applications in the food industry to improve sweetness, solubility, flavor, and digestibility of dairy products. Preparations of β galactosidases have also been exploited for industrial, biotechnological, medical, and analytical applications [12]. Lysozyme is a naturally occurring enzyme found in bodily secretions such as tears, saliva, and milk and has been explored as a food preservative and pharmaceutical. The isoelectric points (pI) of β-galactosidase from *Aspergillus oryzae* and hen egg-white lysozyme are 4.6 and 11.3, and were used as models of acidic and basic globular proteins, respectively [13]. Lyophilized powders of these proteins were mechanically denatured by milling. Their surface energies before and after denaturation were compared in order to understand how the surfaces of the globular protein powders respond to the mechanical denaturation.

2. Materials and methods

2.1. Materials

Micrococcus lysodeikticus (Sigma-Aldrich), 2-nitrophenyl β-D-galacto pyranoside (Sigma-Aldrich), lyophilized powders of β-galactosidase from *A. oryzae* (Sigma-Aldrich) and hen egg-white lysozyme (Biozyme Laboratories, UK) were purchased as indicated. The purchased β-

galactosidase and lysozyme powders were considered to be unprocessed samples and named UNG and UNL, respectively.

2.2. Preparation of mechanically denatured protein powders

Mechanically denatured powders of β-galactosidase and lysozyme were prepared by manually milling. The milling was achieved by rotating a marble pestle over the powder within a marble mortar at ~45 cycles per minute (cpm). Milling times of 60 min were enough to completely denature the protein powders, and this was confirmed by differential scanning calorimetry (DSC) [3]. The mechanically denatured powders of β-galactosidase and lysozyme were named DeG and DeL, respectively. Three batches (2 g each batch) of the mechanically denatured powders were prepared for each protein.

2.3. Microscopy

A Zeiss Axioplan2 polarizing microscope (Carl Zeiss Vision GmbH; Hallbergmoos, Germany) was used to visualize the samples. The accompanying software (Axio Vision 4.2) was then used to determine the projected area diameters of the powders.

2.4. Differential scanning calorimetry (DSC)

Differential scanning calorimetry (DSC) thermograms were obtained using a Perkin-Elmer Series 7 DSC (Perkin-Elmer Ltd., Beaconsfield, UK). Samples (4-7 mg) were sealed in aluminium pans. The escape of water was facilitated by making a pinhole in the lid prior to sealing. The samples were equilibrated at 25 °C and heated to 250 °C at a scan heating rate of 10 °C/min under a flow of anhydrous nitrogen (20 ml/min). Each sample was analysed in triplicate. The temperature

138 axis and cell constant of the DSC cell were calibrated with indium (10 mg, 99.999 % pure, melting
139 point 156.60 °C, and heat of fusion 28.40 J/g).
140
141 *2.5. FT-Raman spectroscopy*
142 FT-Raman spectra of samples were recorded with a Bruker IFS66 optics system using a
143 Bruker FRA 106 Raman module. The excitation source was an Nd: YAG laser operating at 1064
144 nm and a laser power of 50 mW was used. The FT-Raman module was equipped with a liquid
145 nitrogen cooled germanium diode detector with an extended spectrum band width covering the
146 wave number range 1800-450 cm^{-1}. Samples were placed in stainless steel sample cups and
147 scanned 200 times with the resolution set at 8 cm^{-1}. The observed band wave numbers were
148 calibrated against the internal laser frequency and are correct to better than ±1 cm^{-1}. The spectra
149 were corrected for instrument response. The experiments were run at a controlled room
150 temperature of 20±1°C.
151
152 *2.6. Enzymatic assay*
153 The enzymatic activity of lysozyme samples was measured to determine the ability of
154 lysozyme to catalyze the hydrolysis of β-1,4-glycosidic linkages of cell-wall mucopolysaccharides
155 [14]. Lysozyme solution (30 µl, 0.05 % in phosphate buffer, pH = 5.2; 10 mM) was added to
156 *Micrococcus lysodeikticus* suspension (2.97 ml, 0.025 % in phosphate buffer, pH = 6.24; 66 mM).
157 The decrease in the absorbance at 450 nm was monitored by using a UV-Vis spectrophotometer
158 (PU 8700, Philips, UK). The activity was determined by measuring the decrease in the substrate
159 bacterial suspension concentration with time. Hence the slope of the reduction in light absorbance
160 at 450 nm against the time of 3 min, starting when the protein solutions were mixed with the

substrate bacterial suspension, was considered to be the indicator of the lytic activity of lysozyme [15].

The enzymatic activity of β-galactosidase samples was determined using a method relying on the ability of β-galactosidase to hydrolyse the chromogenic substrate *o*-nitrophenyl β-D-galacto pyranoside (ONPG) to *o*-nitrophenol [16]. The results were achieved by adding 20 μl of protein solution (0.05 w/v% in deionised water) to 4 ml of the substrate solution (0.665 mg/ml) in a phosphate buffer (100 mM and pH = 7). The mixture then was incubated for 10 min in a water bath at 30±1 °C. The absorbance at λ = 420 nm was measured to indicate the activity.

The concentrations of the protein solutions had been determined prior to the activity tests using the following equation:

$$[Protein] = Abs_{280\,nm}/E_{280\,nm} \quad (1)$$

where $[Protein]$ is the concentration of protein in the tested solution w/v%, $Abs_{280\,nm}$ is the absorbance of the tested protein solution at 280 nm, and $E_{280\,nm}$ is the absorbance of protein standard solution with concentration 0.05 w/v%. The concentrations of the solutions were diluted to be about 0.05 % w/v so as to give an absorbance value of less than 0.8. The activities of all samples were measured relative to that of a corresponding fresh sample, which was considered as the standard solution.

2.7. Inverse gas chromatography

IGC experiments were performed using an inverse gas chromatography (IGC 2000, Surface Measurement Systems Ltd., UK). A sample (~500 mg) was packed into a pre-silanised

glass column (300 mm × 3 mm i.d.). Three columns of each sample were analysed at 30 °C (the lowest temperature at which the IGC experiments can be performed to avoid thermal stress) and zero relative humidity, using anhydrous helium gas as the carrier. A series of n-alkanes (n-hexane to n-nonane) in addition to chloroform, as a monopolar electron acceptor probe (l_+), and ethyl acetate, as a monopolar donor acceptor probe (l_-), were injected through the columns at the infinite dilution region. Their retention times followed from detection using a flame ionization detector (FID).

2.7.1. Surface energy calculations

Our published methods were used to calculate the surface energies and verify their accuracy [17-19]. These methods describe the surface properties using the dispersive retention factor ($K^a_{CH_2}$), the electron acceptor retention factor (K^a_{l+}), and the electron donor retention factor (K^a_{l-}), which are calculated using the retention times of probes:

$$\ln (t_r - t_0) = (\ln K^a_{CH_2})\, n + C \qquad (2)$$

where n is the carbon number of the homologous n-alkanes, t_r and t_0 are the retention times of the n-alkanes and a non-adsorbing marker, respectively, $K^a_{CH_2}$ is the dispersive retention factor of the analysed powder and C is a constant. The linear regression statistics of equation 2 generate the value of t_0 which gives its best linear fit. The slope of the equation 2 gives the value of $K^a_{CH_2}$.

$$K^a_{l+} = t_{nl+}/t_{nl+,ref} \qquad (3)$$

$$K^a_{l-} = t_{nl-}/t_{nl-,ref} \qquad (4)$$

where t_{nl+} and $t_{nl+,ref}$ are the retention time of l_+ and its theoretical n-alkane reference, respectively, t_{nl-} and $t_{nl-,ref}$ are the retention time of l_- and its theoretical n-alkane reference, respectively.

$$\ln t_{nl+,ref} = \ln t_{nCi} + \left(\frac{\alpha_{l+}\left(\gamma_{l+}^{d}\right)^{0.5} - \alpha_{Ci}\left(\gamma_{Ci}^{d}\right)^{0.5}}{\alpha_{CH_2}\left(\gamma_{CH_2}\right)^{0.5}} \right) \ln K_{CH_2}^{a} \quad (5)$$

$$\ln t_{nl-,ref} = \ln t_{nCi} + \left(\frac{\alpha_{l-}\left(\gamma_{l-}^{d}\right)^{0.5} - \alpha_{Ci}\left(\gamma_{Ci}^{d}\right)^{0.5}}{\alpha_{CH_2}\left(\gamma_{CH_2}\right)^{0.5}} \right) \ln K_{CH_2}^{a} \quad (6)$$

where α_{CH_2} and γ_{CH_2}, α_{Ci} and γ_{Ci}^{d}, α_{l+} and γ_{l+}^{d}, and α_{l-} and γ_{l-}^{d} are the cross–sectional area and the dispersive free energy of a methylene group, an n-alkane, l_+ and l_-, respectively. t_{nCi} is the retention time of the n-alkane.

The retention factors are then used to calculate the surface dispersive (γ_s^d), electron donor (γ_s^-) and electron acceptor (γ_s^+) components of the powders:

$$\gamma_s^d = \frac{0.477\,(T \ln K_{CH_2}^{a})^2}{(\alpha_{CH_2})^2\,\gamma_{CH_2}} \text{ mJ.m}^{-2} \quad (7)$$

$$\gamma_s^- = \frac{0.477\,(T \ln K_{l+}^{a})^2}{(\alpha_{l+})^2\,\gamma_{l+}^{+}} \text{ mJ.m}^{-2} \quad (8)$$

$$\gamma_s^+ = \frac{0.477\,(T \ln K_{l-}^{a})^2}{(\alpha_{l-})^2\,\gamma_{l-}^{-}} \text{ mJ.m}^{-2} \quad (9)$$

where γ_{l+}^{+} is the electron acceptor component of l_+ and γ_{l-}^{-} is the electron donor component of l_-. The units of α are Å^2 and of γ are mJ.m^{-2} in all equations.

The parameters of CH_2 are calculated from the following equation:

$$(\alpha_{CH_2})^2\,\gamma_{CH_2} = -1.869T + 1867.194 \text{ Å}^4\text{.mJ.m}^{-2} \quad (10)$$

The parameters of polar probes are still under debate and different values have been reported [20-25]. In this paper, we used the values which were recently used for ethyl acetate (γ_{l-}^{-} =

19.20 mJ/m^2, γ_{l-}^{d} = 19.60 mJ/m^2, α_{l-} = 48.0 Å^2) and for chloroform (γ_{l+}^{+} = 3.80 mJ/m^2, γ_{l+}^{d} = 25.90 mJ/m^2, α_{l+} = 44.0 Å^2) [17,22]. However, using any other different reported numbers will not change the findings of the comparison.

The percentage coefficient of variation of $\ln K_{CH_2}^{a}$ ($\%CV_{\ln K_{CH_2}^{a}}$) is the indicator of the accuracy of the surface energy measurements. The error of the slope of the equation 2 ($SD_{\ln K_{CH_2}^{a}}$) is used to calculate $\%CV_{\ln K_{CH_2}^{a}}$:

$$\%CV_{\ln K_{CH_2}^{a}} = \left(SD_{\ln K_{CH_2}^{a}} / \ln K_{CH_2}^{a}\right) \times 100 \qquad (11)$$

$\%CV_{\ln K_{CH_2}^{a}}$ should be less than 0.7% to accept the accuracy of the measurement. $\%CV_{\ln K_{CH_2}^{a}}$ is then used to calculate the uncertainty range of γ_s^d:

$$\text{Uncertainty Range of } \gamma_s^d = \left[\left(\frac{100\times\gamma_s^d}{100+7.5\%CV_{\ln K_{CH_2}^{a}}}\right) to \left(\frac{100\times\gamma_s^d}{100-7.5\%CV_{\ln K_{CH_2}^{a}}}\right)\right] \qquad (12)$$

3. Results and discussion

3.1. Microscopy

The photomicrographs of UNL, UNG, DeL, and DeG powders show that they had project-area diameters of ~4 µm (Fig. S1), ~2.5 µm (Fig. S2), ~1.5 µm (Fig. S3), and ~1.5 µm (Fig. S4), respectively. The particle sizes of the original powders were below 5 µm. Therefore, the attrition mechanism was dominant during milling, and so the same original faces did not change [3].

3.2. Differential scanning calorimetry (DSC)

For both proteins, DSC thermograms exhibited broad peaks ranging from ~30 to ~140 °C (Figure 1). These peaks are due to water removal, and their areas depend on water residues in the

242 powders [3]. The enthalpy of the water evaporation peak was 118±11, 124±6, 114±9 and 130±8
243 J/g for UNL, UNG, DeL, and DeG, respectively, and did not significantly change after milling (t-
244 test: $P < 0.05$). The protein powders exchange water with the surrounding air depending on
245 conditions of temperature, relative humidity and exposure time. Therefore, the conditions used
246 during milling did not change the water content of the powders. Also Figure 1 shows that the
247 unprocessed proteins unfolded and a peak was detected at their apparent denaturation
248 temperatures, which varied according to the protein. DSC thermograms of UNL displayed one
249 denaturation peak at ~201 °C, but UNG displayed two denaturation peaks at ~176 °C and ~212
250 °C.
251

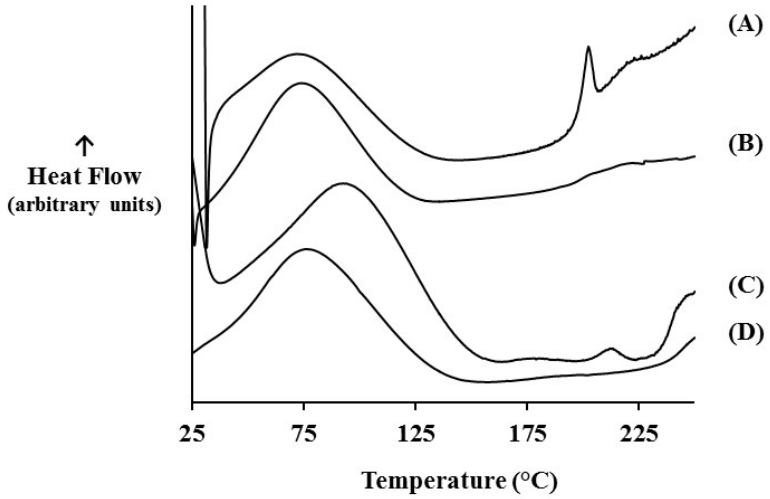


Fig. 1. Example DSC thermograms of protein powders (A) unprocessed lysozyme, (B) mechanically denatured lysozyme, (C) unprocessed β-galactosidase, (D) mechanically denatured β-galactosidase. Conditions: samples heated from 25 to 250 °C; heating rate: 10 °C/min.

252

253 The difference in the thermal denaturation pattern can be due to the difference in the
254 thermal unfolding mechanisms of the proteins. While lysozyme folds in a highly cooperative

manner and so exhibits an all-or-none thermal unfolding transition, β-galactosidase goes through a non-two state thermal unfolding transition resulting in two peaks [26,27]. The unfolding transition peaks were completely lost after mechanical denaturation. Hence there was no peak at ~201 ºC for the milled lysozyme samples and neither were there peaks at ~176 °C and ~212 °C for the milled β-galactosidase. The complete disappearance of the unfolding transition peak from the DSC thermogram indicates the total transition of the protein from its folded state to its unfolded state [3].

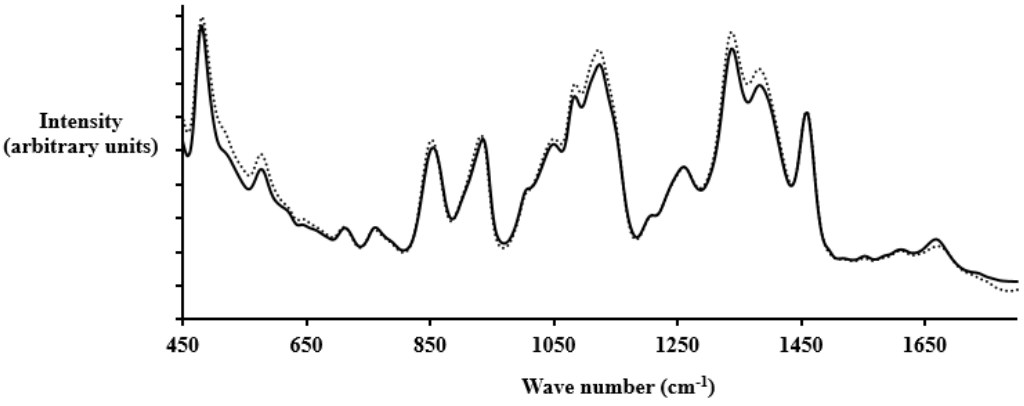
3.3. FT-Raman study

Raman spectroscopy was used to compare the molecular conformation of protein powders before and after mechanical denaturation. The band at ~1450 cm^{-1} indicates the CH bending vibrations of aliphatic side chains, and its intensity and position are unaffected by changes induced in protein structure after dehydration or applying different stresses [28]. Therefore, it was used as an internal intensity standard to normalize Raman spectra before comparison (Figures 2A and 3A). The vibration modes of amide I (C=O stretch) from 1580 to 1720 cm^{-1} (Figures 2B and 3B) and amide III (N-H in-plane bend + C-N stretch) from 1250–1330 cm^{-1} (Figures 2C and 3C) demonstrated the secondary structure of β-galactosidase and lysozyme, respectively. The spectra of the denatured samples show that the modes of the amide I upshifted and broadened for both proteins, and the mode of the amide III intensified and downshifted, especially for lysozyme, but there was no change in the mode of amide III for β-galactosidase. These changes indicated the transformation of α-helix content to β-sheets or a disordered structure which enhances the tendency of proteins to aggregate [3,29]. While β-galactosidase is a beta-type protein containing mainly β-

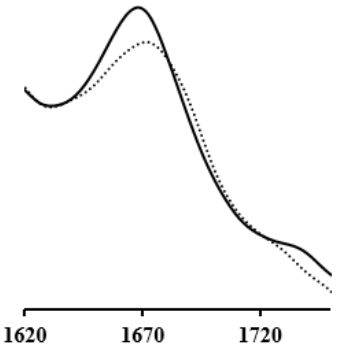
sheet structure and only 5% α-helix [30], the secondary structure of lysozyme consists of 30% α-helix [31]. This explains why no changes in the amide III of β-galactosidase were observed.

The aggregation of denatured proteins combined with changes in the vibration modes of the aromatic residues at ~1550 cm^{-1} in β-galactosidase (Figure 2D), 1320-1380 cm^{-1} in lysozyme (Figure 3D) and 800-900 cm^{-1} in both proteins (Figures 2E and 3E). These changes in the vibration modes of the aromatic residues result from the changes in their micro-environment after denaturation because of their roles in the denaturation processes [29,32]. The aggregates of denatured protein molecules are formed via π-stacking interactions of the aromatic residues [33].

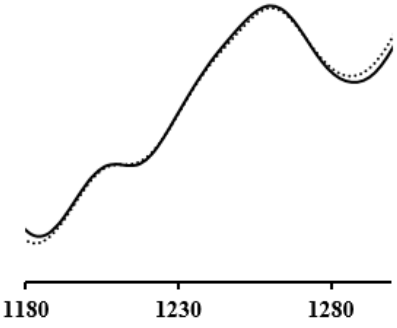
(A)



(B)



(C)



(D)

(E)

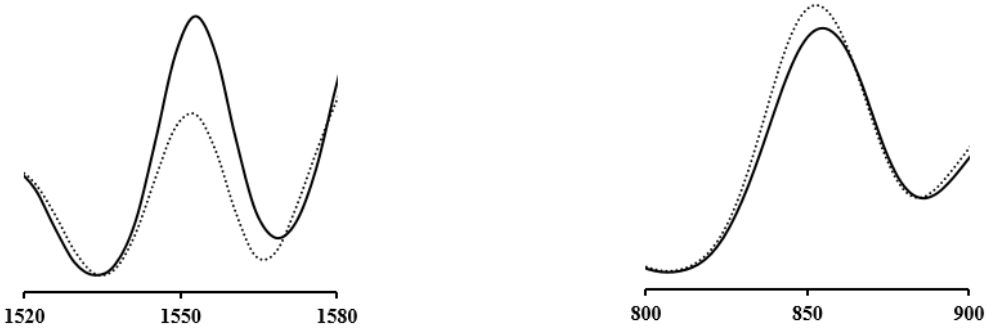
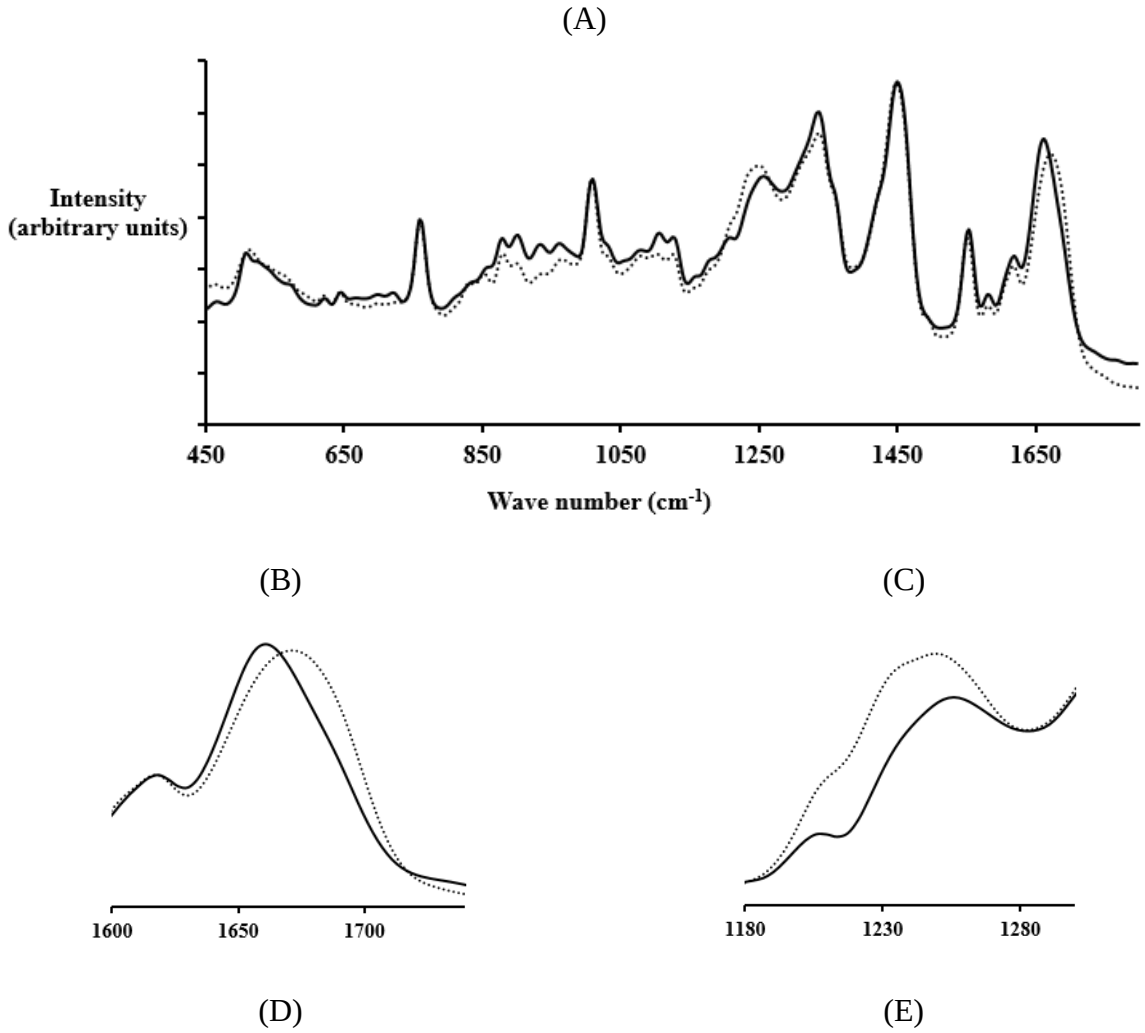


Fig. 2. FT-Raman spectra of β-galactosidase powders, the unprocessed powders (solid lines) and the mechanically denatured powders (dotted lines). Vibration modes of secondary structure are (B) amide I and (C) amide III. Vibration modes of tertiary structure are (D) for Trp and (E) for Trp and Tyr. The spectra were normalized using the methylene deformation mode at ~1450 cm^{-1} as an internal intensity standard.



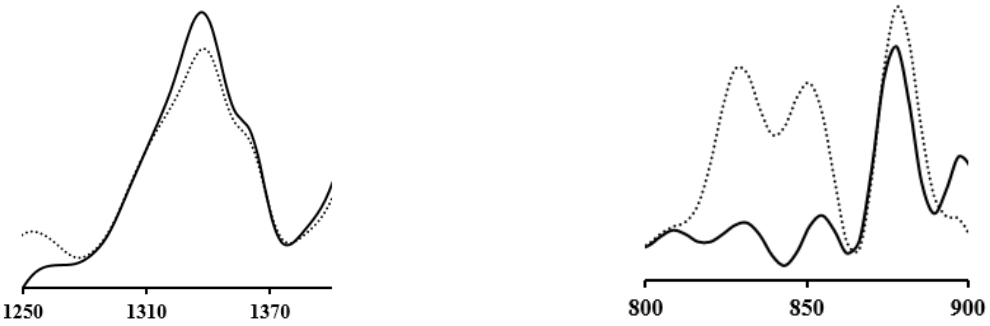


Fig. 3. FT-Raman spectra of lysozyme powders, the unprocessed powders (solid lines) and the mechanically denatured powders (dotted lines). Vibration modes of secondary structure are (B) amide I and (C) amide III. Vibration modes of tertiary structure are (D) for Trp and (E) for Trp and Tyr. The spectra were normalized using the methylene deformation mode at ~1450 cm^{-1} as an internal intensity standard.

3.4. Enzymatic assay

Therapeutic proteins may rapidly denature and lose their enzymatic activity. The structure changes detected using FT-Raman and the absence of Tm detected by DSC have been used to monitor the denaturation of proteins, and the results of Raman and DSC are linked to the results of enzymatic activity [34]. Our DSC and Raman results confirmed the denaturation of both proteins studied. The enzymatic assay showed that the mechanically denatured β-galactosidase samples (DeG) demonstrated no enzymatic activity (Figure 4). However, the mechanically denatured lysozyme samples (DeL) maintained full enzymatic activity when compared to an unprocessed sample (t-test: $P < 0.05$) (Figure 4). This is due to the ability of denatured lysozyme to refold upon dissolution in aqueous media and thus the biological activity of lysozyme is fully recovered following dissolution [3.35].

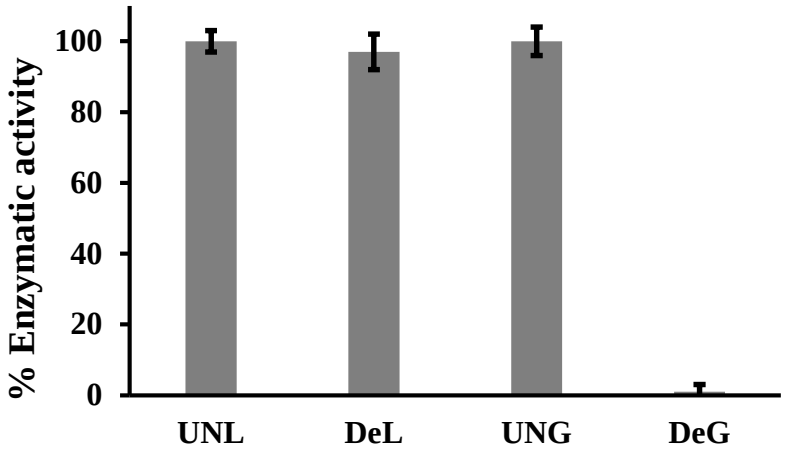


Fig. 4. Enzymatic activity of the unprocessed powders and the mechanically denatured powders of lysozyme and β-galactosidase.

3.5. Surface free energy

The IGC results (Table 1) confirm the acceptable accuracy of the IGC experiments considered in this work with $\%CV_{\ln K^a_{CH_2}}$ values of less than 0.7% [18]. IGC data for the unprocessed powders demonstrated the differences in the surface free energy between β-galactosidase (an acidic protein) and lysozyme (a basic protein). UNG had higher γ_s^d compared to UNL because the uncertainty ranges of γ_s^d of UNG and UNL did not overlap for the three columns [18]. The surface acidity (γ_s^+) and the surface basicity (γ_s^-) of UNG were significantly different from their counterparts of UNL (t-test: $P < 0.05$). The average of γ_s^+ was 16.2±0.2 and 12.4±0.1 mJ.m^{-2} and the average of γ_s^- was 5.5±0.2 and 10.5±0.6 mJ.m^{-2} for UNG and UNL, respectively. This proves that UNG, chosen as a model for acidic proteins, has higher surface acidity and lower surface basicity compared to selected basic protein, UNL.

Table 1. The surface energies (γ_s^d, γ_s^+ and γ_s^-) and retention factors ($K^a_{CH_2}$, K^a_{l+} and K^a_{l-}) of the lyophilized lysozyme powder (UNL), the lyophilized β-galactosidase powder (UNG), the

mechanically denatured lyophilized lysozyme powder (DeL) and the mechanically denatured lyophilized β-galactosidase powder (DeG).

Material	Column	$K^a_{CH_2}$	K^a_{l+}	K^a_{l-}	$\%CV_{\ln K^a_{CH_2}}$	γ_s^d mJ.m^{-2}	Uncertainty Range of γ_s^d mJ.m^{-2}	γ_s^+ mJ.m^{-2}	γ_s^- mJ.m^{-2}
UNL	1	3.099	3.725	34.572	0.144	43.1	41.9-44.4	12.4	10.3
UNL	2	3.095	3.677	34.668	0.094	43.0	42.2-43.9	12.5	10.1
UNL	3	3.089	3.944	33.704	0.077	42.9	42.2-43.6	12.3	11.2
DeL	1	2.937	2.781	33.948	0.127	39.1	38.1-40.2	12.3	6.2
DeL	2	2.965	2.742	31.928	0.147	39.8	38.7-41.0	11.9	6.1
DeL	3	2.944	2.801	31.826	0.117	39.3	38.4-40.3	11.9	6.3
UNG	1	3.235	2.542	55.641	0.141	46.5	45.1-47.8	16.0	5.2
UNG	2	3.222	2.640	58.508	0.076	46.1	45.4-46.9	16.4	5.6
UNG	3	3.228	2.625	56.028	0.158	46.3	44.8-47.9	16.1	5.6
DeG	1	2.926	1.980	43.387	0.205	38.9	37.3-40.6	14.1	2.8
DeG	2	2.958	1.829	41.065	0.160	39.7	38.4-41.0	13.7	2.2
DeG	3	2.948	1.841	39.710	0.221	39.4	37.7-41.3	13.4	2.2

The isoelectric point (pI) of a protein indicates its relative acidity or basicity, the higher the pI, the higher the basicity of the molecule [36]. The isoelectric points (pI) of the β-galactosidase and lysozyme used are 4.6 and 11.3, respectively [13]. The molecule of β-galactosidase contains ~11 w/w% basic amino acids (histidine, lysine, and arginine) and ~22 w/w% acidic (aspartic acid and glutamic acid) residues [37], i.e., approximately double the number of acidic groups compared to basic. Conversely the lysozyme contains ~18 w/w% and ~7 w/w% basic (histidine, lysine, and arginine) and acidic (aspartic acid and glutamic acid) residues, respectively [38]. Detailed information regarding the structures of β-galactosidase and lysozyme can be found in [37,38]. However, this is not the only determinant of energy as the surfaces of both the acidic (UNG) and basic (UNL) protein powders were relatively basic (the values of $\gamma_s^+ > \gamma_s^-$). Therefore to explain our results further, the interaction of protein molecules with surfaces and interfaces, during preparation using lyophilization technique, must be considered.

As protein molecules are surface active containing both polar and nonpolar groups, they tend to adsorb to interfaces via hydrophobic interactions (London), coulombs (electrostatic) and/or

hydrogen bonding, and they reorient their surfaces to the parts which give the optimum attractive force and the most stable state (minimum energy) with a substrate or an interface [39]. Upon lyophilization, protein molecules adsorb to the formed ice via hydrophobic residues but not via hydrophilic residues, and this gives support to the hypothesis that the interaction of proteins with ice involves appreciable hydrophobic interactions [40]. The hydrophobic regions in protein molecules interact spontaneously with the ice faces by an entropy driving force [41]. The rich electron rings of aromatic residues orient so that the ring structures lie flat with the interface in order to maximize the interaction at interfaces and lower the Gibbs free energy of the system [42]. Therefore, lyophilized protein particles expose the rich electron rings of the aromatic residues on their surfaces. Aromatic groups, via their π electrons, which are considered nucleophilic, can form hydrogen bonds with chemical groups (acidic polar probes) being the hydrogen donors [43]. Therefore, exposing these rings to surfaces relatively increases their basicity compared to their acidity irrespective of the acidic or basic nature of the proteins themselves. Also the ring structures can participate in raising the dispersive surface energy via London interactions due to their high polarizability [43]. The aromatic residues (tryptophan, tyrosine, and phenylalanine) make up 16%w/w of the β-galactosidase molecules and 14%w/w of the lysozyme molecules [37,38]. This explains the higher values of γ_s^d of β-galactosidase compared to lysozyme, prior to mechanical denaturation.

UNG was more acidic than UNL. The size and the shape of the molecule can also influence orientation. UNG is larger than UNL, with a globular shape and when some of the chemical groups are preferably exposed to a surface (energetically or entropically), this will expose not only those specific groups but also other closely associated groups which will vary in nature from one protein

366 to another.. Thus, the surfaces of the acidic protein (β-galactosidase) were more acidic compared
367 to the basic protein (lysozyme).
368 Table 1 shows that mechanical denaturation decreased the dispersive free energy and the basicity
369 of the surfaces of protein powders, irrespective of the nature of the protein (acidic or basic).
370 Usually milling induces an increase in the dispersive energy due to the generation of surface
371 amorphous regions or/and creation of higher energy crystal faces because of particle
372 fracture/breakage, thus the surface acidity and basicity change according to the formation of new
373 faces and regions [44,45]. However, in our case, due to lyophilization, the protein powders are
374 amorphous with particle sizes below 5 μm. Therefore, there would be no further size reduction by
375 fracture mechanisms because of brittle ductile transition [3]. Therefore, the denatured protein
376 powders were produced by milling where the attrition mechanism was dominant and so the same
377 original faces did not change. During milling, the extensive mechanical energy completely
378 denatured the protein molecules as confirmed by DSC and Raman results. This denaturation led to
379 aggregation of the protein molecules via non-covalent interactions through π-stacking interactions
380 [33]. This caused a loss of the aromatic groups, which are rich in π electrons, from the surfaces.
381 Therefore, a decrease in the Van der Waals interactions, a major contributor to dispersive energy
382 and nucleophilicity (basicity) occurred, and so γ_s^d and γ_s^- decreased after denaturation for both
383 proteins. Also this loss of aromatic residues from the surface of the denatured powders renders γ_s^d
384 similar for both proteins. This is further evidence that the exposed aromatic residues raise the γ_s^d
385 as outlined previously. The Raman spectroscopic results confirmed that the aromatic residues were
386 involved in the denaturation processes, therefore, supporting the findings and our interpretation of
387 the IGC studies.

388 **4. Conclusions**

The surface energies of the lyophilized protein powders differed according to their amino acid compositions. The absence of the thermal unfolding transition phase for the proteins (lysozyme and β-galactosidase) and the changes in the conformation of the back-bone and side chains confirmed that the mechanical milling process caused denaturation of the protein powders, and this denaturation could potentially be reversible in solution. The acidic protein powder (β-galactosidase) had higher surface acidity (γ_s^+) and lower surface basicity (γ_s^-) compared to the basic protein powder (lysozyme). However, both protein powders had relatively basic surfaces due to the rich electron rings of the aromatic residues which are nucleophilic. During mechanical denaturation, these rings tend to associate through π-stacking interactions and are thus concealed from the surface. Their removal reduced γ_s^- and γ_s^d of the surfaces of both protein powders, and thereby yielded similar γ_s^d for the surfaces of both proteins.

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Supplementary data

Supplementary data associated with this article can be found, in the online version, at http://dx.doi.org/XXXX.

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