Supporting Information

Protein Precoating Modulates Biomolecular Coronas and Nanocapsule–Immune Cell

Interactions in Human Blood

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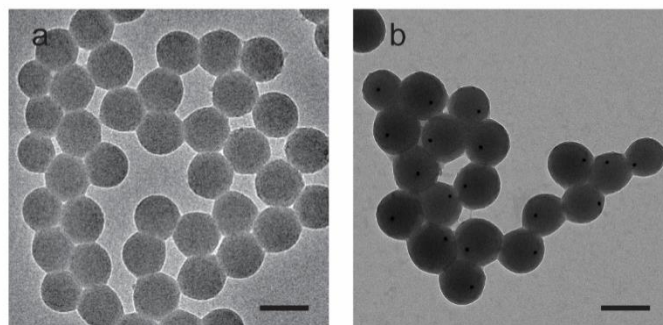
Figure S1. TEM images of 100 nm (a) BDT templates and (b) Au@BDT templates. Scale bars are 100 nm.
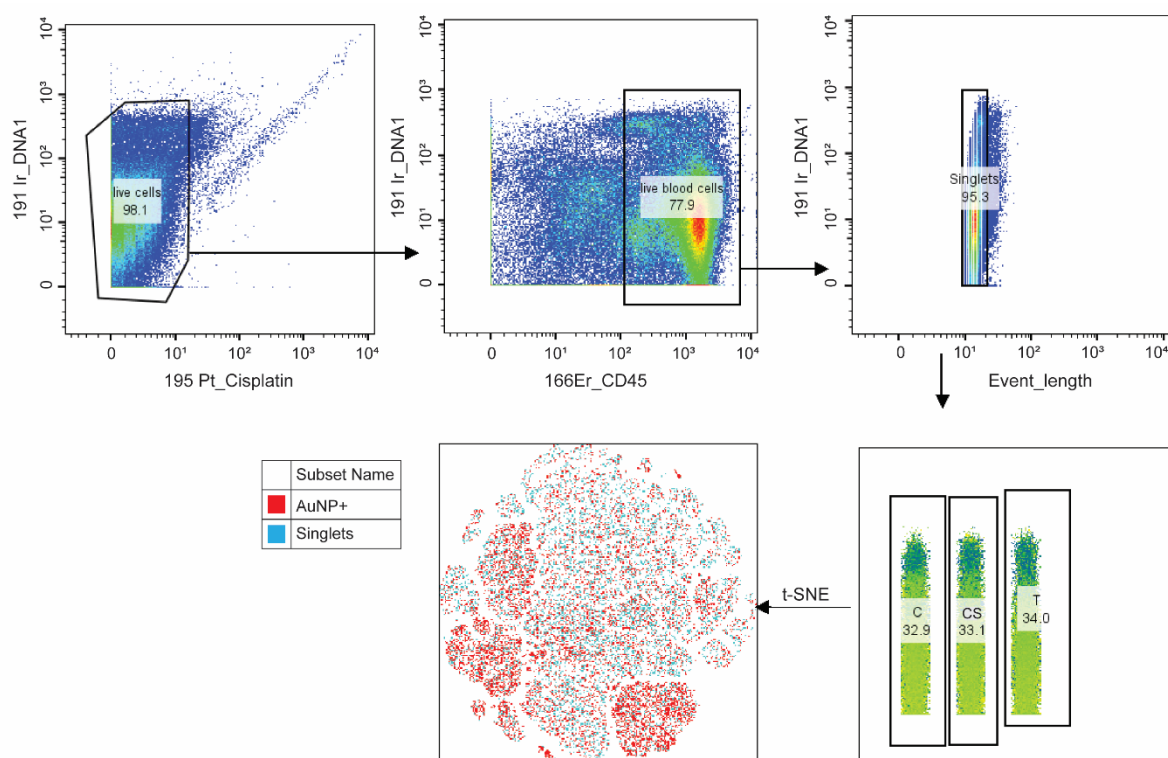
Figure S2. Analysis of mass cytometry data of blood assays. Mass cytometry data from whole blood assays of uncoated nanoparticles were concatenated, and DNA+ (193Ir+) and live (Cisplatin−) blood (CD45+) singlet (Event-Length^{lo}) events were selected. t-SNE was performed on the concatenated file. Events from blood samples of the same nanoparticle type were the selected and cells that had associated nanoparticles were overlaid on the t-SNE plot from the corresponding blood samples.
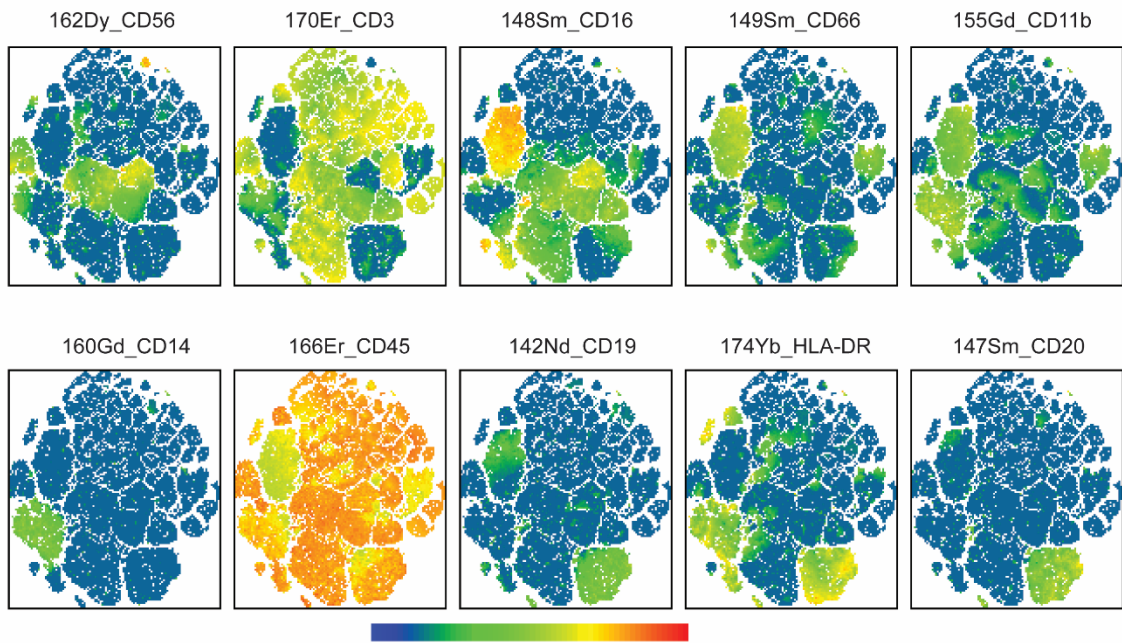
Figure S3. Expression intensity of cell markers in the t-SNE plot of the concatenated sample. Cell populations of different leukocyte types were gated by the expression of specific cell markers.
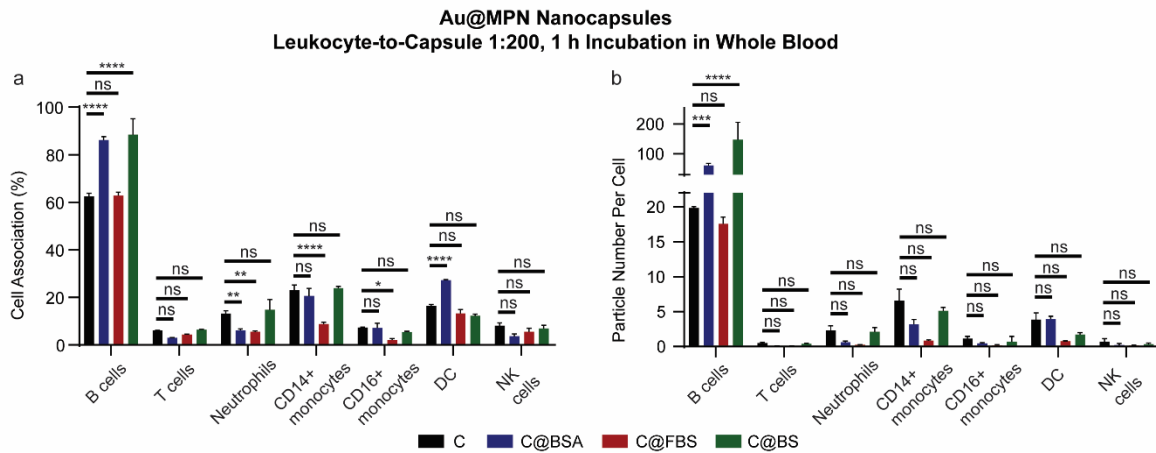
Figure S4. Whole blood association at a leukocyte-to-capsule ratio of 1:200 after 1 h incubation, measured as (a) percentage of association (%) and (b) number of particles per cell, of uncoated 100 nm Au@MPN nanocapsules (C) and BSA-, FBS-, or BS-precoated 100 nm Au@MPN nanocapsules (C@BSA, C@FBS, or C@BS) with B cells, T cells, neutrophils, CD14+ and CD16+ monocytes, DC, or NK cells with statistical analysis included: ns, p-value > 0.05; * p-value < 0.05; ** p-value < 0.01; *** p-value < 0.001; **** p-value < 0.0001 (determined by two-way ANOVA).
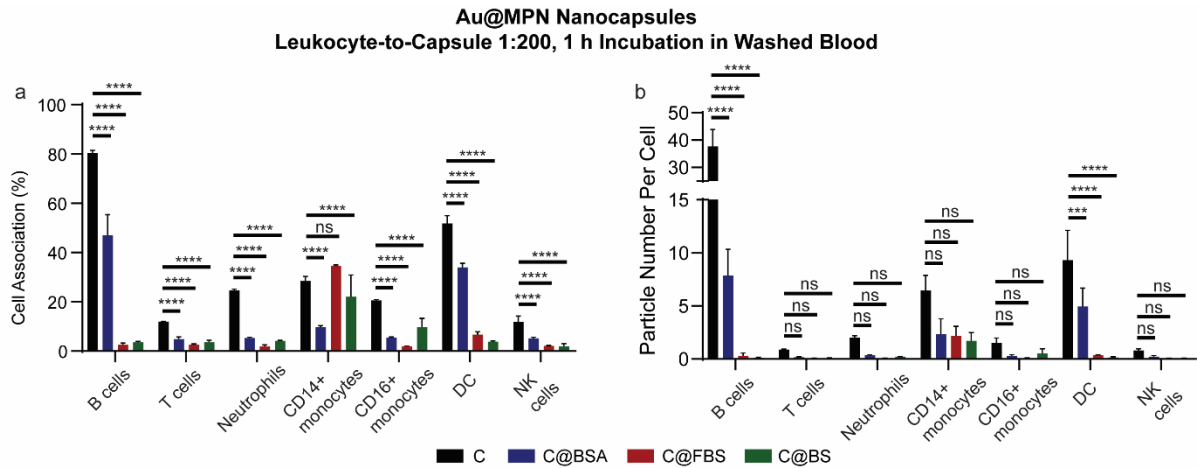
Figure S5. Washed blood association at a leukocyte-to-capsule ratio of 1:200 after 1 h incubation, measured as (a) percentage of association (%) and (b) number of particles per cell, of uncoated 100 nm Au@MPN nanocapsules (C) and BSA-, FBS-, or BS-precoated 100 nm Au@MPN nanocapsules (C@BSA, C@FBS, or C@BS) with B cells, T cells, neutrophils, CD14+ and CD16+ monocytes, DC, or NK cells with statistical analysis included: ns, p-value > 0.05; * p-value < 0.05; ** p-value < 0.01; *** p-value < 0.001; **** p-value < 0.0001 (determined by two-way ANOVA).
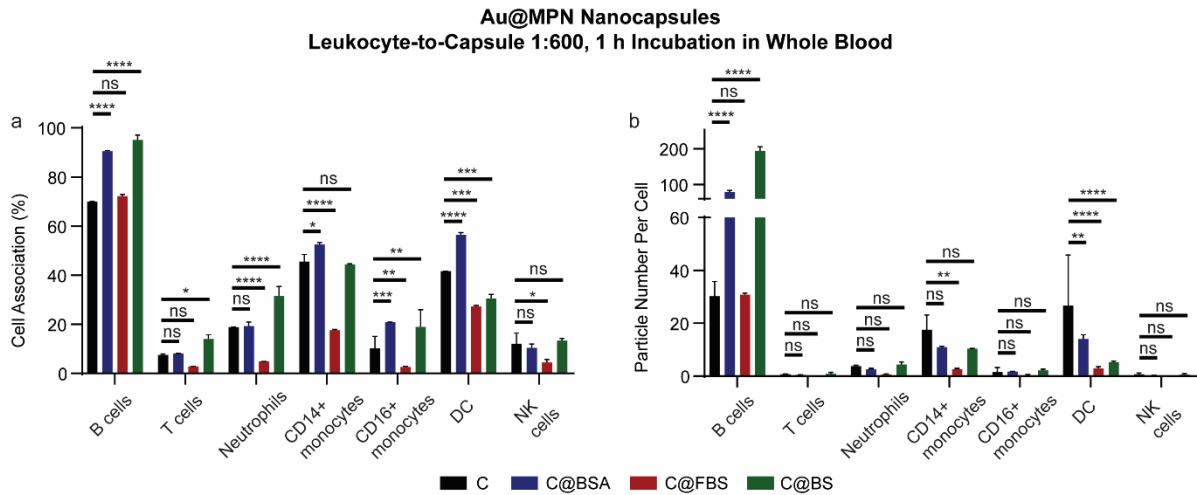
Figure S6. Whole blood association at a leukocyte-to-capsule ratio of 1:600 after 1 h incubation, measured as (a) percentage of association (%) and (b) number of particles per cell, of uncoated 100 nm Au@MPN nanocapsules (C) and BSA-, FBS-, or BS-precoated 100 nm Au@MPN nanocapsules (C@BSA, C@FBS, or C@BS) with B cells, T cells, neutrophils, CD14+ and CD16+ monocytes, DC, or NK cells with statistical analysis included: ns, p-value > 0.05; * p-value < 0.05; ** p-value < 0.01; *** p-value < 0.001; **** p-value < 0.0001 (determined by two-way ANOVA).
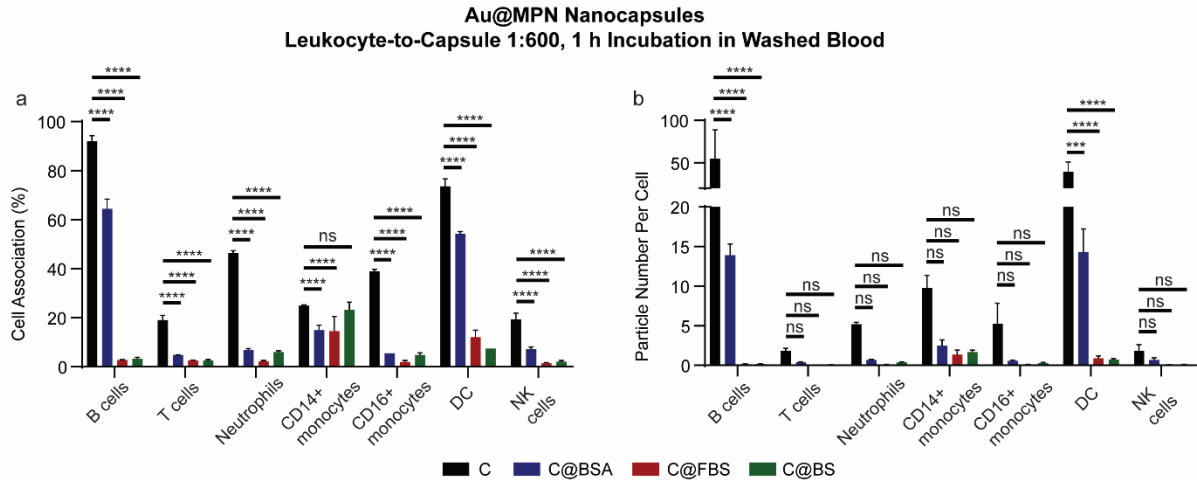
Figure S7. Washed blood association at a leukocyte-to-capsule ratio of 1:600 after 1 h incubation, measured as (a) percentage of association (%) and (b) number of particles per cell, of uncoated 100 nm Au@MPN nanocapsules (C) and BSA-, FBS-, or BS-precoated 100 nm Au@MPN nanocapsules (C@BSA, C@FBS, or C@BS) with B cells, T cells, neutrophils, CD14+ and CD16+ monocytes, DC, or NK cells with statistical analysis included: ns, p-value > 0.05; * p-value < 0.05; ** p-value < 0.01; *** p-value < 0.001; **** p-value < 0.0001 (determined by two-way ANOVA).

Figure S8. Whole blood association cells at a leukocyte-to-capsule ratio of 1:200 after 4 h incubation, measured as (a) percentage of association (%) and (b) number of particles per cell, of uncoated 100 nm Au@MPN nanocapsules (C) and BSA-, FBS-, or BS-precoated 100 nm Au@MPN nanocapsules (C@BSA, C@FBS, or C@BS) with B cells, T cells, neutrophils, CD14+ and CD16+ monocytes, DC, or NK with statistical analysis included: ns, p-value > 0.05; * p-value < 0.05; ** p-value < 0.01; *** p-value < 0.001; **** p-value < 0.0001 (determined by two-way ANOVA).
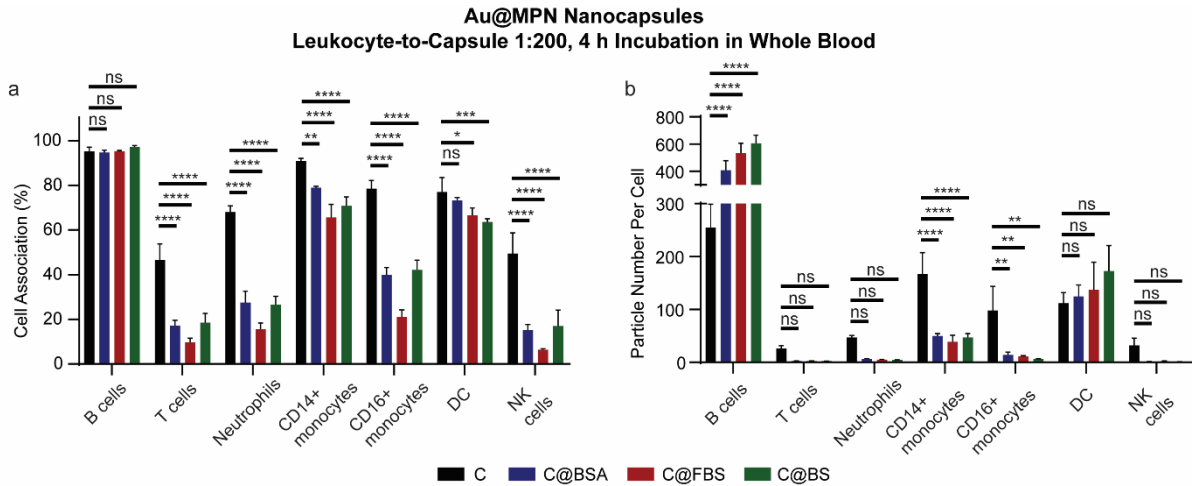
Figure S9. Whole blood association at a leukocyte-to-capsule ratio of 1:600 after 4 h incubation, measured as (a) percentage of association (%) and (b) number of particles per cell, of uncoated 100 nm Au@MPN nanocapsules (C) and BSA-, FBS-, or BS-precoated 100 nm Au@MPN nanocapsules (C@BSA, C@FBS, or C@BS) with B cells, T cells, neutrophils, CD14+ and CD16+ monocytes, DC, or NK cells with statistical analysis included: ns, p-value > 0.05; * p-value < 0.05; ** p-value < 0.01; *** p-value < 0.001; **** p-value < 0.0001 (determined by two-way ANOVA).
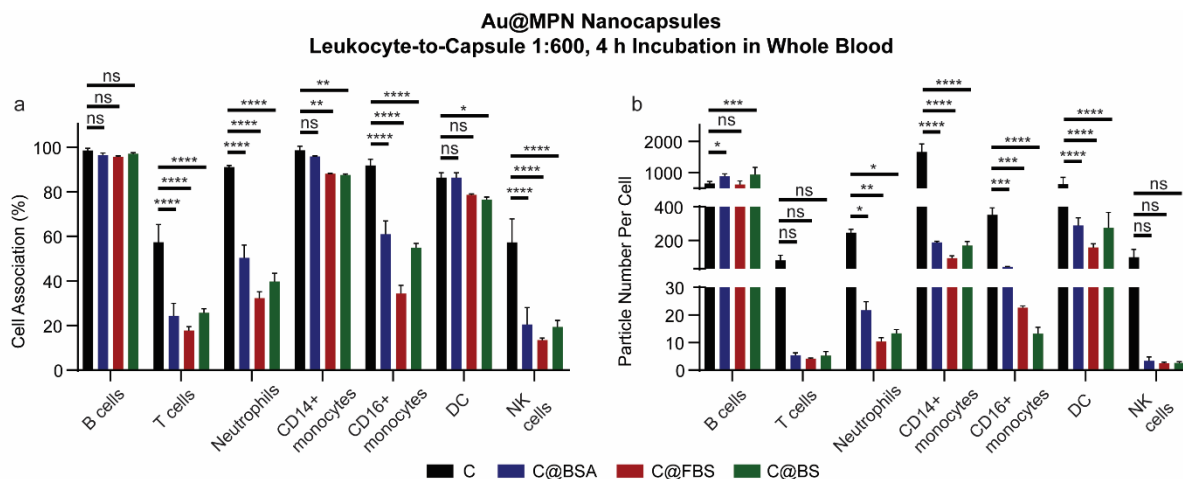

Figure S10. Whole blood association at a leukocyte-to-particle ratio of 1:200 after 1 h incubation, measured as (a) percentage of association (%) and (b) number of particles per cell, of uncoated 100 nm Au@BDT@MPN core–shell nanoparticles (CS) and BSA-, FBS-, or BS-precoated 100 nm Au@BDT@MPN core–shell nanoparticles (CS@BSA, CS@FBS, or CS@BS) with B cells, T cells, neutrophils, CD14+ and CD16+ monocytes, DC, or NK cells with statistical analysis included: ns, p-value > 0.05; * p-value < 0.05; ** p-value < 0.01; *** p-value < 0.001; **** p-value < 0.0001 (determined by two-way ANOVA).

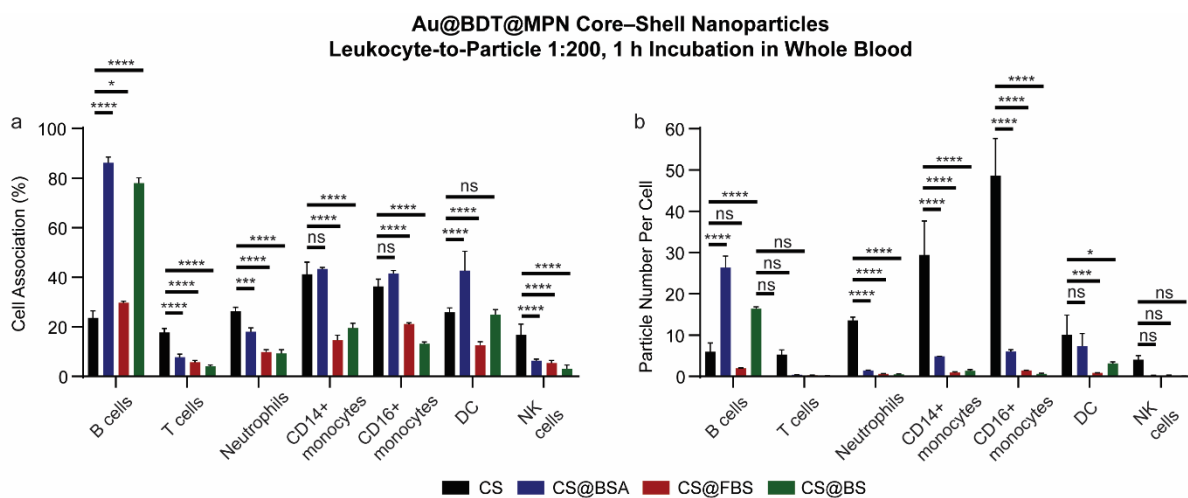**Figure S11.** Washed blood association at a leukocyte-to-particle ratio of 1:200 after 1 h incubation, measured as (a) percentage of association (%) and (b) number of particles per cell, of uncoated 100 nm Au@BDT@MPN core–shell nanoparticles (CS) and BSA-, FBS-, or BS-precoated 100 nm Au@BDT@MPN core–shell nanoparticles (CS@BSA, CS@FBS, or CS@BS) with B cells, T cells, neutrophils, CD14+ and CD16+ monocytes, DC, or NK cells with statistical analysis included: ns, p-value > 0.05; * p-value < 0.05; ** p-value < 0.01; *** p-value < 0.001; **** p-value < 0.0001 (determined by two-way ANOVA).
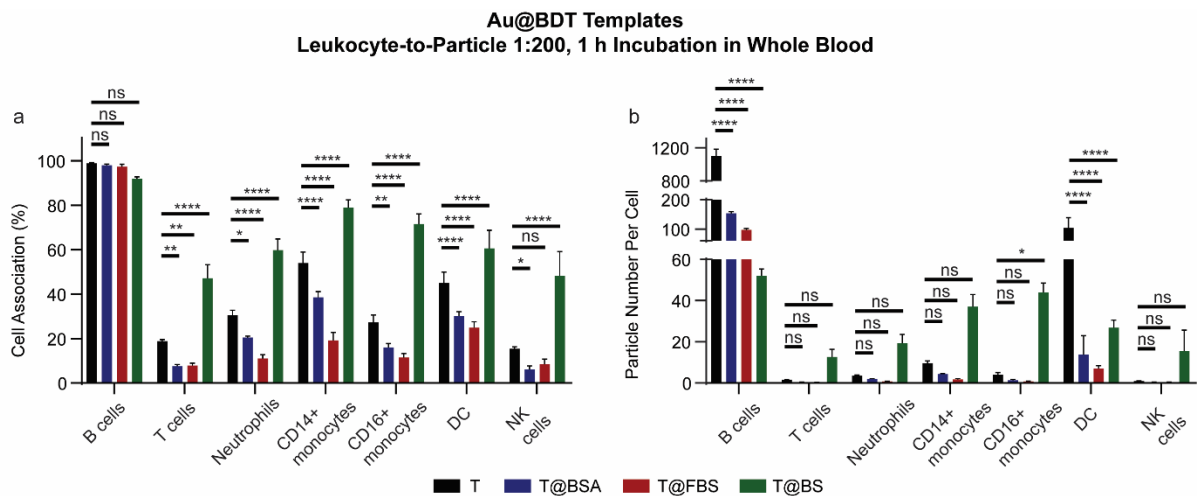
Figure S12. Whole blood association at a leukocyte-to-particle ratio of 1:200 after 1 h incubation, measured as (a) percentage of association (%) and (b) number of particles per cell, of uncoated 100 nm Au@BDT templates (T) and BSA-, FBS-, or BS- precoated 100 nm Au@BDT templates (T@BSA, T@FBS, or T@BS) with B cells, T cells, neutrophils, CD14+ and CD16+ monocytes, DC, or NK cells with statistical analysis included: ns, p-value > 0.05; * p-value < 0.05; ** p-value < 0.01; *** p-value < 0.001; **** p-value < 0.0001 (determined by two-way ANOVA).
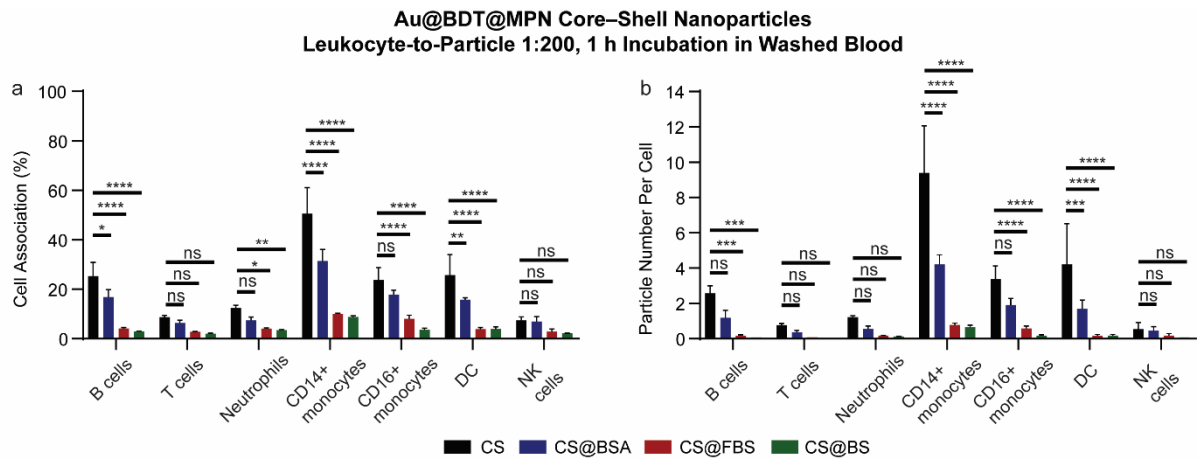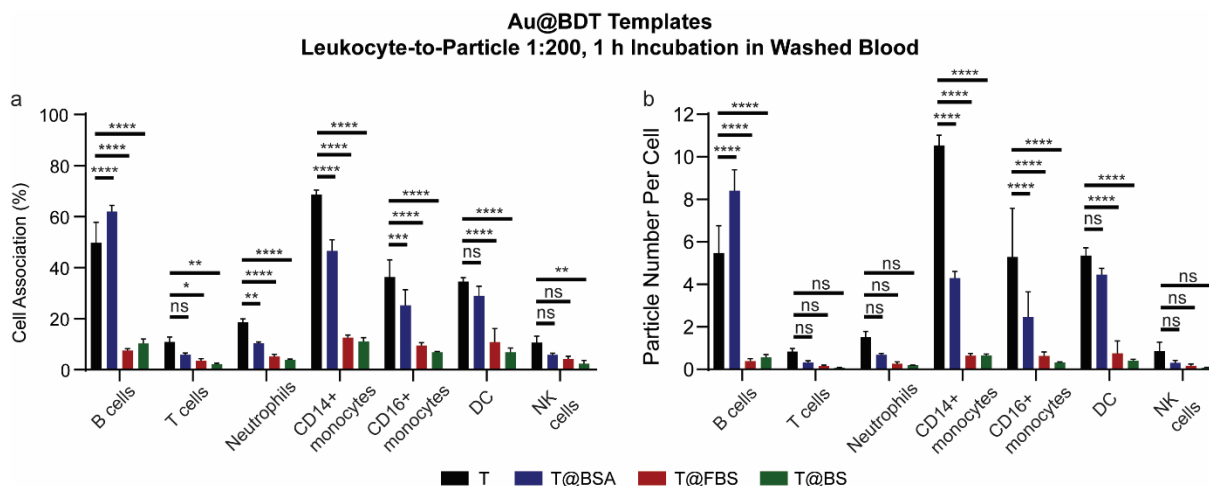
Figure S13. Washed blood association at a leukocyte-to-particle ratio of 1:200 after 1 h incubation, measured as (a) percentage of association (%) and (b) number of particles per cell, of uncoated 100 nm Au@BDT templates (T) and BSA-, FBS-, or BS-precoated 100 nm Au@BDT templates (T@BSA, T@FBS, or T@BS with B cells, T cells, neutrophils, CD14+ and CD16+ monocytes, DC, or NK cells with statistical analysis included: ns, p-value > 0.05; * p-value < 0.05; ** p-value < 0.01; *** p-value < 0.001; **** p-value < 0.0001 (determined by two-way ANOVA).
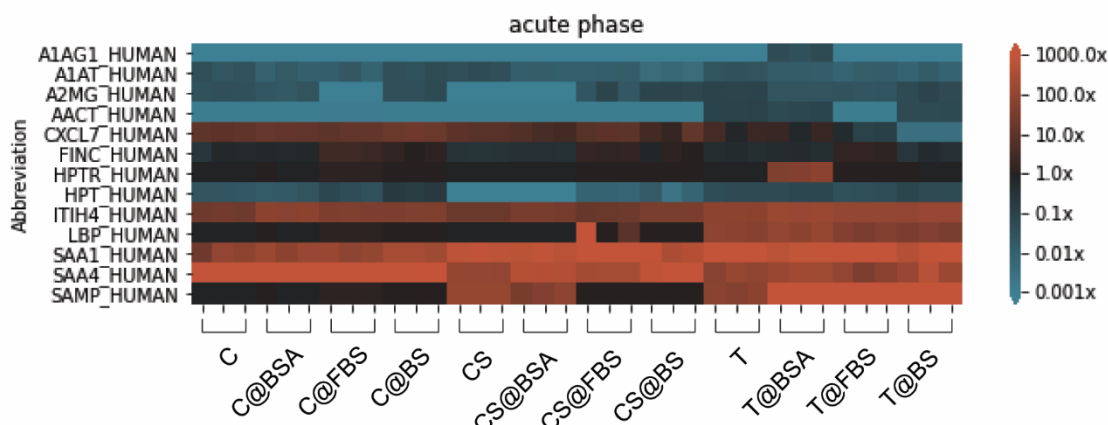

Figure S14. Heatmap of the enrichment indexes of acute phase proteins in the protein coronas of the Au@BDT templates (T), Au@BDT@MPN core–shell nanoparticles (CS), and Au@MPN nanocapsules (C) without and with precoating with BSA, FBS, or BS. The proteins are listed alphabetically in a colorized log scale. Three replicates of each nanoparticle system were examined.
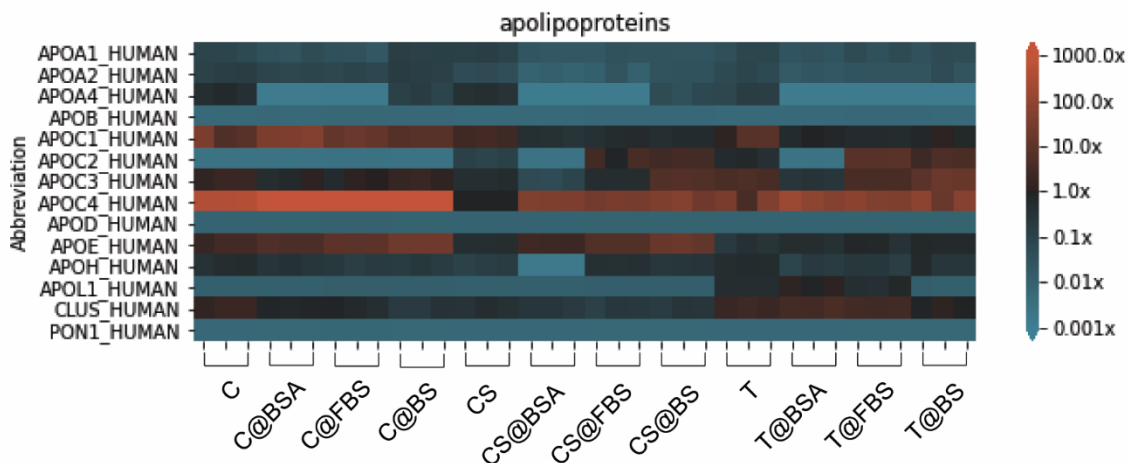
Figure S15. Heatmap of the enrichment indexes of apolipoproteins in the protein coronas of the Au@BDT templates (T), Au@BDT@MPN core–shell nanoparticles (CS), and Au@MPN nanocapsules (C) without and with precoating with BSA, FBS, or BS. The proteins are listed alphabetically in a colorized log scale. Three replicates of each nanoparticle system were examined.
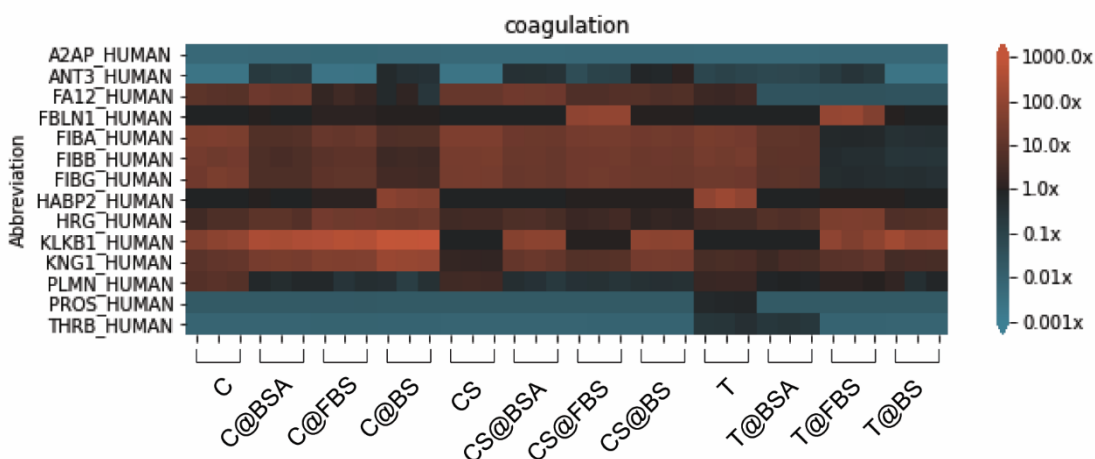
Figure S16. Heatmap of the enrichment indexes of coagulation proteins in the protein coronas of the Au@BDT templates (T), Au@BDT@MPN core–shell nanoparticles (CS), and Au@MPN nanocapsules (C) without and with precoating with BSA, FBS, or BS. The proteins are listed alphabetically in a colorized log scale. Three replicates of each nanoparticle system were examined.
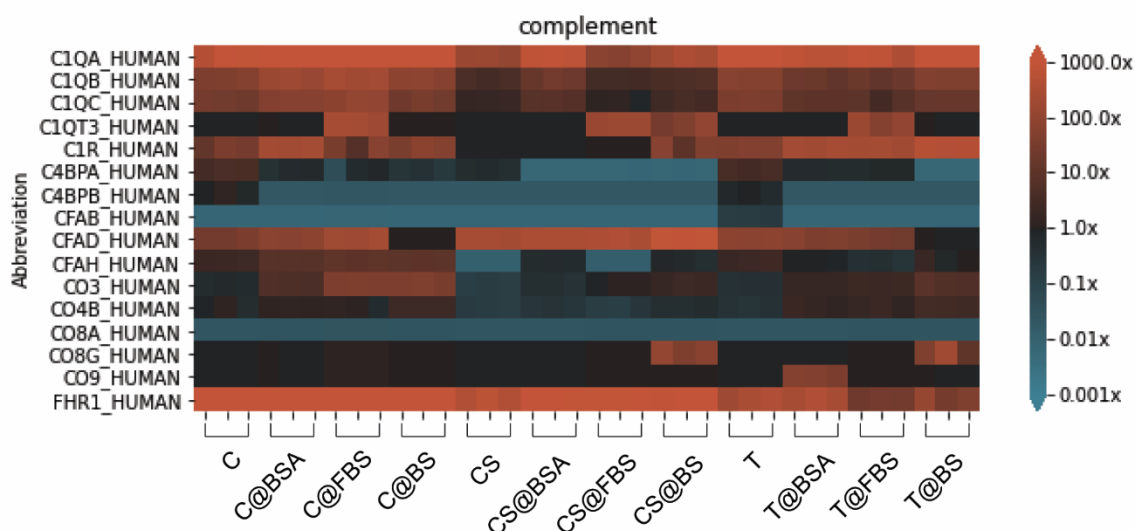
Figure S17. Heatmap of the enrichment indexes of complements in the protein coronas of the Au@BDT templates (T), Au@BDT@MPN core–shell nanoparticles (CS), and Au@MPN nanocapsules (C) without and with precoating with BSA, FBS, or BS. The proteins are listed alphabetically in a colorized log scale. Three replicates of each nanoparticle system were examined.
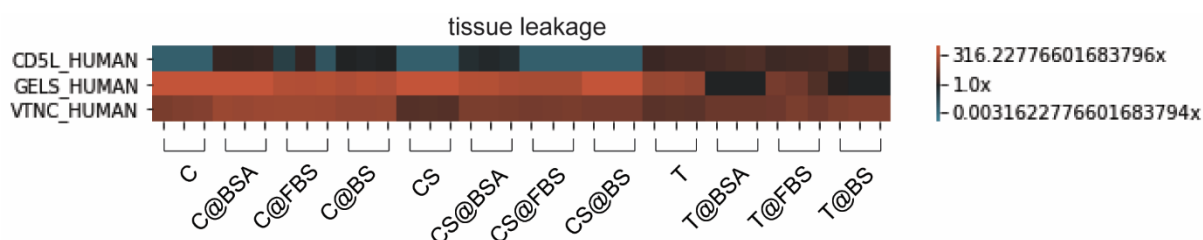
Figure S18. Heatmap of the enrichment indexes of tissue leakage proteins in the protein coronas of the Au@BDT templates (T), Au@BDT@MPN core–shell nanoparticles (CS), and Au@MPN nanocapsules (C) without and with precoating with BSA, FBS, or BS. The proteins are listed alphabetically in a colorized log scale. Three replicates of each nanoparticle system were examined.
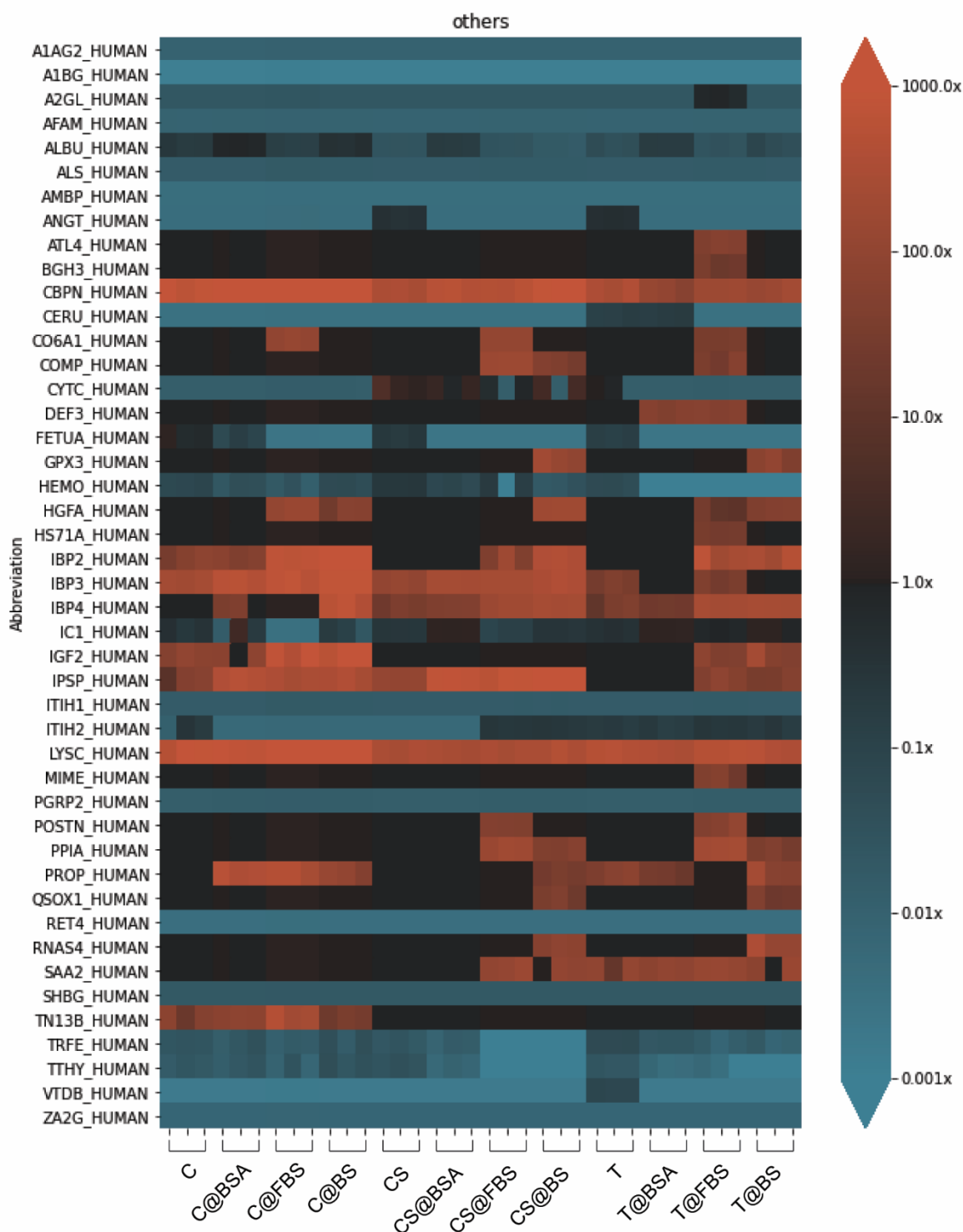
Figure S19. Heatmap of the enrichment indexes of other proteins in the protein coronas of the Au@BDT templates (T), Au@BDT@MPN core–shell nanoparticles (CS), and Au@MPN nanocapsules (C) without and with precoating with BSA, FBS, or BS. The proteins are listed alphabetically in a colorized log scale. Three replicates of each nanoparticle system were examined.

Table S1. Average size, ζ-potential, and thickness of the Au@BDT templates (T), Au@BDT@MPN core–shell nanoparticles (CS), and Au@MPN nanocapsules (C) without and with precoating with bovine serum albumin (BSA), fetal bovine serum (FBS), or bovine serum (BS), followed by incubation in human plasma (HP)

Sample	Average size[a] (nm)	ζ-potential in buffer[b] (mV)	Thickness[c] (nm)
T	98 ± 1	−42 ± 3	−
T@HP	100 ± 1	−16 ± 4	−
T@BSA	99 ± 1	−35 ± 5	−
T@BSA@HP	100 ± 1	−17 ± 5	−
T@FBS	98 ± 2	− 32 ± 4	−
T@FBS@HP	100 ± 2	−18 ± 4	−
T@BS	99 ± 2	−20 ± 4	−
T@BS@HP	102 ± 3	−17 ± 3	−
CS	106 ± 2	−37 ± 5	−
CS@HP	109 ± 5	−16 ± 3	−
CS@BSA	106 ± 3	−30 ± 4	−
CS@BSA@HP	109 ± 4	−16 ± 3	−
CS@FBS	106 ± 3	− 27 ± 5	−
CS@FBS@HP	108 ± 5	−17 ± 3	−
CS@BS	104 ± 4	−18 ± 5	−
CS@BS@HP	104 ± 6	−16 ± 2	−
C	88 ± 2	−31 ± 5	47 ± 6
C@HP	93 ± 5	−16 ± 4	−
C@BSA	85 ± 3	−29 ± 6	−
C@BSA@HP	90 ± 4	−17 ± 4	−
C@FBS	89 ± 2	−22 ± 4	−
C@FBS@HP	93 ± 2	−16 ± 4	−
C@BS	111 ± 7	−16 ± 4	−
C@BS@HP	115 ± 4	−16 ± 4	−

[a] Determined by nanoparticle tracking analysis.
[b] Measured in 10 mM phosphate buffer (pH 7.4) by microelectrophoresis.
[c] Measured from the highest point on the nanoparticle and nanocapsule in dry state to the substrate surface by atomic force microscopy. Ten nanoparticles or nanocapsules were analyzed for each sample.

Table S2. Top 20 proteins identified in the bovine coronas of Au@BDT templates (T), Au@BDT@MPN core–shell nanoparticles (CS), and Au@MPN nanocapsules (C) precoated with BSA, FBS, or BS

Protein ID	Protein name	Gene name	Relative protein abundance (RPA) of top 20 proteins in the bovine coronas (%)								
			T@BSA	T@FBS	T@BS	CS@BSA	CS@FBS	CS@BS	C@BSA	C@FBS	C@BS
Q1RMN8	Immunoglobulin light chain, lambda gene cluster	IGL@	0.05	0.03	20.30	0.14	0.03	7.86	0.08	0.04	8.81
Q3ZBS7	Vitronectin	VTN	0.00	3.38	11.80	0.00	0.06	0.21	0.00	0.63	1.90
P15497	Apolipoprotein A-I	APOA1	0.03	4.29	10.26	0.03	13.45	27.54	0.00	0.62	2.29
P00735	Prothrombin	F2	0.00	1.79	7.93	0.00	0.03	0.60	0.00	0.27	2.48
Q03247	Apolipoprotein E	APOE	0.02	1.74	7.37	0.09	0.34	4.90	0.00	1.02	2.30
Q3T052	Inter-alpha-trypsin inhibitor heavy chain H4	ITIH4	0.02	1.19	6.15	0.00	0.27	3.47	0.70	0.35	1.48
P41361	Antithrombin-III	SERPINC1	0.00	1.72	5.91	0.09	0.08	0.61	0.01	0.31	2.77
P81644	Apolipoprotein A-II	APOA2	0.00	23.54	4.89	0.11	4.14	1.73	0.00	3.07	0.71
Q2KJ62	Kininogen-1	KNG1	0.00	0.09	3.30	0.01	0.02	0.50	0.00	0.01	1.98
Q3SX14	Gelsolin	GSN	0.11	1.40	3.27	1.59	2.56	16.23	2.85	3.29	18.04
P02769	Serum albumin	ALB	94.96	0.63	2.44	93.40	1.20	1.99	95.55	2.34	15.00
Q2UVX4	Complement C3	C3	0.11	0.31	1.66	0.20	0.45	3.03	0.17	3.37	4.59
P01966	Hemoglobin subunit alpha	HBA	0.15	25.97	1.64	0.07	23.62	2.06	0.02	20.56	2.33
Q9N2I2	Plasma serine protease inhibitor	SERPINA5	0.00	1.45	1.49	0.00	1.11	1.72	0.00	1.22	0.95
P02777	Platelet factor 4	PF4	0.00	0.71	1.38	0.00	0.17	1.20	0.00	1.33	8.69
P17690	Beta-2-glycoprotein 1	APOH	0.05	0.29	0.69	0.06	0.71	1.07	0.04	1.35	0.38

Q3SX09	Hemoglobin fetal subunit beta	N/A	0.53	16.79	0.60	0.26	28.44	0.98	0.06	31.98	0.70
P12763	Alpha-2-HS-glycoprotein	AHSG	0.05	9.79	0.11	0.09	14.84	0.15	0.02	12.72	0.91
P34955	Alpha-1-antiproteinase	SERPINA1	0.01	1.10	0.11	0.05	1.11	0.13	0.00	0.82	0.40
P02672	Fibrinogen alpha chain	FGA	0.00	0.39	0.08	0.00	0.90	0.95	0.00	0.59	0.58
P15497, Q03247, P81644, P17690	Apolipoproteins A-I, A-II, E, H	APOA1, APOA2, APOE, APOH	0.1	29.86	23.21	0.29	18.64	35.24	0.04	6.06	5.68

Table S3. Top 20 proteins identified in the human plasma coronas of Au@BDT templates (T), Au@BDT@MPN core–shell nanoparticles (CS), and Au@MPN nanocapsules (C) without precoating and precoated with BSA, FBS, or BS

Protein ID	Protein name	Gene name	Relative protein abundance (RPA) of top 20 proteins of the human plasma coronas (%)											
			T	T@BSA	T@FBS	T@BS	CS	CS@BSA	CS@FBS	CS@BS	C	C@BSA	C@FBS	C@BS
P02671	Fibrinogen alpha chain	FGA	18.94	6.89	0.45	0.27	25.65	11.80	17.95	14.80	24.55	3.81	8.96	3.36
P02679	Fibrinogen gamma chain	FGG	14.53	6.49	0.38	0.32	20.94	10.82	16.13	12.48	21.07	3.23	7.11	2.04
P02675	Fibrinogen beta chain	FGB	15.48	5.43	0.28	0.17	17.46	8.80	12.77	10.44	13.87	2.40	4.98	1.37
P02768	Serum albumin	ALB	1.78	7.13	1.23	2.37	1.15	7.22	1.18	0.69	8.45	32.48	4.74	16.24
P04004	Vitronectin	VTN	1.00	1.94	2.98	4.54	0.79	4.04	3.44	3.10	4.89	16.24	16.88	13.19
P02654	Apolipoprotein C-I	APOC1	1.16	0.16	0.12	0.18	0.55	0.08	0.11	0.11	3.53	8.92	2.75	1.47
P0DOX5	Ig gamma-1 chain C region	IGHG1	7.69	13.01	14.55	17.04	6.04	10.47	8.50	9.03	1.99	0.98	0.44	0.46
P0DOX7	Immunoglobulin kappa light chain	N/A	6.22	11.91	16.98	12.76	6.43	9.94	9.59	7.97	1.61	1.31	0.80	1.28
P35542	Serum amyloid A-4 protein	SAA4	0.04	0.07	0.03	0.10	0.04	0.18	0.09	0.74	1.48	1.83	1.45	2.33
P01042	Kininogen-1	KNG1	0.46	0.38	1.09	0.40	0.18	1.72	0.75	3.24	1.33	3.69	4.81	14.92
P0DOX8	Immunoglobulin lambda-1 light chain	N/A	4.18	6.40	8.31	6.61	2.75	4.48	3.29	3.35	1.24	0.90	0.56	1.79

P02775	Platelet basic protein	PPBP	0.22	0.16	0.03	0.00	0.91	0.44	0.95	0.58	1.12	1.39	1.17	2.09
P02747	Complement C1q subcomponent subunit C	C1QC	1.75	0.46	0.29	0.66	0.08	0.34	0.05	0.14	1.11	2.64	4.11	1.19
P02652	Apolipoprotein A-II	APOA2	0.53	0.15	0.20	0.27	0.38	0.08	0.13	0.23	1.06	0.62	0.57	1.06
P01860	Ig gamma-3 chain C region	IGHG3	0.67	1.19	1.08	2.84	0.53	0.91	0.63	1.40	1.04	0.74	0.34	0.33
P02656	Apolipoprotein C-III	APOC3	2.27	0.15	2.07	7.41	0.27	0.04	0.28	3.25	0.97	0.43	0.45	0.83
P01834	Ig kappa chain C region	IGKC	5.02	10.47	14.09	11.41	4.53	10.04	8.07	8.91	0.90	0.54	0.42	0.36
Q03591	Complement factor H-related protein 1	CFHR1	0.11	0.12	0.01	0.02	0.19	0.41	0.35	0.36	0.89	1.35	0.92	1.54
P02746	Complement C1q subcomponent subunit B	C1QB	1.08	0.31	0.28	0.88	0.07	0.37	0.06	0.09	0.83	2.74	3.90	1.36
P02647	Apolipoprotein A-I	APOA1	0.57	0.25	0.43	0.40	1.03	0.19	0.23	0.23	0.69	0.32	0.24	1.13

Table S4. Top 20 bovine proteins in FBS and BS and top 20 proteins in human plasma

RPA of the top 20 bovine proteins (%)					RPA of the top 20 human proteins (%)			
Protein ID	Protein name	Gene name	FBS	BS	Protein ID	Protein name	Gene name	Human plasma
P02769	Serum albumin	ALB	33.06	38.61	P02768	Serum albumin	ALB	42.54
P12763	Alpha-2-HS-glycoprotein	AHSG	25.34	0.98	P02652	Apolipoprotein A-II	APOA2	7.20
P34955	Alpha-1-antiproteinase	SERPINA1	11.02	1.82	P02787	Serotransferrin	TF	3.60
Q0IIK2	Serotransferrin	TF	5.99	4.67	P0DOX5	Ig gamma-1 chain C region	IGHG1	3.36
Q3SX09	Hemoglobin fetal subunit beta	N/A	4.65	1.50	P02647	Apolipoprotein A-I	APOA1	2.99
Q3SZR3	Alpha-1-acid glycoprotein	ORM1	3.60	7.68	P0DOX7	Immunoglobulin kappa light chain	N/A	4.54
P15497	Apolipoprotein A-I	APOA1	3.22	13.39	P0DOX8	Immunoglobulin lambda-1 light chain	N/A	2.61
Q58D62	Fetuin-B	FETUB	2.13	0.05	P01009	Alpha-1-antitrypsin	SERPINA1	2.21
P81644	Apolipoprotein A-II	APOA2	1.84	2.43	P00738	Haptoglobin	HP	1.98
Q3SZ57	Alpha-fetoprotein	AFP	1.57	0.00	P01859	Ig gamma-2 chain C region	IGHG2	1.72
P01966	Hemoglobin subunit alpha	HBA	1.40	1.11	P02679	Fibrinogen gamma chain	FGG	1.78
Q9TTE1	Serpin A3-1	SERPINA3-1	1.14	4.48	P02675	Fibrinogen beta chain	FGB	1.81

Q2KJF1	Alpha-1B-glycoprotein	A1BG	1.06	1.10	P01834	Ig kappa chain C region	IGKC	1.56
P28800	Alpha-2-antiplasmin	SERPINF2	0.36	0.11	P02671	Fibrinogen alpha chain	FGA	1.55
Q9TRI1	Inter-alpha-trypsin inhibitor HC2 component homolog	N/A	0.28	0.10	P01860	Ig gamma-3 chain C region	IGHG3	1.41
Q3T052	Inter-alpha-trypsin inhibitor heavy chain H4	ITIH4	0.25	1.96	P01023	Alpha-2-macroglobulin	A2M	1.16
Q3MHN5	Vitamin D-binding protein	GC	0.23	0.17	P01871	Ig mu chain C region	IGHM	1.13
Q3SZH5	Angiotensinogen	AGT	0.23	0.10	P01876	Ig alpha-1 chain C region	IGHA1	1.10
P17690	Beta-2-glycoprotein 1	APOH	0.22	0.22	P01024	Complement C3	C3	0.92
P00978	Protein AMBP	AMBP	0.21	0.14	P02790	Hemopexin	HPX	0.84

Table S5. Enrichment indexes of the human plasma corona proteins of the Au@BDT templates (T), Au@BDT@MPN core–shell nanoparticles (CS), and Au@MPN nanocapsules (C) without precoating and precoated with BSA, FBS, or BS (the enrichment indexes for the different nanoparticle systems are listed according to the enrichment indexes of the T nanoparticles sorted from largest to smallest)

Protein ID	Protein name	Gene name	Function	Enrichment index of the human plasma corona proteins											
				T	T@BSA	T@FBS	T@BS	CS	CS@BSA	CS@FBS	CS@BS	C	C@BSA	C@FBS	C@BS
P0DOY2	Immunoglobulin lambda constant 2	IGLC2	immunoglobulins	2867.18	4193.00	7416.84	4807.41	1543.48	3445.98	2248.70	2369.32	0.99	1.00	1.07	1.01
P0DJI8	Serum amyloid A-1 protein	SAA1	acute phase	2579.96	818.98	1799.55	780.96	737.05	677.68	1337.76	545.23	68.63	121.25	113.81	248.03
P02745	Complement C1q subcomponent subunit A	C1QA	complement	2142.64	670.35	637.14	1461.79	132.27	756.62	76.33	277.79	860.57	3245.91	4058.18	1408.54
A0A0C4DH67	Immunoglobulin kappa variable 1-8	IGKV1-8	immunoglobulins	742.25	1233.54	1318.04	697.37	519.63	846.06	842.67	623.48	0.99	1.00	1.07	1.01
P06310	Immunoglobulin kappa variable 2-30	IGKV2D-30	immunoglobulins	681.95	2077.28	3497.60	3295.60	689.73	1181.20	1084.70	1597.77	0.99	1.00	1.07	1.01

A0A0C4DH72	Immunoglobulin kappa variable 1-6	IGKV1-6	immunoglobulins	659.96	1344.58	1452.72	1449.06	712.08	1128.41	852.34	989.35	0.99	1.00	1.07	1.01
A0A075B6K4	Immunoglobulin lambda variable 3-10	IGLV3-10	immunoglobulins	621.21	1189.81	1961.82	434.15	0.99	1341.59	1074.34	315.20	0.99	1.00	1.07	1.01
P61626	Lysozyme C	LYZ	others	494.68	359.06	542.35	435.28	301.21	274.78	286.95	361.23	907.29	968.76	4112.75	3979.90
P15169	Carboxypeptidase N catalytic chain	CPN1	others	341.41	98.21	165.31	171.54	326.67	538.66	507.57	977.46	830.35	3123.96	5082.75	8442.91
Q03591	Complement factor H-related protein 1	CFHR1	complement	287.12	309.01	25.68	65.88	503.56	1097.38	949.73	968.87	2368.61	3636.63	2644.55	4208.02
P01599	Immunoglobulin kappa variable 1-17	IGKV1-17	immunoglobulins	272.25	656.90	797.29	174.07	231.10	288.81	132.53	1.01	0.99	1.00	1.07	1.01
P80748	Immunoglobulin lambda variable 3-21	IGLV3-21	immunoglobulins	237.49	397.57	667.89	520.64	184.40	364.47	263.27	237.94	0.99	1.00	1.07	1.01

A0A075B6S2	Immunoglobulin kappa variable 2D-29	IGKV2D-29	immunoglobulins	207.23	563.56	542.83	647.00	0.99	445.73	188.20	378.02	0.99	1.00	1.07	1.01
P0DP08	Immunoglobulin heavy variable 4-38-2	IGHV4-61	immunoglobulins	198.39	501.41	489.67	894.93	191.46	350.66	246.53	232.29	0.99	1.00	1.07	1.01
A0A0C4DH38	Immunoglobulin heavy variable 5-51	IGHV5-51	immunoglobulins	157.70	171.25	198.88	224.92	103.09	229.20	149.83	175.67	0.99	1.00	1.07	1.01
P01714	Immunoglobulin lambda variable 3-19	IGLV3-19	immunoglobulins	142.34	464.48	508.23	163.54	100.42	372.92	181.82	26.94	0.99	1.00	1.07	1.01
P06396	Gelsolin	GSN	tissue leakage	124.17	0.99	19.73	1.00	1342.94	421.35	272.36	1006.53	1612.52	1708.85	431.67	404.13
A0A0B4J1U7	Immunoglobulin heavy variable 6-1	IGHV6-1	immunoglobulins	115.36	265.21	385.18	271.88	96.67	196.92	128.24	131.26	0.99	1.00	1.07	1.01
P01743	Immunoglobulin heavy	IGHV1-46	immunoglobulins	113.71	153.13	108.73	291.04	0.99	128.36	104.49	84.58	0.99	1.00	1.07	1.01

	variable 1-46														
A0A0C4DH68	Immunoglobulin kappa variable 2-24	IGKV2-24	immunoglobulins	113.05	327.83	359.45	1.00	88.91	332.52	170.79	1.01	0.99	1.00	1.07	1.01
Q14520	Hyaluronan-binding protein 2	HABP2	coagulation	112.06	0.99	1.01	1.00	0.99	0.99	1.01	1.01	0.99	1.00	1.07	55.22
A0A0A0MS15	Immunoglobulin heavy variable 3-49	IGHV3-49	immunoglobulins	109.73	261.71	159.95	189.57	83.77	238.18	101.73	143.41	0.99	1.00	1.07	1.01
P35542	Serum amyloid A-4 protein	SAA4	acute phase	95.37	179.68	70.51	274.94	112.69	480.94	250.66	1992.37	3945.23	4926.36	4174.85	6341.17
Q14624	Inter-alpha-trypsin inhibitor heavy chain H4	ITIH4	acute phase	80.48	150.09	113.74	124.14	18.40	32.01	18.53	36.13	22.89	72.34	41.40	42.38
P00746	Complement factor D	CFD	complement	78.26	50.05	29.02	1.00	263.86	322.73	343.60	860.78	30.17	71.76	211.89	1.01

P0DJI9	Serum amyloid A-2 protein	SAA2	others	74.42	89.09	123.05	73.19	0.99	0.99	124.43	65.65	0.99	1.00	1.07	1.01
P18428	Lipopolysaccharide-binding protein	LBP	acute phase	73.70	102.90	46.79	41.49	0.99	0.99	560.43	1.01	0.99	1.00	1.07	1.01
A0A075B6K0	Immunoglobulin lambda variable 3-16	IGLV3-16	immunoglobulins	73.30	203.21	208.01	239.58	34.40	147.30	119.26	125.04	0.99	1.00	1.07	1.01
P02743	Serum amyloid P-component	APCS	acute phase	70.25	1334.92	1368.38	4842.16	125.49	57.07	1.01	1.01	0.99	1.00	1.07	1.01
P04430	Immunoglobulin kappa variable 1-16	IGKV1-16	immunoglobulins	63.83	229.92	241.34	422.68	0.99	91.59	55.49	61.52	0.99	1.00	1.07	1.01
P27918	Properdin	CFP	others	62.17	25.10	1.01	123.81	0.99	0.99	1.01	31.17	0.99	428.16	406.71	98.21
P02746	Complement C1q subcomponent subunit B	C1QB	complement	59.40	17.05	15.67	48.72	4.11	20.54	3.14	4.83	45.92	151.72	232.16	76.51

P0DP03	Immunoglobulin heavy variable 3-30-5	IGHV3-30-5	immunoglobulins	54.47	81.96	46.18	1.00	0.99	43.08	1.01	1.01	0.99	1.00	1.07	1.01
P00736	Complement C1r subcomponent	C1R	complement	48.83	235.82	233.59	473.12	0.99	0.99	1.01	40.16	25.93	233.70	35.05	56.35
P0DOX6	Immunoglobulin mu heavy chain	N/A	immunoglobulins	45.07	108.13	105.76	59.93	30.15	59.04	51.83	28.42	0.99	1.00	1.07	1.01
A0A0G2J S06	Immunoglobulin lambda variable 5-39	IGLV5-39	immunoglobulins	39.71	141.39	119.21	43.29	43.57	62.69	39.25	25.64	0.99	1.00	1.07	1.01
P02747	Complement C1q subcomponent subunit C	C1QC	complement	38.98	10.31	6.53	14.86	1.78	7.55	1.14	3.07	24.77	58.94	98.66	27.04
A0A087 WSY4	Immunoglobulin heavy variable 4-30-2	IGHV4-30-2	immunoglobulins	37.73	0.99	76.32	69.19	32.82	75.81	61.11	35.60	0.99	1.00	1.07	1.01
P01780	Immunoglobulin heavy	IGHV3-7	immunoglobulins	36.90	93.33	208.00	171.22	0.99	216.23	120.44	122.99	0.99	1.00	1.07	1.01

	variable 3-7													
P17936	Insulin-like growth factor-binding protein 3	IGFBP3	others	35.90	0.99	36.48	1.00	111.51	249.19	249.14	357.27	226.00	542.89	720.95	864.86
P22692	Insulin-like growth factor-binding protein 4	IGFBP4	others	31.60	24.04	245.70	265.25	31.55	46.12	187.23	255.62	0.99	27.16	1.07	603.26
P02671	Fibrinogen alpha chain	FGA	coagulation	29.73	10.82	0.72	0.43	40.20	18.50	28.53	23.54	38.54	6.02	15.18	5.37
P02675	Fibrinogen beta chain	FGB	coagulation	28.00	9.82	0.52	0.31	31.53	15.90	23.39	19.12	25.08	4.37	9.72	2.53
P55056	Apolipoprotein C-IV	APOC4	apolipoproteins	27.04	101.75	54.85	54.00	0.99	44.12	30.91	41.38	420.21	1980.12	3733.19	3362.79
P02679	Fibrinogen gamma chain	FGG	coagulation	20.62	9.22	0.54	0.45	29.68	15.34	23.18	17.95	29.91	4.62	10.89	2.95
P01700	Immunoglobulin lambda	IGKV1-6	immunoglobulins	14.08	23.83	33.64	19.25	7.89	17.98	14.63	9.47	0.02	0.02	0.02	0.55

	variable 1-47														
P04004	Vitronectin	VTN	tissue leakage	8.82	17.06	26.64	40.14	6.96	35.42	30.58	27.55	42.94	143.50	160.00	118.09
P02654	Apolipoprotein C-I	APOC1	apolipoproteins	5.70	0.80	0.61	0.90	2.69	0.37	0.53	0.55	17.37	44.17	14.62	7.37
P02656	Apolipoprotein C-III	APOC3	apolipoproteins	4.16	0.28	3.86	13.65	0.49	0.07	0.52	6.03	1.77	0.78	0.90	1.56
P01042	Kininogen-1	KNG1	coagulation	3.96	3.24	9.45	3.46	1.51	14.61	6.45	27.95	11.33	31.65	44.23	129.70
P01591	Immunoglobulin J chain	IGJ	immunoglobulins	3.60	6.43	4.95	3.46	0.64	0.88	0.86	0.55	0.01	0.01	2.08	1.94
P01834	Ig kappa chain C region	IGKC	immunoglobulins	3.54	7.38	10.11	8.09	3.19	7.07	5.76	6.35	0.63	0.38	0.32	0.25
P04003	C4b-binding protein alpha chain	C4BPA	complement	3.46	0.61	0.71	0.01	0.54	0.01	0.01	0.01	3.96	0.58	0.50	0.30

P04196	Histidine-rich glycoprotein	HRG	coagulation	3.07	5.66	39.25	5.74	2.89	4.37	2.47	1.37	3.99	8.47	23.52	18.65
P0DOX2	Immunoglobulin alpha-2 heavy chain	N/A	immunoglobulins	2.75	5.52	4.99	8.82	1.82	2.66	1.95	2.79	6.16	5.04	2.58	2.22
O43866	CD5 antigen-like	CD5L	tissue leakage	2.37	4.21	2.68	2.55	0.01	0.58	0.01	0.01	0.01	1.71	0.54	0.96
P00748	Coagulation factor XII	F12	coagulation	2.23	0.03	0.03	0.03	14.48	21.90	5.77	5.69	8.12	16.77	2.00	0.75
P08603	Complement factor H	CFH	complement	2.18	0.95	0.39	1.22	0.01	0.59	0.01	0.66	2.15	7.39	10.75	9.77
P02775	Platelet basic protein	PPBP	acute phase	2.09	1.50	0.28	0.00	8.60	4.17	9.18	5.58	10.62	13.32	11.98	20.25
A0A0B4J1X5	Immunoglobulin heavy variable 3-74	IGHV3-74	immunoglobulins	2.08	4.08	4.50	4.66	53.63	11.21	38.01	15.41	0.02	0.02	0.02	0.02
P10909	Clusterin	CLU	apolipoproteins	2.06	3.49	2.80	1.03	0.42	0.26	0.20	0.25	1.74	0.83	0.70	0.25

P01871	Ig mu chain C region	IGHM	immunoglobulins	1.98	3.71	2.34	2.16	0.39	0.49	0.36	0.32	0.45	0.63	0.85	0.44
P01701	Immunoglobulin lambda variable 1-51	IGLV1-51	immunoglobulins	1.93	3.96	2.61	5.91	1.54	2.86	2.40	3.14	0.00	0.00	0.00	0.00
P00747	Plasminogen	PLG	coagulation	1.92	0.94	1.07	0.90	2.73	0.36	0.36	0.40	7.21	0.67	0.51	0.33
P01602	Immunoglobulin kappa variable 1-5	IGKV1-5	immunoglobulins	1.65	5.83	3.23	10.77	0.01	0.44	0.01	0.01	0.01	0.01	0.01	0.01
P0DOX8	Immunoglobulin lambda-1 light chain	N/A	immunoglobulins	1.41	2.16	2.85	2.24	0.93	1.51	1.12	1.14	0.42	0.31	0.20	0.62
P0DOX7	Immunoglobulin kappa light chain	N/A	immunoglobulins	1.28	2.45	3.56	2.64	1.32	2.04	2.00	1.66	0.33	0.27	0.18	0.27
P01624	Ig kappa chain V-III region POM	IGKV3D-7	immunoglobulins	1.27	2.43	3.12	3.58	0.75	1.97	1.54	2.31	0.21	0.14	0.06	0.07

ID	Protein	Gene	Category												
P01619	Immunoglobulin kappa variable 3-20	IGKV3-20	immunoglobulins	1.22	2.46	2.72	2.06	0.80	1.98	1.18	1.36	0.18	0.03	0.08	0.00
A0A0A0MRZ8	Immunoglobulin kappa variable 3D-11	IGKV3D-11	immunoglobulins	1.16	2.22	3.77	3.71	0.69	1.86	2.56	3.31	0.00	0.29	0.00	0.00
P0DOX5	Ig gamma-1 chain C region	IGHG1	immunoglobulins	1.11	1.88	2.15	2.48	0.87	1.51	1.25	1.32	0.29	0.14	0.07	0.07
P06312	Ig kappa chain V-IV region	IGKV4-1	immunoglobulins	1.02	2.85	2.67	2.09	0.64	2.10	0.68	0.83	0.10	0.00	0.16	0.00
P00739	Haptoglobin-related protein	HPR	acute phase	0.99	59.53	1.01	1.00	0.99	0.99	1.01	1.01	0.99	1.00	1.07	1.01
P23142	Fibulin-1	FBLN1	coagulation	0.99	0.99	99.34	1.00	0.99	0.99	97.76	1.01	0.99	1.00	1.07	1.01
P03952	Plasma kallikrein	KLKB1	coagulation	0.99	0.99	71.17	141.58	0.99	69.58	1.01	79.31	73.01	323.14	445.52	944.42
Q9BXJ4	Complement C1q tumor necrosis	C1QTNF3	complement	0.99	0.99	106.39	1.00	0.99	0.99	157.15	60.04	0.99	1.00	233.95	1.01

Accession	Protein name	Gene	Category												
	factor-related protein 3														
P07360	Complement component C8 gamma chain	C8G	complement	0.99	0.99	1.01	86.30	0.99	0.99	1.01	74.45	0.99	1.00	1.07	1.01
P02748	Complement component C9	C9	complement	0.99	48.63	1.01	1.00	0.99	0.99	1.01	1.01	0.99	1.00	1.07	1.01
A2NJV5	Ig kappa chain V-II region RPMI 6410	IGKVA18	immunoglobulins	0.99	0.99	1.01	1.00	0.99	0.99	1.01	1.01	86.49	189.03	137.23	1.01
A0M8Q6	Ig lambda-7 chain C region	IGLC7	immunoglobulins	0.99	322.62	37.18	1.00	0.99	1064.04	36.06	1.01	0.99	1.00	1.07	1.01
P0DOX3	Immunoglobulin delta heavy chain	IGHD	immunoglobulins	0.99	75.01	51.81	1.00	0.99	30.50	1.01	1.01	0.99	1.00	1.07	1.01
A0A0B4J1Y9	Immunoglobulin heavy variable 3-72	IGHV3-72	immunoglobulins	0.99	0.99	1.01	46.40	0.99	0.99	1.01	1.01	0.99	1.00	1.07	1.01

P04432	Immunoglobulin kappa variable 1D-39	IGKV1D-39	immunoglobulins	0.99	279.96	159.14	224.02	0.99	0.99	1.01	1.01	0.99	1.00	1.07	1.01
A0A0C4DH24	Immunoglobulin kappa variable 6-21	IGKV6-21	immunoglobulins	0.99	43.94	54.47	1.00	0.99	0.99	1.01	1.01	0.99	1.00	1.07	1.01
A0A0A0MT36	Immunoglobulin kappa variable 6D-21	IGKV6D-21	immunoglobulins	0.99	69.11	36.98	29.03	0.99	63.35	1.01	1.01	0.99	1.00	1.07	1.01
P01703	Immunoglobulin lambda variable 1-40	IGLV1-40	immunoglobulins	0.99	0.99	157.16	126.55	59.49	107.14	81.70	84.38	0.99	1.00	1.07	1.01
A0A075B6K5	Immunoglobulin lambda variable 3-9	IGLV3-9	immunoglobulins	0.99	32.83	35.04	1.00	0.99	34.13	1.01	1.01	0.99	1.00	1.07	1.01
A0A075B6I9	Immunoglobulin lambda variable 7-46	IGLV7-46	immunoglobulins	0.99	147.81	154.60	87.68	51.04	118.53	54.17	54.95	0.99	1.00	1.07	1.01

A0A0C4DH36	Probable non-functional immunoglobulin heavy variable 3-38	IGHV3-38	immunoglobulins	0.99	60.64	52.31	1.00	0.99	51.94	41.08	1.01	0.99	1.00	1.07	1.01
Q6UY14	ADAMTS-like protein 4	ADAMTSL4	others	0.99	0.99	51.43	1.00	0.99	0.99	1.01	1.01	0.99	1.00	1.07	1.01
P49747	Cartilage oligomeric matrix protein	COMP	others	0.99	0.99	42.06	1.00	0.99	0.99	158.88	40.91	0.99	1.00	1.07	1.01
P12109	Collagen alpha-1(VI) chain	COL6A1	others	0.99	0.99	33.64	1.00	0.99	0.99	112.19	1.01	0.99	1.00	111.51	1.01
P22352	Glutathione peroxidase 3	GPX3	others	0.99	0.99	1.01	73.31	0.99	0.99	1.01	146.10	0.99	1.00	1.07	1.01
P0DMV8	Heat shock 70 kDa protein 1A	HSPA1A	others	0.99	0.99	29.52	1.00	0.99	0.99	1.01	1.01	0.99	1.00	1.07	1.01
Q04756	Hepatocyte growth factor activator	HGFAC	others	0.99	0.99	16.72	50.85	0.99	0.99	1.01	186.32	0.99	1.00	129.90	51.49

P01344	Insulin-like growth factor II	IGF2	others	0.99	0.99	58.36	115.32	0.99	0.99	1.01	1.01	77.70	51.73	787.47	998.65
P18065	Insulin-like growth factor-binding protein 2	IGFBP2	others	0.99	0.99	392.22	332.18	0.99	0.99	89.89	395.95	58.43	55.99	725.77	2497.85
P20774	Mimecan	OGN	others	0.99	0.99	41.89	1.00	0.99	0.99	1.01	1.01	0.99	1.00	1.07	1.01
P59666	Neutrophil defensin 3	DEFA3	others	0.99	56.24	60.80	1.00	0.99	0.99	1.01	1.01	0.99	1.00	1.07	1.01
P62937	Peptidyl-prolyl cis-trans isomerase A	PPIA	others	0.99	0.99	230.16	39.43	0.99	0.99	176.89	49.48	0.99	1.00	1.07	1.01
Q15063	Periostin	POSTN	others	0.99	0.99	75.24	1.00	0.99	0.99	49.94	1.01	0.99	1.00	1.07	1.01
P05154	Plasma serine protease inhibitor	SERPINA5	others	0.99	0.99	66.37	40.79	112.26	786.30	802.80	1421.71	42.10	453.80	300.96	330.48
P34096	Ribonuclease 4	RNASE4	others	0.99	0.99	1.01	198.22	0.99	0.99	1.01	78.85	0.99	1.00	1.07	1.01

O00391	Sulfhydryl oxidase 1	QSOX1	others	0.99	0.99	1.01	30.61	0.99	0.99	1.01	34.67	0.99	1.00	1.07	1.01
Q15582	Transforming growth factor-beta-induced protein ig-h3	TGFBI	others	0.99	0.99	26.18	1.00	0.99	0.99	1.01	1.01	0.99	1.00	1.07	1.01
Q9Y275	Tumor necrosis factor ligand superfamily member 13B	TNFSF13B	others	0.99	0.99	1.01	1.00	0.99	0.99	1.01	1.01	50.11	79.00	313.73	29.20
P01859	Ig gamma-2 chain C region	IGHG2	immunoglobulins	0.88	1.91	1.12	3.15	0.70	1.71	0.77	1.59	0.00	0.00	0.00	0.00
P07225	Vitamin K-dependent protein S	PROS1	coagulation	0.80	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02
P20851	C4b-binding protein beta chain	C4BPB	complement	0.77	0.02	0.02	0.02	0.02	0.02	0.02	0.02	1.04	0.02	0.02	0.02
A0A087WSY6	Immunoglobulin kappa	IGKV3D-15	immunoglobulins	0.74	1.44	0.84	2.12	0.00	1.27	0.00	1.72	0.16	0.32	0.01	0.00

	variable 3D-15														
P01034	Cystatin-C	CST3	others	0.65	0.01	0.01	0.01	2.74	1.43	0.46	2.10	0.01	0.01	0.01	0.01
P02655	Apolipoprotein C-II	APOC2	apolipoproteins	0.60	0.00	8.09	3.79	0.11	0.00	2.46	3.08	0.00	0.00	0.00	0.00
P02749	Beta-2-glycoprotein 1	APOH	apolipoproteins	0.57	0.16	0.21	0.42	0.15	0.00	0.40	0.28	0.48	0.32	0.20	0.19
P02751	Fibronectin	FN1	acute phase	0.53	0.54	1.35	0.44	0.33	0.41	1.52	0.99	0.56	0.73	2.54	1.17
P01860	Ig gamma-3 chain C region	IGHG3	immunoglobulins	0.52	0.93	0.87	2.25	0.42	0.72	0.50	1.12	0.82	0.58	0.29	0.26
O14791	Apolipoprotein L1	APOL1	apolipoproteins	0.51	1.08	0.56	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
A0A0C4DH25	Immunoglobulin kappa variable 3D-20	IGKV3D-20	immunoglobulins	0.48	0.87	1.23	0.72	0.00	0.83	0.00	0.49	0.00	0.00	0.00	0.00

P01019	Angiotensinogen	AGT	others	0.45	0.00	0.00	0.00	0.37	0.00	0.00	0.00	0.00	0.00	0.00	0.00
P01024	Complement C3	C3	complement	0.41	1.80	2.22	6.35	0.16	0.43	1.07	2.09	0.62	4.73	41.38	39.64
P05155	Plasma protease C1 inhibitor	SERPING1	others	0.38	1.30	0.81	1.09	0.26	1.24	0.11	0.29	0.34	0.92	0.00	0.11
P00734	Prothrombin	F2	coagulation	0.35	0.27	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
P0C0L5	Complement C4-B	C4B	complement	0.34	1.65	1.71	2.93	0.17	0.29	0.19	0.51	0.90	1.33	1.02	2.47
P02649	Apolipoprotein E	APOE	apolipoproteins	0.32	0.49	0.66	0.72	0.50	2.30	5.74	15.70	2.62	4.65	9.99	22.12
P01876	Ig alpha-1 chain C region	IGHA1	immunoglobulins	0.31	0.22	0.15	0.06	0.16	0.04	0.02	0.00	0.06	0.07	0.00	0.07
P01614	Immunoglobulin kappa variable 2D-40	IGKV2-40	immunoglobulins	0.26	0.72	1.09	0.00	0.36	1.54	0.84	0.36	0.68	0.62	0.68	0.79

A0A0B4J1V0	Immunoglobulin heavy variable 3-15	IGHV3-15	immunoglobulins	0.23	0.59	0.35	1.23	0.77	0.48	0.20	0.00	0.00	0.00	0.00	0.00
A0A075B6I0	Immunoglobulin lambda variable 8-61	IGLV8-61	immunoglobulins	0.20	0.14	0.34	0.54	0.00	0.10	0.08	0.08	0.00	0.08	0.43	0.69
P19823	Inter-alpha-trypsin inhibitor heavy chain H2	ITIH2	others	0.19	0.18	0.26	0.21	0.01	0.01	0.26	0.25	0.17	0.01	0.01	0.01
P00751	Complement factor B	CFB	complement	0.19	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
P02765	Alpha-2-HS-glycoprotein	AHSG	others	0.14	0.00	0.00	0.00	0.23	0.00	0.00	0.00	0.82	0.10	0.00	0.00
P00450	Ceruloplasmin	CP	others	0.14	0.17	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
P06727	Apolipoprotein A-IV	APOA4	apolipoproteins	0.13	0.00	0.00	0.00	0.39	0.00	0.00	0.05	0.52	0.00	0.00	0.13

P01011	Alpha-1-antichymotrypsin	SERPINA3	acute phase	0.11	0.07	0.00	0.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
P01023	Alpha-2-macroglobulin	A2M	acute phase	0.10	0.03	0.03	0.07	0.00	0.00	0.04	0.08	0.04	0.02	0.00	0.05
P01008	Antithrombin-III	SERPINC1	coagulation	0.09	0.08	0.23	0.00	0.00	0.38	0.09	0.91	0.00	0.20	0.00	0.49
P02774	Vitamin D-binding protein	GC	others	0.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
P02652	Apolipoprotein A-II	APOA2	apolipoproteins	0.07	0.02	0.03	0.04	0.05	0.01	0.02	0.03	0.14	0.08	0.08	0.15
P02647	Apolipoprotein A-I	APOA1	apolipoproteins	0.07	0.03	0.05	0.05	0.12	0.02	0.03	0.03	0.08	0.04	0.03	0.14
P02787	Serotransferrin	TF	others	0.06	0.02	0.01	0.01	0.02	0.01	0.00	0.00	0.03	0.02	0.01	0.03
P00738	Haptoglobin	HP	acute phase	0.06	0.07	0.04	0.07	0.00	0.00	0.01	0.01	0.03	0.02	0.05	0.20

P02790	Hemopexin	HPX	others	0.05	0.00	0.00	0.00	0.25	0.07	0.12	0.03	0.07	0.04	0.02	0.06
P02768	Serum albumin	ALB	others	0.04	0.18	0.03	0.06	0.03	0.18	0.03	0.02	0.21	0.81	0.13	0.41
P01009	Alpha-1-antitrypsin	SERPINA1	acute phase	0.03	0.02	0.01	0.01	0.04	0.01	0.01	0.01	0.03	0.01	0.01	0.04
P07357	Complement component C8 alpha chain	C8A	complement	0.03	0.03	0.03	0.03	0.03	0.03	0.03	0.03	0.03	0.03	0.03	0.03
P02750	Leucine-rich alpha-2-glycoprotein	LRG1	others	0.02	0.02	0.73	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.03	0.02
P02766	Transthyretin	TTR	others	0.02	0.01	0.00	0.00	0.03	0.01	0.00	0.00	0.02	0.02	0.02	0.04
P04278	Sex hormone-binding globulin	SHBG	others	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02
P35858	Insulin-like growth factor-	IGFALS	others	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02

	binding protein complex acid labile subunit														
P19827	Inter-alpha-trypsin inhibitor heavy chain H1	ITIH1	others	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02
Q96PD5	N-acetylmuramoyl-L-alanine amidase	PGLYRP2	others	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.02	0.01
P19652	Alpha-1-acid glycoprotein 2	ORM2	acute phase	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
P43652	Afamin	AFM	others	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
P05090	Apolipoprotein D	APOD	apolipoproteins	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
P25311	Zinc-alpha-2-glycoprotein	AZGP1	others	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01

P01861	Ig gamma-4 chain C region	IGHG4	immunoglobulins	0.01	0.02	0.03	0.03	0.00	0.00	0.00	0.03	0.09	0.04	0.04	0.07
P08697	Alpha-2-antiplasmin	SERPINF2	others	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
P27169	Serum paraoxonase/arylesterase 1	PON1	others	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
P04114	Apolipoprotein B-100	APOB	apolipoproteins	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
P02760	Protein AMBP	AMBP	others	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
P02753	Retinol-binding protein 4	RBP4	others	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
P0DOY3	Immunoglobulin lambda constant 3	IGLC3	immunoglobulins	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.62	1.59	1.06	1.30
P04217	Alpha-1B-glycoprotein	A1BG	others	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

| P02763 | Alpha-1-acid glycoprotein 1 | ORM1 | acute phase | 0.00 | 0.05 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |

Table S6. Key proteins within the protein coronas that are highly correlated to the association of the nanoparticle systems (12 types of nanoparticles i.e., three nanoparticle systems with and without precoating) with B cells, neutrophils, CD14+ monocytes, and CD16+ monocytes[a]

	Protein ID	Protein name	Gene name	correlation coefficient	−log$_{10}$(p-value)
B cells	P02679	Fibrinogen gamma chain	FGG	-0.57	4.20
	P05154	Plasma serine protease inhibitor	SERPINA5	-0.59	4.09
	Q14624	Inter-alpha-trypsin inhibitor heavy chain H4	ITIH4	0.86	10.70
	P01871	Ig mu chain C region	IGHM	0.70	5.70
	P01591	Immunoglobulin J chain	IGJ	0.65	4.80
	P00738	Haptoglobin	HP	0.65	4.80
	P09871	Complement C1s subcomponent	C1S	0.65	4.74
	P01876	Ig alpha-1 chain C region	IGHA1	0.62	4.31
	P10909	Clusterin	CLU	0.60	4.23
neutrophils	P01042	Kininogen-1	KNG1	-0.74	6.72
	P17936	Insulin-like growth factor-binding protein 3	IGFBP3	-0.70	5.78
	P02649	Apolipoprotein E	APOE	-0.68	5.35
	P60709	Actin, cytoplasmic 1	ACTB	-0.65	4.72
	P01876	Ig alpha-1 chain C region	IGHA1	0.60	4.01
CD14+ monocytes	P60709	Actin, cytoplasmic 1	ACTB	-0.72	6.19
	P02649	Apolipoprotein E	APOE	-0.68	5.35
	P02795	Metallothionein-2	MT2A	-0.67	5.12
	P01042	Kininogen-1	KNG1	-0.66	4.87
	P17936	Insulin-like growth factor-binding protein 3	IGFBP3	-0.61	4.17
	P01876	Ig alpha-1 chain C region	IGHA1	0.60	4.01
CD16+ monocytes	P01042	Kininogen-1	KNG1	-0.82	8.94
	P55056	Apolipoprotein C-IV	APOC4	-0.74	6.49

P60709	Actin, cytoplasmic 1	ACTB	-0.71	5.85
P61626	Lysozyme C	LYZ	-0.70	5.70
P17936	Insulin-like growth factor-binding protein 3	IGFBP3	-0.69	5.51
P35542	Serum amyloid A-4 protein	SAA4	-0.67	5.12
Q03591	Complement factor H-related protein 1	CFHR1	-0.65	4.72
P02649	Apolipoprotein E	APOE	-0.65	4.66
P04004	Vitronectin	VTN	-0.63	4.44
P01861	Ig gamma-4 chain C region	IGHG4	-0.63	4.42
P08603	Complement factor H	CFH	-0.62	4.30
P01024	Complement C3	C3	-0.61	4.17
P03952	Plasma kallikrein	KLKB1	-0.61	4.14
P02775	Platelet basic protein	PPBP	-0.61	4.10
P18065	Insulin-like growth factor-binding protein 2	IGFBP2	-0.59	4.08
P01859	Ig gamma-2 chain C region	IGHG2	0.63	4.37
P0DOX8	Immunoglobulin lambda-1 light chain	N/A	0.59	4.04
P0DOX7	Immunoglobulin kappa light chain	N/A	0.59	4.02

[a]Proteins highlighted in blue indicate negative correlation and proteins highlighted in red indicate positive correlation.

Checklist

Minimum Information Reporting in Bio–Nano Experimental Literature

The MIRIBEL guidelines were introduced here: https://doi.org/10.1038/s41565-018-0246-4

The development of these guidelines was led by the ARC Centre of Excellence in Convergent Bio-Nano Science and Technology: https://www.cbns.org.au/. Any updates or revisions to this document will be made available here: http://doi.org/10.17605/OSF.IO/SMVTF. This document is made available under a CC-BY 4.0 license: https://creativecommons.org/licenses/by/4.0/.

The MIRIBEL guidelines were developed to facilitate reporting and dissemination of research in bio–nano science. Their development was inspired by various similar efforts:

- MIAME (microarray experiments): *Nat. Genet.* **29** (2001), 365; http://doi.org/10.1038/ng1201-365
- MIRIAM (biochemical models): *Nat. Biotechnol.* **23** (2005) 1509; http://doi.org/10.1038/nbt1156
- MIBBI (biology/biomedicine): *Nat. Biotechnol.* **26** (2008) 889; http://doi.org/10.1038/nbt.1411
- MIGS (genome sequencing): *Nat. Biotechnol.* **26** (2008) 541; http://doi.org/10.1038/nbt1360
- MIQE (quantitative PCR): *Clin. Chem.* **55** (2009) 611; http://doi.org/10.1373/clinchem.2008.112797
- ARRIVE (animal research): *PLOS Biol.* **8** (2010) e1000412; http://doi.org/10.1371/journal.pbio.1000412
- *Nature*'s reporting standards:
  - Life science: https://www.nature.com/authors/policies/reporting.pdf; e.g., *Nat. Nanotechnol.* **9** (2014) 949; http://doi.org/10.1038/nnano.2014.287
  - Solar cells: https://www.nature.com/authors/policies/solarchecklist.pdf; e.g., *Nat. Photonics* **9** (2015) 703; http://doi.org/10.1038/nphoton.2015.233
  - Lasers: https://www.nature.com/authors/policies/laserchecklist.pdf; e.g., *Nat. Photonics* **11** (2017) 139; http://doi.org/10.1038/nphoton.2017.28
- The "TOP guidelines": e.g., *Science* **352** (2016) 1147; http://doi.org/10.1126/science.aag2359

Similar to many of the efforts listed above, the parameters included in this checklist are **not** intended to be definitive requirements; instead they are intended as 'points to be considered', with authors themselves deciding which parameters are—and which are not—appropriate for their specific study.

This document is intended to be a living document, which we propose is revisited and amended annually by interested members of the community, who are encouraged to contact the authors of this document. Parts of this document were developed at the annual International Nanomedicine Conference in Sydney, Australia: http://www.oznanomed.org/, which will continue to act as a venue for their review and development, and interested members of the community are encouraged to attend.

After filling out the following pages, this checklist document can be attached as a "Supporting Information" document during submission of a manuscript to inform Editors and Reviewers (and eventually readers) that all points of MIRIBEL have been considered.

Supplementary Table 1. Material characterization*

Question	Yes	No
1.1 Are "**best reporting practices**" **available** for the nanomaterial used? For examples, see *Chem. Mater.* **28** (2016) 3535; http://doi.org/10.1021/acs.chemmater.6b01854 and *Chem. Mater.* **29** (2017) 1; http://doi.org/10.1021/acs.chemmater.6b05235		N
1.2 If they are available, **are they used**? If not available, ignore this question and proceed to the next one.		
1.3 Are extensive and clear instructions reported detailing all steps of **synthesis** and the resulting **composition** of the nanomaterial? For examples, see *Chem. Mater.* **26** (2014) 1765; http://doi.org/10.1021/cm500632c, and *Chem. Mater.* **26** (2014) 2211; http://doi.org/10.1021/cm5010449. Extensive use of photos, images, and videos are strongly encouraged. For example, see *Chem. Mater.* **28** (2016) 8441; http://doi.org/10.1021/acs.chemmater.6b04639	Y	
1.4 Is the **size** (or **dimensions**, if non-spherical) and **shape of** the nanomaterial reported?	Y	
1.5 Is the **size dispersity** or **aggregation** of the nanomaterial reported?	Y	
1.6 Is the **zeta potential** of the nanomaterial reported?	Y	
1.7 Is the **density (mass/volume)** of the nanomaterial reported?		N
1.8 Is the amount of any **drug loaded** reported? 'Drug' here broadly refers to functional cargos (e.g., proteins, small molecules, nucleic acids).	not applicable	
1.9 Is the **targeting performance** of the nanomaterial reported, including **amount** of ligand bound to the nanomaterial if the material has been functionalised through addition of targeting ligands?	not applicable	
1.10 Is the **label signal** per nanomaterial/particle reported? For example, fluorescence signal per particle for fluorescently labelled nanomaterials.	Y	
1.11 If a material property not listed here is varied, has it been **quantified**?	not applicable	
1.12 Were characterizations performed in a **fluid mimicking biological conditions**?	Y	
1.13 Are details of how these parameters were **measured/estimated** provided?	Y	
Explanation for **No**: 1.1 The protein corona effect of nanocapsules has not been fully studied in previous literature. 1.7 Density calculations involve the measurement of the weight of a known number of nanoparticles. To minimize measurement errors, a large amount of nanoparticles need to be engineered, which is beyond the production scale in standard laboratories.		

Supplementary Table 2. Biological characterization*

Question	Yes	No
2.1 Are **cell seeding details**, including **number of cells plated, confluency at start of experiment,** and **time between seeding and experiment** reported?	Y	
2.2 If a standardised cell line is used, are the **designation and source** provided?	Y	
2.3 Is the **passage number** (total number of times a cell culture has been subcultured) known and reported?	Y	
2.4 Is the last instance of **verification of cell line** reported? If no verification has been performed, is the time passed and passage number since acquisition from trusted source (e.g., ATCC or ECACC) reported? For information, see *Science* **347** (2015) 938; http://doi.org/10.1126/science.347.6225.938	Y	
2.5 Are the results from **mycoplasma testing** of cell cultures reported?	Y	
2.6 Is the **background signal of cells**/tissue reported? (E.g., the fluorescence signal of cells without particles in the case of a flow cytometry experiment.)	Y	
2.7 Are **toxicity studies** provided to demonstrate that the material has the expected toxicity, and that the experimental protocol followed does not?	Y	
2.8 Are details of media preparation (**type of media, serum,** any **added antibiotics**) provided?	Y	
2.9 Is a **justification of the biological model** used provided? For examples for cancer models, see *Cancer Res.* **75** (2015) 4016; http://doi.org/10.1158/0008-5472.CAN-15-1558, and *Mol. Ther.* **20** (2012) 882; http://doi.org/10.1038/mt.2012.73, and *ACS Nano* **11** (2017) 9594; http://doi.org/10.1021/acsnano.7b04855	Y	
2.10 Is characterization of the **biological fluid** (*ex vivo*/*in vitro*) reported? For example, when investigating protein adsorption onto nanoparticles dispersed in blood serum, pertinent aspects of the blood serum should be characterised (e.g., protein concentrations and differences between donors used in study).	Y	
2.11 For **animal experiments**, are the ARRIVE guidelines followed? For details, see *PLOS Biol.* **8** (2010) e1000412; http://doi.org/10.1371/journal.pbio.1000412	not applicable	
Explanation for **No** (if needed):		

Supplementary Table 3. Experimental details*

Question	Yes	No
3.1 For cell culture experiments: are **cell culture dimensions** including **type of well**, **volume of added media**, reported? Are cell types (i.e.; adherent vs suspension) and **orientation** (if non-standard) reported?	Y	
3.2 Is the **dose of material administered** reported? This is typically provided in nanomaterial mass, volume, number, or surface area added. Is sufficient information reported so that regardless of which one is provided, the other dosage metrics can be calculated (i.e. using the dimensions and density of the nanomaterial)?	Y	
3.3 For each type of imaging performed, are details of how **imaging** was performed provided, including details of **shielding, non-uniform image processing**, and any **contrast agents** added?	not applicable	
3.4 Are details of how the dose was administered provided, including **method of administration, injection location, rate of administration,** and details of **multiple injections**?	not applicable	
3.5 Is the methodology used to **equalise dosage** provided?	not applicable	
3.6 Is the **delivered dose** to tissues and/or organs (in vivo) reported, as % injected dose per gram of tissue (%ID g^{-1})?	not applicable	
3.7 Is **mass of each organ/tissue measured** and **mass of material** reported?	not applicable	
3.8 Are the **signals of cells/tissues with nanomaterials** reported? For instance, for fluorescently labelled nanoparticles, the total number of particles per cell or the fluorescence intensity of particles + cells, at each assessed timepoint.	Y	
3.9 Are **data analysis details**, including **code used** for analysis provided?	Y	
3.10 Is the **raw data** or **distribution of values** underlying the reported results provided? For examples, see *R. Soc. Open Sci.* **3** (2016) 150547; http://doi.org/10.1098/rsos.150547, https://opennessinitiative.org/making-your-data-public/, http://journals.plos.org/plosone/s/data-availability, and https://www.nature.com/sdata/policies/repositories	Y	
Explanation for **No** (if needed):		