

SUPPORTING INFORMATION PARAGRAPH

The Protein Corona of Dendrimers: PAMAM Binds and Activates Complement Proteins in Human Plasma in a Generation Dependent Manner

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EXPERIMENTAL SECTION.

Materials

Polyamidoamine (PAMAM) dendrimer, ethylenediamine core, generation (G) 4, 5, 6 and 7 suspended in methanol were purchased from Sigma Aldrich. Before use, methanol was evaporated under reduced pressure and dendrimer was resolubilised in 10 mM PBS buffer from Sigma Aldrich. TAE buffer (40 mM Tris-HCl, 1 mM EDTA, pH 8.5) was mixed from TrizmaBase and EDTA, purchased from Sigma Aldrich, and pH was adjusted using HCl from Sigma Aldrich. Agarose purchased from Sigma Aldrich was mixed with TAE buffer to form 5% agarose gel. Acrylamide/Bis-Acrylamide, 3xSDS-loading buffer, bromphenol blue, methanol and acetic acid were all purchased from Sigma Aldrich and used without further purification. ColorPlus Prestained Protein Ladder, Broad Range (10-230 kDa) from New England Biolabs, was used as a molecular weight ladder in SDS-PAGE gels. Milli-Q purified water was used in all solutions.

Human plasma

Blood plasma was obtained from Irish Blood Transfusion Service (IBTS), St. James Hospital, Dublin. Plasma was obtained from 6 seemingly healthy donors (3 males and females). Plasma was received at room temperature, mixed and aliquoted in 2 ml eppendorf tubes and stored at -80 °C until use.

Sample preparation

Plasma stored at -80 °C was allowed to thaw at room temperature and centrifuged for 3 min at 16 kRCF before mixed with PAMAM dendrimer. Dendrimer were incubated with high (40 mg/ml) and low (7 mg/ml) plasma concentrations, plasma were diluted with 10 mM PBS, and the final concentration of dendrimer were kept constant at 0.5 mg/ml for all generations (G4, G5, G6, G7). All samples were incubated for 30 minutes at 37 °C with gentle shaking, before electrophoretic separation was performed as it represented a typical protein corona incubation time.

Electrophoretic separation

Immediately after incubation, four part samples were mixed with one part of non-denaturing loading buffer (8 mM Tris-HCl, 0.2 mM EDTA, 50% Glycerol, 0.01% (v/w) bromphenol blue), and equal sample volume were loaded in 0.5% Agarose gel. Gel electrophoresis was performed at 130 V in TAE buffer, using agarose gel equipment (17 cm sized gel) from Biorad for at least 3 h for optimal separation. To prevent heating of the gel, equipment was placed in ice water bath during the separation and the buffer was exchanged at least once every hour. Straight after finished electrophoresis desired bands were cut with a scalpel, thoroughly cleaned with ethanol and MilliQ between each cut, or the gel was stained with coomassie blue staining (40% methanol, 10% acetic acid, 2.5% (w/v) brilliant blue) and subsequently de-stained in (40% methanol, 10% acetic acid). Cut bands were stored at -20 °C until use.

SDS-PAGE

Sample bands from Agarose gel electrophoresis was melted at 100 °C and mixed with 1X SDS-PAGE loading buffer (New england Biolab in 0.1 M DTT in a volume to volume ratio of 2:1. Samples were then boiled for 3 minutes at 100 °C and immediately loaded in 8% (for densitometry) or 12% (for mass spectrometry analysis) polyacrylamide gel. Gel electrophoresis was performed at 130 V for about 60 minutes, until the proteins neared the end of the gel. Each gel contained one lane of a molecular weight ladder standard, ColorPlus Pre-stained Protein Ladder. The gels were subsequently stained using 2D-SILVER STAIN-II (Cosmo Bio CO., LTD) or coomassie blue staining (40% methanol, 10% acetic acid, 2.5% (w/v) brilliant blue) followed by de-staining (40% methanol, 10% acetic acid). Gels were scanned using a Biorad GS-800 calibrated densitometer scanner and gel densitometry was performed using Image J (1.45 version).

Protein Identification by Mass Spectrometry

Bands of interest from SDS-PAGE gels (12%) were excised and digested in-gel with trypsin according to the method of Shevchenko *et al.*¹ The resulting peptide mixtures were re-suspended in 0.1% formic acid and analyzed by electrospray liquid chromatography mass spectrometry (LC MS/MS). An HPLC (Surveyor, ThermoFinnigan, CA) was interfaced with an LTQ Orbitrap (ThermoFinnigan, CA). Chromatography buffer solutions (Buffer A, 0.1% formic acid; Buffer B, 100% acetonitrile and 0.1% formic acid) were run using a 60 minute gradient. A flow rate of 150 µL/min was used at the electrospray source. Spectra were searched using Bioworks Browser 3.3.1 SP1 (ThermoFisher Scientific) using Sequest Uniprot/Swiss-Prot database (www.expasy.org). An exclusion filter was applied to reduce false positives, where peptides with $P < 0.001$, and X correlation

scores of 1.9, 2.5 and 3.2, for single, doubly and triply charged peptides, were retained. MS/MS raw files were exported into Microsoft Excel and protein hits obtained from different raw data files, but belonging to the same gel lane were merged into a unique file. If the same protein identity was detected in multiple bands from the same sample condition, their SpCs were summed to get the total protein amount. Semi-quantitative analysis was performed taking into account the spectral counts of protein identities. Proteins have been grouped according to their functional groups based on GO Ontology and swissprot. Spectral count of proteins belonging to the same functional group have been summed and plotted in histogram.

RESULTS

Table S.1 Theoretical dendrimers surface proprieties

<i>Generatio n</i>	<i>MW</i> *	<i>Concentration</i>	<i>Terminal groups</i> *	<i>Diameter</i> *	<i>Terminal Groups</i> * *	<i>Surface area</i> **	<i>Surface charge density</i> ***
	<i>g/mol</i>	<i>μM</i>		<i>nm</i>	<i>10²¹/mL</i>	<i>(m²/L)</i>	<i>(nm⁻²)</i>
G4	14215	35	64	4.5	1.36	1350	1.0
G5	28826	17	128	5.4	1.34	960	1.4
G6	58048	9	256	6.7	1.33	730	1.8
G7	116493	4	512	8.1	1.32	530	2.5

*Theoretical values taken from manufacturer's homepage.² **The terminal groups and surface area are calculated for a fixed dendrimer concentration of 0.5 mg/mL and assuming a spherical shape. ***The surface charge density was calculated using the theoretical values for number of terminal groups and the surface area and assuming that all terminal groups are protonated³.

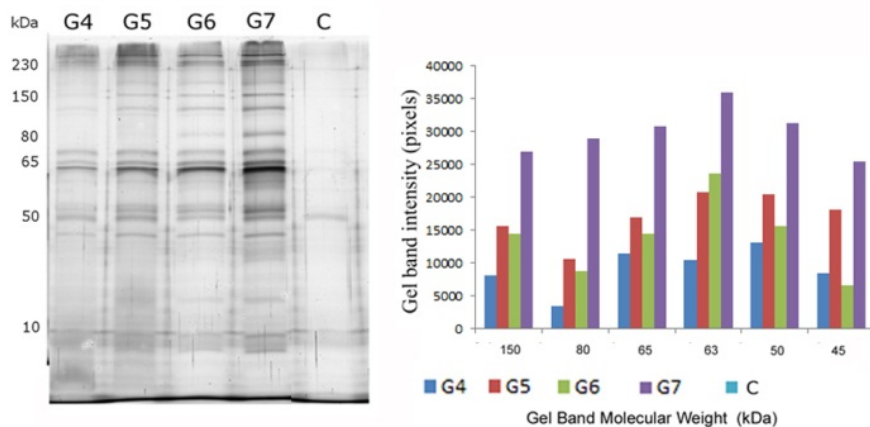


Figure SI.1 SDS-PAGE of human plasma proteins, in low plasma concentration, associated with dendrimer of different generations and plasma control and B) gel band densitometry of most relevant SDS-PAGE gel bands

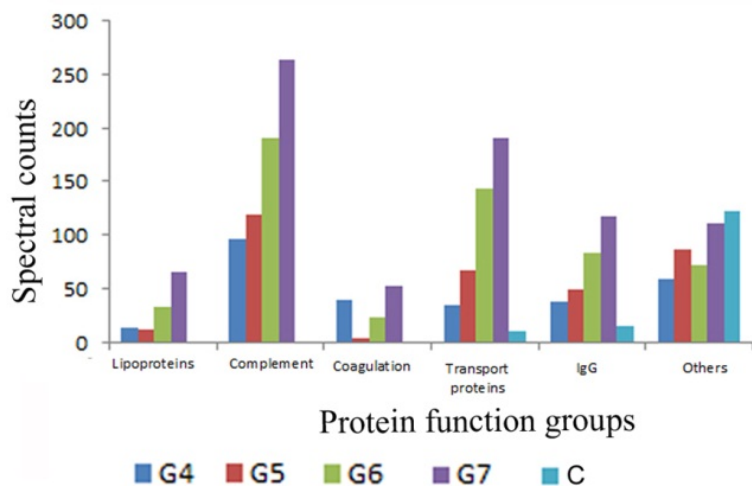


Figure SI.2. Functional classification on identified proteins associated on dendrimers after incubation with high plasma concentration, identified by Mass Spectrometry analysis

Table SI.2 Mass spectrometry analysis of proteins associated to dendrimers after incubation with plasma in high concentration (*in vivo* condition)

Acc num ^a	Protein name	Mw (Da)	G4 ^b	G5 ^c	G6 ^d	G7 ^e	C ^f
P04114	sp P04114 APOB_HUMAN Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=2	515283.6	1	19	63	50	3
P08519	sp P08519 APOA_HUMAN Apolipoprotein(a) OS=Homo sapiens GN=LPA PE=1 SV=1	500996.4	-	-	1	1	-
P15924	sp P15924 DESP_HUMAN Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	331567.8	-	-	1	-	3
Q86YZ3	sp Q86YZ3 HORN_HUMAN Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2	282225.7	2	2	3	2	4
P02751	sp P02751 FINC_HUMAN Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4	262457.6	-	13	30	26	-
P0C0L5	sp P0C0L5 CO4B_HUMAN Complement C4-B OS=Homo sapiens GN=C4B PE=1 SV=1	192671.6	1	1	2	3	-
P0C0L4	sp P0C0L4 CO4A_HUMAN Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=1	192649.5	19	28	61	64	-
P01031	sp P01031 CO5_HUMAN Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4	188185.3	-	1	8	-	-
P01024	sp P01024 CO3_HUMAN Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	187029.3	84	110	152	160	13
P01023	sp P01023 A2MG_HUMAN Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3	163187.4	-	-	2	-	-
P08603	sp P08603 CFAH_HUMAN Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4	139004.4	-	15	34	10	-
P00450	sp P00450 CERU_HUMAN Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1	122127.6	-	35	75	72	-
Q02413	sp Q02413 DSG1_HUMAN Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2	113676.0	-	-	1	-	3
P19823	sp P19823 ITI2_HUMAN Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITI2 PE=1 SV=2	106396.8	-	15	27	24	-
P19827	sp P19827 ITI1_HUMAN Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITI1 PE=1 SV=3	101325.8	-	6	27	28	-
Q06033	sp Q06033 ITI3_HUMAN Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITI3 PE=1 SV=2	99786.6	-	-	5	5	-
P02671	sp P02671 FIBA_HUMAN Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2	94914.3	2	19	32	32	-

P14923	sp P14923 PLAK_HUMAN Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	81692.9	-	2	-	-	2
P00736	sp P00736 C1R_HUMAN Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2	80066.8	-	-	5	1	-
P02788	sp P02788 TRFL_HUMAN Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=6	78132.0	-	-	-	-	-
P23142	sp P23142 FBLN1_HUMAN Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4	77162.4	-	-	1	1	-
P09871	sp P09871 C1S_HUMAN Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1	76634.9	1	8	3	3	-
P08133	sp P08133 ANXA6_HUMAN Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3	75825.7	-	-	-	-	-
P07225	sp P07225 PROS_HUMAN Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1	75074.1	-	3	6	4	-
P01042	sp P01042 KNG1_HUMAN Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2	71912.1	-	-	12	12	-
P03952	sp P03952 KLKB1_HUMAN Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1	71322.8	-	2	2	-	-
P00734	sp P00734 THRB_HUMAN Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2	69992.2	7	23	43	34	-
P02768	sp P02768 ALBU_HUMAN Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	69321.6	7	15	39	32	15
P07359	sp P07359 GP1BA_HUMAN Platelet glycoprotein Ib alpha chain OS=Homo sapiens GN=GP1BA PE=1 SV=1	68912.2	-	-	1	-	-
P04003	sp P04003 C4BPA_HUMAN C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2	66989.4	13	12	24	23	-
P04264	sp P04264 K2C1_HUMAN Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	65998.9	-	-	-	-	-
P35858	sp P35858 ALS_HUMAN Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens GN=IGFALS PE=1 SV=1	65994.0	-	-	6	2	-
P35908	sp P35908 K22E_HUMAN Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	65393.2	-	-	-	-	-
Q08380	sp Q08380 LG3BP_HUMAN Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1	65289.4	1	1	-	-	-
P02748	sp P02748 CO9_HUMAN Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2	63132.8	-	-	4	4	-
Q14520	sp Q14520 HABP2_HUMAN Hyaluronan-binding protein 2 OS=Homo sapiens GN=HABP2 PE=1 SV=1	62630.5	-	-	1	-	-
P13647	sp P13647 K2C5_HUMAN Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	62340.0	-	-	-	-	-
P35527	sp P35527 K1C9_HUMAN Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	62026.7	-	-	-	-	-
P43251	sp P43251 BTD_HUMAN Biotinidase OS=Homo sapiens GN=BTD PE=1 SV=2	61093.3	-	-	1	-	-
P22792	sp P22792 CPN2_HUMAN Carboxypeptidase N subunit 2 OS=Homo sapiens GN=CPN2 PE=1 SV=2	60576.3	-	1	3	6	-
P14618	sp P14618 KPYM_HUMAN Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4	57900.2	-	-	-	-	1
P02675	sp P02675 FIBB_HUMAN Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2	55892.2	6	14	37	32	-
P05155	sp P05155 C1_HUMAN Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2	55119.5	-	2	22	19	-
P00742	sp P00742 FA10_HUMAN Coagulation factor X OS=Homo sapiens GN=F10 PE=1 SV=2	54696.6	-	-	1	1	-
P04004	sp P04004 VTNC_HUMAN Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1	54271.2	1	4	12	12	-
Q9NZP8	sp Q9NZP8 C1RL_HUMAN Complement C1r subcomponent-like protein OS=Homo sapiens GN=C1RL PE=1 SV=2	53464.4	-	-	2	-	-
P01019	sp P01019 ANGT_HUMAN Angiotensinogen OS=Homo sapiens GN=AGT PE=1 SV=1	53120.6	-	-	1	1	-
P10909	sp P10909 CLUS_HUMAN Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	52461.1	-	-	1	2	-
P15169	sp P15169 CBPN_HUMAN Carboxypeptidase N catalytic chain OS=Homo sapiens GN=CPN1 PE=1 SV=1	52253.4	-	-	4	3	-
P04070	sp P04070 PROC_HUMAN Vitamin K-dependent protein C OS=Homo sapiens GN=PROC PE=1 SV=1	52037.5	-	-	2	2	-
P02679	sp P02679 FIBG_HUMAN Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3	51478.9	5	11	21	17	-
P68104	sp P68104 EF1A1_HUMAN Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	50109.2	-	3	-	-	-
Q71U36	sp Q71U36 TBA1A_HUMAN Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1	50103.7	2	3	-	-	1
Q13885	sp Q13885 TBB2A_HUMAN Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1	49875.0	-	-	-	-	-
P14136	sp P14136 GFAP_HUMAN Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1	49849.7	3	3	3	3	3
Q6UXB8	sp Q6UXB8 PI16_HUMAN Peptidase inhibitor 16 OS=Homo sapiens GN=PI16 PE=1 SV=1	49439.6	-	-	1	-	-
P01871	sp P01871 IGHM_HUMAN Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3	49275.6	14	14	24	20	11
P01011	sp P01011 AACT_HUMAN Alpha-1-antichymotrypsin OS=Homo sapiens GN=SERPINA3 PE=1 SV=2	47620.6	-	-	14	10	-
P06733	sp P06733 ENOA_HUMAN Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	47139.4	-	1	-	-	1
P01009	sp P01009 A1AT_HUMAN Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3	46707.1	-	-	3	2	-

P50454	sp P50454 SERPH_HUMAN Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2	46411.3	1	-	-	-	2
P36955	sp P36955 PEDF_HUMAN Pigment epithelium-derived factor OS=Homo sapiens GN=SERPINF1 PE=1 SV=4	46283.4	1	-	4	2	-
P00738	sp P00738 HPT_HUMAN Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=1	45176.6	-	-	2	4	-
P22891	sp P22891 PROZ_HUMAN Vitamin K-dependent protein Z OS=Homo sapiens GN=PROZ PE=1 SV=2	44714.7	-	-	1	-	-
O14791	sp O14791 APOL1_HUMAN Apolipoprotein L1 OS=Homo sapiens GN=APOL1 PE=1 SV=5	43947.0	-	1	1	5	-
Q08431	sp Q08431 MFGM_HUMAN Lactadherin OS=Homo sapiens GN=MFGE8 PE=1 SV=2	43095.5	-	-	-	-	-
Q9BYX7	sp Q9BYX7 ACTBM_HUMAN Putative beta-actin-like protein 3 OS=Homo sapiens GN=POTEKP PE=5 SV=1	41988.9	1	-	1	2	3
P62736	sp P62736 ACTA_HUMAN Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1	41981.8	3	4	-	-	3
Q9BYZ2	sp Q9BYZ2 LDH6B_HUMAN L-lactate dehydrogenase A-like 6B OS=Homo sapiens GN=LDHAL6B PE=1 SV=3	41916.2	-	-	-	-	-
P60709	sp P60709 ACTB_HUMAN Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	41709.7	4	2	3	2	5
P01860	sp P01860 IGHG3_HUMAN Ig gamma-3 chain C region OS=Homo sapiens GN=IGHG3 PE=1 SV=2	41260.4	-	1	2	1	-
P27169	sp P27169 PON1_HUMAN Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3	39706.3	-	1	8	5	-
Q15166	sp Q15166 PON3_HUMAN Serum paraoxonase/lactonase 3 OS=Homo sapiens GN=PON3 PE=1 SV=3	39582.4	-	-	1	-	-
P02765	sp P02765 FETUA_HUMAN Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1	39299.7	-	3	13	7	-
P00739	sp P00739 HPT_R_HUMAN Haptoglobin-related protein OS=Homo sapiens GN=HPR PE=2 SV=2	39004.7	-	1	4	5	-
P02760	sp P02760 AMBP_HUMAN Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1	38974.0	-	-	5	5	-
P51884	sp P51884 LUM_HUMAN Lumican OS=Homo sapiens GN=LUM PE=1 SV=2	38404.8	-	1	3	2	-
P02749	sp P02749 APOH_HUMAN Beta-2-glycoprotein 1 OS=Homo sapiens GN=APOH PE=1 SV=3	38272.7	1	-	4	3	-
O43866	sp O43866 CD5L_HUMAN CD5 antigen-like OS=Homo sapiens GN=CD5L PE=1 SV=1	38063.0	1	2	5	3	-
P01876	sp P01876 IGHA1_HUMAN Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2	37630.7	3	2	11	9	1
P01877	sp P01877 IGHA2_HUMAN Ig alpha-2 chain C region OS=Homo sapiens GN=IGHA2 PE=1 SV=3	36503.0	-	-	1	-	-
P02649	sp P02649 APOE_HUMAN Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	36131.8	1	3	9	7	3
P01857	sp P01857 IGHG1_HUMAN Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	36083.2	9	10	14	13	14
P04406	sp P04406 G3P_HUMAN Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	36030.4	-	1	-	-	-
P01861	sp P01861 IGHG4_HUMAN Ig gamma-4 chain C region OS=Homo sapiens GN=IGHG4 PE=1 SV=1	35917.9	1	-	1	1	1
P01859	sp P01859 IGHG2_HUMAN Ig gamma-2 chain C region OS=Homo sapiens GN=IGHG2 PE=1 SV=2	35877.8	6	6	8	9	6
Q13790	sp Q13790 APOF_HUMAN Apolipoprotein F OS=Homo sapiens GN=APOF PE=1 SV=1	33442.1	-	-	1	1	-
P35030	sp P35030 TRY3_HUMAN Trypsin-3 OS=Homo sapiens GN=PRSS3 PE=1 SV=2	32508.0	3	3	2	2	3
P02647	sp P02647 APOA1_HUMAN Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1	30758.9	3	4	6	9	3
P02746	sp P02746 C1QB_HUMAN Complement C1q subcomponent subunit B OS=Homo sapiens GN=C1QB PE=1 SV=3	26704.5	2	5	3	6	4
P07477	sp P07477 TRY1_HUMAN Trypsin-1 OS=Homo sapiens GN=PRSS1 PE=1 SV=1	26541.1	1	-	-	1	1
P02747	sp P02747 C1QC_HUMAN Complement C1q subcomponent subunit C OS=Homo sapiens GN=C1QC PE=1 SV=3	25757.1	-	1	2	2	1
P02743	sp P02743 SAMP_HUMAN Serum amyloid P-component OS=Homo sapiens GN=APCS PE=1 SV=2	25371.1	-	3	6	5	1
P04792	sp P04792 HSPB1_HUMAN Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	22768.5	-	1	-	-	-
P01591	sp P01591 IGJ_HUMAN Immunoglobulin J chain OS=Homo sapiens GN=IGJ PE=1 SV=4	18087.0	-	-	2	2	-
P12273	sp P12273 PIP_HUMAN Prolactin-inducible protein OS=Homo sapiens GN=PIP PE=1 SV=1	16561.8	-	-	1	1	2
P61626	sp P61626 LYSC_HUMAN Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1	16526.3	-	-	-	-	1
P68871	sp P68871 HBB_HUMAN Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2	15988.3	-	4	1	-	-
P02766	sp P02766 TTHY_HUMAN Transthyretin OS=Homo sapiens GN=TTR PE=1 SV=1	15877.1	-	-	5	5	1
P68431	sp P68431 H31_HUMAN Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2	15394.5	-	-	-	-	-
Q71DI3	sp Q71DI3 H32_HUMAN Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3	15378.5	2	-	-	-	-
P84243	sp P84243 H33_HUMAN Histone H3.3 OS=Homo sapiens GN=H3F3A PE=1 SV=2	15318.5	-	-	-	-	-
P69905	sp P69905 HBA_HUMAN Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2	15247.9	-	2	-	-	-

Q16378	sp Q16378 PROL4_HUMAN Proline-rich protein 4 OS=Homo sapiens GN=PRR4 PE=1 SV=2	15115.6	-	-	-	-	-
P62987	sp P62987 RL40_HUMAN Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2	14719.0	1	-	-	-	-
P62899	sp P62899 RL31_HUMAN 60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1	14453.9	-	-	-	-	-
Q9GZZ8	sp Q9GZZ8 LACRT_HUMAN Extracellular glycoprotein lacritin OS=Homo sapiens GN=LACRT PE=1 SV=1	14237.3	-	-	-	-	-
P04908	sp P04908 H2A1B_HUMAN Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2	14127.0	1	2	-	-	-
P33778	sp P33778 H2B1B_HUMAN Histone H2B type 1-B OS=Homo sapiens GN=HIST1H2BB PE=1 SV=2	13941.6	2	2	1	2	1
P06312	sp P06312 KV401_HUMAN Ig kappa chain V-IV region (Fragment) OS=Homo sapiens GN=IGKV4-1 PE=4 SV=1	13371.6	2	2	1	2	1
P01766	sp P01766 HV305_HUMAN Ig heavy chain V-III region BRO OS=Homo sapiens PE=1 SV=1	13218.4	2	2	4	1	2
P01825	sp P01825 HV207_HUMAN Ig heavy chain V-II region NEWM OS=Homo sapiens PE=1 SV=1	12782.3	-	-	1	-	-
P01781	sp P01781 HV320_HUMAN Ig heavy chain V-III region GAL OS=Homo sapiens PE=1 SV=1	12722.2	-	-	2	1	1
P01614	sp P01614 KV201_HUMAN Ig kappa chain V-II region Cum OS=Homo sapiens PE=1 SV=1	12668.3	-	1	1	2	-
P01625	sp P01625 KV402_HUMAN Ig kappa chain V-IV region Len OS=Homo sapiens PE=1 SV=2	12632.2	2	2	2	2	2
P01764	sp P01764 HV303_HUMAN Ig heavy chain V-III region VH26 OS=Homo sapiens PE=1 SV=1	12574.2	1	1	2	1	1
P04433	sp P04433 KV309_HUMAN Ig kappa chain V-III region VG (Fragment) OS=Homo sapiens PE=1 SV=1	12567.3	-	-	-	-	-
P01765	sp P01765 HV304_HUMAN Ig heavy chain V-III region TIL OS=Homo sapiens PE=1 SV=1	12348.1	1	-	1	2	-
P01617	sp P01617 KV204_HUMAN Ig kappa chain V-II region TEW OS=Homo sapiens PE=1 SV=1	12308.2	-	1	1	-	-
P01763	sp P01763 HV302_HUMAN Ig heavy chain V-III region WEA OS=Homo sapiens PE=1 SV=1	12248.5	-	-	2	1	-
P01613	sp P01613 KV121_HUMAN Ig kappa chain V-I region Ni OS=Homo sapiens PE=1 SV=1	12238.0	2	1	2	2	1
P01593	sp P01593 KV101_HUMAN Ig kappa chain V-I region AG OS=Homo sapiens PE=1 SV=1	11984.9	3	2	2	2	2
P80748	sp P80748 LV302_HUMAN Ig lambda chain V-III region LOI OS=Homo sapiens PE=1 SV=1	11927.8	-	1	1	1	-
P01612	sp P01612 KV120_HUMAN Ig kappa chain V-I region Mev OS=Homo sapiens PE=1 SV=1	11862.8	-	-	1	-	-
P04430	sp P04430 KV122_HUMAN Ig kappa chain V-I region BAN OS=Homo sapiens PE=1 SV=1	11832.8	-	1	1	1	-
P01606	sp P01606 KV114_HUMAN Ig kappa chain V-I region OU OS=Homo sapiens PE=1 SV=1	11769.7	2	2	2	2	-
P01620	sp P01620 KV302_HUMAN Ig kappa chain V-III region SIE OS=Homo sapiens PE=1 SV=1	11767.9	1	1	1	1	4
P01596	sp P01596 KV104_HUMAN Ig kappa chain V-I region CAR OS=Homo sapiens PE=1 SV=1	11696.3	1	2	1	2	1
P01597	sp P01597 KV105_HUMAN Ig kappa chain V-I region DEE OS=Homo sapiens PE=1 SV=1	11653.8	2	2	2	3	2
P01619	sp P01619 KV301_HUMAN Ig kappa chain V-III region B6 OS=Homo sapiens PE=1 SV=1	11627.8	-	-	1	-	-
P01834	sp P01834 IGKC_HUMAN Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1	11601.7	6	10	11	13	9
P01611	sp P01611 KV119_HUMAN Ig kappa chain V-I region Wes OS=Homo sapiens PE=1 SV=1	11600.7	1	-	1	1	-
P01717	sp P01717 LV403_HUMAN Ig lambda chain V-IV region Hil OS=Homo sapiens PE=1 SV=1	11509.6	-	-	-	-	-
P01714	sp P01714 LV301_HUMAN Ig lambda chain V-III region SH OS=Homo sapiens PE=1 SV=1	11385.6	-	-	-	1	-
P62805	sp P62805 H4_HUMAN Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2	11360.4	4	4	-	-	2
P0CG04	sp P0CG04 LAC1_HUMAN Ig lambda-1 chain C regions OS=Homo sapiens GN=IGLC1 PE=1 SV=1	11340.6	2	6	6	7	5
P0CG05	sp P0CG05 LAC2_HUMAN Ig lambda-2 chain C regions OS=Homo sapiens GN=IGLC2 PE=1 SV=1	11286.6	1	2	2	3	-
P81605	sp P81605 DCD_HUMAN Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	11276.8	2	-	1	-	3
P01621	sp P01621 KV303_HUMAN Ig kappa chain V-III region NG9 (Fragment) OS=Homo sapiens PE=1 SV=1	10722.3	-	-	1	1	-

^a Uniprot accession number. *b-f* represents the spectral counting for proteins associated with G4, G5, G6, G7 dendrimers and control sample respectively.

Table SI.3 Mass spectrometry analysis of proteins associated to dendrimers after incubation with plasma in *low concentration* (*in vitro* conditions)

Acc num ^a	Protein name	Mw (Da)	G4 ^b	G5 ^c	G6 ^d	G7 ^e	C ^f
P04114	sp P04114 APOB_HUMAN Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=2	515283.6	1	4	23	50	-
P15924	sp P15924 DESP_HUMAN Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	331567.8	-	4	-	-	-
Q86YZ3	sp Q86YZ3 HORN_HUMAN Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2	282225.7	5	2	1	1	-
P02751	sp P02751 FINC_HUMAN Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4	262457.6	8	14	15	34	-
Q5D862	sp Q5D862 FILA2_HUMAN Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	247926.3	-	1	-	1	-
P35580	sp P35580 MYH10_HUMAN Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3	228856.9	-	-	-	-	1
P35579	sp P35579 MYH9_HUMAN Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	226390.6	-	1	2	-	5
P0C0L5	sp P0C0L5 CO4B_HUMAN Complement C4-B OS=Homo sapiens GN=C4B PE=1 SV=1	192671.6	-	2	1	2	-
P0C0L4	sp P0C0L4 CO4A_HUMAN Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=1	192649.5	11	14	39	49	-
P01031	sp P01031 CO5_HUMAN Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4	188185.3	-	-	-	6	-
P01024	sp P01024 CO3_HUMAN Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	187029.3	69	87	107	137	-
P01023	sp P01023 A2MG_HUMAN Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3	163187.4	-	-	2	13	-
P08603	sp P08603 CFAH_HUMAN Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4	139004.4	4	3	11	30	-
P00450	sp P00450 CERU_HUMAN Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1	122127.6	17	22	41	56	-
Q02413	sp Q02413 DSG1_HUMAN Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2	113676.0	3	4	1	4	-
Q14697	sp Q14697 GANAB_HUMAN Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3	106806.8	-	-	-	-	1
P19823	sp P19823 ITIH2_HUMAN Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2	106396.8	-	4	17	24	-
P12814	sp P12814 ACTN1_HUMAN Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2	102992.7	-	-	-	-	1
P19827	sp P19827 ITIH1_HUMAN Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3	101325.8	-	2	11	20	-
Q08554	sp Q08554 DSC1_HUMAN Desmocollin-1 OS=Homo sapiens GN=DSC1 PE=1 SV=2	99923.8	1	-	-	1	-
Q06033	sp Q06033 ITIH3_HUMAN Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2	99786.6	-	-	1	-	-
P13639	sp P13639 EEF2_HUMAN Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	95277.1	-	-	-	-	4
P02671	sp P02671 FIBA_HUMAN Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2	94914.3	10	13	30	26	-
P08238	sp P08238 HS90B_HUMAN Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	83212.2	-	-	1	-	1
P14923	sp P14923 PLAK_HUMAN Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	81692.9	-	3	-	2	-
P00736	sp P00736 C1R_HUMAN Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2	80066.8	-	-	-	-	-
P02788	sp P02788 TRFL_HUMAN Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=6	78132.0	-	-	-	1	-
P09871	sp P09871 C1S_HUMAN Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1	76634.9	-	-	2	1	-
P08133	sp P08133 ANXA6_HUMAN Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3	75825.7	1	-	1	-	2
P07225	sp P07225 PROS_HUMAN Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1	75074.1	-	-	3	4	-
P01042	sp P01042 KNG1_HUMAN Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2	71912.1	-	-	1	4	-
P00734	sp P00734 THRB_HUMAN Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2	69992.2	6	4	15	24	-
P02768	sp P02768 ALBU_HUMAN Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	69321.6	17	32	58	77	10
P04003	sp P04003 C4BPA_HUMAN C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2	66989.4	9	7	15	12	-
P35858	sp P35858 ALS_HUMAN Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens GN=IGFALS PE=1 SV=1	65994.0	-	-	2	2	-
P02748	sp P02748 CO9_HUMAN Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2	63132.8	-	-	1	3	-
P43251	sp P43251 BTD_HUMAN Biotinidase OS=Homo sapiens GN=BTD PE=1 SV=2	61093.3	-	-	-	1	-
P22792	sp P22792 CPN2_HUMAN Carboxypeptidase N subunit 2 OS=Homo sapiens GN=CPN2 PE=1 SV=2	60576.3	-	-	-	4	-
P14618	sp P14618 KPYM_HUMAN Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4	57900.2	2	2	3	-	4

P02675	sp P02675 FIBB_HUMAN Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2	55892.2	9	17	33	30	-
P05155	sp P05155 IC1_HUMAN Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2	55119.5	-	2	9	16	-
P00742	sp P00742 FA10_HUMAN Coagulation factor X OS=Homo sapiens GN=F10 PE=1 SV=2	54696.6	-	-	1	1	-
P04004	sp P04004 VTNC_HUMAN Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1	54271.2	1	6	7	10	-
P01019	sp P01019 ANGT_HUMAN Angiotensinogen OS=Homo sapiens GN=AGT PE=1 SV=1	53120.6	-	-	2	3	-
P10909	sp P10909 CLUS_HUMAN Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	52461.1	1	-	-	2	-
P15169	sp P15169 CBPN_HUMAN Carboxypeptidase N catalytic chain OS=Homo sapiens GN=CPN1 PE=1 SV=1	52253.4	-	-	1	2	-
P02679	sp P02679 FIBG_HUMAN Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3	51478.9	7	14	19	21	-
P61978	sp P61978 HNRPK_HUMAN Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1	50944.4	-	-	-	-	1
Q9H4B7	sp Q9H4B7 TBB1_HUMAN Tubulin beta-1 chain OS=Homo sapiens GN=TUBB1 PE=1 SV=1	50294.6	-	-	-	1	-
P68363	sp P68363 TBA1B_HUMAN Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1	50119.6	-	-	-	-	2
P68104	sp P68104 EF1A1_HUMAN Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	50109.2	2	1	1	2	5
Q71U36	sp Q71U36 TBA1A_HUMAN Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1	50103.7	4	5	4	3	6
Q13885	sp Q13885 TBB2A_HUMAN Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1	49875.0	1	2	-	1	2
P14136	sp P14136 GFAP_HUMAN Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1	49849.7	3	3	3	3	3
P07437	sp P07437 TBB5_HUMAN Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	49639.0	-	-	-	-	2
P01871	sp P01871 IGHM_HUMAN Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3	49275.6	9	11	14	19	2
P01011	sp P01011 AACT_HUMAN Alpha-1-antichymotrypsin OS=Homo sapiens GN=SERPINA3 PE=1 SV=2	47620.6	-	2	8	12	-
P06733	sp P06733 ENOA_HUMAN Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	47139.4	1	1	1	-	2
P01009	sp P01009 A1AT_HUMAN Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3	46707.1	-	-	1	7	-
P50454	sp P50454 SERPH_HUMAN Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2	46411.3	4	4	3	4	4
P36955	sp P36955 PEDF_HUMAN Pigment epithelium-derived factor OS=Homo sapiens GN=SERPINF1 PE=1 SV=4	46283.4	-	1	2	3	-
P00738	sp P00738 HPT_HUMAN Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=1	45176.6	-	-	2	4	-
O14791	sp O14791 APOL1_HUMAN Apolipoprotein L1 OS=Homo sapiens GN=APOL1 PE=1 SV=5	43947.0	-	-	-	1	-
Q08431	sp Q08431 MFGM_HUMAN Lactadherin OS=Homo sapiens GN=MFG8 PE=1 SV=2	43095.5	-	-	-	-	1
Q9BYX7	sp Q9BYX7 ACTBM_HUMAN Putative beta-actin-like protein 3 OS=Homo sapiens GN=POTEKP PE=5 SV=1	41988.9	2	2	3	3	3
P62736	sp P62736 ACTA_HUMAN Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1	41981.8	5	9	8	7	14
Q9BYZ2	sp Q9BYZ2 LDH6B_HUMAN L-lactate dehydrogenase A-like 6B OS=Homo sapiens GN=LDHAL6B PE=1 SV=3	41916.2	-	-	-	-	1
P60709	sp P60709 ACTB_HUMAN Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	41709.7	5	9	8	4	11
P27169	sp P27169 PON1_HUMAN Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3	39706.3	-	2	5	7	-
Q15166	sp Q15166 PON3_HUMAN Serum paraoxonase/lactonase 3 OS=Homo sapiens GN=PON3 PE=1 SV=3	39582.4	-	-	-	-	-
P51991	sp P51991 ROA3_HUMAN Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2	39570.5	-	-	1	-	6
P02765	sp P02765 FETUA_HUMAN Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1	39299.7	1	4	5	8	-
P00739	sp P00739 HPTTR_HUMAN Haptoglobin-related protein OS=Homo sapiens GN=HPR PE=2 SV=2	39004.7	-	1	1	6	-
P02760	sp P02760 AMB_P_HUMAN Protein AMBP OS=Homo sapiens GN=AMB_P PE=1 SV=1	38974.0	-	-	2	4	-
P07355	sp P07355 ANXA2_HUMAN Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2	38579.8	-	-	1	1	2
P51884	sp P51884 LUM_HUMAN Lumican OS=Homo sapiens GN=LUM PE=1 SV=2	38404.8	-	-	-	1	-
P02749	sp P02749 APOH_HUMAN Beta-2-glycoprotein 1 OS=Homo sapiens GN=APOH PE=1 SV=3	38272.7	-	-	1	-	-
O43866	sp O43866 CD5L_HUMAN CD5 antigen-like OS=Homo sapiens GN=CD5L PE=1 SV=1	38063.0	-	-	-	2	-
P01876	sp P01876 IGHA1_HUMAN Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2	37630.7	1	2	8	7	-
P22626	sp P22626 ROA2_HUMAN Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2	37406.7	1	2	1	1	5
P00338	sp P00338 LDHA_HUMAN L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2	36665.4	-	-	-	-	1
P01877	sp P01877 IGHA2_HUMAN Ig alpha-2 chain C region OS=Homo sapiens GN=IGHA2 PE=1 SV=3	36503.0	-	-	-	1	-

P02649	sp P02649 APOE_HUMAN Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	36131.8	2	-	4	4	-
P01857	sp P01857 IGHG1_HUMAN Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	36083.2	7	11	11	10	3
P01861	sp P01861 IGHG4_HUMAN Ig gamma-4 chain C region OS=Homo sapiens GN=IGHG4 PE=1 SV=1	35917.9	1	1	1	1	-
P01859	sp P01859 IGHG2_HUMAN Ig gamma-2 chain C region OS=Homo sapiens GN=IGHG2 PE=1 SV=2	35877.8	2	4	5	4	1
P25311	sp P25311 ZA2G_HUMAN Zinc-alpha-2-glycoprotein OS=Homo sapiens GN=AZGP1 PE=1 SV=2	34237.1	1	-	-	-	-
Q32P51	sp Q32P51 RA1L2_HUMAN Heterogeneous nuclear ribonucleoprotein A1-like 2 OS=Homo sapiens GN=HNRNPA1L2 PE=2 SV=2	34204.3	-	-	1	-	3
O75636	sp O75636 FCN3_HUMAN Ficolin-3 OS=Homo sapiens GN=FCN3 PE=1 SV=2	32882.0	-	-	1	1	-
Q13151	sp Q13151 ROA0_HUMAN Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens GN=HNRNPA0 PE=1 SV=1	30821.8	-	1	-	-	-
P02647	sp P02647 APOA1_HUMAN Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1	30758.9	3	7	6	10	-
P31944	sp P31944 CASPE_HUMAN Caspase-14 OS=Homo sapiens GN=CASP14 PE=1 SV=2	27662.0	-	1	-	-	-
P02746	sp P02746 C1QB_HUMAN Complement C1q subcomponent subunit B OS=Homo sapiens GN=C1QB PE=1 SV=3	26704.5	3	3	3	5	-
P02747	sp P02747 C1QC_HUMAN Complement C1q subcomponent subunit C OS=Homo sapiens GN=C1QC PE=1 SV=3	25757.1	1	1	1	1	-
P02743	sp P02743 SAMP_HUMAN Serum amyloid P-component OS=Homo sapiens GN=APCS PE=1 SV=2	25371.1	-	3	5	4	-
P62906	sp P62906 RL10A_HUMAN 60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2	24815.5	-	-	-	-	1
P02763	sp P02763 A1AG1_HUMAN Alpha-1-acid glycoprotein 1 OS=Homo sapiens GN=ORM1 PE=1 SV=1	23496.8	-	-	1	1	-
P50914	sp P50914 RL14_HUMAN 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4	23417.0	-	-	-	-	2
P04792	sp P04792 HSPB1_HUMAN Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	22768.5	-	2	-	-	-
P05452	sp P05452 TETN_HUMAN Tetranectin OS=Homo sapiens GN=CLEC3B PE=1 SV=2	22552.3	-	-	-	1	-
P05090	sp P05090 APOD_HUMAN Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1	21261.8	7	-	-	-	-
P84077	sp P84077 ARF1_HUMAN ADP-ribosylation factor 1 OS=Homo sapiens GN=ARF1 PE=1 SV=2	20683.7	1	-	1	-	1
P31025	sp P31025 LCN1_HUMAN Lipocalin-1 OS=Homo sapiens GN=LCN1 PE=1 SV=1	19237.8	-	-	-	1	-
P23528	sp P23528 COF1_HUMAN Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3	18490.7	-	-	2	2	2
P01591	sp P01591 IGJ_HUMAN Immunoglobulin J chain OS=Homo sapiens GN=IGJ PE=1 SV=4	18087.0	-	-	-	2	-
P62937	sp P62937 PPIA_HUMAN Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2	18000.9	-	-	-	-	1
P63241	sp P63241 IF5A1_HUMAN Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2	16821.4	-	1	-	1	-
P12273	sp P12273 PIP_HUMAN Prolactin-inducible protein OS=Homo sapiens GN=PIP PE=1 SV=1	16561.8	1	1	-	2	-
P61626	sp P61626 LYSC_HUMAN Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1	16526.3	1	-	-	1	-
P68871	sp P68871 HBB_HUMAN Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2	15988.3	-	-	-	3	-
P02766	sp P02766 TTHY_HUMAN Transthyretin OS=Homo sapiens GN=TTR PE=1 SV=1	15877.1	-	4	6	5	-
P68431	sp P68431 H31_HUMAN Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2	15394.5	-	1	-	-	-
Q71D13	sp Q71D13 H32_HUMAN Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3	15378.5	2	4	2	1	2
P84243	sp P84243 H33_HUMAN Histone H3.3 OS=Homo sapiens GN=H3F3A PE=1 SV=2	15318.5	-	2	1	1	2
P69905	sp P69905 HBA_HUMAN Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2	15247.9	-	-	-	2	-
Q16378	sp Q16378 PROL4_HUMAN Proline-rich protein 4 OS=Homo sapiens GN=PRR4 PE=1 SV=2	15115.6	-	-	-	1	-
P62987	sp P62987 RL40_HUMAN Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2	14719.0	1	1	-	-	-
P62899	sp P62899 RL31_HUMAN 60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1	14453.9	-	-	-	-	2
Q9GZZ8	sp Q9GZZ8 LACRT_HUMAN Extracellular glycoprotein lacritin OS=Homo sapiens GN=LACRT PE=1 SV=1	14237.3	-	-	-	2	-
P04908	sp P04908 H2A1B_HUMAN Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2	14127.0	1	2	2	1	1
P33778	sp P33778 H2B1B_HUMAN Histone H2B type 1-B OS=Homo sapiens GN=HIST1H2BB PE=1 SV=2	13941.6	2	3	1	2	8
P06312	sp P06312 KV401_HUMAN Ig kappa chain V-IV region (Fragment) OS=Homo sapiens GN=IGKV4-1 PE=4 SV=1	13371.6	-	-	1	-	-
P06702	sp P06702 S10A9_HUMAN Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1	13233.5	-	-	-	1	1
P01766	sp P01766 HV305_HUMAN Ig heavy chain V-III region BRO OS=Homo sapiens PE=1 SV=1	13218.4	1	2	1	2	-
P01781	sp P01781 HV320_HUMAN Ig heavy chain V-III region GAL OS=Homo sapiens PE=1 SV=1	12722.2	-	-	1	2	-

P01614	sp P01614 KV201_HUMAN Ig kappa chain V-II region Cum OS=Homo sapiens PE=1 SV=1	12668.3	1	-	1	-	-
P01625	sp P01625 KV402_HUMAN Ig kappa chain V-IV region Len OS=Homo sapiens PE=1 SV=2	12632.2	1	1	3	3	1
P01764	sp P01764 HV303_HUMAN Ig heavy chain V-III region VH26 OS=Homo sapiens PE=1 SV=1	12574.2	1	1	2	2	-
P04433	sp P04433 KV309_HUMAN Ig kappa chain V-III region VG (Fragment) OS=Homo sapiens PE=1 SV=1	12567.3	-	-	-	1	-
P01765	sp P01765 HV304_HUMAN Ig heavy chain V-III region TIL OS=Homo sapiens PE=1 SV=1	12348.1	1	-	1	1	-
P01613	sp P01613 KV121_HUMAN Ig kappa chain V-I region Ni OS=Homo sapiens PE=1 SV=1	12238.0	-	-	-	1	-
P01593	sp P01593 KV101_HUMAN Ig kappa chain V-I region AG OS=Homo sapiens PE=1 SV=1	11984.9	1	1	1	2	1
P80748	sp P80748 LV302_HUMAN Ig lambda chain V-III region LOI OS=Homo sapiens PE=1 SV=1	11927.8	-	-	-	1	-
P01612	sp P01612 KV120_HUMAN Ig kappa chain V-I region Mev OS=Homo sapiens PE=1 SV=1	11862.8	-	-	-	-	-
P04430	sp P04430 KV122_HUMAN Ig kappa chain V-I region BAN OS=Homo sapiens PE=1 SV=1	11832.8	-	-	-	-	-
P01606	sp P01606 KV114_HUMAN Ig kappa chain V-I region OU OS=Homo sapiens PE=1 SV=1	11769.7	-	-	-	2	-
P01620	sp P01620 KV302_HUMAN Ig kappa chain V-III region SIE OS=Homo sapiens PE=1 SV=1	11767.9	2	1	3	2	-
P01596	sp P01596 KV104_HUMAN Ig kappa chain V-I region CAR OS=Homo sapiens PE=1 SV=1	11696.3	-	-	1	1	-
P01597	sp P01597 KV105_HUMAN Ig kappa chain V-I region DEE OS=Homo sapiens PE=1 SV=1	11653.77	1	1	1	2	1
P01834	sp P01834 IGKC_HUMAN Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1	11601.67	5	4	7	4	4
P01611	sp P01611 KV119_HUMAN Ig kappa chain V-I region Wes OS=Homo sapiens PE=1 SV=1	11600.71	-	-	-	1	-
P01717	sp P01717 LV403_HUMAN Ig lambda chain V-IV region Hil OS=Homo sapiens PE=1 SV=1	11509.6	-	-	-	1	-
P62805	sp P62805 H4_HUMAN Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2	11360.38	3	2	1	2	3
P0CG04	sp P0CG04 LAC1_HUMAN Ig lambda-1 chain C regions OS=Homo sapiens GN=IGLC1 PE=1 SV=1	11340.61	3	3	5	5	2
P0CG05	sp P0CG05 LAC2_HUMAN Ig lambda-2 chain C regions OS=Homo sapiens GN=IGLC2 PE=1 SV=1	11286.55	-	-	1	2	-
P81605	sp P81605 DCD_HUMAN Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	11276.83	3	2	2	6	4
P02656	sp P02656 APOC3_HUMAN Apolipoprotein C-III OS=Homo sapiens GN=APOC3 PE=1 SV=1	10845.5	-	-	-	1	-
P05109	sp P05109 S10A8_HUMAN Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	10827.65	-	1	-	1	-

^a Uniprot accession number. *b-f* represents the spectral counting for proteins associated with G4, G5, G6, G7 dendrimers and control sample respectively

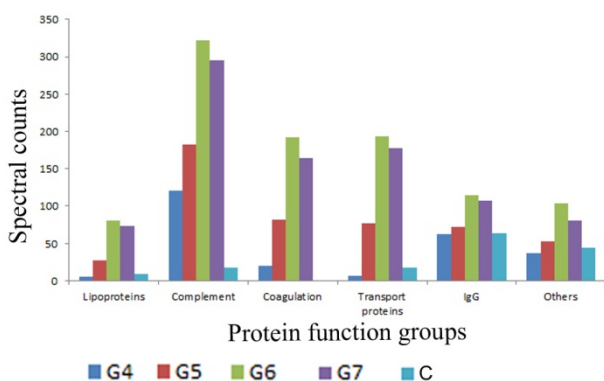


Figure SI.3 Functional classification of human plasma proteins, in low plasma concentration, associated with dendrimers of different generation

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