

# Supramolecular organization and biological interaction of the squalenoyl siRNA nanoparticles

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1	Supramolecular organization and biological interaction of <del>the</del> squalenoyl siRNA
2	nanoparticles
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### 81 Abstract

82 Small interfering RNAs (siRNA) are attractive and powerful tools to inhibit the 83 expression of a targeted gene. However, their extreme hydrophilicities combined with a 84 negative charge and short plasma half-life counteract their use as therapeutics. Previously, we 85 chemically linked siRNA to squalene (SQ) which self-assembled as nanoparticles (NPs) with 86 pharmacological efficiency in cancers and recently in a hereditary neuropathy. In order to 87 understand the siRNA-SQ NP assembly and fate once intravenously injected, the present 88 study detailed characterization of siRNA-SQ NP structure and its interaction with serum 89 components.

We discovered that the siRNA-SQ bioconjugate self-assembled as 11-nm diameter core/shell supramolecular assemblies, which are connected one to another to form spherical nanoparticles of around 130-nm diameter. The siRNA-SQ NPs were stable in biological media and interacted with serum components, notably with albumin and LDL. The high specificity of siRNA to decrease or normalize gene expression and the high colloidal stability when encapsulated into squalene nanoparticles offer promising targeted therapy with wide applications for pathologies with gene expression dysregulation.

### 97 **1. Introduction**

98 Small interfering RNAs (siRNA) discovered by Fire and Mello at the end of the 90s 99 (Fire, Xu et al. 1998), are small double-stranded RNAs composed of 19-21 bases pairs with 100 3'-cohesive ends. The antisense strand is complementary to a targeted messenger RNA 101 (mRNA), leading to its degradation and gene silencing (Elbashir 2001, Elbashir, Martinez et 102 al. 2001). Despite their specificity and efficiency at low doses, their intrinsic parameters 103 constitute the main hurdles for in vivo delivery (Caillaud, El Madani et al. 2020). Indeed, in 104 blood, naked siRNAs are rapidly degraded by nucleases and cleared by glomerular filtration, 105 resulting in short plasmatic half-life (less than 15 mins) (Thompson, Kornbrust et al. 2012, 106 Ozpolat, Sood et al. 2014). Moreover, their hydrophilic and polyanionic nature prevents 107 efficient cellular uptake (Whitehead, Langer et al. 2009, Kanasty, Dorkin et al. 2013).

We previously developed an original approach for the conjugation of siRNA to squalene (SQ), a precursor of the cholesterol's biosynthesis. The so-called "Squalenoylation" technology consists of the bioconjugation of this lipid to a biologically active molecule, adopting a compact molecular conformation in aqueous media (Couvreur, Stella et al. 2006,

112 Couvreur, Reddy et al. 2008, Desmaele, Gref et al. 2012). Squalene was initially covalently 113 coupled to siRNA via maleimide-sulfhydryl chemistry and the resulting siRNA-SQ 114 nanoparticles (siRNA-SQ NPs) showed significant results in reducing tumor growth in two 115 cancer models with fusion oncogenes: RET/PTC1 and RET/PTC3 (present in papillary 116 thyroid carcinoma) and TMPRSS2-ERG (found in prostate cancer) (Raouane, Desmaele et al. 117 2011, Ali, Maksimenko et al. 2014, Ali, Urbinati et al. 2014, Urbinati, Ali et al. 2015, 118 Urbinati, de Waziers et al. 2016). The conjugation method has been further improved, 119 implementing strain-promoted azide-alkyne cycloaddition. This copper-free (Cu-free) click 120 chemistry approach increased the bioconjugation yield while preserving the antineoplastic activity of siRNA TMPRSS2-ERG-SQ NPs in a xenografted cancer model (Massaad-121 122 Massade, Boutary et al. 2018). Recently, we succeeded in delivering squalenoyl siRNA 123 targeting PMP22, an overexpressed gene causing hereditary neuropathy, *i.e.* the Charcot-124 Marie-Tooth 1A (CMT1A) disease. The intravenous administration of siRNA PMP22-SQ 125 NPs restored both motor and neuromuscular activities in transgenic mouse models (Boutary, 126 Caillaud et al. 2021). Moreover, the targeted gene expression normalization indicated that the 127 NPs successfully entered into the targeted tissue, the sciatic nerve and more specifically inside 128 Schwann cells.

129 To better understand the siRNA-SQ NPs fate, their structure, as well as their 130 biological behavior once intravenously injected into the circulating bloodstream should be investigated. Indeed, characterization of size, shape, surface properties and structure of 131 132 siRNA-SQ NPs is important because these parameters may dramatically affect their biological 133 outcome such as tissue accumulation and cell uptake (Kang, Kim et al. 2016, Dormont, 134 Rouquette et al. 2019). In our previous studies, basic physicochemical parameters, like overall 135 size and surface charge, were determined. However, their supramolecular organization, 136 another key issue for the therapeutic efficiency in terms of availability and release of the 137 active molecule (Lepeltier, Bourgaux et al. 2014, Kang, Kim et al. 2016), had never been 138 investigated. Therefore, in the present study, high-resolution small-angle scattering has been 139 performed to obtain new insights on the supramolecular organization of these nanoparticles.

*In vivo* interactions of nanoparticles with blood components represent another key point for biomedical applications. The interaction with serum biomolecules has already been investigated with squalenoyl conjugates bearing a small active functional group, like gemcitabine, doxorubicin (Sobot, Mura et al. 2017, Sobot, Mura et al. 2017, Yesylevskyy, Ramseyer et al. 2018) or adenosine (Gobeaux, Bizeau et al. 2020) but, never so far with macromolecules such as siRNA. Consequently, understanding the interaction between siRNA-SQ NPs and blood proteins is mandatory for further development towards clinical
applications. Among serum components interacting with NPs, we have focused our attention
on albumin and lipoproteins (LPs).

149 Albumin is the most abundant serum protein (55%) and acts as carrier for several other 150 endogenous proteins, such as steroids and fatty acids (Sleep 2015, Mariam, Sivakami et al. 151 2016, Lamichhane and Lee 2020). Human albumin has been investigated and approved in 152 clinics to deliver paclitaxel, a chemotherapy drug, to cancer cells (Abraxane®) or to extend 153 the plasmatic half-life of insulin hormone linked to a fatty acid (Levemir®), which allows for 154 98% binding to this protein (Kratz 2008). On the other hand, lipoproteins (LPs) are the third 155 most abundant plasma molecules in humans. They consist of an assembly of lipids and 156 proteins. Low-density lipoproteins (LDL) are the main carriers for cholesterol (75%) and fatty 157 acids in mammals (Schumaker and Adams 1969). Thanks to their apolipoproteins 158 (amphiphilic protein) embedded in the outer membrane, LPs bind to lipoprotein receptors 159 resulting in cellular uptake by clathrin-mediated endocytosis (Chaudhary, Bower et al. 2019). 160 These macromolecules interact in the bloodstream with lipophilic drugs and deliver them to 161 tissues, such as the liver and tumors (Wolfrum, Shi et al. 2007, Wasan, Brocks et al. 2008, 162 Chaudhary, Bower et al. 2019).

In the present study, we first fully characterized the external and internal structure of siRNA-SQ NPs at the supramolecular level and we assessed the interactions between siRNA-SQ NPs and serum components, notably albumin and LDL.

### 167 **2. Materials and Methods**

### 168 **2.1. Chemicals**

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170 All chemicals used were of highest analytical grade and purchased from Sigma–Aldrich. The 171 anhydrous solvents were dried and distilled before use (tetrahydrofuran (THF) on 172 Na/benzophenone) and reactions sensitive to air or humidity were performed under nitrogen 173 pressure.  $D_2O$  (99.85% D) for small angle neutron scattering (SANS) experiments was 174 purchased from Eurisotop (France).

Modified siRNAs for the Cu-free click chemistry reactions were purchased from Eurogentec
(France). Azido-Squalene and cationic squalenaldehyde hydrazinoguanidinium acetate salt
(SQ<sup>+</sup>) were synthetized according to our previous studies (Bertrand, Lucas et al. 2015,
Massaad-Massade, Boutary et al. 2018). Dulbecco's modified Eagle medium (DMEM), OptiMEM, fetal bovine serum (FBS) were purchased from Fisher Scientific (Illkirch, France).
UltraPure<sup>TM</sup> distilled water (Dnase and Rnase free water) purchased from Invitrogen. Water
was purified using a Milli-Q system.

LDLs from human plasma [dissolved in 10 mM Tris, 150 mM NaCl, 0.3 mM EDTA pH 8.3 and 2 mM NaN<sub>3</sub>] were purchased from Invitrogen (Thermo Fisher Scientific). For small-angle scattering and fluorescence experiments, lyophilized BSA powder was dissolved to a 200  $\mu$ M concentration in 0.2 M Phosphate Buffer Saline (PBS) then in H<sub>2</sub>O for standard experiments and in D<sub>2</sub>O for SANS experiments. BSA solutions were dialyzed overnight against at least a 10-fold volume PBS/D<sub>2</sub>O (or PBS/H<sub>2</sub>O) solution, then stored at 4 °C. FBS was also dialyzed overnight against PBS/D<sub>2</sub>O just after bottle opening.

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### 2.2. siRNAs used and chemical modifications

191 The siRNA targeting RET/PTC1 and PMP22 used in the experiments were previously 192 described (Ali, Maksimenko et al. 2014, Massaad-Massade, Boutary et al. 2018, Boutary, 193 Caillaud et al. 2021). All single-stranded RNAs were synthesized by Eurogentec (France) and 194 purified by RP-HPLC. Single-strand RNAs were synthesized as 19-mers with two 3'-195 overhanging 2'-deoxynucleotide residues to provide stabilization against nucleases, as 196 described by Tuschl et al. (Tuschl 2002). To allow conjugation with squalene, a 197 dibenzocyclooctyne (DBCO) reactive group and a linker N-(hexamethylenyl)-6-198 oxohexanamide spacer (C6) were introduced at the 5'-end of the sense strand of each siRNA 199 (Massaad-Massade, Boutary et al. 2018).

To anneal naked siRNA (*i.e.* siRNA not coupled to SQ), equimolar amounts of sense and antisense strands were mixed with the hybridization buffer [30 mM HEPES-KOH (pH 7.4), 2 mM Mg acetate, 100 mM K acetate]. The mixture was incubated for 3 min at 95°C and then for 45 min at room temperature before being stored at -80°C.

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### 2.3. Preparation of siRNA-SQ nanoparticles

206 Cu-free click chemistry, a 1,3-dipolar cycloaddition was developed by our lab as previously 207 described (Massaad-Massade, Boutary et al. 2018, Boutary, Caillaud et al. 2021). Then, the 208 siRNA-SQ NPs were prepared by inverse nanoprecipitation in acetone/water as sketched in Figure S1. Practically, annealed siRNA-SQ bioconjugates in UltraPure<sup>TM</sup> distilled water 209 210 (Dnase and Rnase free water) were added drop wisely to a stirred organic phase (acetone) 211 with a volume/volume ratio of 1 [organic phase]: 2 [aqueous phase]. Then acetone was 212 evaporated using nitrogen flux for 30 min to obtain an aqueous suspension of pure siRNA-SQ 213 NPs.

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### 2.4. Physicochemical characterization of siRNA-SQ nanoparticles

217 Hydrodynamic diameter, PDI and  $\zeta$ -potential were measured by dynamic light scattering 218 (DLS) using the Malvern Zetasizer Nano ZSP (Malvern Instrument) with a scattering angle of 219 173° for size measurements. Samples were analyzed at 10  $\mu$ M concentration in RNase-free 220 water.

221 Cryogenic Transmission Electron Microscopy (cryo-TEM) was performed with a JEOL 2100 222 electron microscope at the Electronic Microscopy Platform (IBPS/Institut de Biologie Paris-223 Seine, Université P. et M. Curie, Paris, France). A 4 µL drop of the concentrated siRNA-SQ 224 NPs (166 µM) was deposited on a carbon-coated copper grid. Excess liquid was removed 225 with blotting filter paper, and the samples were quickly vitrified by plunging them into liquid 226 ethane using a guillotine-like frame. The samples were then transferred to a cryo-sample 227 holder. Observations were made at an acceleration voltage of 200 kV under a low electron 228 dose. Analysis was performed with Image J software.

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### 2.5. Preparation of siRNA-SQ/SQ<sup>+</sup> NPs

Cationic squalenaldehyde hydrazinoguanidinium acetate salt ( $SQ^+$ ) was dissolved in acetone at a concentration of 1 mg/mL and added dropwisely to a suspension of already prepared siRNA-SQ NPs at a molar ratio of 1 [NPs]:100 [ $SQ^+$ ]. The organic solvent was then evaporated for 30 min under stirring using the nitrogen flow to obtain siRNA-SQ/SQ<sup>+</sup> NPs in aqueous solution. Then size and  $\zeta$ -potential were measured.

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### 2.6. Cell lines and culture

BHP 10-3 is a papillary thyroid carcinoma cell line harboring the fusion oncogene *RET/PTC1* and MSC80 is a mouse Schwann cell line expressing *PMP22*. Both cell lines were maintained at 37 °C in an atmosphere of 5% CO<sub>2</sub> and 95% humidity in complete DMEM supplemented with 10% heat-inactivated FBS, with 100 units/mL penicillin, and 100  $\mu$ g/mL streptomycin.

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### 2.7. In vitro cell transfection

One feature of siRNA-SQ NPs is that they cannot spontaneously enter into cells *in vitro* without the help of a transfection agent (Raouane, Desmaele et al. 2011, Ali, Maksimenko et al. 2014, Urbinati, Ali et al. 2015, Massaad-Massade, Boutary et al. 2018, Boutary, Caillaud et al. 2021). Therefore, Lipofectamine 2000 was used to assess naked siRNA and siRNA-SQ NPs efficiency *in vitro*.

To study the effect of surface charge,  $3 \times 10^5$  cells of BHP 10-3 and MSC80 were seeded, 24 249 250 h before transfection, in six-well plates in DMEM supplemented with 10% FBS, penicillin 251 (100 U/mL), and streptomycin (10 µg/mL). The next day, the cell medium was replaced with 252 2mL of Opti-MEM medium (Gibco Life technologies, ref. 11058021). The siRNA-SQ NPs 253 and naked siRNA were transfected using Lipofectamine 2000, according to the supplier's 254 recommendations, in the reduced Opti-MEM medium for a final concentration of 50 nM/well. 255 Similarly, siRNA-SQ/SQ<sup>+</sup> NPs and siRNA-SQ NPs alone (as a negative control) were added 256 to Opti-MEM and incubated with the cells. 4h later, the medium was replaced by complete 257 DMEM and 48 h later the experiments were stopped, and RNA was extracted to analyze 258 silencing of targeted genes RET/PTC1 and PMP22. Each experiment was performed at least 259 twice in duplicate.

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### 2.8. mRNA Extraction and Real-Time PCR (RT-qPCR) experiments

Total RNA was extracted from BHP 10-3 and MSC80 cells using the RNeasy mini-kit (Qiagen, Courtaboeuf, France). Reverse transcription was performed using the M-MLV RT buffer pack (Invitrogen, Charbonnières-les-Bains, France). Then, real-time PCR (qPCR) was carried out with the CFX96TM Real-time system (Biorad) using the Maxima Syber Green Rox qPCR master Mix (Thermo Scientific, Villebon-sur-Yvette, France), according to the manufacturer's instructions. Samples were run in duplicate; gene expression was determined by the  $2^{-\Delta\Delta Ct}$  method. Relative mRNA levels of targeted genes (*RET/PTC1* and *PMP22*) were compared to non-treated (NT) cells after normalization regarding control gene levels in at least 2 independent experiments.

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### 2.9. Small-Angle Neutron Scattering (SANS)

273 SANS experiments were carried out on the D33 spectrometer at ILL (doi: 10.5291/ILL-274 DATA.9-13-781). Samples prepared in D<sub>2</sub>O were placed in 1-mm size Hellma quartz cells 275 and thermostated at 20°C. The raw data were radially averaged, corrected for electronic 276 background and normalized by water scattering using the LAMP software (Richard, Ferrand et al. 1996). Three configurations were used to cover a q range going from 0.0013 to 0.27 Å<sup>-1</sup>: 277 1) wavelength:  $\lambda = 13$  Å, sample detector distance D = 12 m, collimation:  $\Phi = 12.8, 2$   $\lambda = 4.6$ 278 279 Å, D = 12 m, collimation:  $\Phi$  = 7.8 and 3)  $\lambda$  = 4.6 Å, D = 2 m, collimation  $\Phi$  = 7.8, for small, medium and large angles, respectively. 280

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### 2.10. Small-Angle X-ray Scattering (SAXS)

Small-angle X-ray scattering patterns (SAXS) were obtained on the SWING beamline of the SOLEIL synchrotron (Saint-Aubin, France). The scattering vector range q of  $2 \times 10^{-3}$  Å<sup>-1</sup> to 2.5 Å<sup>-1</sup> was obtained with an energy of 16 keV and two sample-to-detector distances (6 and 0.50 m for the SAXS and the wide-angle X-ray scattering ranges, respectively). The data were recorded by a two-dimensional Eiger 4M (Dectris) detector. Data reduction was performed using Foxtrot software, an application developed at SOLEIL. The sample was placed in a 1.5mm diameter quartz capillary sealed with kerosene wax.

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## 2.11. siRNA-SQ NPs internal structure characterization

Analysis of the SANS and SAXS patterns of siRNA PMP22-SQ NPs in aqueous solution 292 293 allows to draw a first sketch of the shape and internal structure of the NPs. The scattering 294 curves were fitted by SASview software (www.sasview.org/) to a lognormal sphere 295 distribution model for the siRNA-SQ particles and a cylinder model for the siRNA moiety. 296 The fitting of the experimental curves of siRNA led to a cylindrical shape whose volume was 297 given by the following formula: V(siRNA) =  $\pi \times \text{radius}^2 \times \text{height}$ . Fitting of the curves of 298 siRNA-SQ NPs gave a spherical distribution. The nanoparticle volume corresponded to: (4/3) x  $\pi$  x radius<sup>3</sup>. Consequently, the ratio between the volume of the siRNA-SQ nanoparticle and 299 300 the volume of the siRNA made it possible to determine the number of siRNAs linked to SQ in 301 a nanoparticle.

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# 2.12. Electrophoresis of siRNA PMP22-SQ NPs incubated in FBS or with serum components

306 Interactions between siRNA PMP22-SQ NPs and FBS or with one of its main components 307 (BSA or LDL) were performed by incubating increasing amounts of FBS, BSA (molar ratio) 308 or LDL (mass ratio) with 5 µM siRNA PMP22-SQ NPs for 30 min at 37°C. The same volume 309 of each aliquot was loaded into 4% agarose electrophoresis gel stained with Midori Green 310 Advance (Nippon Genetic Europe, Germany) that only reveals the oligonucleotides. The 311 molecular weight (MW) size marker served as an evidence to testify the migration of siRNA 312 PMP22-SQ NPs. Bands were revealed by camera under UV lamp illumination and recorded 313 by Visio-capt 14.2 software.

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### 2.13. BSA Fluorescence quenching

317 A series of BSA solutions at a fixed concentration (5 µM) incubated with an increasing 318 amount of siRNA PMP22-SQ NPs (BSA/siRNA PMP22-SQ molar ratios = 0.5, 1, 2, 4 and 8) 319 were analyzed. Solutions were filled into Hellma quartz Ultra-Micro cells and placed in a 320 Cary Eclipse fluorimeter (Varian, Oxford, UK) for measurements. The samples were excited 321 at 280 nm and emission scans were recorded between 300 and 550 nm. Spectra were averaged 322 over 5 measurements. Quenching experiments could affected by the inner filter effect, where 323 the sample could attenuate both the excitation beam and the emission spectrum. However, in 324 our case, we worked with rather low concentrations of both BSA and siRNA PMP22-SQ NPs, 325 and the optical density of the solutions was below 0.1; thus, this effect could be ruled out.

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### 2.14. Steady-state fluorescence

To a fixed concentration of siRNA PMP22-SQ NPs (5  $\mu$ M, *i.e.* 0.065 mg/mL), the BSA (100 µM stock solution) or LDL (2.5 mg/mL stock solution) were gradually added to achieve a final molar ratio of 1 [siRNA PMP22-SQ]:1 [BSA 5  $\mu$ M] or mass ratio of 1 [siRNA PMP22-SQ]:2 [LDL 0.12 mg/mL]. Briefly, 1 mL of a 5  $\mu$ M or 0.065 mg/mL siRNA PMP22-SQ NPs solution was filled into a Hellma Ultra-Micro quartz cell and 2  $\mu$ L of BSA or LDL were progressively added until reaching the final ratio. In parallel, BSA and LDL were added to water to reach the same final concentration. After each addition, samples were excited at 280 336 nm and the fluorescence emission spectra were recorded from 300 to 400 nm using a Horiba337 Jobin Yvon Fluorolog 3 spectrometer.

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### 2.15. Synchrotron radiation circular dichroism (SRCD)

340 Synchrotron radiation circular dichroism (SRCD) experiments were performed on the DISCO 341 beamline at the SOLEIL Synchrotron (Saint Aubin, France). The conformation of naked 342 siRNA PMP22 at two stages of NPs preparation (before and after the nanoprecipitation) was 343 performed, as well as, the study of the interaction with BSA by mixing siRNA PMP22-SQ 344 NPs and BSA at a volume/volume ratio of 1 [siRNA PMP22-SQ]:1 [BSA]. Four µL droplets 345 of the samples were placed in 3.7 µm path length CaF<sub>2</sub> cells (Hellma). The raw spectra were 346 acquired with a 1 nm spectral resolution. The spectra presented in this study were treated with 347 CDTool software that can be freely downloaded at http://www.cdtools.cryst.bbk.ac.uk/ (Miles 348 and Wallace 2018). Each is the average of three spectra. A background (water or 349 corresponding buffer spectrum recorded under the same conditions) was subtracted. Intensity 350 calibration was obtained with a camphor sulfonic acid CSA scale standard sample. Intensities 351 were converted from millidegrees ( $\theta$  machine units) into  $\Delta \varepsilon$  using the formula  $\Delta \varepsilon =$ 352  $\theta \times (0.1 \times MRW)/(3298 \times l^*C)$ , where MRW is the mean residue weight of the BSA (protein 353 weight/number of residues = 114 Da), l is the path length of the CaF<sub>2</sub> cell in cm and C is the 354 protein concentration in mg/ml. In some cases, we have added a smoothing function.

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### 2.16. Statistical analysis

358 Statistics were computed with GraphPad Prism 8.3.0 software. When we had two groups to 359 compare, the Mann-Whitney analysis was performed to assess the statistical difference. For 360 studies requiring grouped analyses, a one-way ANOVA followed by Bonferroni multiple 361 comparison test was performed. A value of p<0.05 was considered significant.

**3**63 **3. Results** 

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366 367 3.1. Structure determination of siRNA-SQ NPs

3.1.1. The physico-chemical characteristics of squalenoyl siRNA nanoparticles are nucleoside sequence-independent

368 To obtain nanoparticles, an inverse nanoprecipitation method (Bilati, Allémann et al. 369 2005) was performed by the addition of the aqueous solution containing the siRNA-SQ 370 bioconjugates into acetone as an organic solvent, where siRNA-SQs were not soluble. The 371 size and polydispersity of two resulting nanoformulations with siRNA RET/PTC1 or siRNA 372 PMP22 were measured by DLS (Figures 1A and 1B). For the siRNA RET/PTC1, 373 conjugation to SQ led to 180 nm NPs with a homogeneous distribution as indicated by the 374 polydispersity index (PDI; less than 0.2). Surface charge of NPs was negative, around -35 375 mV, which favors colloidal stability of the NP suspension (Figure 1C). For siRNA PMP22, 376 the results were similar: NPs size was 218 nm, PDI < 0.2 and surface charge -40 mV. No 377 significant difference was observed between siRNA RET/PTC1-SQ and siRNA PMP22-SQ 378 NPs in terms of size, polydispersity index and  $\zeta$ -potential (Figures 1A, 1B and 1C). As no 379 significant difference was found concerning the physicochemical parameters of both siRNAs 380 (PMP22 or RET/PTC1) and previously with the siRNA TMPRSS2-ERG (Massaad-Massade, 381 Boutary et al. 2018), it was decided to continue further experiments with the siRNA PMP22-382 SQ NPs. This resolution is also supported by our recent findings showing that the siRNA 383 PMP22-SQ NPs could lead to a targeted therapy for CMT1A neuropathy (Boutary, Caillaud 384 et al. 2021).

Then, the siRNA PM22-SQ NPs were observed by cryo-TEM (**Figure 1D**). Spherical nano-objects of around 130 nm in size were observed. Interestingly, the shape and size were in accordance with our previous observations (Massaad-Massade, Boutary et al. 2018).



388 Figure 1: Physicochemical characterization of siRNA-SQ NPs. After inverse nanoprecipitation of siRNA RET/PTC1-SQ NPs and siRNA PMP22-SQ NPs the size (A) and 389 390 polydispersity index (B) were measured by dynamic light scattering and the surface charge 391 (C) by electrophoretic light scattering. Three measurements were performed and the average 392 diameter  $\pm$  standard error of the mean (SEM) of more than 5 independent nanoformulations, 393 was calculated. Using the Mann and Whitney test, no significant difference between the two 394 nanoformulations was found. D) Micrography of siRNA PMP22-SQ NPs by cryoTEM. The 395 siRNA-SQ NPs are spherical with a diameter of around 130 nm.

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- 3.1.2. Inversion from negative to positive charge of siRNA-SQ NPs improves their transfection
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400 To understand the impact of surface charge on the internalization of siRNA-SQ NPs, 401 several experiments were conducted in vitro. Previously, we showed that the siRNA-SQ NPs 402 were unable to enter cultured cells spontaneously without any cationic transfection agent 403 (Raouane, Desmaele et al. 2011, Ali, Maksimenko et al. 2014, Boutary, Caillaud et al. 2021). 404 We postulated that the negative surface charge of siRNA-SQ NPs prevented cell uptake due 405 to electrostatic repulsion with the negative plasma membrane. It is well known that cationic 406 nanoparticles had a higher internalization rate than neutral and negative nanoparticles. This 407 difference can be explained by Coulomb's law, where opposite charges are attracted to each 408 other. Thus, the cationic nanoparticles can be delivered to the cytoplasm by electrostatic 409 attraction with the negatively charged cell membranes. To confirm this assumption, we 410 modified the nanoparticle charge by addition of cationic guanidium-squalene to the siRNA-SQ NPs (Figure 2A). The resulting positive nanoparticles were then incubated with BHP 10-411 412 3 and MSC80, two cell lines of different origins (tumoral and normal). Interestingly, the 413 inhibition of the targeted gene expression without using lipofectamine testified that the uptake

414 of the nanoparticle is facilitated by the use of a cationic compound (Figures 2B and 2C).



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Figure 2: Positively charged siRNA-SQ NPs are successfully cell internalized. A) 416 417 Physicochemical characteristics of NPs. No statistical difference was observed between siRNA-SQ NPs and siRNA-SQ NPs: SQ<sup>+</sup> for their size and PDI. Using the Mann-Whitney 418 419 test, a statistical difference was found concerning the zeta potential between the siRNA-SQ 420 NPs and siRNA-SQ NPs:SQ+ (p < 0.001). B and C) mRNA inhibition. BHP 10-3 B) and 421 MSC80 C) cells were transfected with 50 nM siRNA RET/PTC1 or PMP22-SQ NPs with or 422 without SQ<sup>+</sup>. NT: non-treated cells. Lipofectamine was also used to transfect the naked 423 siRNA and siRNA RET/PTC1 or PMP22-SQ NPs (positive controls). 48 hours later, cells were harvested, RNA was extracted, and RT-qPCR performed. One-way Anova followed by a 424 425 Bonferroni test was used to assess the significant difference between treatments: \*\*\* p < p426 0.0001, compared to NT and untransfected targeted gene-SQ NPs ; \$ p < 0.0001 when 427 compared to transfected naked siRNA RET/PTC1 and siRNA RET/PTC1-SQ NPs by 428 lipofectamine.

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### 3.1.3 Spherical nanoparticles contain core/shell assemblies

Based on our previous results showing impressive therapeutic results in several tumor models (thyroid and prostate cancers (Ali, Urbinati et al. 2012, Urbinati, Hafiz et al. 2013, Ali, Maksimenko et al. 2014, Ali, Urbinati et al. 2014, Urbinati, Ali et al. 2015, Urbinati, de Waziers et al. 2016) as well as in monogenic neuropathy (CMT1A (Boutary, Caillaud et al. 2021)) and considering that cationic lipid have a higher *in vivo* toxicity (Caillaud, El Madani et al. 2020), we decided to deeply characterize the conjugated siRNA-SQ nanoparticles. 437 To verify that the conjugation to SQ and the formulation as nanoparticle did not induce 438 changes in siRNA conformation, circular dichroism measurements were performed. As shown 439 in Figure S2A, naked siRNA PMP22 and siRNA PMP22-SQ both before and after 440 nanoprecipitation displayed the same spectrum type, confirming that the  $\alpha$ -helix structure of 441 the siRNA was kept intact after chemical conjugation to SQ and formulation as nanoparticles. 442 Small-angle scattering methods are prominent tools for characterizing such nanometric 443 colloidal suspensions. Taking advantage of the high difference of the scattering length density 444 between hydrogen and deuterium, small-angle neutron scattering (SANS) represents, indeed, 445 a method of choice to characterize the size distribution of hydrogenated colloids in a 446 deuterated solvent and it has been proven previously to be a good way of characterizing the 447 size of the squalene-based nanoparticles (Saha, Testard et al. 2015, Rouquette, Ser-Le Roux et 448 al. 2019, Gobeaux, Bizeau et al. 2020). On the other hand, small-angle X-ray scattering 449 (SAXS), which is sensitive to contrasts in electron densities, offered a description of the 450 squalenovl siRNA nanoparticles with deeper access to their internal structure. In the case of 451 siRNA PMP22-SQ NPs, it was relevant to combine SANS and SAXS analysis since the 452 former would be capable of detecting a larger contrast between the solvent and the full 453 squalene derivative, and the latter between the solvent and the siRNA moiety (Figure 3A). The SANS of a 45 µM suspension of siRNA PMP22-SQ NPs is shown in Figure 3B. This 454 455 pattern was not sensitive to dilution and the nanoparticle size remained stable under a dilution factor of two (Figure S2B). The absence of structural peaks in the wide-angle region (q >456 0.04 Å<sup>-1</sup>) indicated that the nanoparticle core displayed no regular crystal-like structure, in 457 accordance with cryo-TEM images (see Figure 1). In the medium q-range (0.006 to 0.02 Å<sup>-1</sup>), 458 the scattering intensity followed a power-law in  $q^{-3.44}$  slightly deviating from the  $q^{-4}$  expected 459 for sharp interfaces (Porod's Law (Guinier, Fournet et al. 1955)) between particle surfaces 460 461 and solvent. If such observation may eventually indicate a slightly diffuse or fractal interface, 462 it was however unlikely, given that the siRNA PMP22-SQ NPs surface appeared rather 463 smooth in the cryo-TEM images. At the lowest wavevectors, the scattering intensity reached 464 the onset of a plateau indicating a finite size. A simple Guinier analysis gave a gyration radius  $(R_g)$  of 80 nm that corresponded to a hydrodynamic radius (as it would be determined by 465 466 DLS) of 103 nm for a spherical shape. Overall, this scattering pattern could be fitted by 467 considering a lognormal distribution of spheres (black line on red pattern in Figure 3B), with 468 a median radius of 61.9 nm and a polydispersity index (PDI) of 0.25. The corresponding 469 diameter distribution resulting from this fit is presented in Figure 3C.

470 The SAXS pattern of a 263 µM solution of siRNA PMP22-SQ NPs (blue pattern) is 471 presented in Figure 3D. Again, no specific structural peak could be observed in the large qregion ( $q > 0.3 \text{ Å}^{-1}$ ). On the contrary to the SANS pattern, two large oscillations were visible 472 in the middle q-range (0.007 < q < 0.3 Å<sup>-1</sup>), that could be attributed to siRNA moieties in the 473 474 nanoparticle or at least to electronic density heterogeneities in the particle. As a matter of 475 comparison, the SAXS pattern of the siRNA PMP22 moiety (224 µM) was also plotted (green 476 pattern). The scattering pattern originating from the naked siRNA PMP22 dispersion 477 exhibited an oscillation in the same q-range and could be fitted by a cylindrical form factor (L 478 = 7.1 nm, R = 1.1 nm), in accordance with the SANS analysis of similar siRNA strands 479 reported by Ristori et al. (Ristori, Ciani et al. 2012) (Table S1). This characteristic shape was 480 found again in the oscillation, visible in the large q of the siRNA PMP22-SQ pattern, 481 yielding the following dimensions: L = 4 nm and R = 1.1 from the fitting by a cylindrical form 482 factor. The other oscillation (at lower q) could be fitted by spheres with a radius of 5.5 nm. 483 Since these spheres could accommodate the siRNA strands, we suggested that the siRNA 484 PMP22 moieties were segregated and surrounded by the squalene moiety in core/shell 485 assemblies with interconnections of the squalene moieties within the NPs. The obtained 486 dimensions indicated a heterogeneity in electronic density inside the NPs, but without long 487 range ordering.



488

Figure 3: Structural characterization of siRNA PMP22-SQ NPs by small-angle
 scattering.

492 A) Scattering length densities show that the SANS approach allows to characterize the overall 493 structure of the nanoparticles and the SAXS analysis to characterize the siRNA encapsulated 494 within the NPs. The solvent used are  $H_2O$  and  $D_2O$  for SAXS and SANS, respectively. **B**) 495 SANS pattern for siRNA PMP22-SQ NPs (open circles) depicting a fit with a lognormal 496 distribution of spheres (black trace). C) SANS view software analysis of the fit B showed that 497 the corresponding siRNA PMP22-SQ NPs diameters are 124 nm. D) SAXS patterns of the 498 naked siRNA PMP22 (green circles) and of siRNA PMP22-SQ NPs (blue circles) with their 499 corresponding fits (black traces). The naked siRNA PMP22 can be fitted by a 7 nm-long cylindrical shape and a scattering in  $q^{-3}$  in the low q range (a signature of aggregation). A 500 combination of 4 nm cylindrical and 11 nm spherical shapes was found for the internal 501 organization of the siRNA PMP22-SQ NPs. 502

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3.1.4. A 130 nm nanoparticle can encapsulate around 60 000 siRNAs

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506 The structural model of siRNA PMP22-SQ NPs is illustrated by the sketch in **Figure** 507 **4**. The siRNA PMP22-SQ bioconjugate monomer is represented by a green cylinder for the 508 siRNA moiety and a yellow lipid tail for the squalene moiety (**Figure 4A**). The 509 supramolecular organization inside the nanoparticle is represented by 11-nm core/shell 510 spheres with the lipidic moieties surrounding the hydrophilic siRNAs (Figure 4A). As no 511 specific inner structure was apparent in the cryo-TEM images, the core/shell structures were 512 supposed to be randomly distributed inside the whole nanoparticle volume. Therefore, 513 representation of a top view nanoparticle cross-section depicts a random pattern of circular 514 motifs (Figure 4B). Since the formation of squalene-based nanoparticles was clearly driven 515 by hydrophobic interactions (Lepeltier, Bourgaux et al. 2014), we assumed that the squalene 516 shells around the hydrophilic siRNA core could be interpenetrated and formed a continuous 517 lipophilic network and it is most likely that some charged hydrophilic siRNA strands point 518 towards the solvent (represented by the green circle around the yellow one in Figure 4B). By 519 a simple geometrical calculation (volume of nanoparticle/volume of siRNA), we could 520 estimate that one nanoparticle contained on average 60,000 siRNA PMP22-SQ bioconjugates.



521 522 Figure 4: Graphical representation of a siRNA PMP22-SQ nanoparticle as determined 523 by the fit of the scattering patterns. A) Sketch of siRNA PMP22-SQ monomer. The siRNA 524 moiety (green) of the bioconjugate can be viewed as a cylinder (siRNA not to scale in 525 comparison to others chemical entities). The squalene moiety is depicted in yellow. The 526 SAXS pattern reveals 11-nm spherical structures inside the nanoparticle that we view as self-527 assembled core/shell domains with a siRNA core surrounded by squalene which could 528 interpenetrate with the other squalene moieties. B) Representation of a cross-section of 2D 529 siRNA PMP22-SQ nanoparticle. The core/shell spheres of 11-nm each are randomly arranged 530 inside the nanoparticle. The 2D cross section is the cause of the difference in the core/shell 531 sphere size in the sketch. 532

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### 3.2. siRNA PMP22-SQ NP interactions with serum and its components

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3.2.1. Serum components stabilize siRNA PMP22-SQ NPs

537 SANS was performed to determine the influence of fetal bovine serum (FBS), a 538 biological medium with high ionic strength containing several proteins, on the structure of siRNA PMP22-SQ NPs. In the low q range (q < 0.003 Å<sup>-1</sup>), the resulting SANS patterns did 539 540 not show strong deviation from the scattering intensity of the siRNA PMP22-SQ suspension 541 (at similar concentration) (Figure 5A). No intensity increase was observed, as it could be 542 expected when particles are growing or when attractive interactions appear between particles. 543 It demonstrates that siRNA PMP22-SO NPs were colloidally stable and did not aggregate in 544 this complex mixture. On the contrary, the scattering intensity arising from the siRNA 545 PMP22-SQ NPs slightly decreased. As confirmed by the fitting curve (black line on Figure 5A), the SANS pattern of the mixture appeared to be a linear combination of the two 546 reference patterns. If we consider the formula:  $I_{fit} = A \times I_{single}(siRNA PMP22-SQ NPs)_{ini} +$ 547 548  $B \times Isingle(FBS)_{ini}$ , the best fit was obtained for A = 0.87 and B = 0.98, demonstrating that 549 only 13% of the siRNA PMP22-SQ signal had disappeared. The same result has been 550 observed after incubation of siRNA PMP22-SQ NPs with a high concentration of bovine 551 serum albumin (BSA) (200 µM, green pattern in Figure 5B). As with FBS, SANS patterns of 552 BSA alone (red pattern) or siRNA PMP22-SQ NPs alone (blue pattern) were also recorded. 553 Likewise, the scattering intensity was not much modified at small q. Thus, neither siRNA 554 PMP22-SQ NPs nor FBS or BSA were significantly affected by the presence of each other. 555 Therefore, it was concluded that siRNA PMP22-SQ NPs had a high colloidal stability in both 556 biological media.



**Figure 5: The siRNA PMP22-SQ NPs are stable in FBS and in the presence of high BSA concentration**. **A**) SANS pattern of siRNA PMP22-SQ NPs/FBS mixture (yellow circles). Blue circles: 23  $\mu$ M [siRNA PMP22-SQ] in D<sub>2</sub>O, red circles: FBS dialyzed against D<sub>2</sub>O and diluted by a factor of 2 to reach the same concentration as in siRNA PMP22-SQ NPs/FBS mixture. The smooth black curve corresponds to a linear combination of the FBS and siRNA PMP22-SQ NPs curves. **B**) SANS pattern of siRNA PMP22-SQ NPs/BSA mixture (green circles). Blue circles: 23  $\mu$ M [siRNA PMP22-SQ] in D<sub>2</sub>O, red circles: 200  $\mu$ M [BSA] in D<sub>2</sub>O. 565

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3.2.2. Serum neutralizes the siRNA-SQ NPs surface charge

568 The ζ-potential increased progressively towards neutrality when siRNA PMP22-SQ 569 NPs were incubated with 0.2 % to 100 % of FBS (Figure 6A). The 100% of FBS represent its 570  $\zeta$ -potential and is used as a control to discriminate the  $\zeta$ -potential of the nanoparticles from 571 the undiluted FBS. These results highlighted the strong interaction occurring between some 572 FBS components and siRNA PMP22-SQ NPs. Interaction with serum components was also 573 confirmed by electrophoresis (Figure 6B). A progressive slowdown of migration reflected by 574 a delay in their electrophoretic mobility was observed when siRNA PMP22-SQ NPs were 575 incubated in FBS (respectively around 350 kb for NPs with FBS as against around 150 kb for 576 NPs in  $H_2O$ ). Interestingly, this phenomenon was observed at very low FBS concentration 577 (2%). Taken together, these results showed that FBS modified the surface charge and 578 electrophoretic mobility of siRNA-SQ NPs.



**Figure 6: siRNA PMP22-SQ NPs interact with serum components. A)** Measurements of the siRNA-PMP22-SQ NPs  $\zeta$ -potential in the presence of increasing concentrations of FBS (from pure water (0% FBS) to pure FBS (100%). \* p < 0.05, \*\*p<0.001 and \*\*\*\*p<0.00001 by using One-way Anova followed by a Bonferroni test. B) The siRNA PMP22-SQ NPs were incubated with increased concentration of FBS and loaded onto 4% agarose electrophoresis gel, then stained by Midori, a nucleotide maker. Migration slows down when FBS is added to

the siRNA PMP22-SQ NPs (red arrow, wells 3 to 8), compared to siRNA PMP22-SQ NPs in

587 water (black arrow, well 1).

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3.2.3. siRNA PMP22-SQ NPs interact with BSA

589 Albumin is the main serum component, representing around 55% of total protein 590 content. BSA has intrinsic fluorescence, due to its amino acid, tryptophan, which can be 591 recorded by fluorescence emission spectroscopy. Thus, the interaction between BSA and 592 siRNA PMP22-SQ NPs was investigated by two fluorescence spectroscopic approach: Stern-593 Volmer quenching and steady-state fluorescence. First, by using the Stern-Volmer quenching 594 experiment, we showed an interaction between siRNA PMP22-SQ NPs and BSA (Figure 595 7A). Indeed, when BSA was incubated with increasing siRNA PMP22-SQ concentrations, the 596 intrinsic fluorescence of BSA was quenched, represented by a reduction of fluorescence 597 emission compared to BSA alone at 5 µM (red curve in Figure 7A). These results were 598 determined according to the Stern-Volmer equation described in Supplementary 599 information, equation A. The value obtained for the quenching rate constant,  $K_{q}$ , was higher than  $10^{10}$  mol.L<sup>-1</sup>.s<sup>-1</sup>, suggesting a static mechanism with the formation of a complex between 600 601 BSA and siRNA PMP22-SQ NPs (Table 1). The equivalent of the affinity constant for the kinetic intermediate, the Stern-Volmer constant, was equal to  $2.60 \pm 0.80 \times 10^5$  L.mol<sup>-1</sup>. All 602 603 the obtained values are presented in Table 1.

604Table 1: Numerical values based on linear fit of Stern-Volmer and Steady-state605equations

Constants		Value	Unit	
Quenching rate constant	Kq	$2.60\pm0.80$	$\times 10^{13} \text{ L.mol}^{-1}.\text{s}^{-1}$	
Stern-Volmer constant (kinetic intermediate)	K <sub>sv</sub>	$2.60 \pm 0.80$	$\times 10^5 \text{ M}^{-1}$	
Overall affinity constant (final thermodynamic complex)	Ka	2.34 ± 0.59	x 10 <sup>7</sup> M <sup>-1</sup>	

In the steady-state fluorescence approach, BSA was progressively titrated against siRNA PMP22-SQ NPs suspension, to a final molar ratio of 1 [siRNA PMP22-SQ]:1 [BSA]. In parallel, BSA was added to distilled water at the same concentration and the final spectra were compared. The presence of siRNA PMP22-SQ NPs led to a significant modification of the BSA emission spectrum (red curve in **Figure 7B**) compared to that of BSA alone in water (black curve in **Figure 7B**). Indeed, we observed a smaller fluorescence intensity under the final experimental conditions and a shift in the maximum fluorescence intensity (from 351 nm

for BSA alone to 349 nm for NPs-BSA), which indicated the formation of a complex between the two species (*i.e.*, siRNA PMP22-SQ NPs and BSA). The interaction mechanism could be probed by several equations according to the species in solution that are dependent on pH and temperature (**Supplementary information, equation B**). The linear least-squares regression showed good correlation between siRNA PMP22-SQ NPs and BSA (**Figure 7C**). The calculated overall apparent dissociation constant, K<sub>obs</sub>, was equal to  $4.95 \pm 1.38 \times 10^{-8}$  M (n = 3; pH 7) with an overall affinity constant, K<sub>a</sub>, of  $2.34 \pm 0.59 \times 10^{7}$  M<sup>-1</sup>.

620 Using both spectroscopic approaches, we showed the formation of a complex between siRNA PMP22-SQ NPs and BSA. However, there was a disparity between the affinity 621 622 constants obtained. This could be explained by the experimental conditions, especially the 623 time (Figure 7D). Indeed, with Stern-Volmer quenching, a kinetic intermediate (BSA-NPs)' was obtained with  $K_a$ ' of 2.6 x 10<sup>5</sup> M<sup>-1</sup>. The slow titration of the steady-state fluorescence led 624 to the final thermodynamic complex between BSA and NPs: BSA-NPs ( $K_a = 2.34 \pm 0.59 \text{ x}$ 625 10<sup>7</sup> M<sup>-1</sup>). Therefore, the intermediate complex underwent a conformational change which 626 627 allowed to attempt its final thermodynamic state by increasing even more the stability of the 628 complex by a factor of 100.



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Figure 7: Spectroscopic analysis of siRNA PMP22-SQ NPs/BSA mixtures. A) SternVolmer quenching of BSA in the presence of siRNA PMP22-SQ NPs. The fluorescence
intensity of BSA decreases progressively in the presence of siRNA PMP22-SQ NPs. B)
Steady-state experiment showing the emission fluorescence spectra at the end of the

experiment, excitation wavelength ( $\lambda_{ex} = 280$  nm), pH 7.4 at 37°C: BSA (5  $\mu$ M, black curve) 634 and BSA (5  $\mu$ M) + siRNA PMP22-SQ (5  $\mu$ M) in red. The maximal fluorescence intensity 635 decreases, and the emission wavelength shifts by 2 nm (from 351 nm to 349 nm) when BSA 636 interacts with siRNA PMP22-SQ NPs. Fluorescence intensity has been normalized on BSA 637 maximum peak. C) Linear least-squares regression of the formula given in the 638 Supplementary information, equation 2 ( $R^2 = 0.9972$ ). D) Graphical representation 639 640 showing the relationship between Stern-Volmer and steady-state approaches, showing the affinity constants, Ka' and Ka 641

642 The interaction between BSA and siRNA PMP22-SQ NPs was further investigated by 643 circular dichroism spectroscopy (Figure 8A). Incubation of BSA with siRNA PMP22-SQ 644 NPs resulted in a decrease of 8% to 10% in the absolute signal intensity. Secondary structure 645 quantifications of BSA was performed by using BestSel software, showing a slight decrease 646 in the number of  $\alpha$ -helices, similarly to concentrated BSA (Figure S3). This interaction 647 between BSA and siRNA PMP22-SQ NPs was also tested by electrophoresis gel. Migration 648 of siRNA PMP22-SQ NPs was slowed down after incubation with increasing concentrations 649 of BSA (Figure 8B). At molar ratio [siRNA PMP22-SQ] 1: 4 [BSA], migration delay was 650 maximum and we estimated that around 10 BSA molecules surrounded 1 nanoparticle 651 (Supplementary information, equation C). Taken together, both results highlighted the 652 formation of a NPs-BSA complex. However, this complex was not able to modify the BSA 653 secondary structure.





**Figure 8: siRNA PMP22-SQ NPs interact with BSA. A)** Circular dichroism spectrum of BSA alone (orange curve) and in the presence of siRNA PMP22-SQ NPs (red curve). In water, BSA spectra exhibits one positive peak at 192 nm and two negative bands at 210 and 224 nm, both characteristic of the  $\alpha$ -helical structure. A decrease in the BSA signal in the presence of siRNA PMP22-SQ NPs is observed. **B)** Gel electrophoresis representing the migration of the siRNA PMP22-SQ NPs (5  $\mu$ M) incubated at 37°C with increasing BSA

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### 3.2.4. siRNA-SQ NPs interact with LDL.

667 Finally, we focused on the low-density lipoproteins (LDL), that carry 75% of blood 668 cholesterol in humans. Incubation of siRNA PMP22-SQ NPs with increasing amounts of LDL 669 showed a slowdown of the gel electrophoresis migration testifying an interaction between the 670 two species (Figure 9A). In addition,  $\zeta$ -potential measurements revealed a significant 671 progressive increase of the NPs surface charge with increasing LDL concentration (Figure 672 **9B**). These results were confirmed by the fluorescence spectrum of the LDL (Figure 9C), which weakened in the presence of the NPs and was accompanied by a 5-nm shift in the peak 673 674 emission wavelength. This clearly confirmed the formation of a siRNA PMP22-SQ NPs -675 LDL complex.

concentration loaded on 4% agarose gel. Migration progressively slows down (red arrow,

wells 4 to 8), compared to siRNA PMP22-SQ NPs in water (black arrow, well 1).

676



677 Figure 9: siRNA-SQ NPs interact with LDLs. A) Gel electrophoresis showing the 678 migration of siRNA PMP22-SQ NPs incubated at 37°C with increasing LDL concentration 679 680 loaded on 4% agarose gel. Migration progressively slows down (red arrow, wells 5 to 7), 681 compared to siRNA PMP22-SQ NPs in water (black arrow, well 1). B) ζ-potential measurement after incubation with growing concentrations of LDL. \*\*\* p < 0.0001 vs siRNA 682 683 PMP22-SQ NPs (One-way Anova followed by a Bonferroni test). C) Emitted fluorescence 684 spectrum of LDL in the absence (black curve) or presence of siRNA-SQ NPs (red curve). The maximal fluorescence intensity decreases and there is a 5 nm shift of emission peak (from 337 685 686 nm to 342 nm) when LDL interacts with siRNA PMP22-SQ NPs. Fluorescence intensity has 687 been normalized to LDL peak maximum.

688 689 3.2.5. siRNA PMP22-SQ NPs interact via the squalene moiety with serum components

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NPs made from small molecules linked to squalene, including nucleoside analogs,
interact with serum components *via* the SQ moiety (Sobot, Mura et al. 2017, Sobot, Mura et al. 2017, Yesylevskyy, Ramseyer et al. 2018). To confirm that similar interaction could occur

with siRNA PMP22-SQ NPs and FBS or its components (*i.e.*, BSA and LDL), naked siRNA
PMP22 (*i.e.* not conjugated with SQ) was incubated with increasing amounts of whole serum,
BSA or LDL, before electrophoresis were performed. Contrary to siRNA PMP22-SQ NPs,
migration of serum and serum components did not slow down (Figure 10). This confirmed
that the interaction of nanoparticles with serum components occurred well *via* the squalene
moiety and not *via* the oligonucleotide moiety.



Figure 10: Naked siRNA PMP22 do not interact with total serum, BSA and LDL. 4%
non-denaturated agarose electrophoresis were performed after incubation of naked siRNA
PMP22 with increasing amounts of FBS (A), BSA (B, molar ratio) and LDL (C, mass ratio).
No slowdown of migration was observed.

705 **4. Discussion** 

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706 Conjugation of siRNA to squalene by Cu-free click chemistry, has been previously 707 demonstrated to protect the double-strand oligonucleotide from degradation and to treat 708 different experimental diseases such as cancer with fusion oncogene or peripheral neuropathy 709 (Massaad-Massade, Boutary et al. 2018, Boutary, Caillaud et al. 2021). To be injectable and 710 efficient *in vivo*, squalenovl siRNAs needed to be formulated as nanoparticles. However, due 711 to the different molecular weight of the two bioconjugate moieties (*i.e.*, ~ 13,000 Da for 712 siRNA /~ 494 Da for SQ forming a ratio of 26/1 between hydrophilic siRNA and lipophilic 713 squalene) and because the siRNA-SQ bioconjugates were not soluble in organic solvents but 714 totally soluble in water, an inverse nanoprecipitation protocol has been optimized by adding 715 the aqueous phase to the organic one, before solvent evaporation to obtain the final siRNA-716 SQ NPs suspension (Bilati, Allémann et al. 2005).

The size and size distribution of the nanoparticles are important parameters for drug delivery systems. Using DLS, a rapid method for determination of nanoparticles size, we found that the diameter of squalenoyl siRNA nanoparticles were nucleoside sequence independent. Indeed, both siRNA PMP22-SQ and RET/PTC1-SQ nanoparticles displayed similar dimension, around 200 nm with a negative charge less than -30 mV; they were stable for a month at 4 °C (Massaad-Massade, Boutary et al. 2018, Boutary, Caillaud et al. 2021). As no significant difference was found concerning their physicochemical parameters, it was decided to use the siRNA PMP22-SQ NPs for all further experiments. This resolution was
also supported by our recent findings concerning the therapeutic efficiency of siRNA PMP22SQ NPs as a targeted therapy for CMT1A neuropathy (Boutary, Caillaud et al. 2021).

727 Then, the siRNA PM22-SQ NPs were observed by cryo-TEM. Spherical nanoobjects of 728 around 130 nm in size with no specific internal structure were observed similar to our 729 previous observation on siRNA TMPRSS2-ERG-SQ NPs, which confirmed once again that 730 the size was independent of the nucleoside sequence (Massaad-Massade, Boutary et al. 2018). 731 Of note, cryoTEM is more specific than DLS, since it provides additional information on 732 shape and morphology. The smaller nanoparticles size observed by cryoTEM was explained 733 by the fact that laser light scattering measured the hydrodynamic size when cryoTEM allowed 734 to visualize the nanoparticle core only. Small-angle neutron scattering (SANS) confirmed the 735 observed size and shape of the siRNA PMP22-SQ nanoparticles. Altogether DLS, cryo-TEM 736 and SANS analysis represented complementary approaches, giving an ensemble picture of the 737 siRNA PMP22-SQ NPs.

738 To describe more precisely the internal composition and the siRNA organization inside of 739 the NPs, SAXS analysis have been performed, which depicted that the siRNA PMP22-SQ 740 bioconjugates self-organized in water into small core/shell domains of 11-nm size with the 741 lipidic moiety exposed to the outside and the siRNA located in the core, without modification 742 of the  $\alpha$ -helix structure of the nucleic acid. We assume that hydrophobic interactions are the 743 main driving force leading to the self-assembly of the nanoparticle into a 130-nm size 744 spherical random structure with some hydrophilic siRNA moieties being exposed onto the 745 nanoparticle surface for solubility reasons. To our knowledge, this unique random 746 supramolecular structure, composed of typical 11-nm size spheres with internal electronic 747 density heterogeneities, has only been observed with siRNA PMP22-SQ NPs. It confirms the 748 diversity of the squalencyl nanostructures and the flexibility of the hydrophobic squalene 749 chain which allows to self-assemble into nanoparticles, even when a hydrophilic 750 macromolecule of much higher molecular weight was attached to the SQ.

We then assessed the interaction of siRNA PMP22-SQ NPs with blood components, specifically albumin and lipoproteins. Indeed, once administered intravenously, siRNA-SQ NPs encounter different blood components that can adsorb to the NPs surface, either stabilizing or destabilizing their structure and this may dramatically impact their *in vivo* fate in terms of biodistribution, pharmacokinetics, toxicity and therapeutic efficiency (Aggarwal, Hall et al. 2009, Lesniak, Fenaroli et al. 2012, Monopoli, Aberg et al. 2012, Gao and He 2014, Marichal, Giraudon-Colas et al. 2019, Marichal, Degrouard et al. 2020). 758 It was observed that siRNA PMP22-SQ nanoparticles interacted hydrophobically, via the 759 squalene moiety, with serum components, especially BSA and LDL. Interestingly, it has been 760 reported that BSA may display some dysopsonin-like activity (Ogawara, Furumoto et al. 761 2004). These interactions with serum components can undergo conformational changes on the 762 NPs surface which could also affect their biological fates (Gunawan, Lim et al. 2014). This 763 hypothesis was assessed by SANS experiments performed in FBS and in presence of high 764 BSA concentrations. No significant modifications in the SANS pattern of the nanoparticles 765 could be observed. This proved that the siRNA PMP22-SQ NPs kept high colloidal stability 766 in biological media, contrarily to previous studies performed with small chemical molecules 767 conjugated to squalene showing a destabilization of the squalenoyl NPs in the presence of 768 blood components, with an insertion of these bioconjugates, as molecular entities, into the 769 LDL and BSA fractions (Ambike, Rosilio et al. 2011, Sobot, Mura et al. 2017, Yesylevskyy, 770 Ramseyer et al. 2018, Gobeaux, Bizeau et al. 2020). Thus, the present study clearly suggests 771 that the biological behavior of squalene-based nanoparticles may depend on the nature of the 772 associated biologically active molecule. Such different behavior of squalenoyl NPs may be 773 explained by: i) the respective molecular weight of the linked drug versus the squalene (i.e., a 774 ratio of 1 or 2 vs 26 with siRNA-SQ), ii) the different physicochemical parameters (siRNA-775 SQ is highly negatively charged) and, iii) the supramolecular organization.

776 Since LDL and HDL are the main transporters of cholesterol, an important lipid for tumor 777 cell proliferation (Chaudhary, Bower et al. 2019) and myelin synthesis (Zhou, Bazick et al. 778 2019), we hypothesize that the interaction of LDL with siRNA PMP22-SQ NPs may trigger a 779 natural nanoparticles functionalization for targeting these pathological tissues. Additionally, 780 such specific biodistribution may be amplified by the inflammation of the pathological 781 tissues, resulting in histological modifications such as defective endothelial cells with wide 782 fenestrations in cancer tissues (Tatiparti, Sau et al. 2017, Hoogenboezem and Duvall 2018) 783 and edema with lymphocyte infiltration in neurodegenerative diseases (Weis, Claeys et al. 784 2017). Especially, albumin accumulate preferentially in these type of tissues (Hoogenboezem 785 and Duvall 2018). Thus, siRNA-SQ NPs are expected to extravasate through damaged tissues, 786 as supported by our previous studies for cancers and a disease of the peripheral nervous 787 system (CMT1A), where in both pathologies a significant inhibition of the targeted gene was 788 observed in the tissues concerned (Massaad-Massade, Boutary et al. 2018, Boutary, Caillaud 789 et al. 2021).

### 790 **5.** Conclusions

791 The present study has provided an important contribution to better understand the 792 physico-chemical structures of siRNA squalene-based nanoparticles, as well as their 793 interactions with some biological components encountered after intravenous administration. 794 The high specificity of siRNA to decrease or normalize gene expression offers new outlooks 795 to cure pathologies with gene expression dysregulation such as fusion oncogene cancer or 796 hereditary monogenic peripheral neuropathy. In this area, siRNA-SQ NPs are promising new 797 potential drug candidates with wide therapeutic applications thanks to their high colloidal 798 stability. 799

### 800 **6. Credit author statement**

801 M.C. designed and performed the experiments and wrote the manuscript, F.G. contributed 802 and performed the experiments of SAXS and SANS studies, M.H. developed the 803 Fluorescence quenching experiments, S.B. contributed to the synthesis and characterization of 804 the siRNA-SQ NPs, P.G. contributed to study design and discussion, D.D developed the 805 azido-squalene synthesis, P.C. contribute on the discussion of the results and to the writing of 806 the manuscript, F.W. and I.G. performed with MC and FG the SRCD experiments, F.T. 807 contributed and performed the experiments of SAXS and SANS studies and, L.M. is the PI of 808 the study, she supervised, designed the study and contributed to the writing of the manuscript.

### 809 7. Declaration of Competing Interest

810 The authors declare that they have no known competing financial interests or personal 811 relationships that could have appeared to influence the work reported in this paper.

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998

Figure S1: Sketch of siRNA-SQ nanoparticles preparation. The siRNA-SQ bioconjugates were obtained after Cu-free click chemistry and annealing to the antisense strand. Then, the siRNA-SQ NPs were prepared by inverse nanoprecipitation : siRNA-SQ bioconjugates in water were added drop wisely to a stirred organic phase (acetone) with a volume/volume ratio of 1 [organic phase, acetone]: 2 [aqueous phase, siRNA-SQ bioconjugate]. Then acetone was evaporated using nitrogen (N2) flux to obtain an aqueous suspension of pure siRNA-SQ NPs.

- 1005
- 1006



1007 A Wavelength (nm) B Figure S2: Circular dichroism spectrum of siRNA. A) Naked siRNA (blue curve); siRNA-SQ 1009 NPs (orange) siRNA-SQ bioconjugates before nanoprecipitation (grey). Intensity difference 1010 (y-axis) is due to the use of different sample concentrations. B) Small-angle neutron scattering 1011 patterns of two dilutions of siRNA-SQ suspensions. Red circles: 45  $\mu$ M; yellow circles: 23 1012  $\mu$ M. The small-angle region corresponds to values of q < 0.002 Å<sup>-1</sup>, mean angles 0.002 to 1013 0.04 Å<sup>-1</sup> and the large-angle q > 0.04 Å<sup>-1</sup>.





1016 1017 Figure S3: Quantification of the secondary structure of BSA. After circular dichroism 1018 analysis, quantifications of BSA were performed by BestSel program 1019 (http://bestsel.elte.hu/index.php). The histogram represents the comparison of two BSA 1020 concentrations (123 µM in blue and 62 µM in orange) alone or in presence of siRNA-SQ NPs (in grey) with BSA at  $62 \mu$ M. No difference was observed for the different conditions. 1021

## Table S1: Table comparing siRNA size estimation

1024

"Source"	Dimensions (nm)		
22 base pairs x 3.5 Å	L = 7  nm		
SANS pattern Ristori <i>et al</i> .	Cylindrical form factor L = 5.2  nm R = 1.1  nm		
SAXS pattern of siRNA strands	Cylindrical form factor L = 7 nm R = 1.1 nm		
SAXS pattern of siRNA-SQ	Cylindrical form factor L = 4  nm R = 1.1  nm		

1025 The scattering pattern originating from the naked siRNA PMP22 dispersion exhibited an 1026 oscillation in the same *q*-range in accordance with the SANS analysis of similar siRNA 1027 strands reported by Ristori *et al.* (Ristori, Ciani et al. 2012).

1028

### Supplementary information, equation A

1030 1031

$$\frac{F_0}{F} = 1 + K_{sv}[siRNA PMP22-SQ] = 1 + K_q \tau_0[siRNA PMP22-SQ]$$

### 1032

1033 **Equation A. Stern-Volmer equation**:  $F_0$  and F are fluorescence intensities of BSA in 1034 absence and presence of quencher (siRNA-SQ NPs), [siRNA PMP22-SQ] the molar 1035 concentration of siRNA PMP22-SQ (in M),  $K_{sv}$  (M<sup>-1</sup>) the Stern-Volmer constant which 1036 depends on  $K_q$  (M<sup>-1</sup>.s<sup>-1</sup>) and  $\tau_0$  (s) the average lifetime of tryptophan fluorescence in the 1037 absence of quencher, equals 10<sup>-8</sup> s.

1039 Supplementary information, equation B 1040 Interaction between the siRNA-SQ nanoparticles (NPs) and BSA can be probed in the 1041 following formula: siRNAPMP22-SQ NPs + n(BSA)  $\leftrightarrow$  [siRNA PMP22-SQ NPs-(BSA)<sub>n</sub>] 1042 (**B**1) 1043 According to this equation we can determine the apparent dissociation constant (K<sub>obs</sub>) at pH 7 1044 and at 25°C. 1045  $K_{obs} = \frac{[siRNA PMP22-SQ][BSA]}{[siRNA PMP22-SQ-(BSA)]}$ 1046 (B2) 1047 Based on equation (1), the intrinsic fluorescence intensity of the mixture is expressed as a 1048 function of the concentrations of all species in solution, weighted by experimental factors  $f_1$ , 1049 f<sub>2</sub> and f<sub>3</sub> for [siRNA PMP22-SQ], [BSA] and |siRNA PMP22-SQ-BSA] respectively: 1050 1051  $F = f_1[siRNA PMP22-SQ] + f_2[BSA] + f_3[siRNA PMP22-SQ-(BSA)_n]$ (B3) 1052 1053 In absence of BSA, the initial fluorescence intensity is given by:  $F_0 = f_1 [siRNA PMP22-SQ]_{initial}$ 1054 1055 The experimental conditions are as follow: 1) ratio [BSA]: [siRNA-SQ] < 1; 2) the 1056 1057 fluorescence intensity emitted by the siRNA PMP22-SQ NPs + BSA mixture should be 1058 completely adsorbed BSA, therefore 3) the intensity emitted from free BSA ( $f_2$ |BSA]) can be 1059 neglected. 1060 The experimental factor  $f_3$  is calculated based on raw data. From the variation in fluorescence 1061 emission  $\Delta F = F - F_0$  of equation (3) the K<sub>obs</sub> (2) can be calculated from the linear least-1062 squares regression: 1063 (B4)  $\frac{f_3 - f_1}{\Delta F} = \frac{1}{[siRNA PMP22 - SQ]_{initial}} + \frac{K_{obs}}{[siRNA PMP22 - SQ]_{initial}([BSA] - \frac{\Delta F}{f_3 - f_3})}$ 1064 1065 1066

1067	Supplementary information, equation C				
1068					
1069	1) Mass calculation of one nanoparticle				
1070	As serum components will interact with the squalene moiety which surround the				
1071	nanoparticle, we postulated that the mass of one nanoparticle is based on its density ( $\rho_{SQ}$ =				
1072	$858 \text{ kg/m}^3$ ) and the nanoparticle volume:				
1073	(C1)	$m_{NP} = \rho_{SQ} V_{NP}$			
1074					
1075	Number of NPs can be calculated as follow:				
1070					
1077	(C2)	$N_{\rm NP} = \frac{C_{\rm m}({\rm siRNAPMP22-SQ})}{m_{\rm NP}}$			
1078 1079 1080	2) <u>Determ</u>	ination of the number of proteins			
1081	Based on e	lectrophoresis experimental conditions and molecular weight of the BSA, we			
1082	can calculate the	he total mass of BSA:			
1083 1084	(C3)	$m_{\text{total BSA}} = [BSA]MM_{BSA}V$			
1085 1086 1087	Where [BSA] is the molar concentration of BSA, MM <sub>BSA</sub> the BSA molecular weight g/mol) and V the volume used for incubation before electrophoresis.				
1087 1088 1089	Number of BSA proteins can be determined as follow:				
1090	(C4)	$\mathrm{N}_{\mathrm{BSA}} = rac{\mathrm{m}_{\mathrm{totalBSA}}}{\mathrm{M}\mathrm{M}_{\mathrm{BSA}}}\mathrm{N}\mathrm{A}$			
1091 1092 1093 1094	Where N is the entities contain	e BSA protein number and $N_A$ the Avogadro number (number of elementary ned in a mole of matter, equal to 6.023 x $10^{23}$ ).			
1094 1095 1096	<ul> <li>3) Determination of BSA proteins per nanoparticle</li> </ul>				
1097 1098 1099	Based on (2) and (4), we can calculate the number of BSA interacting with one nanoparticle:				
1100	(C5)	Number $BSA/_{NP} = \frac{N_{BSA}}{m_{NP}}$			
1101					
1102 1103					