SUPPORTING INFORMATION

In silico profiling nanoparticles: predictive nanomodeling using universal nanodescriptors and various machine learning approaches

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Fig. S1 QNAR model performance of consensus modeling results in (a) GNP-enzyme binding affinities (b) Cellular uptake potentials by HEK293 cell (c) ROS levels in HEK293 cell (d) Cellular uptake potentials by A549 cell (e) logP (f) Zeta potentials in water (g) Zeta potentials in phosphate buffer. Red dots are GNPs in the training set, and blue dots are those in the test set. The results were obtained from one-time simulation. Correlation coefficients (R^2) from consensus modeling results are also shown.



Fig. S2 QNAR model performance of consensus modeling results in (a) GNP-enzyme binding affinities (b) Cellular uptake potentials by HEK293 cell (c) ROS levels in HEK293 cell (d) Cellular uptake potentials by A549 cell (e) logP (f) Zeta potentials in water (g) Zeta potentials in phosphate buffer. Red dots are GNPs in the training set, and blue dots are those in the test set. The results were obtained from leave-one-out (LOO) validation. Correlation coefficients (R²) from consensus modeling results are also shown.

Modeling set	kNN		RF		Consensus	
	5-fold cross validation	Eternal validation	5-fold cross validation	External validation	5-fold cross validation	External validation
1	0.85	-	0.57	-	0.76	-
2	0.86	-	0.76	-	0.84	-
3	0.80	-	0.51	-	0.70	-
4	0.78	0.87	0.68	0.81	0.78	0.86
5	0.81	0.86	0.69	0.76	0.79	0.82
6	0.89	0.81	0.76	0.86	0.85	0.84
7	0.81	0.93	0.83	0.93	0.84	0.94

Table S1. Correlation coefficients (R^2) from *k*NN, RF and consensus modeling results of seven modeling sets. The results were obtained from one-time simulation.

Table S2. Correlation coefficients (R^2) from *k*NN, RF and consensus modeling results of seven modeling sets. The results were obtained from leave-one-out (LOO) validation.

Modeling set	kNN	RF	Consensus
1	0.51	0.51	0.53
2	0.90	0.81	0.87
3	0.67	0.54	0.63
4	0.84	0.76	0.83
5	0.86	0.73	0.81
6	0.86	0.86	0.87
7	0.85	0.89	0.88