

Data-Driven Design of Protein-Like Single-Chain Polymer Nanoparticles

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ABSTRACT

The functional structure of proteins is heavily influenced by their folding behavior. AlphaFold, a powerful artificial intelligence (AI) program trained on information from the Protein Data Bank (PDB), was developed to predict the 3D structure of proteins from its amino acid sequence. Inspired by this, we aim to elucidate structural features of synthetic single-chain polymer nanoparticles (SCNPs) based on compositional information (monomers, chain length, molecular weight, charge, and valency) by machine learning (ML). Specifically, we demonstrate the effectiveness of ML to improve the efficiency of SCNP design and uncover important polymer design attributes to mimic protein-like structural features. To start, we randomly screened over

1000 synthesized SCNPs through a combination of high-throughput dynamic light scattering (DLS) and small-angle X-ray scattering (SAXS) and compared these results to simulated protein data from the PDB. Then, utilizing evidential neural networks (ENets), we predicted, synthesized, and characterized 30 novel compact SCNPs. Incredibly, this data-driven approach yielded 58% of the predicted SCNPs with Porod exponent ≥ 3.5 as opposed to 5% of SCNPs from the random screen. Using Shapely additive explanation (SHAP) values, we further uncovered interesting contributions of monomer content on Porod exponent and radius of gyration. From this work, we have shown that an ML-guided approach proves effective for the challenging, unintuitive problem of nanoparticle design.

INTRODUCTION

Proteins are remarkably complex macromolecules with specific functionality. The ultimate principle in protein science is that amino acid sequence impacts the structure which in turn enables function.¹⁻⁵ Protein structure and folding requires a combination of hydrophobic interactions, electrostatics, and hydrogen bonding.^{2, 4, 6, 7} A key requirement is dehydration whereby hydrophobic amino acids form a hydrophobic core surrounded by solvent-accessible amino acids. Additional intra- and intermolecular interactions permit even greater structural control.⁶⁻⁸ Further, concentration effects exist since below a characteristic concentration, the entropic cost of chain collapse and chain-chain repulsion is greater than the benefit of avoiding contact with water.^{3, 6} This extensive theoretical knowledge about protein folding along with significant information in the Protein Data Bank (PDB) paved the path for AlphaFold, an artificial intelligence (AI) platform that provides protein structural predictions given only the corresponding amino acid sequence.⁹

While this landmark advancement has significantly closed the gap in our ability to predict how protein sequence organization impacts its ultimate morphology, these advancements beg the question – is it possible to bridge the gap between design features and structural attributes for synthetic macromolecules which lack the precise organization of globular proteins?

A class of synthetic macromolecules that mimic proteins are referred to as single-chain polymer nanoparticles (SCNPs) which can collapse into higher ordered structures.¹⁰⁻¹⁸ These nanoparticles have potential as enzyme^{19, 20} or protein mimetics,^{16, 21, 22} sensing nanomaterials,²³ and drug delivery systems.²⁴⁻²⁶ Of particular interest is the use of SCNPs as multivalent therapeutics because of their biophysical tunability and therefore ligand presentation.^{27, 28} Multivalent strategies provide avidity or accumulated binding strength from presentation of multiple ligands and can be explained mathematically using statistical thermodynamics. Greater valency theoretically increases permutation entropy, or number of possible ligand-receptor interaction pairs, and thus results in a more negative or favorable binding free energy. This effect tends to be more pronounced for weaker binding ligands (*e.g.* peptides) which have a faster off-rate and allow for more potential interactions.²⁹ Providing some optimal amount of polymer scaffold flexibility can impart sufficient conformational freedom for ligands to position towards receptors and be in position to interact and bind. Recently, Chapman and co-workers utilized a similar strategy with end-functionalized star polymer-peptide conjugates to mimic the chemotherapeutic protein TNF-related apoptosis-inducing ligand (TRAIL).²² Multivalency has also been implemented to improve binding affinity and biological activity of erythropoietin (EPO) mimetic peptides, illustrating the appeal of this approach.³⁰⁻³⁴

To effectively mimic protein therapeutics, there is a requirement to further optimize SCNPs design features that affect downstream signaling such as compactness, flexibility, and valency.³⁵⁻

³⁷ While complexity in the form of orthogonal chemistry may be required,^{14, 38} a polymer coil-to-globule transition is largely driven by hydrophobic collapse to form a core that is shielded from aqueous solvent. Hydrogen bonding, π - π stacking, and electrostatics can both stabilize SCNPs and enhance solubility.⁶ There is an obvious relationship between polymer chain flexibility and compactness: flexible polymers undergo intra-chain cross-linking and collapse and interacting segments tend to increase in stiffness with reduced conformational degrees of freedom.²⁹

Despite our fundamental understanding of polymer physics, there is no established protocol to design polymers with a desired conformation because of the inability to experimentally probe the entire chemical design space. Traditional polymer chemistry techniques such as reversible addition-fragmentation chain transfer (RAFT) polymerization and atom transfer radical polymerization (ATRP) must be conducted in inert conditions.^{39, 40} Introduced within the last decade were air-tolerant photoinduced electron/energy transfer-RAFT (PET-RAFT),⁴¹⁻⁴⁵ enzyme-assisted ATRP,⁴⁶ enzyme-assisted RAFT (Enz-RAFT),^{47, 48} and ring-opening polymerization (ROP) through water⁴⁹ which have enabled polymerizations to be carried out directly in microplate format. To further the ability to complete combinatorial chemistry, our group previously demonstrated the potential of a plate-based gel filtration purification,⁵⁰ high-throughput structural characterization of SCNPs,⁵¹ and the adaptation of liquid handling robotics to complete polymer synthesis and post-polymerization functionalization.^{52, 53} Others such as Gibson and co-workers have also utilized liquid handling robotics for preparing and testing polymer libraries.⁵⁴⁻⁵⁶

However, utilizing only high-throughput approaches to synthesize and characterize SCNPs runs the risk of inefficiency, false positives and negatives, and difficulty with interpreting large datasets.⁵⁷ In previous work, we conducted high-throughput screening of a large combinatorial library (> 450 copolymers) via dynamic light scattering (DLS) and small-angle X-ray scattering

(SAXS) to identify compact nanostructures.⁵¹ Due to polymer hydrophobicity and having a relatively small dataset, we were unable to define a model to quantitatively inform further design, thus serving as a motivation for this study. For such complex and non-intuitive material design problems,⁵⁸⁻⁶⁰ machine learning (ML) is emerging as an exciting approach for informing design. ML has seen success in small-molecule organic synthesis⁶¹⁻⁶³ and is being introduced for synthetic polymers^{64, 65} to accelerate discovery of new materials with desired structural or functional properties.^{63, 64, 66} In particular, ML can be exploited to classify large datasets, uncover hidden patterns, and reduce the number of variables for a multivariate dataset.⁶⁷ By accomplishing these tasks, a data-driven approach can make predictions about material features of interest and further our understanding of how these features can be designed in future experiments.⁶⁸⁻⁷⁰

In this study, we combined high-throughput polymer synthesis and characterization with ML to aid the design of novel SCNPs that are compact and exhibit similar flexibility to ordered proteins. We hypothesized that an ML-guided approach can be leveraged in an SCNPs synthetic workflow to identify difficult-to-design compact and rigid nanoparticles. First, we synthesized over 1000 amphiphilic random heteropolymer backbones containing varied composition (neutral, cationic, and hydrophobic monomers), degree of polymerization (DP) (200, 300, and 400), functionalization (2 kDa PEG, TRAIL mimetic peptide, or EPO mimetic peptide), and valency (2, 5, and 10 mol%). Synthesized copolymers were characterized by SAXS and DLS to provide compactness and flexibility information that was then compared against a parallel dataset of over 300 protein structures extracted from the PDB with analogous theoretical compactness and flexibility. The dataset of over 1000 synthesized copolymers were leveraged to train evidential neural networks (ENets) to provide novel predictions for compact SCNPs.^{71, 72} This approach successfully identified novel SCNPs structures that demonstrated remarkable compactness. Further, we

performed post hoc analysis of our data to understand how copolymer features influence SCNP compactness and flexibility (**Figure 1**).

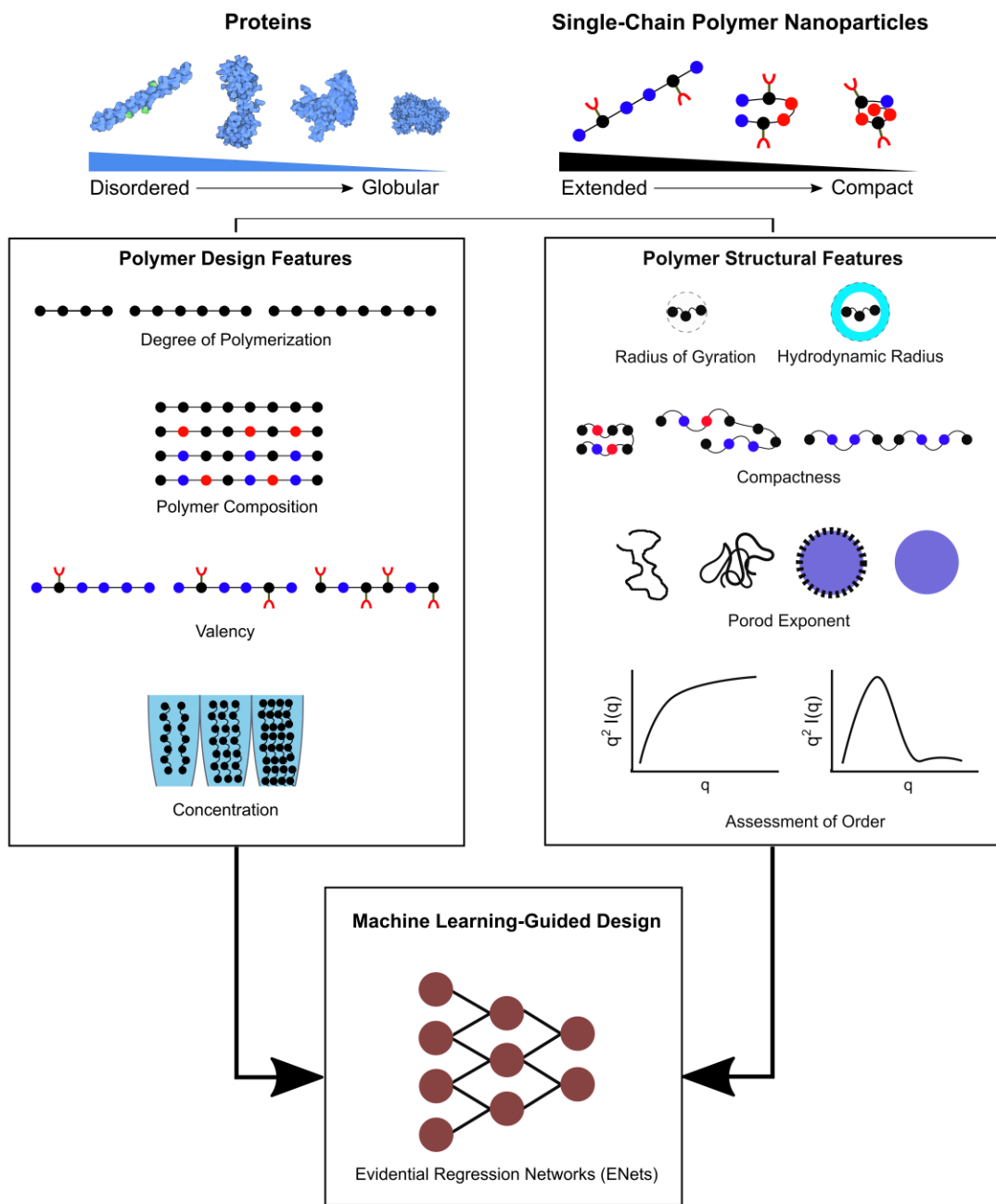


Figure 1. Schematic of ML-guided approach for designing SCNPs. Proteins undergo a complex folding process and possess a high level of structural order. Using synthetic materials, a ML approach is utilized to model important design (DP, polymer composition, valency, and concentration) and structural features (R_h , R_g , compactness as R_g/R_h , and Porod exponent) to provide predictions for synthesizing novel copolymers with desired properties.

RESULTS AND DISCUSSION

Random Screen of Copolymer Backbones and Polymer Conjugates

We began by investigating our initial library of copolymer backbones, copolymer-PEG conjugates, and copolymer-peptide conjugates that we will refer to as a random screen. To explore a broad compositional space, we employed *N,N*-dimethylacrylamide (DMA) as a neutral monomer, [2-(methacryloyloxy)ethyl]trimethylammonium chloride (TMAEMA) as a cationic monomer, and methyl methacrylate (MMA) and butyl methacrylate (BMA) as hydrophobic monomers. All representative monomer, copolymer, and copolymer conjugate structures are provided (**Figures S1-S4**). Additionally, we varied DP (200, 300, and 400) and valency of SPAAC-functionalized PEG or peptide (2, 5, and 10 mol%). For polymer-peptide conjugates, we focused on two peptides that have been previously validated and characterized for binding with an objective of enabling nanoparticle design.^{22, 30-34, 73} All characterization data of PDB simulated proteins (simulation details provided in Materials and Methods), copolymer backbones, PEG-SCNPs, EPO-SCNPs, and WDCL-SCNPs are provided in **Tables S3-S7**.

After synthesis and characterization of copolymer backbones and copolymers conjugated with PEG, EPO, and WDCL, various approaches were taken to visualize attributes of the large dataset. Compactness (R_g/R_h) and flexibility (Porod exponent) are two parameters of interest in the realm of SCNP design. **Figure 2** illustrates kernel density estimation (KDE) and principal component analysis (PCA) that were completed for the dataset to observe differences in flexibility between subgroups. Compared to copolymer backbones, the conjugation of the EPO peptide on average seemed to shift behavior towards that of proteins. These EPO-SCNPs tended towards increased Porod exponent compared to that of copolymer backbones, showing greater similarity to the behavior of the PDB proteins. The other subgroups of synthesized SCNPs (PEG and WDCL)

displayed more of a disparity with PDB proteins compared to EPO-SCNPs (**Figure 2A**). R_g/R_h seems to have greater complexity as the two groups of polymer-peptide conjugates, the EPO-SCNPs and WDCL-SCNPs, have greater overlap with compactness of PDB proteins than copolymer backbones and PEG-SCNPs (**Figure 2B**). This is also reflected in the shift in median R_g/R_h and Porod exponent, respectively, between the groups: Backbone (1.13, 1.8), PEG-SCNPs (0.98, 1.8), WDCL SCNPs (0.91, 2.1), EPO-SCNPs (0.88, 2.8), and PDB proteins (0.85, 3.6). Individual physical characterization data including values obtained from SAXS and DLS along with feature information (molecular weight, charge, and hydrophobicity) are also provided (**Tables S3-S7**).

While KDE plots in **Figure 2A-C** quantitatively show the influence of composition on structure, 2D PCA in **Figure 2D-F** seems to reflect that there are three distinct groups within the dataset (**Figure 2C**) when we featurize the data using all known values (R_g , R_h , R_g/R_h , molecular weight, total charge, total positive charge, total negative charge, $\log P$, and HLB) (representation of explained variance is provided in **Figure S12**). We also observe that when the data is featurized by only polymer design features (DP, mol% DMA, mol% TMAEMA, mol% MMA, mol% BMA, mol% NHS methacrylic acid, mol% DBCO, mol% PEG, mol% EPO, mol% WDCL, and molecular weight) and colored by Porod exponent and R_g (**Figure 2D,E**), there does not seem to be a clear gradient or dependency. These illustrations reveal that SCNP structural design contains non-linear complexities that cannot be explained by simple feature correlations alone. Additional two-dimensional KDE plots are provided for only chemical descriptors and experimentally derived features (**Figures S13 and S14**).

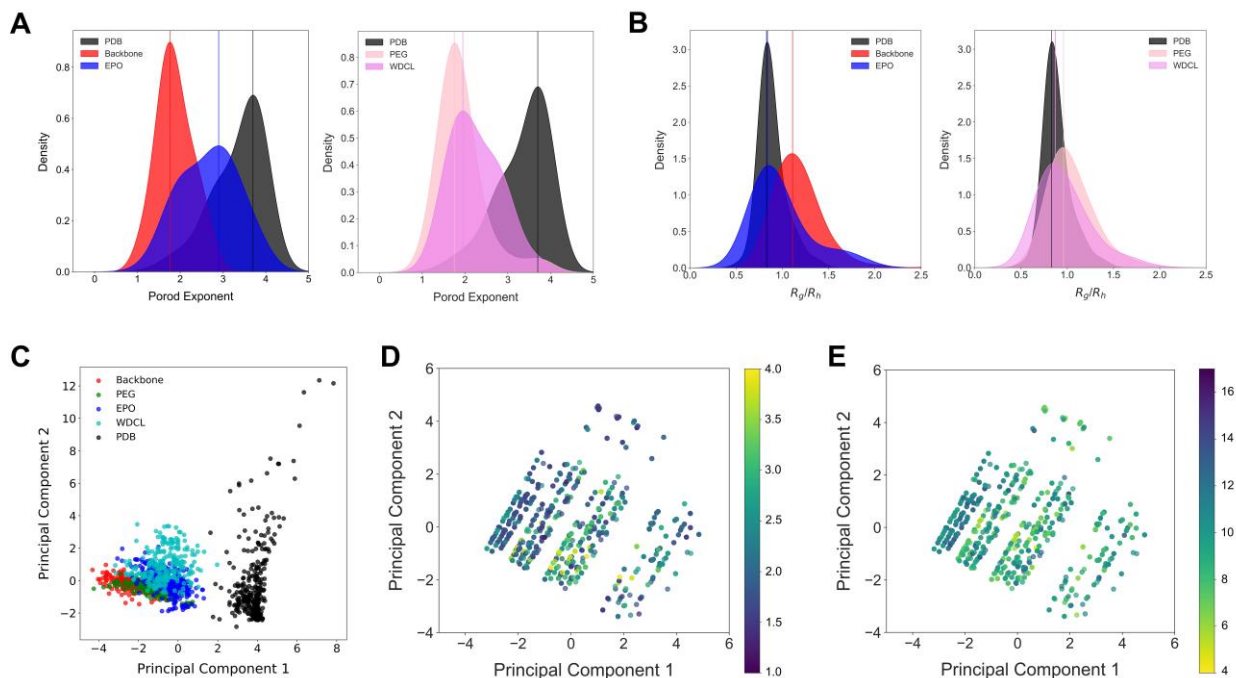


Figure 2. KDE and PCA of copolymers, copolymer conjugates, and proteins. KDE and PCA were used to determine differences between the subgroups: proteins simulated from the PDB, copolymer backbones (Backbone), PEG-SCNPs (PEG), EPO-SCNPs (EPO), and WDCL-SCNPs (WDCL). (A) The probability densities associated with Porod exponents of PDB proteins, copolymer backbones, and EPO-SCNPs along with PDB proteins, PEG-SCNPs, and WDCL-SCNPs are shown. (B) The probability densities associated with R_g/R_h of PDB proteins, copolymer backbones, and EPO-SCNPs along with PDB proteins, PEG-SCNPs, and WDCL-SCNPs are provided. (C) PCA was completed for all groups using all features (R_g , R_h , Porod exponent, Porod volume, R_g/R_h , molecular weight, total charge, total positive charge, total negative charge, $\log P$, and HLB) with explained variance of 0.608. PCA was also done using only polymer design features (DP, % DMA, % TMAEMA, % MMA, % BMA, % NHS methacrylic acid, % DBCO, % PEG, % EPO, % WDCL, and molecular weight), colored by (D) Porod exponent and (E) R_g .

Comparisons of the random experimental screen of copolymer backbones and copolymer conjugates with the PDB protein dataset is important, however, some limitations should be noted. While our PDB dataset would ideally contain a large percentage of both disordered and globular proteins, intrinsically disordered proteins (IDPs) that lack secondary or tertiary structure only comprise about 30% of the eukaryotic proteome.⁷⁴ Also a large fraction of the structural information in the PDB are for globular proteins with almost 90% of structures from crystallography while the other 10% are from solution NMR and electron microscopy.⁷⁵ Although we attempted to diversify our PDB dataset, it still included approximately 64% of structures from X-ray crystallography. CRY SOL is a powerful program in the ATSAS package that enables computation of theoretical SAXS curves given a PDB structure file as an input.^{76, 77} While other groups have also implemented this program to obtain information about IDPs,^{74, 78-80} CRY SOL is limited by size or D_{max} due to its use of spherical harmonics which can make the program challenging for generating SAXS profiles of extended proteins.⁸⁰ Especially for IDPs, the maximum number of harmonics (50) should be selected, but there remains the possibility to provide experimental scattering data to CRY SOL to improve fitting.

Additionally, KDE allows us to visualize the chemical space of our dataset in terms of total charge, HLB, and $\log P$ compared to the simulated PDB proteins (**Figures S18-S20**). While copolymer backbones are somewhat similar in total charge to a large portion of the PDB protein population, there are differences between the two subgroups in HLB and $\log P$. EPO-SCNPs and WDCL-SCNPs appear to shift copolymer HLB closer to that of proteins, and these plots represent that a combination of descriptors are likely required for the complex task of SCNP design. For analysis and interpretation of SAXS and DLS data, we focused on two parameters of interest in the realm of therapeutic receptor binding: compactness (R_g/R_h) and flexibility (Porod exponent).

From the KDE plots, there seems to be three distinct groups based on distributions of PDB proteins (narrow compact range with Porod exponent > 3.0), copolymer backbones and PEG-SCNPs (with extended conformation and Porod exponent ≤ 2.0), and EPO-SCNPs and WDCL-SCNPs (favor compactness with a broad range of flexibility and intermediate Porod exponent from 2.0-3.0). The data also indicates that peptidic side chains seem to shift copolymer behavior closer to that of proteins in terms of both R_g/R_h and Porod exponent (**Figure 2A,B**).

We supplemented the PCA analysis displayed in **Figure 2** by separating each subgroup and labeling by features of interest (Porod exponent or R_g). In contrast to PDB proteins which displayed greater Porod exponent throughout, the copolymer backbones and conjugates contained distinct pockets of lower flexibility regions indicative of higher order that even differed between each synthetic subgroup (**Figure S15**). This implies that it would be nearly impossible to logically formulate a *de novo* framework for designing similarly structured compact copolymers. Conversely, R_g seems to have relatively more consistency between these regions of compact structures (**Figure S16**). Simply focusing the PCA on SCNPs allowed us to expand our feature set to include more polymer specific characteristics, resulting in greater spread within the EPO and WDCL groups and demonstrating the utility of including relevant polymer descriptors in data visualization and interpretation (**Figure S17**). While PCA and KDE are powerful tools for dimensionality reduction or drawing conclusions about the overall dataset, they cannot provide us feature importance or predictive capability which is why we must turn to other methods.⁸¹

ML Investigation of SCNPs

While many copolymer conjugates were investigated in our initial study, only a small fraction of SCNPs demonstrated significant compactness and flexibility. This is not surprising as designing

self-folding behavior in synthetic macromolecules remains challenging. To facilitate further control over these higher order behaviors, we utilized ML techniques to identify samples that demonstrate compactness and protein-like flexibility. To do so, we began by training multiple ENets to make predictions on SCNP parameters of interest (R_g , R_h , R_g/R_h , Porod exponent) directly from chemical representations of polymer conjugate chemistry and chosen molecular descriptors (see Materials and Methods). Predictions of R_h and R_g/R_h demonstrated low accuracy on held-out validation data during training (**Figure S5**) and prediction accuracy of R_g and Porod exponent was significantly greater, leading us to utilize these models in our future design. The tuning of the ENet regularization parameter is illustrated in **Figure S6**. To generate compactness and flexibility predictions of copolymer conjugates similar to our synthesized samples, respective ENet models were used to predict expected mean and variance of R_g and Porod exponent for ~700,000 copolymer conjugate chemistries *in silico*. Comparable to our observations of compactness and flexibility in our measured data of SCNPs, predictions of PEG, WDCL, and EPO suggested EPO-SCNPs generally exhibited high Porod exponent and PEG-SCNPs were anticipated to demonstrate the lowest R_g (**Figure S7**).

As we were particularly interested in designing compact samples with protein-like features, 30 EPO-SCNPs were proposed for synthesis and characterization with low predicted R_g and high predicted Porod exponent (see Materials and Methods). Since many of these samples demonstrated limited solubility, likely due to large hydrophobic monomer fractions (**Table S8**), DLS and SAXS characterization were completed on 12 of 30 samples. Remarkably, **Figure 3A** demonstrates that ML-informed design appropriately identified numerous EPO-SCNPs exhibiting more similar physical measurements to the PDB sampled proteins than prior EPO-SCNPs measured during our random screen. While only 5% of SCNPs in the random screen demonstrated Porod exponent $\geq$

3.5, ~58% of EPO-SCNPs proposed by the ENets demonstrated Porod exponents above this threshold. Further, these differences are readily observed in the distinction in median R_g and Porod exponent between initial EPO-SCNPs (8.4 nm and 2.7) and ENet proposed EPO-SCNPs (5.7 nm and 3.5). As R_g and Porod exponent shifted towards more protein-like values, R_h remained large for EPO-SCNPs (**Figure S9**). The R_g/R_h of an ideal sphere is 0.775, however, some of the characterized SCNPs exhibited $R_g/R_h < 0.775$. This phenomenon was even more prevalent in the ML predicted EPO-SCNPs. A few potential reasons for this include adoption of a core-shell structure or molten globule with tight packing of the hydrophobic alkyl side chain surrounded by a more dispersed shell.^{82, 83}

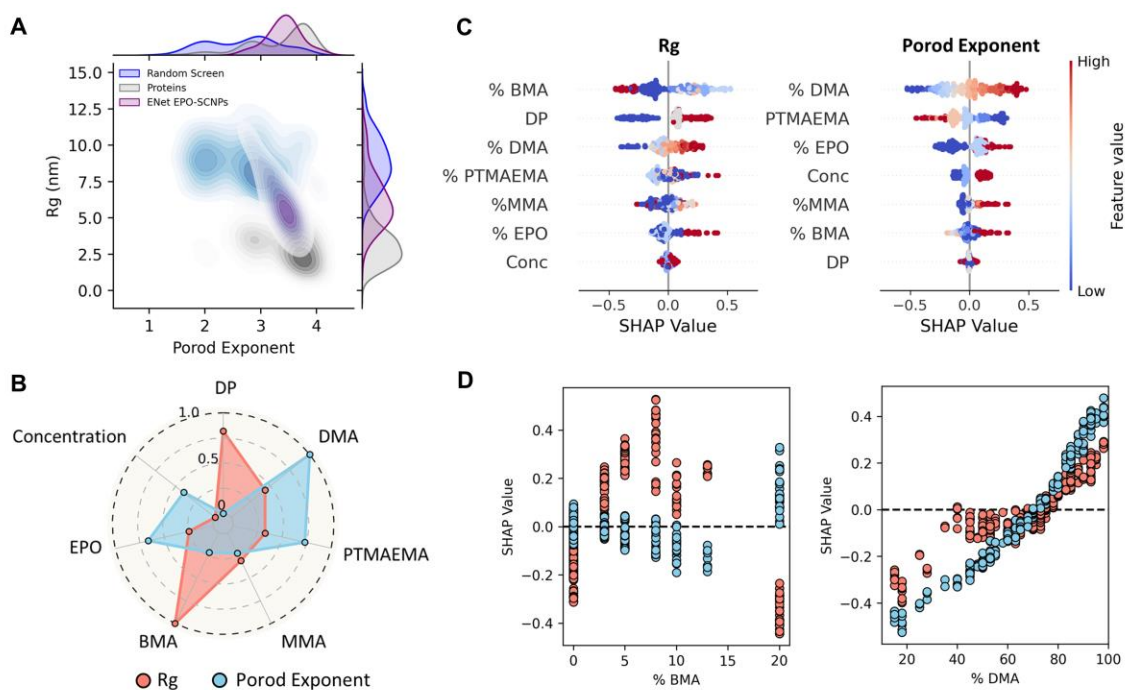


Figure 3. ML guided design of compact SCNPs. (A) Joint distribution plot comparing R_g and Porod exponent of random screen EPO-SCNPs, ML predicted EPO-SCNPs, and PDB proteins. (B) Normalized mean absolute Shapely additive explanation (SHAP) values calculated for Porod exponent and R_g . (C) Summary of SHAP values calculated for all SCNP features for Porod exponent and R_g , respectively. (D) Porod exponent and R_g SHAP values for BMA and DMA monomer content.

Because ENet models were generally successful in predicting more compact EPO-SCNPs, we sought to understand the underlying chemical designs that led to compactness within our study. For this, we computed Shapely additive explanations (SHAP) values to quantify the impact of model features (monomers, peptide, DP) on prediction of both R_g and Porod exponent.^{84, 85} In these interpretations, positive SHAP values indicate a positive contribution to predicted R_g or Porod exponent, and negative values indicate a negative contribution. Further, mean absolute SHAP values for individual features are used as a metric for overall feature importance. **Figure 3B** demonstrates that different EPO-SCNP features play primary roles in the predictions of R_g or Porod exponent. For example, while BMA is measured to be the most impactful parameter for predicting R_g , DMA demonstrates the largest absolute SHAP value for predictions of Porod exponent. To further investigate these differences, we compare all SHAP values for predictions of R_g and Porod exponent (**Figure 3C**). As our objective in this study was to identify highly compact SCNPs, we anticipated that EPO-SCNPs hydrophobicity would be important to induce single chain folding through induction of a hydrophobic core. Interestingly, BMA, a highly hydrophobic monomer, not only demonstrates the largest feature importance for R_g but also demonstrates a large negative SHAP for R_g at high levels of incorporation, in line with our design objective of minimizing R_g (**Figure 3D**). Additionally, despite not being as impactful to the ENet model for Porod exponent, BMA demonstrates a positive SHAP contribution to Porod exponent at high monomer incorporation. This suggests that high incorporation of BMA is ultimately synergistic to both design objectives. In contrast to this synergistic behavior for BMA, DMA, the chemical feature with highest absolute SHAP value for predicted Porod exponent, demonstrated competing behavior in predicting high Porod exponent and small R_g . Highly correlated SHAP values for DMA between Porod exponent and R_g demonstrate that high DMA incorporation leads to positive SHAP

values for Porod exponent (in line with our objective), yet high DMA also leads to positive SHAP values for R_g , a parameter we aimed to minimize.

Structural Characterization of Predicted SCNPs

Once ML guided design was completed, individual copolymer backbones and copolymer conjugates were further inspected for interesting structural characteristics. **Table 1** contains a summary of BSA, EPO-SCNPs from the random screen, and a ML predicted EPO-SCNP with design features (DP, valence, molecular weight, and HLB). Other quantities included were those obtained by a combination of SAXS and DLS (R_g , R_h , R_g/R_h , and Porod exponent). BSA, widely used as a model compact and ordered protein, is presented alongside other copolymer conjugates that displayed evidence of compactness from the random screen (EPO119, EPO163, EPO166, and EPO172). We have also included the ML predicted compact EPO-SCNP (ML EPO24). Conversely, the extended and water-soluble polymer PEG 35 kDa is presented alongside other EPO SCNPs that exhibited extendedness (EPO18, EPO59, EPO229, and EPO308). In terms of the copolymer design features provided in **Table 1** (monomer composition, DP, valence, molecular weight, and HLB), there is no clear distinction in the physicochemical characteristics between these two groups, although extended copolymers and copolymer conjugates tended to exhibit greater hydrophilicity with a higher weighted HLB. This is further evidence that the problem of SCNP design does not contain a simple solution with a single parameter. We can, however, visualize a clear gap between these two groups of samples in terms of measured R_g/R_h and Porod exponent as compact macromolecules tended towards $R_g/R_h \sim 0.775$ and Porod exponent from 3.0-4.0, while extended ones tended towards $R_g/R_h > 1.00$ and Porod exponent < 2.0 . The gap suggests that incorporation of experimental data may be useful in defining a framework for SCNP structural

design. Also, SEC-MALS was completed to quantify molecular weight and $\bar{D}$ for copolymer backbones (**Table S1** and **Figure S10**) while UV-vis spectroscopy was conducted to determine DBCO incorporation which has implications for valency (**Table S2**).

Table 1. Physical characterization data of highlighted random screen and ML predicted EPO-SCNPs along with BSA and PEG.

ID	Polymer Composition	DP	Valence	MW _{theoretical} (kDa)	HLB	R_g (nm)	R_h (nm)	R_g/R_h	Porod Exponent
BSA	--	--	--	66.5	--	3.07	4.00	0.775	3.9
ML EPO24	DMA 47.5% / TMAEMA 12.5% / BMA 35%	275	2.5%	53.5	--	7.31	12.10	0.604	4.0
EPO119	DMA 85% / TMAEMA 5% / MMA 5%	200	5%	48.6	14.0	8.38	10.90	0.769	3.2
EPO163	DMA 88% / MMA 10%	200	2%	33.1	12.7	7.81	9.70	0.805	3.6
EPO166	DMA 93% / BMA 5%	200	2%	31.3	10.5	8.16	10.39	0.785	3.7
EPO172	DMA 93% / MMA 5%	300	2%	46.4	11.9	9.17	11.76	0.780	3.8
PEG	PEG 100%	794	0%	35.0	10.9	5.10	4.50	1.13	1.5
EPO18	DMA 45% / TMAEMA 25% / MMA 17% / BMA 3%	300	10%	121.4	17.4	11.35	6.54	1.74	2.2
EPO59	DMA 45% / TMAEMA 25% / MMA 12% / BMA 13%	400	5%	108.2	14.6	9.37	7.26	1.29	1.5
EPO229	DMA 73% / TMAEMA 15% / BMA 10%	200	2%	35.0	12.6	6.75	3.60	1.88	2.3
EPO308	DMA 50% / TMAEMA 25% / BMA 20%	400	5%	109.3	14.6	9.89	9.40	1.05	2.1

Further, SAXS data are illustrated for the same compact and extended EPO-SCNPs from the random screen and ML-guided design alongside controls BSA and PEG 35 kDa (**Figure 4**). This includes the SAXS intensity profiles, normalized Kratky plot, and Porod plot of the compact copolymer conjugates (ML EPO24, EPO119, EPO163, EPO166, and EPO172) and BSA (**Figure 4A-C**). The same was included for extended copolymer conjugates (EPO18, EPO59, EPO229, and EPO308) and PEG 35 kDa (**Figure 4D-F**). There was reasonable overlap in SAXS intensity profiles of the synthesized copolymers and copolymer conjugates with the controls. Further, characteristic behavior of macromolecular compactness and flexibility were exhibited through respective intensity, Kratky, and normalized plots (**Figures S21-S23**). Compact and extended SCNPs displayed SAXS features similar to highly ordered protein BSA and the extended polymer PEG, respectively. While the SAXS intensity profiles show agreement between synthesized SCNPs and their respective compact and extended controls, normalized Kratky plots qualitatively

confirm that the degree of order is also in reasonable agreement. Interestingly, the ML EPO24 SCNP exhibits order more similar to that of BSA when compared against other SCNPs from the random screen (**Figure 4B**). These normalized Kratky plots can be useful in the case of combinatorial libraries that may contain various measured concentrations and thus differences in scattering intensity at zero angle, referred to as $I(0)$. Therefore, deviations from BSA in terms of peak broadness and intensity in the normalized Kratky plot reflect on the varying degrees of order. This work also illustrates that we can synthesize a wide range of SCNPs using ML-predicted compositions to obtain the desired compactness and flexibility utilizing PET-RAFT and click chemistry (**Figures 2 and 4**).

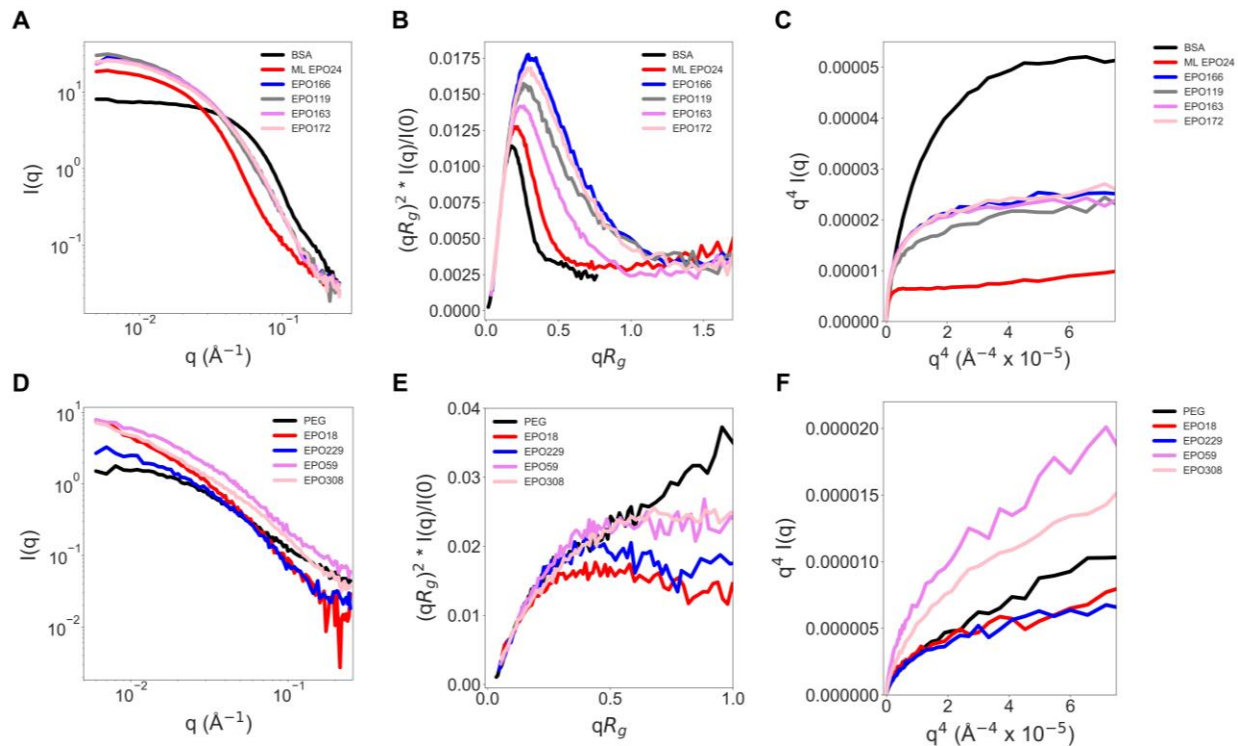


Figure 4. SAXS summary of compact and extended EPO-SCNPs from the random screen and ML prediction. (A) SAXS intensity plot of compact protein BSA, ML predicted compact EPO-SCNP (ML EPO24), and randomly screened compact EPO-SCNPs (EPO166, EPO119, EPO163, and EPO172). Compact behavior is revealed with characteristic (B) normalized Kratky and (C) Porod plots. (D) SAXS intensity plot of extended PEG 35 kDa and randomly screened extended EPO-SCNPs (EPO18, EPO229, EPO59, and EPO308). Extendedness is illustrated through characteristic (E) normalized Kratky and (F) Porod plots.

CONCLUSION

While AlphaFold supplies protein structural information from specific amino acid sequences, a design-structure gap exists for synthetic macromolecules. As high-throughput polymer chemistry provides new opportunity for data-driven design, we aimed to bridge the gap between synthetic SCNP design features and structural characteristics (compactness and flexibility) where sequence-level control is not yet possible. It is clear from this large dataset of copolymers and copolymer conjugates that the synthesis and design of SCNPs is a multi-objective problem with high complexity as there are design features and measured characteristics that are interrelated.⁸⁶ SCNPs contain nearly an infinite chemical space with the potential to select features such as DP, monomer composition, architecture, and valency, but the question remains of how to select an initial polymer library. In this work, we intuitively selected copolymers based on theoretical $\log P$ and attempted to prescreen these combinations using DLS. Employing our own logic can result in inefficiencies and may require a more iterative process which can be difficult to implement experimentally especially with a technique such as SAXS.^{86, 87} Another challenge with complex copolymer conjugates involves deconvoluting physical contributions between polymer and peptide which would require other techniques such as NMR or small-angle neutron scattering (SANS).⁸⁸ In addition to all of these factors, it is likely difficult to synthesize structures with the same level of order and folding as proteins mainly because of the lack of sequence-level control.^{6, 18, 67, 87, 89, 90} Until advances are made to achieve this level of control with synthetic ease, polymer chemists may need to rely on quantifying reactivity ratios,⁹¹⁻⁹³ illustrating compositional drift,⁹⁴ and potentially designing for molecular weight distribution.⁹⁵ Others are even making efforts to increase complexity with polymer design,^{25, 96} biologically inspired monomers,^{97, 98} and multi-orthogonal

approaches.^{53, 99} Combining informative approaches such as ML, simulations, and structural characterization can only strengthen the SCNP design paradigm.

In summary, our objective was to demonstrate the utility of a data-driven design approach for identifying compact SCNPs that are challenging to design *de novo*. We first completed a random screen of over 1000 SCNP random heteropolymers and copolymer conjugates with varied DP, composition, valence, and functionality. In this random screen, we characterized SCNPs by DLS and SAXS to quantify macromolecular compactness and flexibility. Data visualization approaches (KDE and PCA) demonstrated that this is a complex multi-objective problem that cannot be understood by simple chemical design principles alone and seemed to indicate that polymer-peptide conjugates served as an intermediate between disordered copolymers and folded proteins. We proceeded to employ ENets to predict compact EPO-SCNPs with $R_g < 7$ nm and Porod exponent from 3.7-4.0 and randomly sampled 30 EPO-SCNPs which were synthesized and characterized to validate the model. While the initial random screen only resulted in 5% of SCNPs with Porod exponent ≥ 3.5 , about 58% of the ENets predicted SCNPs exhibited a Porod exponent ≥ 3.5 . Not only did this ML-guided approach improve SCNP design efficiency, SHAP analysis uncovered interesting design features such as the importance of DMA and BMA monomer content on Porod exponent and R_g . In conclusion, our work has illustrated that data-driven design provides a much-needed solution to the often-unintuitive problem of nanoparticle design and provides an potential framework for understanding synthetic macromolecule design-structure relationships.

MATERIALS AND METHODS

Materials

The monomers DMA (Sigma-Aldrich), MMA (Alfa Aesar), BMA (Alfa Aesar), and TMAEMA (Fisher Scientific) were sourced from a variety of vendors. The chain transfer agent 4-cyano-4[(dodecylsulfanylthiocarbonyl)sulfanyl] pentanoic acid and initiator zinc tetraphenylporphyrin (ZnTPP) were purchased from Sigma-Aldrich and Fisher Scientific, respectively. Dibenzocyclooctyne-amine (DBCO-NH₂) which was used for click chemistry was purchased from Click Chemistry Tools while 4-dimethylaminopyridine (DMAP) was purchased from Sigma-Aldrich. Traditional Fmoc amino acids (CEM Corporation), Fmoc-L-lysine-N₃ (Lys-N₃) (Chem-Impex International), and the spacer Fmoc-*N*-amido-PEG₂-acid (PEG₂) (BroadPharm) were utilized for solid-phase peptide synthesis. Methoxypolyethylene glycol azide with M_n = 2000 Da (PEG-N₃) (Sigma-Aldrich) was the other molecule conjugated onto the synthesized copolymers.

Automated PET-RAFT

Automated PET-RAFT was completed using oxygen-tolerant PET-RAFT chemistry^{41, 44} coupled with adaptation of the Hamilton Microlab STARlet liquid handling robot to complete this chemistry.⁵² The DMA, MMA, BMA, and TMAEMA monomers were prepared at a 2 M concentration in DMSO and deinhibited by passing solutions through columns containing inhibitor remover beads (Sigma-Aldrich), glass wool (Fisher Scientific), and aluminum oxide (Sigma-Aldrich). Meanwhile, the methacrylic acid NHS monomer was prepared in anhydrous DMSO at 0.4 M with 1 mol equivalent acetic acid/NHS. The degree of polymerization (DP) of the polymer was varied between 200, 300, and 400 by shifting the final monomer:CTA molar ratios (200:1,

300:1, and 400:1) and fixing the final CTA:ZnTPP molar ratio (50:1). All reagents were loaded into 1.5 mL centrifuge tubes, dispensed by the liquid handling robot into a 96-well polypropylene plate, and photoinitiated by a 560 nm LED light for 16 h. Representative monomer, copolymer, and copolymer conjugate structures were also included (**Figures S1-S4**).

Solid-Phase Peptide Synthesis

The WDCL (WDCLDNRIGRRQCV-{Lys-N3}-L-amide) (Cyc 3, 13) (99% purity) and EPO (GGTYSCHFGPLTWVCKPQ-{PEG2}-SS-{Lys-N3}-amide) (Cyc 6, 15) (99% purity) peptides were synthesized by solid-phase peptide synthesis. HPLC chromatograms demonstrating peptide purity are provided (**Figure S11**). This was completed using a Liberty Blue automated microwave peptide synthesizer (CEM Corporation) on Rink Amide ProTide Resin with 0.16 mmol/g loading (CEM Corporation). 1 M Oxyma and 1 M DIC were used as the base and activator along with 20% (v/v) piperazine in DMF as the deprotection solution. Both cysteine-containing peptides were cleaved off the resin by bubbling for 4 h in a 95% (v/v) trifluoroacetic acid (TFA), 2.5% (v/v) triisopropylsilane (TIS) (Fisher Scientific), and 2.5% (v/v) ultrapure H₂O with 2.5% (w/v) dithiothreitol (DTT) (Sigma-Aldrich). The solution was collected, the resin was washed three times with DCM, and the solution was rotary evaporated to remove TFA. Peptide was precipitated in cold diethyl ether and centrifuged at 3000 g for 10 min with a total of three wash steps. Overnight vacuum desiccation left solid pellets of peptide.

Peptide Purification and Cyclization

The peptide pellets were dissolved in water/0.1% (v/v) TFA (at a concentration of about 5 mg/mL) and purified using the CombiFlash RF200 Flash Chromatography instrument (Teledyne Isco) equipped with a 50 g RediSep Rf Gold Reversed-Phase C18 column. 5 mL of peptide solution was loaded for each round of purification. At a 40 mL/min flow rate with H₂O/0.1% TFA (solvent A) and acetonitrile (solvent B), the gradient used was: 0% solvent B from 0-3 min, ramped up to 100% solvent B at 9 min, ramped down to 0% solvent B at 11 min, and held at 0% solvent B until 15 min. Collected sample fractions were rotary evaporated to remove acetonitrile and trace amounts of TFA before lyophilizing. For cyclization, lyophilized peptides were reconstituted in a 10 mM borate buffer (pH 8.5) and stirred for 24 h. These peptides were then purified and lyophilized a second time.

Automated Post-Polymerization Modification

DBCO-NH₂ addition was completed in an automated fashion using the Hamilton Microlab STARlet liquid handling robot.⁵² Both DBCO-NH₂ and DMAP were prepared at 0.1 M in DMSO. Inputting custom user-defined reagent addition scripts allowed for addition of DBCO-NH₂ and DMAP directly into the 96-well plates based on methacrylic acid NHS content (molar ratio of DBCO-NH₂:DMAP:NHS of 1:1:1). This reaction was left overnight to completion in sealed 96-well plates.

Purification, Peptide Addition, and Sample Preparation

After DBCO-NH₂ and DMAP addition, all copolymers were purified using 96-well Zeba filter plates (Thermo Fisher Scientific) manually packed with Sephadex G-25 superfine, following a previously published protocol.⁵⁰ Incorporated DBCO concentration was quantified by measuring absorbance at the characteristic wavelength of 310 nm and comparing to a DBCO-NH₂ standard curve. Addition of WDCL and EPO peptides to conjugate onto copolymers by strain-promoted azide-alkyne cycloaddition (SPAAC) was performed using the same automated reagent addition scripts as the DBCO-NH₂ and DMAP addition step and left overnight for reaction completion. Polymer-peptide conjugates were then diluted 3x in DMSO and 10x in ultrapure H₂O before being dialyzed into H₂O using Spectra/Por 6 RC 18 mm dialysis tubing (Repligen). Dialysis was completed with three H₂O changes over a period of two days. The remaining solutions were then lyophilized.

Size-Exclusion Chromatography-Multi-Angle Light Scattering (SEC-MALS)

SEC-MALS was completed on two separate systems (organic and aqueous) to quantify polymer backbone molecular weight and dispersity ($\bar{D}$) depending on solubility. A 1200 series Agilent GPC was used to run all SEC-MALS. An organic system running on DMF with 50 mM LiBr mobile phase and an aqueous system running on 0.5x PBS (BioShop) with 0.02% (w/v) sodium azide were utilized depending on polymer solubility. The organic system separated copolymers by passing through two Agilent PLgel 5 μ m columns in series (10^3 and 10^4 Å, 300 x 7.5 mm). The aqueous system utilized a Superose 12 10/300 GL 11 μ m column (300 x 10 mm). Both systems contained a pre-column stainless steel filter with a 2 μ m pore size (VWR). Following the columns

are an Agilent UV detector, Wyatt Technology miniDAWN TREOS MALS detector, and Agilent 1260 Series differential refractive index (RI) detector. SEC calibration and MALS detector normalization was carried out with polyethylene oxide standards (Agilent). All copolymers were prepared at approximately 2 mg/mL and filtered with a 0.45 μ m PTFE filter for organic SEC-MALS and a 0.45 μ m nylon filter for aqueous SEC-MALS.

High-Throughput Dynamic Light Scattering (DLS)

Initial DLS screening of copolymers was conducted in 384-well plates using the DynaPro DLS Plate Reader III (Wyatt Technology) which uses a wavelength of 830 nm and scattering detector angle of 173°. For this, copolymers were diluted directly from the reaction volume into HBS-EP+ buffer (10 mM HEPES, 150 mM NaCl, 3 mM EDTA, 0.05% P20 at pH 7.6) (VWR) such that solutions contained 1% (v/v) DMSO. Hydrodynamic radius (R_h) and diffusion interaction parameter (k_D) of copolymers was quantified by cumulants analysis by using auto-attenuation with 20 acquisitions, 5 s/acquisition, and four concentrations depending on the molecular weight of the copolymer. This screening enabled selection of copolymers, polymer-PEG conjugates, and polymer-peptide conjugates for later SAXS characterization. For this, copolymers and copolymer conjugates had to be lyophilized to allow for proper SAXS buffer matching. DLS data was collected for lyophilized samples in 384-well plates using the same acquisition settings for concentrations of 1, 2, 5, and 10 mg/mL for polymer backbones and 1, 2, and 5 mg/mL for copolymer conjugates. All samples were centrifuged at 10,000 g for 10 min before loading the supernatant into 384-well plates for data collection. A data filter was applied to all data to assess data quality, following the Wyatt Technology default parameters (minimum amplitude = 0, maximum amplitude = 1, and baseline limit = 1 ± 0.01).

High-Throughput Small-Angle X-ray Scattering (SAXS)

SAXS experiments were conducted at beamline 16-ID of the National Synchrotron Light Source II (NSLS-II) at Brookhaven National Laboratory (Upton, NY) which is for Life Science X-ray Scattering (LiX). Copolymers and copolymer conjugates were lyophilized and prepared at different concentration ranges (1-10 mg/mL and 1-5 mg/mL, respectively). All samples were centrifuged at 10,000 g for 10 min. Copolymers and copolymer conjugates were transferred from PCR plates to PCR tubes manually on-site using multichannel pipettes. In this format, samples and buffer blanks were loaded into custom sample holders where a robotic arm can handle a sequence of sample holders (1 buffer for every 3 samples). This beamline contains three Pilatus 1M detectors which have a q range of 0.005-3.13 $\text{\AA}^{-1}$ ($q = 0.005\text{-}0.25 \text{\AA}^{-1}$ was taken as the small-angle region).¹⁰⁰⁻
¹⁰² All background subtracted data were analyzed using BioXTAS RAW 2.1 with ATSAS 2.8.4 to perform Guinier analysis and indirect Fourier transform (IFT) in the same manner as previously done.^{51, 76, 103, 104} Porod analysis was also utilized to quantify the flexibility of each copolymer chain in BIOSIS ScÅtter 4.0.^{105, 106} Once the hyperbolic Porod region was identified, the linear region of the $q^4 I(q)$ vs q^4 Porod-Debye plot was selected to determine the Porod exponent.¹⁰⁷⁻¹¹⁰

Simulated PDB Dataset

Because proteins are well-characterized and this work takes inspiration from protein design, we compiled a set of 304 PDB files of single protein species. These PDB files were used as an input to obtain simulated SAXS $I(q)$ vs q . The simulated data was generated in CRY SOL, a program in the ATSAS software suite.^{76, 77} For a q range of 0-0.25 $\text{\AA}^{-1}$, default parameters were used except for the number of points in the q range which was increased to 200 points. With the simulated SAXS data, the same analysis was completed as was done for experimental data of copolymers

and copolymer conjugates to compute R_g , $D_{\max}$, Porod exponent, and Porod volume. These structure files were also input into HullRad which can calculate hydrodynamic size with a convex hull model.¹¹¹ The FASTA files associated with each PDB entry selected were then used to calculate chemical parameters such as molecular weight, total charge, total positive charge, total negative charge, $\log P$, and HLB.

ML Models

Data obtained from random screening SAXS and DLS experiments were utilized to train evidential regression networks (ENets);^{71, 72} a type of deep neural network for prediction of R_g , R_h , R_g/R_h , and Porod Exponent. In this approach, a neural network is trained to predict the hyperparameters (γ , ν , α , β) of a normal-inverse gamma (NIG) distribution representative of labeled data. This enables efficient prediction of complex data, while also learning uncertainty within data. To train the networks, relative incorporation of monomers, peptides, and degree of polymerization of SCNPs were represented as one-hot encoding vectors and normalized using Sci-Kit Learn's RobustScaler transform. ENets were trained to predict the normalized values of R_g , R_h , R_g/R_h , and Porod exponent after RobustScaler transformation. To determine effective ENet hyperparameters, we performed 10-Kfold cross-validation utilizing the Python KerasTuner package to minimize a combined loss function of negative log-likelihood (NLL) loss, a regularization coefficient, and mean squared error (MSE) as described elsewhere.¹¹² Optimal hyperparameters that were identified on nine of ten folds were then utilized to make predictions on target R_g , R_h , R_g/R_h , and Porod Exponent values from the remaining fold. This process was repeated for each fold until predictions on all held-out folds were made. These 10 sets of held-out predictions were then utilized to validate model performance and determine a final set of

hyperparameters for forward predictions of EPO-SCNPs (**Figure S5**). To determine an appropriate value for our loss function regularization coefficient (L^R), values from 1e-5:1 were evaluated by observing model confidence on held-out data predictions. An L^R of 0.1 was selected for further hyperparameter optimization as it demonstrated effective calibration of uncertainty on held out data (**Figure S6**).

Prediction and Selection of Compact SCNPs

To propose candidate SCNPs for synthesis and characterization, ENets trained on Porod exponent and R_g respectively were utilized to predict NIG distributions for ~750,000 SCNP candidates representative of similar chemical constraints during our random screen. As we observed that predictions for EPO-SCNPs demonstrated an overall greater Porod Exponent than WDCL-SCNPs and PEG-SCNPs (**Figure S7**), we limited our selection to EPO-SCNPs for synthesis. From the remaining predictions, candidates were filtered to require predicted $R_g < 7$ nm, Porod exponent of 3.7 - 4.0, and exist in the lowest quartile of predicted variance for Porod exponent predictions. These criteria filtered possible candidates to 336 SCNP chemistries, from which 30 were randomly sampled for final synthesis and characterization. Additionally, to ensure that proposed EPO-SCNPs were not highly similar to previously synthesized SCNPs in our random screen, three-dimensional PCA analysis was performed on ENet proposed EPO-SCNPs in comparison to EPO-SCNPs evaluated during random screen (**Figure S8**). Distinct differences between model proposed EPO-SCNPs and random screened samples are observed.

ASSOCIATED CONTENT

Supporting Information for “Data-Driven Design of Protein-Like Single-Chain Polymer Nanoparticles”

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DATA AVAILABILITY STATEMENT

The data that supports the findings of this study is openly available on Github at <https://github.com/GormleyLab/Data-Driven-Design-of-SCNPs>.¹¹³

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