



## Historical Perspective

## Small-angle X-ray and neutron scattering applied to lipid-based nanoparticles: Recent advancements across different length scales

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## ABSTRACT

Lipid-based nanoparticles (LNPs), ranging from nanovesicles to non-lamellar assemblies, have gained significant attention in recent years, as versatile carriers for delivering drugs, vaccines, and nutrients. Small-angle scattering methods, employing X-rays (SAXS) or neutrons (SANS), represent unique tools to unveil structure, dynamics, and interactions of such particles on different length scales, spanning from the nano to the molecular scale. This review explores the state-of-the-art on scattering methods applied to unveil the structure of lipid-based nanoparticles and their interactions with drugs and bioactive molecules, to inform their rational design and formulation for medical applications. We will focus on complementary information accessible with X-rays or neutrons, ranging from insights on the structure and colloidal processes at a nanoscale level (SAXS) to details on the lipid organization and molecular interactions of LNPs (SANS). In addition, we will review new opportunities offered by Time-resolved (TR)-SAXS and -SANS for the investigation of dynamic processes involving LNPs. These span from real-time monitoring of LNPs structural evolution in response to endogenous or external *stimuli* (TR-SANS), to the investigation of the kinetics of lipid diffusion and exchange upon interaction with biomolecules (TR-SANS). Finally, we will spotlight novel combinations of SAXS and SANS with complementary on-line techniques, recently enabled at Large Scale Facilities for X-rays and neutrons. This emerging technology enables synchronized multi-method investigation, offering exciting opportunities for the simultaneous characterization of the structure and chemical or mechanical properties of LNPs.

## 1. Introduction

Lipid-based NPs (LNPs) embrace a broad class of self-assembled nanomaterials with different levels of structural complexity (Fig. 1). These span from liposomes, where single or multiple lipid bilayer shells enclose an internal aqueous pool, to multicompartment nanostructured particles with exotic liquid-crystalline mesostructures, where the lipid bilayer assumes a non-lamellar arrangement [1–6]. Cubosomes represent a key example in the field [7–9], where a polymeric shell stabilizes an internal lipid cubic phase with 3-dimensional periodicity and co-existence of lipid and aqueous domains. The most common structures encountered in cubosomes include bicontinuous cubic phases with crystallographic space group symmetries Pn3m (Q [224]), Im3m (Q [229]), and Ia3d (Q [230]) or discrete micellar cubic phases with space groups Pm3n (Q [223]), Fm3m (Q [225]) and Fd3m (Q [227]) [10–13].

Other classes of non-lamellar LNPs include hexosomes [11,14], with internal direct (H<sub>I</sub>) or inverse (H<sub>II</sub>) hexagonal phase, or “spongeosomes” [15,16], featuring a bicontinuous fluid L<sub>3</sub> sponge phase core.

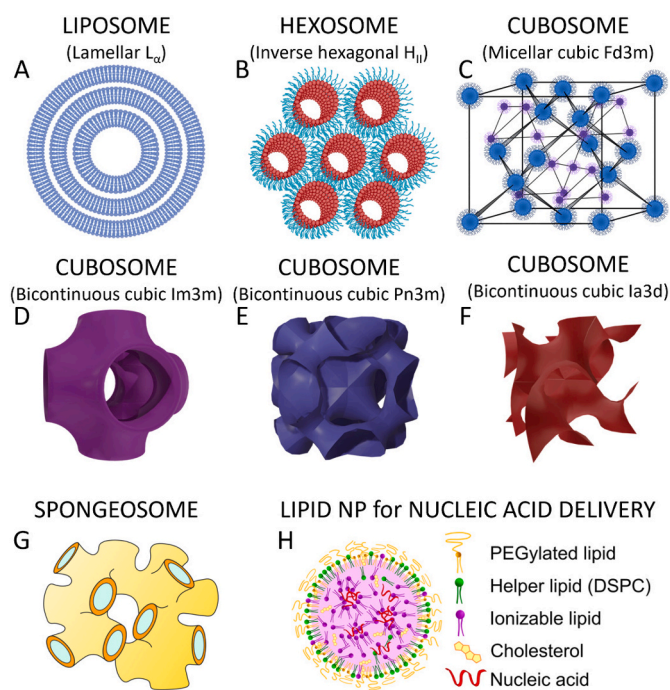
Additionally, nucleic acids-containing LNPs, recently employed to deliver antigen mRNA in COVID-19 vaccines, represent the state-of-the-art of non-viral gene delivery vectors [17,18]. These LNPs contain a mixture of nucleic acids, cationic ionizable lipids, helper lipids (such as phospholipids), cholesterol, and PEGylated lipids. Such systems typically exhibit a core-shell structure, featuring distinctive compositions of the core and of the inner and outer shell [17].

This structural versatility, coupled with the biocompatibility of the lipid matrix and ability to encapsulate hydrophilic and hydrophobic molecules, makes LNPs ideal candidates for application in different fields of Nanomedicine. In this respect, many excellent literature reviews summarize recent advancements in the design of lamellar and

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**Fig. 1.** Most common nanostructures found in LNPs: (A) Lamellar structure (liposomes); (B)  $H_{II}$  inverse hexagonal phase (hexosomes); (C) discontinuous micellar cubic phase Fd3m (cubosomes); (D) bicontinuous cubic Im3m phase (cubosomes); (E) bicontinuous cubic Pn3m phase (cubosomes); (F) bicontinuous cubic Ia3d phase (cubosomes); (G)  $L_3$  sponge phase (spongesomes); (H) Core-shell structure of LNPs for nucleic acid delivery.

non-lamellar LNPs for drug delivery [7,17,19–27], biomedical imaging [2,21] and biosensing [7,28,29]. In spite of this, the number of LNPs currently available on the market is surprisingly limited and primarily restricted to liposome-based formulations [19,30,31], or novel LNPs formulated with cationic ionizable lipids for gene transfection, recently employed in COVID-19 vaccines [17,18].

*Elucidating the link between structure and biomedical functions in LNPs* is key to bridge this translational gap and fully harness the medical potential of LNPs. The structure of LNPs has been found to control their stability under physiological conditions [32,33], encapsulation efficiency [34–36] and release kinetics of incorporated drugs [37,38]. For instance, the inherent nanostructure of cubosomes and hexosomes offers several benefits over liposomes, such as improved mechanical robustness and larger lipid bilayer-water interfacial area for enhanced drug loading capacity [11,21]. In addition, the tortuous nanostructure of non-lamellar LNPs ensures prolonged release of encapsulated molecules for sustained drug delivery applications [39,40]. In this respect, the structure of the lipid matrix controls the molecular diffusion and release kinetics of drugs [39,40]; for instance, inverse bicontinuous cubic phases promote a faster release than inverse hexagonal phases, due to the larger size of the water channels and enhanced surface area [38,41]. Similarly, micellar cubic phases of discontinuous nature exhibit slower release rates than bicontinuous cubic or hexagonal phases [37]. These differences may be harnessed to control the release of drugs through structural transitions in the lipid scaffold, potentially triggered by either external or endogenous *stimuli* [42]. Moreover, non-lamellar structures in LNPs proved to favor the conjugation with antibodies compared to liposomal analogues, making them more attractive for targeted delivery of chemotherapeutics [43]. Pioneering studies also reported that the lipid structure regulate cellular uptake [44,45], endosomal escape [46], biodistribution [47] and toxicity [48] of LNPs, shaping their biological fate and medical performance. Adding to the complexity, LNPs undergo dynamic structural alterations in biological environments, responding to natural pH gradients and/or interactions with biological molecules and

interfaces [40,49]. When in biological fluids, the surface of LNPs gets readily covered with a layer of biomolecules, called “protein corona” [50,51]. This layer redefines the surface identity of LNPs, affecting their chemical and biological functions, such as blood circulation time, cellular uptake and endosomal escape ability [52–55]. Recent reports highlighted a mutual interplay between nanoparticles structure and protein corona formation, i.e., the morphology of nanoparticles may affect the composition and structure of the protein corona [56,57], while the adsorption of biomolecules can similarly modify the internal structure of LNPs [58,59]. Understanding such structural changes is key to predict the behavior of LNPs in living organisms and to improve their medical efficacy. Additionally, the structural responsiveness to endogenous *stimuli* (e.g., pH variations throughout the body) can be harnessed to design “smart” LNPs, able to deliver and release actives at specific locations or (sub)cellular compartments in living organisms [60–63]. Investigating the structure of LNPs is also instrumental to elucidate LNPs-drugs mutual interactions, impacting molecular loading and release [64], as well as to thrive the development of hybrid LNPs for controlled drug delivery, where incorporated inorganic nanomaterials introduce responsiveness to external *stimuli* (e.g., light, or magnetic fields) [65–70].

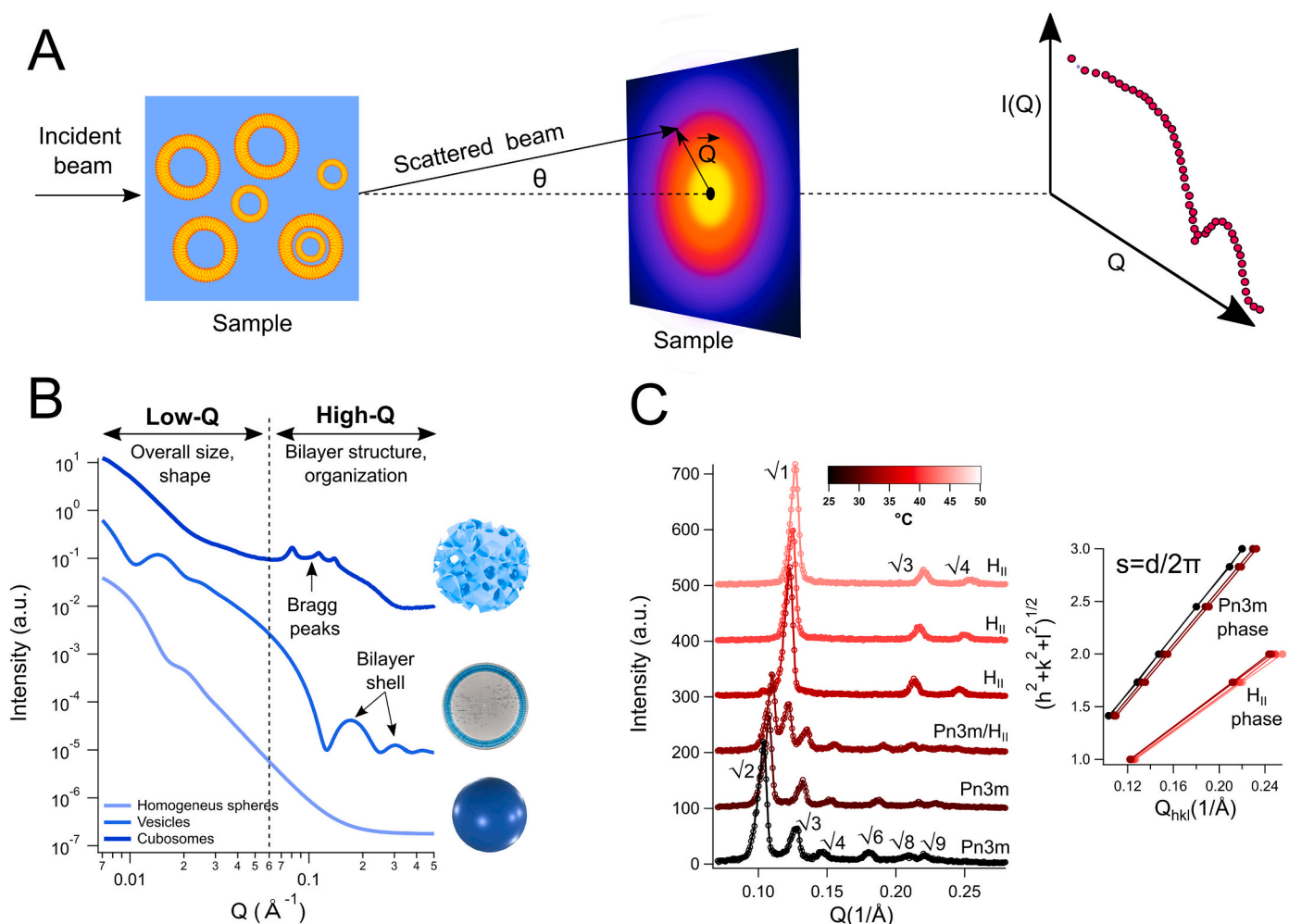
Small-angle X-ray scattering (SAXS) and small-angle neutron scattering (SANS) are excellent tools to investigate the structure of LNPs and their interactions at the nanoscale. These methods leverage X-ray or neutron probes and collect the scattering from the sample at small angles, which enables to resolve structures ranging from 1 nm to over 100 nm [71]. Compared to microscopic techniques with similar resolution, scattering methods allow sampling a vast number of scattering objects in a single experiment, leading to statistically significant ensemble-averaged structural information. In addition, no sample pre-treatment is required (e.g., drying, freezing or other invasive procedures, possibly leading to sample perturbation), and samples are conveniently characterized as particle dispersions in glass capillaries (SAXS) or quartz cuvettes (SANS). On the other side, background scattering and sample polydispersity may pose serious challenges in characterizing solution-based samples, which need to be addressed to generate reliable data. The signal recorded from a particle dispersion contains the scattering from LNPs, but also a scattering background originating from the solvent, sample holder and instrumental set-up. To remove this background, the scattering of the solvent (without the sample) must be acquired and subtracted from the signal of the sample, recorded within the same sample holder and under identical experimental conditions. The background subtraction is a critical step, especially for samples with a weak scattering signal [72]. For example, LNPs in water typically exhibit weak X-ray scattering intensities as compared to inorganic NPs, due to the small difference in the electron density between the lipids and the water medium. Such difference may decrease even more upon addition of components to the aqueous buffer of LNPs, inducing a further reduction in the scattering signal [72]. Under these circumstances, even small discrepancies in the composition of sample and control buffers may affect background subtraction and, in turn, the quality of data analysis. Ensuring a good match between the buffer for background subtraction and the sample solvent is thus a prerequisite for generating usable data. In addition, sample polydispersity may involve significant challenges for precise analysis of scattering data. When LNPs populations of different sizes coexist in the same sample, their signals sum-up inducing a smearing of the scattering profile, potentially causing a loss of the structural fingerprints of individual LNPs populations. The presence of aggregates is particularly crucial, as the scattering is proportional to the square of the NP volume [72]. Thus, even a relatively small number of aggregates might partially -or fully- cover the scattering features of single LNPs. Therefore, controlling LNPs polydispersity and limiting aggregation is essential to generate usable data and simplify their interpretation.

In the following, we will introduce the basic working principles of small-angle scattering, shared by SAXS and SANS (Section 1.1). A more

exhaustive description of these methods can be found in references [73–75]; then, we will focus on the main differences between SAXS and SANS (Section 1.2), including specific sample/probe interactions, experimental details and instruments availability, as well as different information accessible with the two methods. Next, we will provide recent examples of applications of SAXS to investigate the structure and interactions of LNPs at the nanoscale level (Section 2). A specific emphasis will be placed on Synchrotron SAXS, as a powerful tool for a fast readout of structural details of LNPs. We will then review recent literature on SANS applied to unveil lipid organization and molecular interactions of LNPs (Section 3). Finally, we will review recent advancements in the field of small-angle scattering applied to LNPs (Section 4), including the investigation of dynamic processes through Time-Resolved (TR)-SAXS and SANS. In this respect, TR-SAXS and TR-SANS provide complementary information at different length scales, i.e., from structural transformations at the nanoscale (SAXS) to alterations in molecular diffusion and exchange (SANS). Innovations in combined multi-technique approaches will be also discussed, enabling the simultaneous characterization of structural and physicochemical properties of samples.

### 1.1. Introduction to small-angle X-ray and neutron Scattering

In a small-angle scattering experiment, a collimated beam of X-rays (with wavelength 0.01–0.2 nm) or neutrons (0.1–2 nm) impinges on a sample, which will partially adsorb, transmit and scatter the beam (Fig. 2A). The scattering contribution arises from the interaction of the beam with the atoms in the sample; in particular, X-rays selectively interact with the *electrons* of an atom through electromagnetic forces [73,74], while neutrons interact with the *nucleus* through short-range nuclear forces [76]. Irrespective of the type of interaction, this results in the scattering of X-rays or neutrons from individual atoms. When the sample contains a nanoscale organization (1–1000 nm size), the waves scattered by different atoms form an interference pattern, which encloses structural information. Such pattern is collected on a 2-D detector, while the transmitted beam is blocked by a beam-stop (Fig. 2A). For a nanoparticle dispersion with a random distribution, the 2-D scattering pattern is isotropic and, thus, it can be radially averaged to obtain a 1-D curve (Fig. 2A), where the scattering intensity ( $I$ ) is expressed as a function of the modulus of the momentum transfer, also called scattering vector ( $Q$ ,  $\text{\AA}^{-1}$ ).



**Fig. 2.** (A) Scheme of a Small-angle scattering set-up, showing the interference pattern from the scattering of X-rays or neutrons by a lipid vesicles sample, collected on a 2D detector and radially averaged to obtain an  $I(Q)$  versus  $Q$  1D profile. (B) Simulated Small-angle X-ray scattering curves from diluted homogeneous spheres (diameter = 500Å, polydispersity = 0.2 and SLD =  $9 \cdot 10^{-6} \text{\AA}^{-2}$ ) and unilamellar vesicles (diameter = 500Å, polydispersity = 0.2 and shell SLD =  $8.3 \cdot 10^{-6} \text{\AA}^{-2}$ ) in water (calculated with SasView), together with the experimental curve of glycerol monooleate cubosomes, functionalized with Pluronic F-127 (diam =  $2300 \pm 500 \text{\AA}$ ), with internal cubic Pn3m liquid crystalline phase (reprinted from [65]). Curves are shifted for the sake of clarity; (C) Small-angle X-ray scattering profiles of glycerol monooleate/oleic acid/oleylamine mesophases, showing different Bragg peak patterns as a function of temperature, corresponding to different liquid crystalline structures. The inset reports linear plots of  $(h^2 + k^2 + l^2)^{1/2}$  versus experimental  $Q_{hkl}$  for the different Bragg reflections, whose slope relates to  $d$  through  $s = d/2\pi$ . Readapted from [66].

The latter represents the difference between the incident wave vector and the scattered wave vector for elastically scattered X-rays or neutrons, and its modulus is described as follows:

$$Q = \frac{4\pi}{\lambda} \sin\left(\frac{\theta}{2}\right) \quad (1)$$

with  $\lambda$  wavelength of the probe and  $\theta$  scattering angle.

Remarkably,  $Q$  is inversely proportional to the probed length scale ( $d$ ), through the following relation (derived from the Bragg law [77]):

$$Q = \frac{2\pi}{d} \quad (2)$$

Thus, the lower- $Q$  region of the scattering intensity curve yields information on the sample's larger length scales (e.g., particle size and overall shape), while the high- $Q$  part captures structural details of smaller size (e.g., bilayer's arrangement and structure). This different structural information is contained in the scattering intensity curve as a function of  $Q$ , expressed as follows:

$$I(Q) - I_{\text{background}} = \nu(\Delta\rho)P(Q)_{\text{NP}}S(Q)_{\text{NP}} \quad (3)$$

where  $\nu$  is the volume fraction of nanoparticles and  $\Delta\rho$  (i.e., the contrast of the experiment) is a constant, represented by the difference in the scattering length density ( $\rho$ ) between NPs and the solvent (discussed in Section 1.2).  $P(Q)$  and  $S(Q)$  describe the  $I(Q)$  functional dependency and are the so-called "intra-particle" form factor and "inter-particle" structure factor of the NPs, respectively.  $P(Q)$  describes the overall size and shape of LNPs, alongside smaller structural details, selectively resolved in different  $Q$ -regions.  $S(Q)$  is a dimensionless oscillatory function, which tends to 1 at high  $Q$  and describes inter-particle interactions (i.e., between different NPs in the systems), which can be attractive, repulsive, or excluded volume. A detailed description of  $S(Q)$  is beyond the scope of this review, and can be found elsewhere [73,74,78]. The  $S(Q)$  contribution to  $I(Q)$  is generally more pronounced at low- $Q$ , as interparticle-interactions often occur at longer length scales compared to the size of the single particle. Thus,  $S(Q)$  can be normally neglected when  $2\pi/d_{\text{NP}} \ll Q_{\text{min}}$ , where  $d_{\text{NP}}$  is the particle diameter and  $Q_{\text{min}}$  the smallest  $Q$  measured [79]. In addition, for a sufficiently diluted dispersion of LNPs, inter-particle interactions are negligible ( $S(Q) = 1$ ) and the  $I(Q)$  functional dependency is exclusively governed by  $P(Q)$ . Unless there is a specific interest in measuring  $S(Q)$ , this condition is normally the most convenient, as it strongly simplifies data analysis. The concentration threshold at which  $S(Q) = 1$  depends on the strength of inter-particle interactions [79], e.g., it is lower for charged particles than for uncharged ones. A good strategy to find the highest concentration for which  $S(Q) = 1$  is to probe the sample at varying concentrations, until the normalized scattering intensity as a function of  $Q$  becomes constant. Given that  $P(Q)$  does not depend on concentration, a constant normalized scattering intensity means  $S(Q) = 1$  and, hence, negligible interactions between LNPs.

### 1.1.1. Scattering from lipid vesicles

Analytical expressions of  $P(Q)$  are known for a wide range of particle shapes, such as homogeneous spheres, cylinders, discs and spherical shells (e.g., lipid vesicles) [73,80,81], and can be combined with polydispersity functions accounting for particle's size distribution. Fig. 2B provides simple examples of  $P(Q)$ , calculated for diluted dispersions of homogeneous spheres (light blue) and lipid vesicles (middle blue), of same size and polydispersity. The low- $Q$  region the two profiles contain scattering features related to the size and the overall morphology of the particles. In contrast, the high- $Q$  region highlights structural differences occurring at a smaller length-scale; here, the  $P(Q)$  of lipid vesicles features a series of bumps (absent for a homogeneous sphere), accounting for the vesicles' shell, i.e., the lipid bilayer, with thickness  $\sim 1/20$  of the particle size.

Similar and more sophisticated models for  $P(Q)$  can be conveniently

used to simulate LNPs systems, or fit experimental data to obtain information on real samples. Several open-source software packages are available for this, including SasView [82], SASfit [83], and the Igor-Pro based NCNR SANS (from the NIST Center for Neutron Research) [84] and *Irena* [85], each of them including comprehensive documentation on fitting models and useful guides to data analysis.

Additionally, Guinier and Porod model-free approaches can be applied across a limited range of  $Q$  [86]. The Guinier approximation [80] provides an estimation of particle size in terms of its radius of gyration ( $R_g$ ), and it is defined as follows (only holding at small  $Q$  values, i.e.,  $QR_g < 1$  for spherical particles):

$$I(Q) = Ge \left( \frac{-Q^2 R_g^2}{3} \right) \quad (4)$$

where  $G$  is a scale factor.

Instead, the Porod law [86] provides an approximate shape and surface structure for the particles, through the following relation, holding at high  $Q$  values ( $Q < \frac{2\pi}{d_{\text{min}}}$ , with  $d_{\text{min}}$  smallest inhomogeneity present in the system):

$$I(Q) = \frac{C}{Q^p} \quad (5)$$

where  $C$  is the scale factor and  $p$  the Porod exponent. Different  $p$  values identify particles with varying physical forms, from spheres with a smooth surface, to spherical particles with a rough surface and rigid rods.

Beside these theoretical considerations, accessing simultaneous information on vesicles size, shape and bilayer's structure may be challenging in practice. As discussed above, these structural features correspond to different  $Q$  values, and the  $Q$  range required to capture all of them might not be accessible with standard instrumentation. Conventional SAXS and SANS instruments typically cover a  $Q$  range of approximately  $0.006$ – $0.6 \text{ \AA}^{-1}$ , which roughly corresponds to a probed length scale interval of  $1$ – $100 \text{ nm}$  (Eq. (2)). While suitable for vesicles smaller than  $100 \text{ nm}$ , this  $Q$  range doesn't allow for probing the size and overall morphology of bigger particles. In this respect, recent advances in the instrumentations have opened new opportunities for LNPs investigation through Ultra-small angle X-ray and neutron scattering (USAXS and USANS, respectively). Such methods allow for accessing wider  $Q$  ranges and minimum  $Q$  values well below  $0.001 \text{ \AA}^{-1}$ , to probe length scales from  $100 \text{ nm}$  to above  $1 \text{ \mu m}$  [87–89]. Remarkably, when used in combination with SAXS and SANS, they can cover the size range  $1 \text{ nm}$ – $20 \text{ \mu m}$  [87–90]. Despite being less available than standard SAXS and SANS technology (see Section 1.2.2), USAXS and USANS offer several benefits for the field of LNPs, such as access to the whole form factor of large size LNPs or the possibility to investigate LNPs-LNPs interactions and aggregation processes occurring in the nano and micro size range.

### 1.1.2. Scattering from non-lamellar lipid NPs

LNPs of non-lamellar nature generate a characteristic fingerprint of the high- $Q$  region, i.e., a pattern of sharp peaks called "Bragg peaks" (Fig. 2B, dark blue curve), associated to their ordered internal structure. In non-lamellar NPs, the lipid bilayer folds in the 2- or 3-D space originating complex arrangements with structural periodicity [91–94]. Resembling solid crystals, these systems consist in a unit cell repeated in the space, leading to a periodic lattice. The distribution of atoms in the unit cell dictates the symmetry of the lattice, which is identified by its crystallographic space-group. Each symmetry is associated with a series of parallel planes (lattice planes) of atomic arrangements, each indicated with the Miller indices  $h k l$  [95]. The separation distance between different lattice planes is the characteristic spacing of the lattice, i.e., the lattice parameter ( $a$ ). Importantly, since a size is comparable with the wavelength of X-rays and neutrons, the lattice planes act as diffraction



$$\phi_w = \frac{C_w}{C_w + (1 - C_w) \left( \frac{\rho_w}{\rho_l} \right)} \quad (16)$$

where,  $m$  is the mass of a lipid molecule (e.g.,  $5.92 \cdot 10^{-22}$  g for glycerol monooleate (GMO)),  $C_w$  is the water weight fraction,  $\rho_w$  is the density of water and  $\rho_l$  is the density of the lipid (e.g.,  $0.942 \pm 0.05$  g cm<sup>-3</sup> for GMO [99,100]).

Moreover, being based on periodic minimal surfaces, the Pn3m, Im3m and Ia3d cubic phases in cubosomes are related through the “Bonnet transformation”, i.e., they can isometrically transform one into the other [101–103]. Consequently, the ratio of the lattice parameters of two coexisting bicontinuous cubic phases at the equilibrium, i.e., the so-called Bonnet ratio, is fixed and equal to 1.279 for  $a_{\text{Im3m}}/a_{\text{Pn3m}}$  and 1.576 for  $a_{\text{Ia3d}}/a_{\text{Pn3m}}$  [101–103].

Beside the internal nanostructure, the scattering profile of non-lamellar LNPs also contains information on their size and shape. Although theoretically possible, the simultaneous investigation of LNPs lattice structure and size/shape is practically challenging. Among the most significant issues, the size of non-lamellar LNPs such cubosomes is usually around 200–300 nm [8,21,26], while their lattice parameter is typically more than one order of magnitude smaller. The relatively narrow Q range of standard SAXS and SANS devices cannot simultaneously capture such a broad range of length scales. Moreover, as discussed in Section 1.1.1, the size of non-lamellar LNPs is typically bigger than the larger length scale accessible with these instruments. In this respect, USAXS and USANS represent a valuable alternative, enabling access to lower Q values. In addition, when used in combination with SAXS or SANS, USAXS and USANS can potentially provide simultaneous access to the whole form factor of non-lamellar LNPs and their lattice structure, yielding a complete structural and morphological fingerprint of particles. However, a major drawback of these methods is that they are currently less available in number than standard SAXS and SANS set-up (see Section 1.2.2). Another issue is that the form factor of LNPs can partially overlap with lattice structure factor, i.e., the Bragg peaks pattern; this overlap can significantly complicate or even hinder the analysis of the particle form factor through model free approaches or fitting operations. Among the strategies to tackle this issue, Förster et al. [104] recently proposed a mathematical framework to model the scattering from a wide range of ordered meso- and nanoscale materials, including non-lamellar liquid crystalline particles. The model account for the lattice structure factor (comprising of expressions for the unit cell dimensions, finite domain sizes and peak shape) and for the particle form factor, including functional dependencies from particle size, size distribution and shape. The analytical expressions derived from this model could be potentially used to fit experimental data, enabling simultaneous analysis of morphology, size and internal structure of LNPs.

## 1.2. SAXS or SANS?

SAXS and SANS employ different probes, leading to diverse information achievable from a measurement, as well as experimental differences (e.g., experimental times and feasibility).

### 1.2.1. Probe-related differences

X-rays are electromagnetic waves (also referred to photons), while neutrons are subatomic particles. Both X-rays and neutrons have a spin and no charge. X-rays and neutrons interact with matter in a different way, i.e., either probing electrons via electromagnetic interactions (X-rays) or atomic nuclei through short-range nuclear forces (neutrons). Additionally, neutrons interact with unpaired electronic spins via magnetic dipole interactions [109]. A discussion on magnetic neutrons-electrons interactions is beyond the scope of this review and can be found elsewhere [110,111].

In simple mathematical terms, the difference in X-ray and neutrons interactions is encoded in  $\rho$  (Å<sup>-2</sup>) (Eq. (3)), which, for a molecule, is expressed as [112]:

$$\rho = \frac{\sum_i^n b_i}{V_{\text{mol}}} = \frac{\delta N_A}{M} \sum_i^n b_i \quad (17)$$

where  $V_{\text{mol}}$  is the molecular volume (Å<sup>3</sup>),  $\delta$  the bulk physical density of the molecule (expressed in g/Å<sup>3</sup>),  $M$  the molecular weight (g/mol),  $N_A$  is Avogadro's number ( $6.022 \cdot 10^{23}$  mol<sup>-1</sup>) and  $b_i$  is the X-ray or neutron scattering length of the  $i$ -th atom in the molecule (expressed in Å). The scattering length is connected to the cross section of the atom ( $\sigma$ ), as follows [113]:

$$\sigma = 4\pi b^2 \quad (18)$$

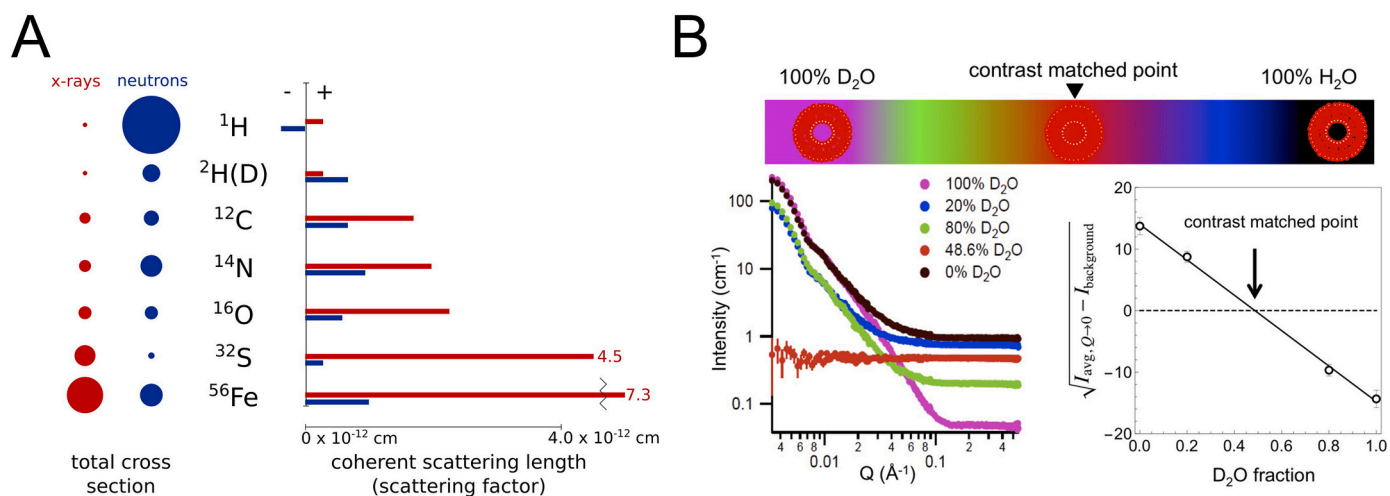
$\sigma$  represents the probability that the scattering process will occur and gives information on the “strength” of the interaction between the atom and the probe. X-rays and neutrons are associated with different cross-sections for the same atom, leading to different scattering lengths.

In addition, neutrons can discriminate between isotopes of the same element (e.g., hydrogenous and deuterium, Fig. 3A), which is a major advantage of SANS over SAXS. In SAXS experiments,  $\Delta\rho$  is fixed for a specific sample/solvent combination, while, instead, it can be easily manipulated in SANS by varying the H<sub>2</sub>O/D<sub>2</sub>O ratio of the solvent (“contrast variation” approach) (Fig. 3B). This allows disentangling different scattering contributions in multicomponent systems, by selectively enhancing or matching the contrast of individual compartments. Contrast variation is often combined with deuteration (i.e., replacement of hydrogen with deuterium in selected molecules) to further enhance selectivity to specific molecular components [114,115]. These features make neutrons unique, able to provide structural information which cannot be obtained through other means. Recent studies benefiting from these approaches will be illustrated in Section 3.

Another important advantage of neutrons is that, interacting through short-range nuclear interactions, they can penetrate the matter far more than X-rays, without inducing sample damage and allowing for sample recovery after the measurement. On the other hand, matter scatters neutrons less than X-rays, determining intrinsically lower signal intensity. In addition, available neutron sources exhibit lower intensities than X-ray sources (i.e., typical flux of  $10^4$  neutrons/s/mm<sup>2</sup>, against  $10^{18}$  photons/s/mm<sup>2</sup> offered by Synchrotron X-ray sources [116]). Consequently, neutron scattering is a signal-limited technique, associated with significantly higher acquisition times (i.e., typically hours for neutrons versus minutes or seconds for X-rays).

### 1.2.2. X-ray and neutron sources availability

Finally, neutrons and X-rays are produced in different ways, which determines a different level of availability of the two probes. Neutrons are either produced in nuclear reactors through the fission process or in proton accelerator-based facilities, exploiting the spallation process [117]. Such neutron sources are only available at specific institutions, most of which are user facilities (i.e., open to external users), providing beamtime through a proposal evaluation system and a high level of support during experiments. In this context, Europe hosts two of the world-leading neutron sources, i.e., the reactor-based Institut Laue Langevin, ILL (Grenoble, France) and the accelerator-based ISIS Neutron and Muon Source (Oxfordshire, UK), together with several other large-, middle- and small-scale neutron facilities [118,119]. In addition, the European Spallation Source, ESS (Lund, Sweden), currently under construction, is expected to provide the next generation source of neutrons for Europe [119]. This consists of a spallation target station and a high-power proton accelerator, delivering a unique long-pulse source of slow neutrons. Leveraging the inherent high flux, flexible resolution, and large bandwidth of its long-pulse source, ESS will house a suite of 22 neutron beam instruments with breakthrough scientific capabilities,



**Fig. 3.** (A) X-ray and neutron scattering cross sections for different elements, together with corresponding scattering lengths. Reprinted from [112]; B) Top: representative scheme of lipid vesicles in different solvents, determining a variation in the experimental contrast. Bottom left: Scattering from deuterated 1-palmitoyl-2-oleoyl-sn-glycero-3-phosphocholine vesicles in aqueous solvents with different  $\text{D}_2\text{O}/\text{H}_2\text{O}$  ratios, where vesicles are fully contrast-matched for 48.6/52.4 v/v %  $\text{D}_2\text{O}/\text{H}_2\text{O}$ . Bottom right: Square root of the background subtracted average low  $Q$  intensity vs  $\text{D}_2\text{O}/\text{H}_2\text{O}$  ratio. The linear fit identifies the contrast-matched point (0.486  $\text{D}_2\text{O}$  fraction), where vesicles display a flat scattering intensity in this solvent condition (red curve on the left plot). Reprinted from [114], with permission from Elsevier. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

currently unmatched at other facilities. Other key examples include the Spallation Neutron Source, SNS (Oak Ridge, Tennessee) and the NIST Center for Neutron Research (Gaithersburg, Maryland) in USA, the Australian Centre for Neutron Scattering, ACNS (ANSTO, Sydney) in Australia and Japan Spallation Neutron Source, JSNS (J-PARK, Tokai, Japan) in Asia. USANS and SANS combinations are available at some of these facilities, including the NIST Center for Neutron Research, the Oak Ridge National Laboratory, ANSTO, the Helmholtz-Zentrum Berlin (HZB), ILL and the Jülich Centre for Neutron Science (JCNS) [90].

X-ray sources are more easily accessible, as SAXS experiments can be conveniently performed in-house with commercially available SAXS laboratory instruments. However, LNPs characterization with lab instruments remains challenging, due to the relatively low difference in electron density between lipids and water media, yielding low experimental contrasts. For instance, the Bragg peak pattern of non-lamellar LNPs is only detectable with the state-of-the-art laboratory SAXS instruments, equipped with either a MetalJet source, or a rotating anode tube [87], providing X-ray fluxes up to  $10^9$  photons  $\text{s}^{-1}$  in a few hundreds of  $\mu\text{m}^2$ . Alternatively, Synchrotron X-ray sources provide a fast and high-resolution readout of LNPs structure and are available worldwide (<http://www.lightsources.org/>), accessible via project proposal mechanisms. These employ relativistic electrons to provide X-rays of high brilliance and flux (several order of magnitude more than for lab instruments) [ ]. These sources offer unique possibilities, such as a high-throughput and high-resolution readout of LNPs structure (Section 2), analysis of samples of low concentrations and volumes, real-time monitoring of processes with very fast dynamics (Section 4), and extremely versatile sample environments (Section 4). Additionally, several Synchrotron facilities feature advanced USAXS set-up, such as the ID02 beamline at the European Synchrotron Radiation Facility (ESRF) [89].

## 2. SAXS applied to the investigation of lipid-based LNPs

### 2.1. SAXS for the characterization of the nano-structure of LNPs

SAXS is among the most powerful methods for the characterization of lipid systems, providing structural information with high accuracy, in a label-free and high-throughput manner. Due to this unique features, SAXS is nowadays widely used to probe the shape and morphology of

LNPs and the degree of their internal structure, aimed at guiding the rational design and development of lipid formulations for drug delivery, imaging, and many other applications in Nanomedicine [23,64].

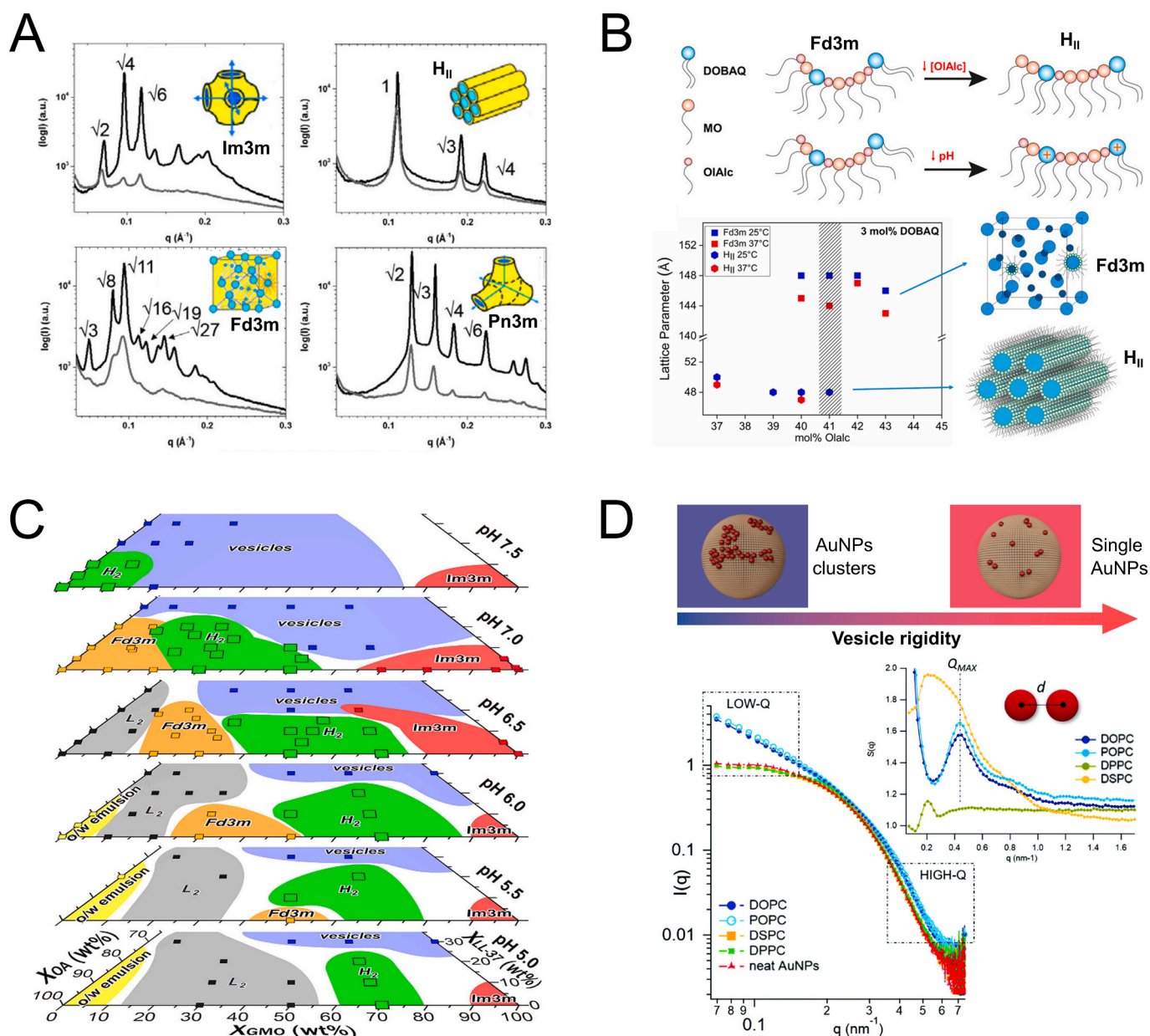
Over the past decades, SAXS has found widespread use in the characterization of lipid vesicles [121–124], including structural effects of stabilizing agents [125,126] and embedded cargoes [64,125,127–130]. In addition, recent literature reviews collected the latest advancements in scattering data analysis from multilamellar liposomes [131–133] or compositionally complex unilamellar vesicles, mimicking relevant biological membranes [134]. The latter include models to analyze the scattering from lipid vesicles with an asymmetric distribution of lipids across inner and outer bilayer leaflets [134–136] or featuring the presence of nanosized compositional heterogeneities, i.e., “lipid rafts” [137,138].

In addition, SAXS was recently applied to investigate the structure of unilamellar or multilamellar vesicles prepared through innovative microfluidic approaches [139–143]. Other recent advancements feature the application of SAXS for the characterization of natural lipid vesicles, such as synaptic vesicles [144,145] and Extracellular vesicles derived from human erythrocytes [146], cord Mesenchymal Stem Cells [147], skeletal muscle cells [148], saliva [149] and bacteria [150].

On the other hand, X-ray scattering from non-lamellar LNPs is usually analyzed through model-free approaches, enabling the detection of their inner structure through the pattern of associated Bragg peaks (Section 1.1.2). Following this approach, the phase behavior of non-lamellar LNPs has been widely explored as a function of lipid composition [151–154], stabilizing agents [155–158], and embedded guest molecules [159–163]. In a recent example, Kulkarni et al. [164] described the self-assembly of Phytantriol and Dimodan U/J LNPs mixed with solubilized tetradecane (Fig. 4A). SAXS analysis revealed a rich polymorphism of such binary mixtures, featuring different liquid crystalline internal phases as a function of the tetradecane concentration. Authors also employed SAXS to investigate the structural response of such systems to hydrostatic pressure, aimed at assessing their robustness for technological applications involving high pressures.

Furthermore, SAXS is systematically applied to monitor the structural response of LNPs to different environmental conditions, such as pH [61,63,105,167–169], ionic strength [170] and solvents [171], temperature [65,66,172–174] and pressure [164].

In this context, Tyler et al. [61] recently engineered pH-responsive



**Fig. 4.** A) SAXS profiles and identification of lipid-based bulk (black curves) and dispersed nanoparticles (gray curves) for Dimodan U/J or Phytantriol NPs mixed with solubilized tetradecane at different concentrations, at 25 °C and ambient pressure. The different lipid phases assumed by the ternary mixtures are sketched in the right insets, and spacings between corresponding Bragg reflections are indicated for each phase. Adapted with permission from [164]. Copyright {2016} American Chemical Society; (B) Phase behavior and lattice parameter GMO LNPs, mixed with 3 mol% of a pH-sensitive lipid, as a function of oleyl alcohol concentration, at pH 7.4. The dashed region highlights the composition explored in this study as a function of pH. The top inset sketches the effects of increasing amounts of oleyl alcohol or pH lowering on the lipid bilayer curvature, leading to the formation of different lipid mesophases. Reprinted from [61]; (C) Phase diagram for pH-sensitive oleic acid/GMO/LL-37 LNPs, extracted from SAXS measurements and reported as a stack of partial tertiary phase diagrams under different pH conditions. Black squares represent single SAXS measurements. Reprinted with permission from [165]. Copyright {2021} American Chemical Society; (D) SAXS profile of AuNPs with and without vesicles (1:8 vesicles/AuNPs molar ratio) of different composition, determining diverse membrane rigidities. The power law dependence at low-q is connected to the presence of AuNPs clusters and to their morphology, while the structure factor  $S(q)$ , extracted from the high-q region, relates to AuNPs interparticle distance. The sketch on the top illustrates how the stiffness of lipid vesicles modulates AuNPs self-assembly onto their surface. Redapted from [166].

LNPs composed of glycerol monooleate (GMO), oleic acid, and an ionizable lipid. Through SAXS, authors determined the phase behavior of such ternary mixtures as a function of composition (Fig. 4B). In addition, SAXS investigation revealed that pH variations can trigger a reversible transition in the structural connectivity of the system from the inverse micellar cubic Fd3m phase (at neutral pH) to the inverse hexagonal H<sub>II</sub> phase (at acidic pH). These findings pave the way to developing stimuli responsive LNPs that reversibly modify their structure at low pH, often connected to human diseases.

Other recent investigations employed SAXS to validate novel preparation methods for LNPs [175], often involving microfluidics [176–178], or to characterize innovative LNP formulations incorporating specific functionalities [179–181]. The work by Jones et al. [180] is a relevant example in this field, where authors employed SAXS to characterize the first example of light-responsive cubosomes composed of mixtures of monoolein and photoswitchable amphiphiles. These authors showed that UV irradiation resulted in a fast squeezing of the cubic lattice induced by the isomerization of photoswitchable amphiphiles



within cubosomes. This squeezing enabled the release of guest molecules from cubosomes, highlighting the potential of such systems as carriers for photo triggerable drug release.

## 2.2. SAXS for the investigation of the interactions with biomolecules

SAXS can effectively investigate interactions between LNPs and various bioactive molecules, e.g., nucleic acids and peptides in Sections 2.2.1 and 2.2.2, respectively. Within this framework, SAXS demonstrated particularly valuable for investigating non-lamellar LNPs, whose structure is highly responsive to the interaction with biomolecules and encapsulation of guest species.

### 2.2.1. Interaction with nucleic acids

Recently, there has been a growing interest in developing novel non-viral vectors for gene therapy, specifically for the delivery of nucleic acids. Lipid-based vectors have emerged as highly promising in mRNA delivery, especially in the context of anti-SARS-CoV-2 vaccines [182]. While SAXS has been extensively employed to investigate lamellar vectors and their interaction with nucleic acids [183–188], non-lamellar LNPs have emerged as effective systems for encapsulating and transporting nucleic acids only recently. Recent studies addressed non-lamellar LNP interaction with nucleic acid cargoes through SAXS [177,189–192]. Among these, Kim et al. [190] prepared cubosomes of ~500 nm size based on GMO, 1,2-dioleoyl-3-trimethylammonium propane (DOTAP), and GMO-Polyethylene glycol (PEG) loaded with siRNA (referred to as “cuboplexes”). SAXS investigation demonstrated that cubosomes with an internal Im3m phase could encapsulate siRNA with higher efficiency compared to liposomal analogs. In a following study [177], the same authors developed a microfluidic platform to produce cuboplexes with smaller sizes (75 nm) and narrower distribution, to fulfill drug delivery requirements. Here, a combination of Synchrotron SAXS with Cryo-TEM revealed the mechanism of cubosomes' formation within the microfluidic device and how their size can be controlled by tuning the amount of PEG stabilizer. In addition, comparing the scattering of cuboplexes with the one exhibited by empty cubosomes, authors showed that the inclusion of siRNA shifted the Bragg peak pattern to higher Q, indicating a squeezing of the Im3m cubic phase unit cell due to siRNA-induced screening of the cationic lipid electrostatic repulsion. In another recent study, Sarkar et al. [191] systematically investigated the encapsulation and release of double-stranded (ds) DNA in cationic GMO-based cubosomes. Synchrotron SAXS was employed for a high-throughput characterization of GMO cubosomes formulated with six different cationic lipids at varying concentrations, and to investigate the structural effects of the encapsulation of different dsDNA ladders. This study showed that the Im3m phase was preserved upon the addition of cationic lipids in the 0–2 mol% concentration range. Moreover, a decrease in the lattice parameter was observed for pure GMO cubosomes with increasing dsDNA size due to the dehydration of the GMO hydroxyl groups induced by negatively charged dsDNA. Conversely, cationic cubosomes displayed a swelling of the lattice parameter with increasing dsDNA size, due to partial neutralization of their positive charge, which promoted hydration.

### 2.2.2. Interaction with peptides

In the last decades, LNPs have been widely investigated as potential carriers for peptides, aimed at increasing their bioavailability and achieving controlled delivery and release. In this context, antimicrobial peptides (AMPs) attracted significant interest, owing to their innate defence capabilities against bacterial infections. In particular, several works focused on the application of SAXS to develop liposomal carriers for AMPs [193–196]. Recent reports in this field include the work from Utterström et al. [194], where authors employed SAXS to investigate the structural destabilization of cholesterol-rich phosphatidylcholine (PC) vesicles induced by an AMP-mimetic peptide, as possible strategy to control and trigger the release of cargoes. They found that the binding to

the liposomal surface, followed by peptide folding, triggered a lipid phase separation, involving high local peptide concentration at the bilayer surface, and abrupt release of cargo.

In latest years, pioneer researches also focused on the development of non-lamellar carriers and characterization of optimal structural features for peptides delivery [197–202]. Among these, Meikle et al. [159] investigated the incorporation of hydrophobic and amphiphilic AMPs within cubosomes of different compositions, i.e., from monoolein, to monopalmitolein, monovaccenin, and phytantriol. Authors employed SAXS to determine optimal peptide loading ranges over which cubic symmetry was retained, providing useful information for the future development of peptide carriers for drug delivery. Similarly, Zabara et al. [203] employed SAXS to validate new formulations of stabilizer-free cubosomes as carriers for the LL-37 AMP, while Gontsarik et al. [165] designed pH-responsive GMO/oleic acid cubosomes for the delivery of the same peptide. Aimed at targeting sites of bacterial infection with abnormal pH levels, authors employed SAXS to build-up a detailed pH-lipid composition phase diagram (Fig. 4C). Results showed that lipid composition controls the pH at which cubosomes undergo the structural transformations of interest for drug delivery, providing guidelines for the design of adaptable nanocarriers for patient-optimized pH-targeted AMP delivery.

## 2.3. SAXS applied to hybrid LNPs formulation

The combination of LNPs with engineered systems (from inorganic NPs to polymeric matrices and hydrogels) represents an innovative research area, where the biocompatibility and structural responsiveness of lipids is combined with functional properties of inorganic or polymeric matrices, leading to versatile hybrid platforms for multiple biomedical purposes. In this respect, SAXS is instrumental in deciphering structure-function relationships in hybrids LNPs, aimed at informing their rational design. In addition, SAXS can be applied to explore events occurring at the interface between engineered systems and LNPs as models for biological membranes, aimed at unravelling complex membrane-related phenomena [204–211].

In this field, recent reports employed SAXS to investigate the spontaneous clustering of citrated-gold nanoparticles (AuNPs) onto lipid vesicles [166,208]. In particular, Caselli et al. [166] focused on PC vesicles of varying membrane rigidity, to gain insights into the structure of AuNPs clusters adsorbed on their surface (Fig. 4D). For soft fluid-phase bilayer vesicles, the power-law dependence in the low-Q region of the double-logarithmic scattering plot relates to the presence of AuNPs aggregates with increasing fractal dimension as the stiffness of vesicles decreases. Conversely, the absence of such power-law for stiff gel-phase liposomes hints to non-aggregated AuNPs, preserving their original diameter. In addition, the analysis of the S(Q) structure factor vs Q, extracted from the high-Q region of SAXS profiles (right inset in Fig. 4D), revealed increasing AuNP center-to-center distances with enhancing membrane stiffness, highlighting that membrane rigidity controls the assembly of AuNPs.

Other studies employed SAXS to investigate the combination of lamellar and non-lamellar LNPs with different classes of inorganic nanoparticles, from metallic [179,212–215] to iron oxide [65–68,216] NPs. These investigations showed that, depending on their physico-chemical properties, inorganic NPs may preserve the structural integrity of the lipid assemblies or induce structural changes, ultimately controlling the properties and possible end-use of hybrid LNPs. In this respect, Meikle et al. [214] functionalized GMO- and Phytantriol cubosomes with a series of magnetite, copper oxide and silver nanocrystals. The SAXS investigation demonstrated that the lipid cubic phase can be retained up to 20 w/w % nanocrystals concentration, opening new possibilities for efficient dual delivery of nanocrystals and conventional drugs embedded within the same lipid nanocarrier. Other recent research employed SAXS to characterize zinc-functionalized LNPs, i.e., “metallo-cubosomes”, for RNA delivery [179] and

cubosomes co-encapsulating inorganic up-converting  $\text{Er}^{3+}$  and  $\text{Yb}^{3+}$  co-doped  $\text{NaYF}_4$  NPs for photodynamic therapy [181]. In another key example, Szlezak et al. [216] used SAXS to confirm the successful incorporation of hydrophilic and hydrophobic magnetic NPs within cubosomes for magnetically-guided drug delivery, occurring with full preservation of the cubic lipid structure.

Investigating the interaction of LNPs with polymers [172,217–220] as LNPs stabilizing agents, represents another field of intensive research. LNPs generally require steric stabilizers to improve colloidal stability in aqueous media and to enhance their pharmacokinetics and bio-distribution profile in living organisms [221]. Poly(ethylene glycol) (PEG)-conjugated lipids are among the most common stabilizers for LNPs, recently also employed in the BioNTech/Pfizer and Moderna SARS-CoV-2 mRNA-LNPs vaccines [222]. The PEG moiety prevents LNPs aggregation and opsonin targeting, for prolonged LNPs circulation time in the blood. Alternatively, commercially available non-ionic triblock copolymers, such as Pluronics® or Poloxamers, are frequently used to stabilize non-lamellar LNPs, e.g., cubosomes and hexosomes, due to their high stabilization ability and low cost. The nature and concentration of the steric stabilizer deeply affects LNPs size, shape and phase behavior, which can be conveniently studied through SAXS. For instance, SAXS investigations showed that the stabilization of GMO cubosomes with the widely used Pluronic F127 produces well-dispersed particles, which, however, exhibit a different internal structure than the corresponding bulk assemblies in excess water (i.e., an Im3m cubic phase instead of the Pn3m cubic structure observed in bulk systems) [66,223]. Conversely, the Pn3m structure is preserved in Pluronic F127-stabilized phytantriol cubosomes [223] or in GMO cubosomes stabilized with Pluronic F108 [224]. Further studies investigated Tween 80 as potential stabilizing agent for LNPs, potentially providing enhanced LNPs penetration across the blood–brain barrier [156,225]. This stabilization strategy yields cubosomes with internal Im3m cubic phase and high colloidal stability, achieved at higher concentrations of Tween 80 than conventional Pluronics. More recently, Yu et al. [226] extended this investigation to phytantriol-based LNPs formulation, including two of the most popular ionizable lipids (ALC-0315 and SM-102) used in mRNA delivery [62]. In this study, the authors investigated the impact of different stabilizers (Pluronic F127, Pluronic F108 and Tween 80) in the pH-dependent phase behavior of LNPs. Incorporating Pluronic F108 and Tween 80 within the LNP formulation instead of the conventional F127 resulted in slightly larger LNPs, whereas the impact of stabilizers appeared to be only marginal in the phase behavior of LNPs, primarily governed by the lipid composition. This was attributed to the spatial distribution of stabilizers, predominantly localizing at the outer surface of LNPs rather than within their internal core.

In addition to conventional stabilizers, the latest years have witnessed an increasing interest in developing customized stabilizing agents, offering enhanced biosafety and/or specific functionalities [221]. The work of Balestri et al. [172] represents a relevant example in the field, where SAXS was employed to assess the structure of novel cubosomal formulations stabilized with the copolymer poly(*N,N*-dimethylacrylamide)-*block*-poly(*N*-isopropylacrylamide), introducing thermo-responsivity for advanced drug-delivery applications.

In the context of LNPs formulation for drug delivery, anomalous small-angle X-ray scattering (ASAXS) represents a significant advancement in the Synchrotron technology, which opens new opportunities for the characterization of LNPs interactions with stabilizers and guest active principles. In this technique, selecting a single wavelength (and corresponding energy) of the X-ray beam and working near the X-ray absorption edge of an element of interest results in a contrast variation method [64,227]. Consequently, this approach allows to highlight specific elements in the sample under investigation and gain insight into the spatial distribution of different components within LNPs, such as the lipid bilayer, guest molecules (e.g., metal ions or drugs often containing heavy metals) and stabilizing agents [125,228–230]. In combination with SAXS, it is also possible to perform X-ray absorption near-edge

structure (XANES) spectroscopy, which can be exploited to monitor the chemical state of metal ions (e.g., as components of guest drugs) entrapped within LNPs, which can be connected to drug release processes [206,231]. For instance, Henriksen et al. recently employed XANES to investigate the molecular coordination of the positron emitter  $^{64}\text{Cu}^{2+}$  loaded within several liposome formulations containing a specific chelator for copper, for application in in vivo positron emission tomography (PET) imaging [232].

Further SAXS investigations focused on the integration of LNPs into organic matrices, such as and hydrogels [233,234]. Among recent examples, Villalva et al. [234] prepared phytantriol cubosomes immobilized in chemically cross-linked hydrogels of partially oxidized hyaluronic acid, as biocompatible and biodegradable hybrids for sustained drug release. SAXS analysis confirmed the structural integrity of cubosomes when incorporated into hydrogels with varying degrees of chemical cross-linking. SAXS was also recently used to elucidate structural transformations of PC vesicles when exposed to synthetic and natural hydrogels, mimicking the extracellular matrix [235]. In this study, Bandara et al. demonstrated that the hydrogels cause a transition from unilamellar vesicles to multilamellar vesicles aggregates, due to an osmotic driving force from the hydrogel environment. This restructuring effect, which was less pronounced in the case of PC liposomes with a PEG corona, might have significant implications in the properties and fate of vesicles in biological tissues.

### 3. SANS applied to the investigation of lipid-based NPs

#### 3.1. SANS for the characterization of the molecular structure of LNPs

SANS is the method of election to investigate the structure of LNPs at a molecular level [75,76], providing information not accessible with SAXS or, in several cases, any other technique. In the last decades, SANS has been widely employed to study the bilayer's structure in single-component phospholipid vesicles, e.g., made of phosphatidylcholines (PC) [236–239], phosphatidylglycerols (PG) [240,241], phosphatidylethanolamines (PE) [240], phosphatidylserines (PS) [242], cardiolipin [243] or sphingomyelins [244]. These investigations unveiled information such as bilayer thickness, area per lipid molecule and intrabilayer structural parameters under different experimental conditions, e.g., as a function of temperature [243,245–247] or ionic strength [248,249]. SANS has been also applied to synthetic systems of higher complexity, e.g., vesicles with a heterogeneous bilayer composition to mimic bacterial membranes [250]. Many other studies employed SANS to address the effect of cholesterol on the molecular packing of synthetic phospholipid bilayers [251–256], providing insights on its biological role in natural membranes.

In addition, SANS represents an ideal method to characterize some structural fingerprints of lipid membranes, such as lateral heterogeneities (i.e., “lipid rafts”) occurring in multicomponent synthetic and natural bilayers [257–259]. In this context, contrast variation (Section 1.2), combined with the selective deuteration of molecular components, enables to systematically highlight, or hide, micro- or nanodomains with different lipid composition [260–262]. Heberle et al. [263] provided a proof of concept of this approach, employing four-component vesicle models, containing cholesterol and a mixture of saturated and unsaturated PC. By contrast-matching the solvent, headgroups and hydrophobic chains of the lipids, they isolated the scattering contribution arising from lateral segregations in the acyl chain region, induced upon domain formation. Through systematic variations in lipid composition, authors correlated variation in the SANS signals with domain size and structure. Later studies further extended this strategy [264–267], e.g., applying it to determine the bending modulus of lipid nanodomains in synthetic vesicles [268].

In addition to lateral heterogeneity, SANS also proved as a powerful tool to study the asymmetric distribution of lipids across the bilayer (commonly encountered in natural plasma membranes) and related

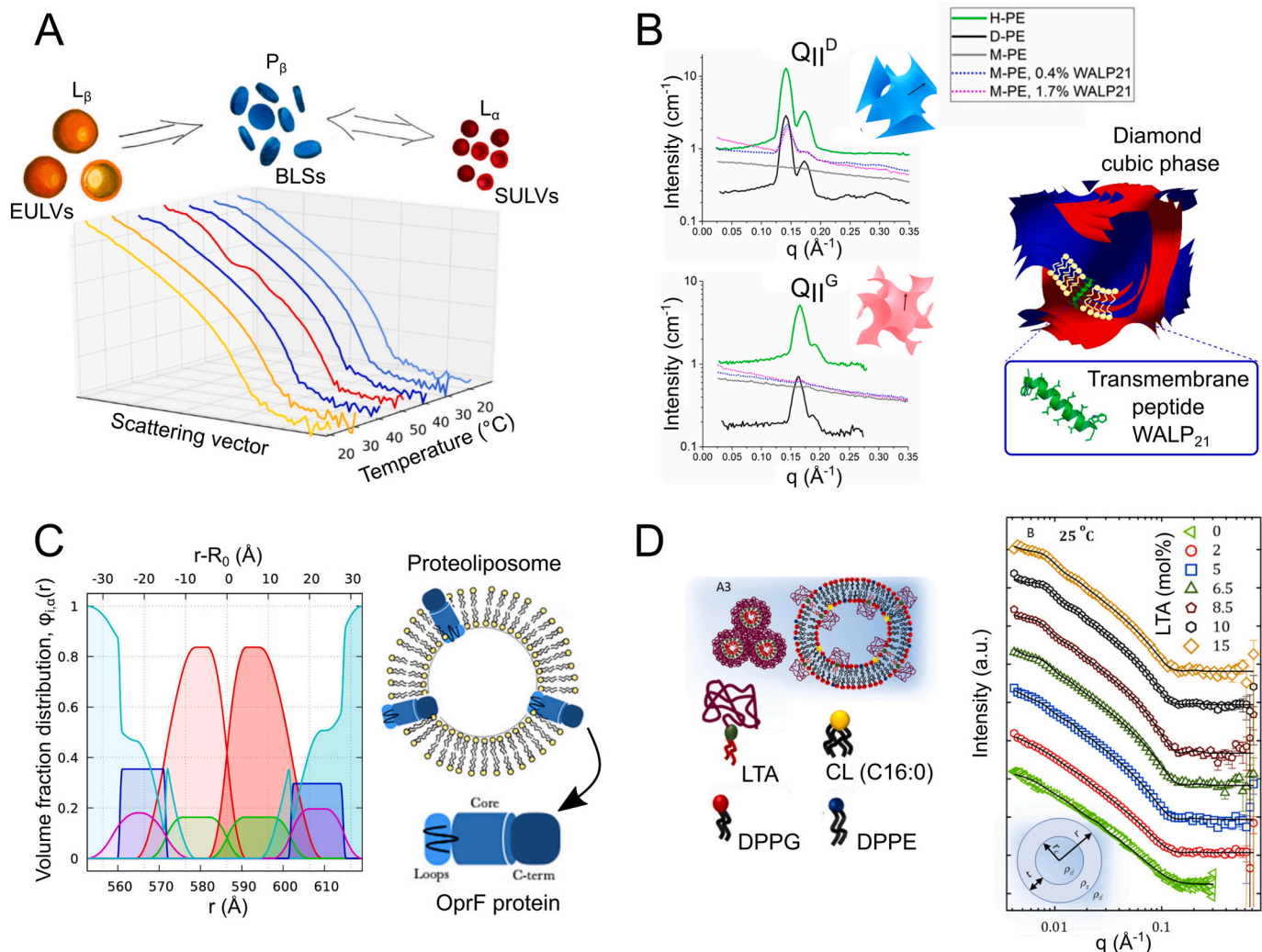
inter-leaflet coupling phenomena, by introducing isotopic differences between inner and outer membrane leaflets [136,269–272].

### 3.2. SANS for the investigation of the interactions with biomolecules

SANS offers unique possibilities to explore the interactions of LNPs with biological molecules, providing information on their partitioning into the lipid matrix and structural rearrangements occurring at the molecular length scale. This information is instrumental for fundamental studies employing LNPs as synthetic models for cell membranes and for the application of NPs in different technological fields, from food science to drug delivery.

#### 3.2.1. Interaction with peptides

In recent years, SANS has been intensively applied to investigate the interaction of synthetic lipid vesicles with different classes of peptides [273], ranging from antimicrobial [195,274–276] to amyloid-forming [277–281] and fusion peptides [282,283]. In the context of antimicrobial peptides, Silva et al. [274] recently investigated bacteria-mimicking PG/PE unilamellar vesicles interacting with a cecropin A-melittin hybrid peptide. Through SANS, they showed that the peptide induces the formation of tightly packed onion-like multilamellar structures, held together by intercalated peptides. Analysis of the associated Bragg progression demonstrated that this process involves membrane condensation, occurring through a fluid to gel phase transition of the lipid bilayer. The effects of similar antimicrobial peptides (i.e., melittin



**Fig. 5.** (A) SANS data on 1,2-dipalmitoyl-sn-glycero-3-phosphocholine (DPPC)/Amyloid-Beta Peptide (25–35) ( $A\beta_{25-35}$ ) assemblies as a function of temperature. The best fit model to describe the SANS curves are indicated with colours corresponding to the structures schematically illustrated above. Reprinted from [279]; (B) SANS profiles for hydrogenated (H-), deuterated (D-) phytanoyl monoethanolamide (PE), as well as for a proper H-PE/D-PE mixture to achieve fully contrast matched PE (M-PE), all at 25 °C. SANS curves of M-PE containing different amounts of the transmembrane peptide WALP<sub>21</sub> are also shown. Data for systems in excess D<sub>2</sub>O, having a diamond cubic  $Q_{II}^D$  phase, are reported in the top graph, while the bottom graph collects SANS profiles systems featuring a gyroid cubic  $Q_{II}^G$  phase, at hydration 13% w/w D<sub>2</sub>O. The right inset illustrates a diamond cubic  $Q_{II}^D$  phase with bilayer-embedded WALP<sub>21</sub>. Reprinted with permission from [284]. Copyright 2022 American Chemical Society; (C) Volume fraction distributions calculated from the SANS data for proteoliposomes as a function of (i) the radial distance from the vesicle centre ( $r$ ), bottom horizontal axis and (ii) the radial distance from the average vesicle radius ( $r-R_0$ , with  $R_0$  average vesicle radius, top horizontal axis). Filled areas with lower transparencies refer to the inner monolayer, while higher intensities to the outer one. Red, blue, and light blue distributions represent the lipid hydrophobic group, lipid polar group and water, respectively. On the contrary, green and magenta distributions relate to the protein hydrophobic and polar groups, respectively. The right inset sketches a proteoliposome with embedded Oprf proteins. Reprinted with permission from [285]. Copyright 2022 American Chemical Society; (D) SANS profiles for liposomes containing 0–15 mol% Lipoteichoic acid (LTA) at 25 °C, fitted according to a spherical core-shell model, illustrated in the bottom inset. The left inset schematically illustrates mixed lipid/LTA vesicles (0–15 mol% LTA) and segregated LTA micelles at LTA >15 mol%. Readapted from [286]. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

and alamethicin) on PC/PG mixed vesicles was also investigated by Quian et al [275]. Employing SANS coupled with selective deuterium labelling, they observed a peptide-induced recruitment of negatively charged PG into the outer leaflet of the bilayer, creating an asymmetric distribution of lipids across the membrane.

The interaction of lipid vesicles with amyloid-forming peptides represents another very active area of research, aimed at gaining insights on the onset of neurodegenerative pathologies. Among recent studies in this field, Ivankov et al. [279] investigated PC vesicles with incorporated amyloid-beta peptide, a key factor in Alzheimer's disease. By means of SANS, they found that the peptide triggered membrane damage, resulting in spontaneous reorganization of unilamellar vesicles to discoidal bicelle-like structures and small unilamellar vesicles (Fig. 5A), occurring during the thermodynamic phase transitions of lipids.

Other recent investigations employed SANS to address the effects of cell-penetrating [287] or fusion peptides [282,283] on model lipid vesicles. Santamaria et al. [282] investigated the process of membrane fusion for selected SARS-CoV-2 Spike fusion peptides, and how this is modulated by cholesterol and calcium ions. Complementing SANS with dynamic information from quasi-elastic and spin-echo neutron spectroscopy, they revealed different functions encoded in the Spike fusion domain and proposed a mechanism for the initiation of viral infection.

Despite most studies so far focused on vesicles, the application of SANS has been recently extended to investigate molecular interactions of non-lamellar lipid NPs. Van't Hag et al. [284] pioneered the field by developing a lipid deuteration strategy to obtain perfectly contrast-matched cubic phases in D<sub>2</sub>O (Fig. 5B), having negligible effects on the phase behavior of cubic phase-forming lipids. This strategy potentially enables to determine the location and distribution host molecules (e.g., proteins and peptides) within non-lamellar lipid phases, crucial for their applications in technological fields, such as in *meso* crystallization and drug delivery. Additionally, Conn et al. [288] recently showed that contrast-matched bicontinuous cubic phases can also be successfully used to elucidate specific membrane protein conformations using SANS. This approach can be conveniently applied to characterize membrane structures of proteins that are typically too small for Cryogenic Electron Microscopy (Cryo-EM), or too large for Nuclear magnetic resonance (NMR) studies.

While the above studies [284,288] provided a proof of concept of the applicability of this method to bulk cubic mesophases, Yepuri et al. [289] extended it non-lamellar lipid NPs, i.e., phytantriol-based cubosomes. The work of Milogrodzka [202] represents the last advancement in this field, where authors investigated the interaction of monoolein cubosomes of high content of cholesterol and phospholipids, encapsulating a Coronavirus fusion peptide. The SANS investigation showed that cholesterol and phospholipids were essential to prompt the interaction with the peptide. Moreover, increasing concentrations of the fusion peptide enhanced membrane's negative curvature, due to the oblique insertion of the peptide, leading to an alteration of the bilayer structure and phase behavior.

### 3.2.2. Interaction with proteins

Beyond peptides, SANS has been widely used to characterize the interaction of LNPs with full-length proteins [59,285,290–294], vitamins [295] and hormones [254,296].

For instance, Spinozzi et al [285] focused on lipid vesicles with embedded outer membrane protein F (i.e., the main porin of *Pseudomonas aeruginosa*), recently identified as potential vaccines against antibiotic-resistant bacteria [297]. Employing a systematic variation of the solvent deuteration grade, coupled with a newly developed volume fraction-based approach for data analysis, they obtained quantitative structural information to optimize the design of this delivery system, such as the average amount and location of the protein in the lipid bilayer and effects of its incorporation on the bilayer's structure (Fig. 5C).

In another recent work, Holme et al. [293] investigated the interaction of PC vesicles with biologically relevant enzymes, i.e., the lipid-cleaving phospholipases C and D. Combining SANS with all-atom molecular dynamics simulations, they obtained a multi-scale structural information to guide the bottom-up design of sensitive liposome-based systems for therapy and diagnosis of phospholipases-dysregulating diseases.

Other studies applied SANS to sophisticated bacteria-mimicking vesicles, e.g., containing molecular components extracted from bacteria. In this context, Bharatiya et al. [286] focused on model lipid vesicles containing Lipoteichoic acid (LTA), a surface associated polymer tethered to the cytoplasmic membrane of Gram-positive bacteria. Here, SANS revealed the impact of increasing amount of LTA on the bilayer thickness and overall size of lipid vesicles (Fig. 5D); in addition, it pinpointed a threshold concentration for the incorporation of LTA after which self-aggregation occurs, which nicely correlates to LTA concentrations generally found in real bacterial membranes.

## 3.3. SANS applied to LNPs formulation

### 3.3.1. Drug loading

In the last decades, many investigations applied SANS to study the effects of host drug molecules on the structure of LNPs [64,298–302], aimed at guiding the rational design of lipid carriers for drug delivery.

Recent advances in this field include the work of Truzzi et al. [303], where the authors developed multilamellar liposomes co-loaded with isoniazid and rifampicin, for inhaled anti-tubercular therapy. By means of SANS, they obtained information on the carrier-cargo structures and interactions, such as multi-lamellae number and spacings, particle stability and drug localization. In addition, they demonstrated that isoniazid/rifampicin co-loading stabilized the multilamellar liposome architecture, increasing the drug loading capacity.

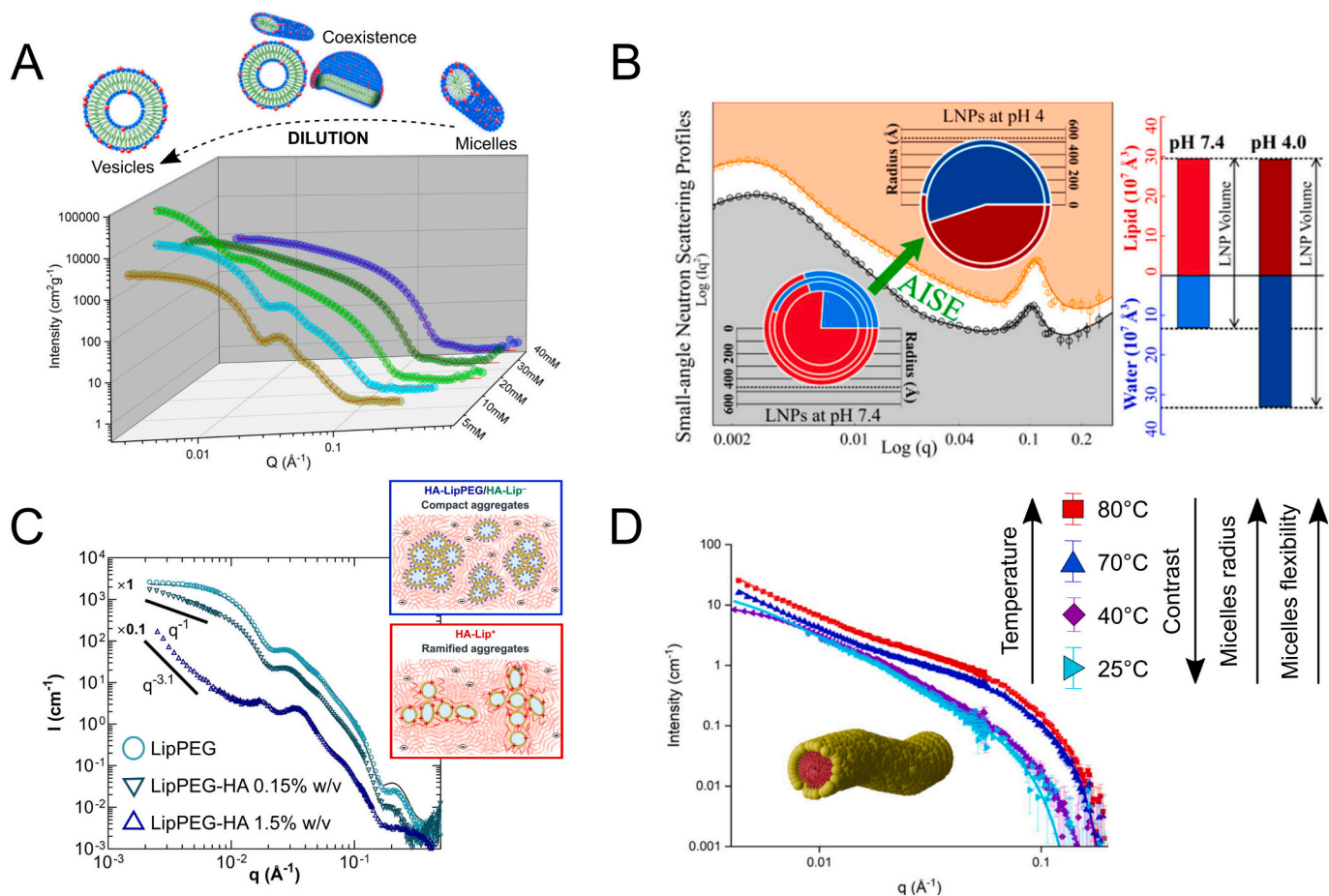
In another recent study, Motlaq et al. [304] investigated the co-assembly of PC lipids with ricyclic antidepressant drug amitriptyline hydrochloride (AMT). SANS analysis highlighted the formation of different structures as a function of sample concentration, from rod-like micelles to bilayer disks and vesicles (Fig. 6A). Remarkably, they detected spontaneous formation of ultrasmall unilamellar mixed vesicles (i.e., with diameter <15 nm) at low concentrations, characterized by excellent colloidal stability in physiological saline solution. Such systems were proposed as promising candidates for applications in drug delivery, owing to their high drug solubilization capacity, biocompatibility and good transport properties.

### 3.3.2. Interaction with LNPs stabilizing agents

Other studies focused on the mutual interaction between LNPs and their stabilizing agents, to optimize LNPs formulations for application in Nanomedicine [289,308–311].

In this context, several recent works applied SANS to investigate the effects of PEGylation (i.e., a widely employed LNPs stabilization strategy) on the structure of LNPs. To name a few, Xiao et al. [310] employed SANS to validate a new preparation protocol of azide-functionalized PEGylated liposomes with encapsulated drug nanocrystals for anti-cancer targeted delivery. Similarly, Nele et al. [312] performed an in-depth SANS investigation to characterize the effects of PEGylation, as well as preparation method and lipid composition, on the lamellarity of PC liposomes for drug delivery.

Other recent investigations focused on different polymeric stabilizers for LNPs. For instance, Yepuri et al. [289] investigated non-lamellar LNPs dispersed by the non-ionic surfactants Tween 80 and Pluronic F-127. Through SANS, they found that the liquid-crystalline structure of LNPs controls the arrangement of these surfactant within phytantriol cubosomes. In addition, Tsengam et al. [313] recently investigated the interaction between PC vesicles and Tween 80, often found together in formulations for drug delivery. By combining SANS with a Cryo-TEM investigation, they observed a surfactant-induced transformation of



**Fig. 6.** (A) SANS profiles with best curve fits for 1,2-di-(9Z-octadecenoyl)-sn-glycero-3-phosphocholine (DOPC)/ amitriptyline hydrochloride (AMT), with fixed 0.25 DOPC mole fraction and total DOPC+AMT concentration in the range 5–40 mM. The top inset illustrates the different structures encountered upon dilution. Readadapted from [304]; (B) SANS profiles and best fit curves for lipid nanoparticles (LNPs) in D<sub>2</sub>O at pH 7.4 (black symbols and solid line) and 4.0 (orange symbols and solid line). The pie-charts show the changes of the lipid mixture (red) and water (blue) in the different regions of LNPs at pH 7.4 (gray area) and 4.0 (orange area), obtained from SANS analysis. The bar-charts show corresponding volume changes in the lipid mixture and water. Reprinted from [305]; (C) SANS profiles, together with best curve fits, for PEGylated liposomes (LipPEG) in suspensions, or in hyaluronic acid (HA) at 0.15% or 1.5% w/v, obtained in D<sub>2</sub>O. The right insets sketch the structure of anionic and PEGylated liposomes (top) or cationic liposomes (bottom) in HA. Reprinted from [306] with permission from Elsevier; (D) SANS data and best curve fits for POPC in 99% w/w of D<sub>3</sub>EAN in the temperature range 25–80 °C, fitted according to a flexible homogenous cylinder model. The increase in temperature determines an increase in the flexibility and radius of the micelles and a decrease in the contrast of the experiment. Reprinted from [307]. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

vesicles into spherical micelles, and elucidated the structural aspects connected to it.

### 3.3.3. Stimuli-responsive NPs formulations

Recent studies applied SANS to investigate the structural responsivity to external *stimuli* in smart preparations of LNPs.

The work of Matviykov et al. [314] represents a distinguished example, where authors prepared liposomes made of artificial phospholipids with a dedicated backbone chemistry and tail length, that form interdigitated bilayers. Such chemical features produce metastable non-spherical liposomes, endowed with mechanical and thermal responsivity for controlled-release applications. By means of SANS, the authors investigated temperature-induced structural changes of selected artificial liposomes and identified suitable preparations for use in the medically relevant temperature range (22–42 °C). Instead, Yuan et al. [315] focused on light-activatable PC liposomes, whose structure can be altered via plasmonic photothermal effect upon laser-irradiation to achieve a controlled release of cargoes. Through SANS, they highlighted that cholesterol inclusions play a key role in driving membrane destabilization and drug-release upon laser irradiation.

Moreover, Barriga et al. [316] recently investigated LNPs made of a

mixture of cholesterol, phosphatidylcholines, phosphatidic acids and Pluronic F127. They used SANS to link LNPs composition with internal structure and to monitor the interaction with phospholipase D. The investigation highlighted a promising potential of such LNPs as enzyme-responsive structures to treat diseases involving phospholipase D dysregulation. Similarly, Li et al. [305] formulated LNPs with PC, cholesterol, PEGylated and ionizable lipids, incorporating plasmid DNA for gene-delivery. In this study SANS was used to investigate structural changes occurring upon acidification (from pH 7.4 to 4.0), faced by NPs while undergoing endocytosis in living organisms. Results detected structural responsivity, encompassing protonation of ionizable lipids, volume expansion and redistribution of aqueous and lipid domains (Fig. 6B). A good correlation between such structural variations and *in-vitro* expression efficiency was observed, disclosing promising application of pH-responsive LNPs in Nanomedicine.

### 3.3.4. Novel formulation strategies

SANS also represents a powerful tool to explore structural and morphological properties of novel LNPs formulations.

In this context, Liu et al. [317] recently developed a method to fabricate asymmetric lipid vesicles, which relies on lipid exchange

between lipid coated silica nanoparticles and originally symmetric vesicles. The efficiency of this approach was demonstrated through SANS, which detected asymmetry in vesicles composed of isotopically distinct PC lipids. The work of Jaudoin et al. [306] represents one of the first applications of SANS to hybrid vesicles-polymer systems, where authors investigated the microstructure of liposomes mixed with hyaluronic acid for drug delivery. Here, the SANS investigation aimed at assessing how the polymer affected the integrity and organization of liposomes, as well as the impact of hydrophilic drugs encapsulated within the hybrid system. Authors found that the integrity of liposomes was preserved in the polymer matrix and that liposomes surface (neutral, cationic, anionic, or anionic-PEGylated) is a key factor in controlling the overall microstructure of the hybrids (Fig. 6C).

Finally, recent studies pioneered the preparation and physicochemical characterization of lipid vesicles in ionic liquid [307,318–321]. Ionic liquids are a novel class of solvents of interest as a potential replacement of organic solvents in a vast range of chemical processes. In addition, they enable the self-assembly of a vast range of surfactants (including lipids) and, as such, represent a possible alternative to water in biotechnological applications. In this context, Bryant et al. [319] investigated the structure and properties of PC of varying composition in a library of different protic ionic liquids. Findings from SANS analysis showed that, as in water, longer acyl chain lengths determine increased bilayer melting temperatures and thicknesses. However, as a difference from the water phase behavior, the stability and structure of vesicles primarily depend on the underlying amphiphilic nanostructure of the ionic liquid, controlled by its anionic and cationic components. More recently, Manni et al. [307] detected a complex phase behavior of PC lipids in the ionic liquid ethylammonium nitrate, significantly different from the one in water. Specifically, SANS investigation showed that 1,2-distearoyl-sn-glycero-3-phosphocholine underwent a  $L_b$ - $L_c$  phase transition upon heating, while 1-palmitoyl-2-oleoyl-sn-glycero-3-phosphocholine formed  $L_1$  worm-like at high solvation (Fig. 6D). This was explained considering the larger solvation volume of the ionic liquid compared to water, inducing alterations in the lipid packing. In addition, recent investigations highlighted different membrane flexibility for PC vesicles when formed in ionic liquids [318,321]. In particular, Miao et al. [318] combined SANS with Neutron Spin-Echo to investigate egg PC vesicles in two different ionic liquids, and their water mixtures. They observed a decrease in the bilayer's bending modulus up to an order of magnitude compared to in water, while no significant changes in the structure of the vesicles' bilayer were detected.

#### 4. Advances in SAXS and SANS methodologies to investigate lipid-based NPs

SAXS and SANS have been recently emerged as powerful techniques to probe dynamic processes involving LNPs. In particular, the high brilliance of Synchrotron X-ray sources allows for real-time monitoring of LNPs structural evolution, with resolution down to a few milliseconds. In addition, modern neutron sources enable the investigation of dynamic processes occurring at the molecular scale (i.e., within the lipid bilayer), through time-resolved SANS with smallest temporal step in the sub-second range. Such advancements in SAXS and SANS methods will be discussed in Sections 4.1 and 4.2, respectively. Finally, Section 4.3 will discuss innovative multi-techniques approaches recently introduced at Large Scale Facilities for X-rays and neutrons, enabling simultaneous in-situ combinations of SAXS and SANS with spectroscopic, calorimetric, and light scattering methods, as well as synchronized SAXS/SANS investigation.

##### 4.1. Synchrotron TR-SAXS to probe the structural evolution of LNPs

With recent advances in Synchrotron radiation sources, TR-SAXS has emerged as an attractive approach for the real-time detection of dynamic structural transitions of LNPs, involving relatively fast processes

within a few hundreds of milliseconds. The structural evolution of these lipid nano self-assemblies can be observed under different conditions: (i) upon exposure to *stimuli*, such as pH and ionic strength variations or application of light and electromagnetic fields (Section 4.1.1); (ii) upon interaction with biologically relevant molecules and engineered systems of interest for biomedical applications (Section 4.1.2). In this context, TR-SAXS is often combined with advanced set-ups [322,323] and dedicated microfluidic platforms [139,140,324,325], allowing for the continuous production and in situ structural characterization of LNPs, designed for drug delivery, diagnostic and theranostic applications.

##### 4.1.1. Structural response to external stimuli

Nowadays, the advancements in time-resolved SAXS allows to characterize the dynamic structural response induced upon external *stimuli* [65,180,326] or *endogenous* stimuli, simulating specific processes and environments within the body [323,325,327,328]. Investigating such processes real-time is key for guiding the rational design of "smart" *stimuli*-responsive LNPs, as well as for gaining insights in the complex and dynamic transformations faced by LNPs in living organisms.

In this context, Hempt et al. [322] investigated the generation and evolution of lipid nanostructures during the process of milk digestion. To this purpose, they developed an experimental setup, shown in Fig. 7A, which enabled to combine flow-through TR-SAXS with an in vitro cell co-culture model simulating the small intestine. This set-up allowed to remotely trigger digestion by pumping pancreatic extract and monitor structural variations in the lipid phase of the milk emulsion droplets via Synchrotron TR-SAXS. Measurements revealed subsequent formation of different non-lamellar phases (i.e., from inverse micellar ( $L_2$ ), to a lamellar ( $L_\alpha$ ), and inverse hexagonal ( $H_{II}$ ) phase, coexisting with an  $Im3m$  cubic phase), possibly acting as carriers for poorly water-soluble milk components.

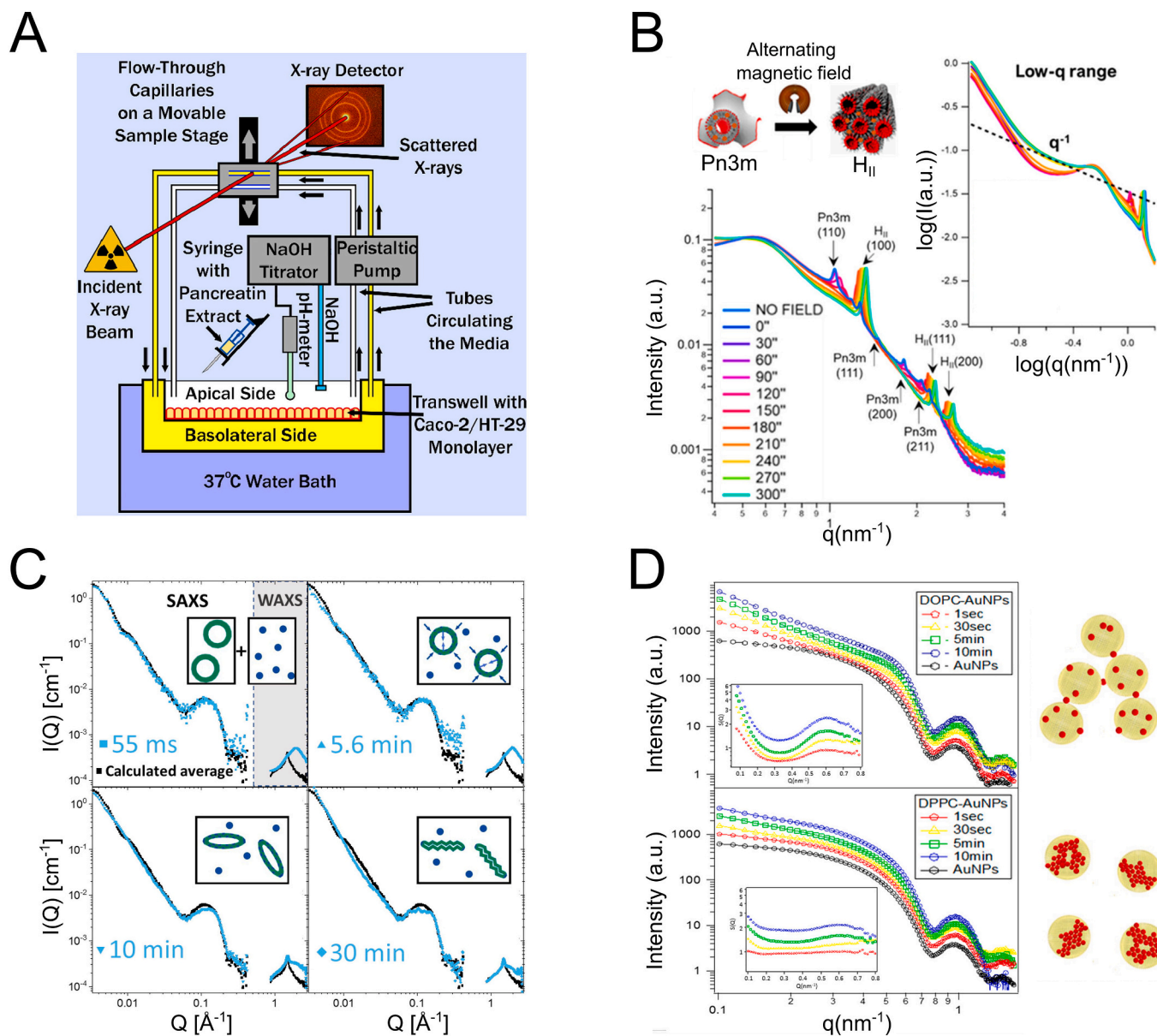
Similarly, Fong et al. [330] applied TR-SAXS to investigate the lipolysis of PC and PE vesicles, occurring during intestinal digestion. Results showed that lipid composition controls the structural transformation of lipid vesicles upon hydrolysis with the enzyme Phospholipase C, providing insights for the design of enzyme-responsive LNPs for drug delivery applications.

In addition, TR-SAXS has been applied to monitor pH-driven structural transition in LNPs in the physiological pH window. In this context, Yu et al. [62] recently combined TR-SAXS with rapid flow mixing to investigate the structural responsivity of LNPs containing two ionizable lipids widely employed for COVID-19 vaccine formulations, occurring upon gradual acidification as encountered in endosomes. TR-SAXS experiments provided direct evidence for the formation of structures with increasing membrane curvature (from inverse micellar, to inverse hexagonal and bicontinuous cubic, to lamellar phases) upon acidification, shedding lights on the link between the structure and endosomal escape of LNPs.

Moreover, recent investigations employed TR-SANS to elucidate the structural responsivity of LNPs to external *stimuli* (e.g., light or magnetic fields), aimed at developing lipid devices for controlled 'on-demand' drug release [65,180,326]. In this context, Caselli et al. [65] exploited real-time SAXS to monitor the structural changes in GMO cubosomes hybridized with superparamagnetic iron oxide nanoparticles (SPIONs) upon application of an alternating magnetic field (AMF). SAXS analysis revealed a transition from the cubic  $Pn3m$  to the inverse hexagonal phase within cubosomes, remotely triggered upon AMF application (Fig. 7B). This phase transformation, resulting from the local heat released by SPIONs upon AMF exposure, can be effectively applied to prompt the release of guest molecules from the water channels of cubosomes for controlled drug delivery applications.

##### 4.1.2. Structural response to the interaction with molecules and engineered systems

TR-SAXS has been recently applied to shed light on the dynamic structural behavior of both lamellar and non-lamellar LNPs when



**Fig. 7.** (A) Experimental setup used for the in situ study of the milk digestion in the presence of a Caco-2/HT-29 co-culture. The formation of lipid nanostructures was simultaneously monitored through online SAXS on the apical and basolateral side of the cell layer. Reprinted from [322]; (B) SAXS profiles of monoolein cubosomes containing  $9.5 \cdot 10^{-5}$  SPIONs per monoolein molecule, recorded at 25 °C under different times of exposure to the AMF. The Bragg reflexes of Pn3m and H<sub>II</sub> phases are indexed in the graph with the corresponding Miller indices. The inset reports the detail of the low- $q$  region of SAXS profiles, highlighting the rearrangement SPIONs into linear aggregates (identified by the emergence of a  $q^{-1}$  scattering feature) upon field exposure. Reprinted from [65]; (C) Time-resolved Small and Wide-Angle X-Ray Scattering (SAXS and WAXS, respectively) profiles of a 1:1 mass ratio mixture of DPPC and TX-100. Calculated average sum of the individual DPPC and TX-100 scattering patterns is also shown. The insets in the graphs illustrate the possible steps in the formation of the rippled bilamellar nanodiscs, involving increasing attraction between adjacent bilayers as TX-100 molecules insert into the vesicles, subsequently leading to a collapse of the spherical lipid vesicles into a flat doubled bilayer, followed by the formation of ordered ripples. Readapted from [329]; (D) TR-SAXS profiles of AuNPs-DOPC (top) and AuNPs-DPPC (bottom) hybrids collected at different times over 10 min of incubation. The inset shows the structure factor of the samples, with correlation peaks related to the center-to-center interparticle distances. Reprinted from [213].

interacting with biological and synthetic molecules, such as proteins [331,332], surfactants [329], and drug molecules [333].

In this context, Bjørnstad et al. [334] examined the interaction between unilamellar dipalmitoylphosphatidylcholine (DPPC) liposomes and Triton X-100 (TX-100, i.e., a non-ionic surfactant mostly used for biotechnological applications) at low temperatures, where the DPPC bilayer is resistant to solubilization. TR-SAXS investigation revealed the kinetics of collapse of DPPC vesicles upon addition of TX-100, leading to the formation of ordered rippled bilamellar disc structures (Fig. 7C), which prevent solubilization. Authors suggested that the bilayer ripple

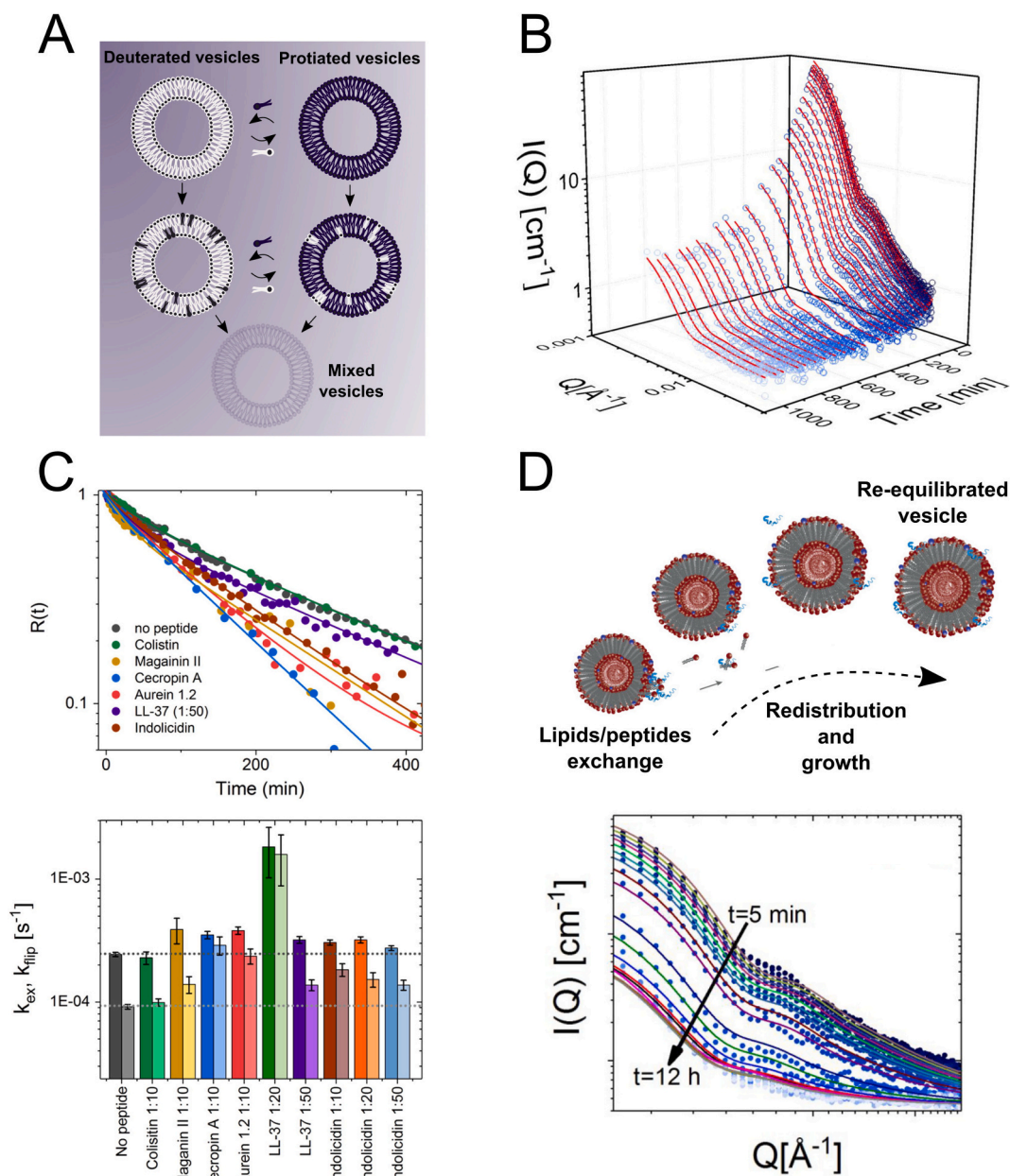
phase was adopted to counter-balance the packing constraints due to the insertion of TX-100 molecules, while the vesicles collapse was attributed to concomitant osmotic pressure and water structure destabilization effects. TR-SAXS also proved to be an effective tool to monitor interactions with more complex biomacromolecules, such as enzymes. In a recent work, Thorn et al. [332], explored GMO-based cubosomes as efficient bacterial-triggered drug delivery systems. They demonstrated that the release of different antibiotics from cubosomes can be triggered in the presence of bacteria by lipase-mediated digestion and disruption of the lipid nanocarriers. Specifically, TR-SAXS analysis showed that

non-regiospecific lipases induced the swelling and degradation of cubosomes via single-phase digestion kinetics, leading to the formation of lamellar structures with subsequent release of embedded drugs. Conversely, regiospecific lipases drove a two-phase digestion process, featuring a cubic to inverse hexagonal phase transition, which resulted in less effective drug release.

Further TR-SAXS investigations focused on the interaction of LNPs with engineered systems, from synthetic molecules to inorganic NPs, aimed at understanding relevant events at the nano-bio interface and

inspiring the design of functional hybrid nanomaterials for biomedical applications.

The work of Cardellini et al. [213] represents a recent example, where authors investigated the temporal evolution of AuNPs adhesion and clustering onto fluid-phase and gel-phase PC target membranes, using TR-SAXS in combination with a stopped-flow apparatus. This investigation showed that AuNPs underwent fast aggregation onto fluid-phase PC vesicles, leading to fully AuNPs-decorated liposomes within few tens of seconds. In addition, the analysis of SAXS profiles over the



**Fig. 8.** (A) Conceptual scheme illustrating the methodology used to resolve intravesicle “flip–flop”, and intervesicle exchange processes. This consists in mixing fully deuterated and hydrogenated vesicles in a 50/50% H<sub>2</sub>O/D<sub>2</sub>O mixture, which matches the average scattering length density of vesicles. Over time, contrast is lost due to molecular exchange processes, leading to a mixed population of vesicle and subsequent gradual decrease in neutron scattering intensity (as the one shown in Fig. 7B). Reprinted from [336]; (B) TR-SANS profiles with best curve fits for mixed 1,2-dimyristoyl-sn-glycero-3-phosphocholine (DMPC)/1,2-Dimyristoyl-sn-glycero-3-phosphoglycerol (DMPG) vesicles at 37 °C, obtained through the deuteration strategy described in Fig. 7A, showing a continuous decrease in the scattering intensity over time due to molecular rearrangements. Readapted from [336]; (C) Top: Rate of contrast decay  $R(t)$  and best curve fits for deuterated and hydrogenated vesicles, mixed in the absence and in the presence of different antimicrobial peptides. Bottom: Corresponding rate constants for intervesicle exchange (darker colours) and flip-flop (lighter colours) obtained from  $R(t)$  curve fittings (the top graph). Dotted lines indicate the intervesicle exchange and flip-flop constants for lipid vesicles without peptides. Reprinted from [334]; (D) TR-SANS profiles with best curve fits as a function of time obtained for deuterated and protiated DMPG/DMPG/1,2-Dimyristoyl-sn-glycero-3-phosphoethanolamine (DMPE)-PEG vesicles, mixed in the presence of indolicidin, at 37 °C. The top inset schematically illustrates the mechanism of size growth observed over time, induced by lipids/peptides molecular exchange and rearrangement. Reprinted from [336].



0–30s time-range (Fig. 7D), revealed a structural evolution of AuNPs aggregates from 1D to 2D clusters. In contrast, a slower and weaker interaction was observed onto gel-phase PC vesicles, suggesting partial NPs aggregation on the lipid membrane in the form of less densely packed AuNPs clusters. These TR-SAXS measurements highlighted that the physical state of vesicles controls the adhesion and aggregation of AuNPs onto the lipid shell, providing insights on the role of membrane physico-chemical features in nanobiointeractions.

#### 4.2. TR-SANS to probe lipid diffusion in lipid-based NPs

In the last decade, TR-SANS has proved to be a powerful method to probe the dynamics of molecular diffusion in lipid vesicles (Section 4.2.1). In addition, it is label-free and non-headgroup specific, which represents a major advantage over other available methods for measuring kinetics of lipid exchange. Furthermore, recent investigations also applied TR-SANS to investigate how the dynamics of lipid exchange is affected upon interaction with relevant biological molecules, which will be discussed in Section 4.2.2.

##### 4.2.1. Dynamics of transfer of lipids and sterols

TR-SANS can probe the diffusion of lipids in the bilayer, including transversal exchange across outer and inner bilayer leaflets (i.e., lipid flip-flop) or inter-vesicles lipid exchange.

This was proved for the first time by Nakano et al. [335], who applied TR-SANS to unilamellar PC vesicles. They demonstrated that the rates of inter-bilayer and trans-bilayer exchange can be independently determined with a single experiment, with a relatively simple approach. This relies on mixing two populations of vesicles with different isotopic composition, i.e., one with hydrogenated and the other with deuterated chain PC. While providing good contrast for fully hydrogenated or deuterated vesicles, the solvent D<sub>2</sub>O/H<sub>2</sub>O ratio is strategically set to match the SLD of vesicles with 50/50 hydrogenated/deuterated lipids (Fig. 8A). Upon mixing, lipid exchange and flip-flop induce a continuous decrease in the scattering intensity over time, as the SLD of vesicles approaches the contrast match point (Fig. 8B). The real-time monitoring of such intensity losses yields quantitative information on the kinetics of lipids transfer.

Later studies applied this strategy to other types of PC vesicles [337] or different environments [338]. For instance, Nguyen et al. [338] found that PC flip-flop is dramatically accelerated in methanol, a widely used solubilizing agent for lipid mixtures. Other groups extended the investigation to the transport of cholesterol in lipid membranes [114,339,340]. For instance, Breidigan et al. [340] applied TR-SANS to investigate the effects of different membrane environments on the inter- and intra-membrane movement of cholesterol. They found that the transport rate decreased with the degree of saturation of membrane lipids and by replacing PC with sphingomyelins.

##### 4.2.2. Effects of the interaction with biomolecules

More recently, TR-SANS was applied to isolate and exclusively study the lipid flip-flop contribution and how this is affected by the interaction with different biological molecules, such as peptides or proteins [334,336,341–343]. This can be achieved by employing asymmetric vesicles with hydrogenated lipids in the inner leaflet and deuterated lipids in the outer. Among the examples, Nguyen et al. [341] investigated flip-flop exchange in asymmetric vesicles, made of hydrogenated (inner leaflet) and deuterated (outer leaflet) PC. They found that the interaction with different antimicrobial peptides (i.e., gramicidin, alamethicin, melittin) strongly enhances the rate of transversal lipid exchange. In addition, they highlighted that peptides adsorbed to the membrane surface might be more effective in eliminating asymmetry than when incorporated within the bilayer. A few years later, Nielsen et al. [334] investigated the effects of a wide library of natural antimicrobial peptides on bacteria-mimicking PC/PG/PE vesicles. Except for colistin, all the peptides accelerated phospholipid flip-flop (Fig. 8C),

without involving membrane structural destabilization or pore-formation. These findings highlighted a common mechanism for the interaction of peptides with lipid membranes, possibly connected to their mode of action and *in vivo* antimicrobial activity. Marx et al. [344] extended the investigation to other antimicrobial peptides, namely frog peptides L18W-PGLa and magainin 2, and the lactoferricin derivative LF11–215. They found that the acceleration of lipid flip-flop in asymmetric PG/PE vesicles is highly peptide-specific, occurring at the fastest rate for L18W-PGLa.

In another recent study, Nielsen et al. [336] developed a new scattering model to analyze full Q-range TR-SANS profiles, allowing for simultaneous investigation of lipid flip-flop and vesicular growth. As a proof of concept, they applied this method to neat PC/PG/PE vesicles and to the same systems incubated with an accelerating substrate, i.e., indolicine. They found that indolicine increases the lipid flip-flop rate, while simultaneously prompting vesicles' size growth (Fig. 8D). This was explained in terms of peptide-induced lipid partial dissolution and reorganization, leading to larger and more polydisperse vesicles. In addition, TR-SANS experiments were performed on partially labelled lipid mixtures to isolate the dynamics of different lipid components. Thanks to this strategy, the authors pinpointed a faster exchange kinetics for PG than for PC lipids, while comparable increases in flip-flop rates were observed upon peptide addition.

Finally, recent works applied TR-SANS to investigate interactions with systems other than peptides, such as surfactants [329] or proteins [345]. In this context, Maric et al. [345] studied the kinetics of lipid exchange between PC vesicles and human lipoproteins. They discovered that lipid exchange occurs through two distinct mechanisms, i.e., particle collision and particle tethering to the lipid membrane. Moreover, they highlighted that these two modes of binding depend on the lipoprotein type and have different effects on lipid exchange.

#### 4.3. Simultaneous multi-technique approaches

Recent technological advancements in neutron and synchrotron facilities enabled the combination of SANS or SAXS with complementary on-line techniques for a multi-method characterization occurring simultaneously on the same sample. These approaches offer unique possibilities to directly correlate the structural evolution occurring in a sample with modifications in its physical and chemical properties. Obtaining complementary data sets at the same time is vital for the study of processes with fast dynamics, for which *ex-situ* characterization of intermediates is not feasible and time-synchronization is required for a reliable integration of data from different techniques [346,347].

The high brilliance of Synchrotron sources offers a flexible environment for simultaneous characterization approaches, which were readily developed starting from the '90s [231,348,349]. Nowadays, these represent routine approaches at Synchrotron radiation facilities and include combinations of SAXS with Differential Scanning Calorimetry (DSC) [350], which allows for measuring heat exchanges within the samples during controlled temperature programs and relate them to specific structural transformations, e.g., bilayer melting transitions or mesoscale reorganizations in lipid systems [351]. In addition, SAXS can be integrated with on-line liquid chromatography [352,353]; this method is often employed to characterize polydisperse protein samples, allowing for isolating components of different size and collecting the scattering from homogeneous sub-populations, which strongly facilitates data analysis and interpretation. In addition, the concentration of specific protein subpopulations within the sample can be conveniently increased to enhance their scattering signal, which is particularly useful for weakly scattering samples or precious materials available in limited amounts. This approach could be potentially translated to the field of LNPs, e.g., to enable on-line purification and separation of vesicles of different size in polydisperse biological samples (e.g., of Extracellular Vesicles) or to identify different LNPs populations in synthetic formulations. Combinations of SAXS and TR-SAXS with spectroscopic

techniques, such as Raman [354,355], UV-Visible [356] and Fourier-transform infrared (FTIR) [357–359] spectroscopies, are also available, and can be used to simultaneously monitor the structure and the chemical state of a sample while undergoing transformations. While mostly applied to polymeric materials so far, integrated spectroscopic and scattering methods hold significant potential for the field of LNP. This includes opportunities to investigate structural and conformational changes in lipid systems, monitor cargo encapsulation and elucidate specific interactions between lipid membranes and incorporated biomolecules or drugs.

SAXS can be also combined with Dynamic Light Scattering (DLS), for simultaneous investigation of nanoparticles structure and size. In this respect, the BioSAXS endstation of the EMBL beamline P12 at PETRA III (DESY, Hamburg, Germany) offers an advanced SAXS/DLS set-up featuring a multi-receiver four-channel DLS system to collect DLS data prior and during X-ray exposure [360]. This instrumentation provides an online screening of the hydrodynamic radius and polydispersity of particles, which can be readily combined with SAXS structural information for a multiscale investigation of particles properties. The combination of SAXS with rheology (Rheo-SAXS) represents another advancement in the field, which enables to monitor real-time structural deformations occurring in a sample in response to an applied shear stress [361]. This approach has been employed to probe the relationship between structure and rheological properties for a wide range of systems, including lamellar surfactant systems [362,363], colloidal suspensions [364,365] and polymer solutions [366].

Compared to X-ray, simultaneous multi-technique approaches involving neutrons have been only enabled in last years, thanks to recent technological advancements in high-intensity SANS instruments.

Among these, Jordan et al. [367] reported the first implementation of in situ size exclusion chromatography (SEC) on a SANS instrument, i. e., D22 (ILL, Grenoble, France). More recently, Johansen et al. [368] demonstrated that this dedicated SEC-SANS set-up is particularly useful to investigate complex soft matter systems, consisting in phospholipid nanodisc particles with embedded membrane proteins. Here, in situ SEC provided high sample homogeneity and purity, allowing for reducing the smearing of the scattering signal due to structural dispersity. This enabled a high-resolution structural analysis of originally polydisperse particles at a relatively low concentration, not achievable through a conventional SANS apparatus. Moreover, apparatus for simultaneous SANS and FTIR have been developed in recent years, and currently available at the instruments KWS2 [369] (Heinz Maier-Leibnitz Center (MLZ), Garching, Germany) and TAIKAN [370] (Material and Life Science Experimental Facility (MLF), Japan Proton Accelerator Research Complex (J-PARC), Tokai, Japan).

Similarly, SANS has been recently combined with Raman Spectroscopy at the NG7 30 m SANS instrument (NIST Center for Neutron Research (NCNR, Gaithersburg, MD) [371].

The integration of SANS with in situ DSC, a long-available feature in Synchrotron facilities, has faced several challenges connected to the lower flux of neutron sources, but also to scattering geometry and thermal control. These issues have been overcome only recently, with the development of a combined SANS/DCS system placed at Quokka instrument [372] (OPAL, ANSTO, Sydney, Australia), with accessible temperature range – 150–500 °C.

In addition, novel in situ DLS setups have been installed at SANS instruments in different Large Scale Facilities, including D11 [373] (ILL, Grenoble, France), ZOOM and LOQ [374] (ISIS Pulsed Neutron and Muon Source, Didcot, UK), SANS-I [375] (SINQ spallation source at Paul-Scherrer Institute (PSI) Villigen, Switzerland) and KWS2 [347] (MLZ, Garching, Germany). In this respect, Nawroth et al. [376] used synchronous time-resolved DLS and SANS at D11, combined with a stopped-flow device, to investigate the structural evolution of a bile salt-phospholipid micellar solution upon dilution, as model for the flow of bile secretion into the human digestive system. Crossed beam experiments of TR-DLS and TR-SANS revealed a stepwise formation of lipid

vesicles, triggered upon digestion. The dynamics of the micelles to vesicles transition was characterized at a multiscale level, enabling direct correlation between particle size and molecular structure.

Analogously to Rheo-SAXS, combinations of SANS with rheology (Rheo-SANS) were made available at Large Scale Facilities, aimed at probing the microstructure–rheology relationship in soft matter samples [377,378]. In the context of surfactants, former SANS studies performed in-flow highlighted orientational transitions in lyotropic lamellar phases [379,380] or formation of multilamellar vesicles under shear stress [381]. Nowadays, TR-SANS in combination with rheology is widely used to investigate the dynamics of transformations and/or nonequilibrium microstructural transitions in surfactant systems under shear flow [382–384], which has relevant implications in the field of LNPs formulation. Recent advancements in this field feature the development of Capillary Rheo-SANS (CRSANS) [385], which uses pressure-driven flow through a long and flexible silica capillary to generate higher shear rates than in conventional Rheo-SANS experiments. The application of this method to LNPs would potentially enable to characterize their nanostructure and rheology at industrially-relevant shear rates, encountered under processing conditions such as extrusion, coating, spraying, or lubrication. Additionally, an in situ magnetorheological SANS setup has been recently installed at ILL [386], enabling simultaneous monitoring of the structural and rheological response of samples under magnetic field and shear flows. This new set-up offers intriguing possibilities for the investigation of hybrid LNPs containing magnetic inclusions, of relevance in the field of magnetically-guided drug delivery and/or magnetic fluid hyperthermia.

Finally, SAXS/SANS simultaneous analysis represents the latest frontier of in situ multi-technique characterization, recently introduced at D22 (ILL, Grenoble, France) [387,388]. Here, an advanced portable SAXS system, mounted on a standalone metal rack, has been successfully installed and tested in combination with SANS. Through this setup, SAXS and SANS data can be acquired from the same sample volume and fitted simultaneously using a common structural model. Remarkably, this novel instrumentation will allow in situ TR-SANS and SAXS, revealing complementary information on structural evolution occurring in the sample, i. e., from molecular to nanoscale rearrangements. Moreover, probing the same sample under different contrasts (i. e., provided by neutron and X-ray probes) will allow for accessing simultaneous information on different compartments in multicomponent systems. Overall, this SAXS/SANS combination represents a promising avenue to explore innovative LNPs of hybrid nature, and to investigate their molecular interactions with unprecedented accuracy.

## 5. Conclusions

LNPs represent the most promising class of nanocarriers for the delivery of hydrophobic and hydrophilic drugs, peptides, proteins, nucleic acids, and imaging agents. In addition, they offer opportunities for smart hybrid platforms engineering, where inorganic nanomaterials are incorporated within a structurally responsive lipid matrix.

Recent years have witnessed a tremendous growth in LNPs research, especially aimed at developing non-lamellar LNPs for next-generation Nanomedicine. Despite this, LNPs currently approved for clinical use are relatively few and primarily limited to liposome-based formulations. Understanding the structure-function relationship in LNPs, especially in physiological environments and upon interaction with biologically relevant molecules, represents a first step to overcome this translation bottleneck. *In this respect, more efforts should be devoted to couple biological investigation and performance studies on LNPs with a systematic screening of LNPs structure and transformations in biologically relevant conditions.* Small-angle X-ray and neutron scattering are robust and versatile techniques that serve perfectly to this purpose, offering ensemble-averaged and label-free structural information. The relevance of SAXS and SANS in this research field is increasingly recognized, as attested by the rapid broadening of users at Large Scale facilities,

including researchers from biomedical and pharmaceutical communities.

In this review, we discussed the state-of-the-art in SAXS and SANS applied to LNPs research, aimed at highlighting benefits and unique opportunities that these techniques bring to the field. A user-friendly description of small-angle scattering, including a basic introduction to data analysis, was also included (Section 1) to assist new users or researchers with diverse backgrounds. Throughout the review, a special focus was placed on structural information and interactions of LNPs with biomolecules and/or relevant physiological environments, of interest for their application in the medical field.

Overall, the spreading of SAXS and SANS across the biomedical community, along with the ongoing advancements in scattering technology, foretells a rapid evolution in LNPs research in the coming years. In addition, the emergence of new advanced approaches, outlined in Section 4, will open new avenues to explore dynamic transformations in LNPs within biological environments, possibly bridging the gap between conceptual design and clinical translation of LNPs.

### CRedit authorship contribution statement

**Lucrezia Caselli:** Conceptualization, Methodology, Supervision, Writing – original draft, Writing – review & editing. **Laura Conti:** Writing – original draft. **Ilaria De Santis:** Writing – original draft. **Debora Berti:** Conceptualization, Funding acquisition, Methodology, Supervision, Writing – original draft, Writing – review & editing.

### 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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### Data availability

No data was used for the research described in the article.

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