

Electronic Supporting Information

Pore structure and particle shape modulates the protein corona of mesoporous silica particles

Kalpeshkumar Giri, Inga Kuschnerus, Michael Lau, Juanfang Ruan, Alfonso Garcia-Bennett

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Experimental Section

All chemicals were purchased from Sigma-Aldrich (Sydney, Australia) and used as received.

Mesoporous Particle Synthesis

The method used for the preparation of **AMS-6S** mesoporous particles has been described previously and was used here with slight modification.¹ In the synthesis, the surfactant, N-Lauroyl-L-Alanine (1.25 g), was first added to 250 mL deionized water in a polypropylene bottle and kept in this bottle at 80 °C (200 rpm) for 12 hours. The surfactant solution was stirred for 10 min at 1000 rpm before adding a co-structure directing agent 3-aminopropyl triethoxysilane (1.25 g APES) and tetraethyl orthosilicate (6.25g TEOS) as the silica source. After addition, above the solution was stirred at 1000 rpm for 1 hour. The speed was reduced to 500 rpm after 12 hours and stopped stirring and kept the bottle at RT for 12 hours. The surfactant was removed by calcination at 550 °C (3 hours in flowing air).

The synthesis of **AMS-6F** followed a modified protocol previously reported.² N-Lauroyl-L-Alanine (0.80 g, C12AlaA) was dissolved in 160 g of water and left in static conditions in a

closed polypropylene bottle at 80 °C for one day, in order to allow the surfactant to dissolve completely. To the surfactant solution, co-structure directing agent (3-aminopropyl) trimethoxysilane (0.68 g, APMS) was added under vigorous stirring at 80°C for 1 minute. A polymeric non-ionic dispersant solution was prepared using Pluronic P123 (0.51 g) in 60 g of water in a separate polypropylene bottle and left to stir at room temperature for at least 12 hours. The dispersant solution was added to the surfactant solution and allowed to stir at 80°C for 12 min. After 12 min, TEOS (4.15 g) of was added to the solution and stirred for a further 10 min and subsequently stored at 80°C under the static condition for a period of 48 hours. The sample was hydrothermally treated at 100 °C for 24 hours, filtered, and dried at 95 °C overnight. The surfactant was removed by calcination at 550 °C (3 hours in flowing air) to give the final porous material.

The synthesis of **SBA-15** material followed the protocol previously reported.³ Briefly, P123 (3.9 g), water (135 g), Hydrochloric acid (9.8 g, HCl), TEOS (8.2 g) was added into a propylene bottle and stirred at 40 °C for 20 hours. The bottle was then placed inside an oven at 100 °C for 48 hours. After 48 hours, the sample was filtered and dried at 60 °C overnight. The products were calcined as described above for AMS-6. The synthesis of **aminopropyl-functionalised SBA-15** followed the protocol described above but with the addition of APTES (0.4 g) together with TEOS.

Solvent extraction of as synthesised AMS-6S, AMS-6F, and SBA-15 (aminopropyl-functionalised) in HCl(37%)/EtOH solution (30:70) at 70 °C, (ratio 1 g:250 ml solution). After 12 hours the remaining solid was filtered and washed with ethanol before drying. The extracted amine functionalised AMS-6S, AMS-6F and SBA-15 materials was conjugated to rhodamine by reflux in ethanolic solution (at pH of 11 adjusted with 1M NaOH) for 6 hours at 90 °C.

Cellular uptake study

Immortalized murine microglia cells (BV2) was kindly donated by Dr Lindsay Parker (Macquarie University, Centre for Nanoscale Biophotonics, Australia). Microglia cells were cultured in Dulbecco's Modified eagle media supplemented with 10% Fetal bovine serum (Thermo Fisher Scientific, Australia) and 1% Penicillin/Streptomycin (Thermo Fisher Scientific, Australia) at 37 °C, 5% CO₂, and 95% fresh air. Cells of passage length between 10 to 15 days was used for the in vitro cell experiments.

The cellular uptake of rhodamine conjugated functionalised MSPs was quantified by the CytoFLEX S flow cytometer (Beckman coulter, Australia). BV2 cells were seeded on 24 well plates at an approximate seeding density of 180,000 cells. After 24 hour incubation with MSPs, cells were washed with PBS, and detached using TrypLE Express (Thermo Fisher Scientific, Australia). Cells were resuspended in PBS, and ten thousand events were collected for each sample and results analysed by CytExpert software (Beckman coulter).

Material Characterisation

Powder X-ray diffraction (XRD)

Powder X-ray diffraction (XRD) studies were performed on loaded samples and free drug to evaluate the crystallinity by a powder diffractometer (Bruker D8 Discover diffractometer) using Cu-K α radiation as X-Ray source ($\lambda = 1.5406 \text{ \AA}$). The diffraction patterns were recorded between $1-70^\circ 2\theta$. The data were collected and analysed with DIFFRAC.SUITE™ software.

Nitrogen adsorption/desorption isotherms

Textural properties were characterised using Nitrogen isotherms measurement on calcined and drug-loaded silica samples at liquid nitrogen temperature (-196°C) using a Micromeritics TriStar II volumetric adsorption analyzer (Micromeritics Instrument Corporation, GA, USA). Before the measurements, all samples were dried and degassed for 12 hours at 100°C . (40°C for drug loaded samples to avoid drug degradation). Specific surface areas were calculated by applying the Brunauer–Emmett–Teller (BET) method in the relative pressure range between 0.05 and 0.2. The total mesopore volume was considered from the amount of gas adsorbed at $P/P_0 = 0.95$.

Scanning Electron Microscopy (SEM) and cryo Transmission electron microscopy (cryo-TEM)

SEM was used to study morphology and topography of the particles and their surfaces as well as their size by using a JSM-7401F scanning electron microscope (JEOL Ltd., Tokyo, Japan) operating at $1-2 \text{ kV}$ with no gold coating. For cryo-TEM imaging, $4.5 \mu\text{l}$ of sample was placed onto a glow-discharged Quantifoil copper grid followed by blotting with filter paper for 2.5 seconds. The grid was plunged into liquid ethane with a Leica EM GP freeze plunger (Leica, Germany) and stored in liquid nitrogen. Electron micrographs were obtained with a FEI Talos Arctica TEM (Thermo Fisher Scientific, USA) operating at 200 kV .

Dynamic light scattering (DLS)

Hydrodynamic diameter and zeta potential measurements were performed by DLS a Zetasizer ZS (Malver Instrument, UK) at 25°C with a He-Ne laser (633 nm , 4 mW output power) as a light source. NP dispersions ($10 \mu\text{L}$, 1 mg/mL) were measured in 1 mL in filtered phosphate buffer saline (PBS).

Protein corona formation and analysis:

Sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE)

Particles were incubated with bovine serum 100% for 10, 30 and 120 mins. Subsequently, the samples were washed to remove the unbound and loosely bound proteins (soft corona), and then the hard corona coated mesoporous silica particles were mixed with $20 \mu\text{L}$ of lysis buffer,⁴ and boiled for 5min at 95°C . Samples were then loaded in NUPAGE 4-12% BT GEL of 12 wells (Life Technologies), and the gel was run for 55-60 min at 200 mV in 20 times diluted MOPS SDS Running Buffer ($10\times$, Thermo Scientific). Staining was performed with Coomassie Brilliant Blue R-250 Staining Solutions Kit (Bio-Rad) for 2 hours, followed by washing in Milli-Q water for 2–3 days.

Mass spectrometry

After performing SDS-PAGE, gel bands were excised (4 fraction per lane) from the gel and dehydrated using acetonitrile, followed by vacuum centrifugation. Dried gel pieces were reduced with 10 mM dithiothreitol and alkylated with 55 mM iodoacetamide. Gel pieces were then washed alternately with 25 mM ammonium bicarbonate, followed by acetonitrile. This process was repeated, and the gel pieces dried by vacuum centrifugation. Samples were digested with trypsin overnight at 37 °C. Peptide extraction was performed using a formic acid (2%) and acetonitrile (50%) solution. The extracted peptide solution was dried using a vacuum centrifuge, and peptides were reconstituted in 0.1% formic acid solution. Peptide extraction was performed using a formic acid (2%) and acetonitrile (50%) solution. The extracted peptide solution was dried using a vacuum centrifuge and peptides were reconstituted in 0.1% formic acid solution. Analysis of peptides and peptide fragments was performed using liquid chromatography-tandem mass spectrometry (LC-MS/MS) on a Q-Exactive hybrid Quadrupole Orbitrap mass spectrometer (Thermo). An in-house packed trap (Halo® 2.7 µm 160 Å ES-C18, 100 µm x 3.5 cm) and analytical column (Halo® 2.7 µm 160 Å ES-C18, 75 µm x 10 cm) were used for sample application. Prior to the mass spectrometry, high performance liquid chromatography (HPLC) separation was performed using nanoflow liquid chromatography (EASY-nLC™ II, Thermo). A linear gradient of buffers A (2% v/v acetonitrile, 0.1% v/v formic acid) and B (99.9% v/v acetonitrile, 0.1% v/v formic acid) was used for the elution of peptides. The starting gradient was 1-50% buffer B for 50 minutes followed by increase in buffer B concentration from 50 to 85% for two minutes and column washing at 85% of buffer B for 8 minutes. The flow rate was kept constant at 300 nl/min during the gradient. The mass spectrometry spectral acquisition was performed in the scanning range of 350-2000 m/z in positive mode. For the tandem mass spectrometry analysis, HCD fragmentation of the top 10 most intense precursor ions was performed at a normalised collision energy of 30% (Xcalibur, Thermo). Three technical replicates per samples were performed. Each replicate was injected once for LCMS experiment Raw data files, obtained from Xcalibur software (3.1.66.10 Version), were submitted to MaxQuant 1.5.2.8 which incorporated the Andromeda search engine for protein identification and label free intensity- based quantification. Data were searched against the Bos Taurus (Bovine) Uniprot complete proteome reference database downloaded on September 09, 2017. Above, searches specified trypsin as the proteolytic enzyme with up to two missed cleavages. Carbamidomethylation of cysteine and oxidation of methionine were set as fixed and variable modification, respectively. The monoisotopic mass tolerance for precursor ions and fragmentation ions were set to 10 ppm and 0.5 Da, respectively. One peptide per protein with maximum false discovery rates set 0.01 on peptide and protein levels. The outputs from MaxQuant were then filtered to remove known contaminants such as trypsin, human keratin. Protein abundance as a function of intensity was calculated from all qualified peptides corresponding to a particular protein. An average of triplicate analysis of adsorbed proteins was used for the calculation. The proteins were then listed in order of decreasing relative protein abundance (RPA). Protein

abundance/quantity calculated by this method was represented by unit-less numerical values.

Fig. S1. XRD patterns of as-synthesized, amine functionalised and calcined samples of AMS-6S, AMS-6F, and SBA-15 mesoporous silica particles.

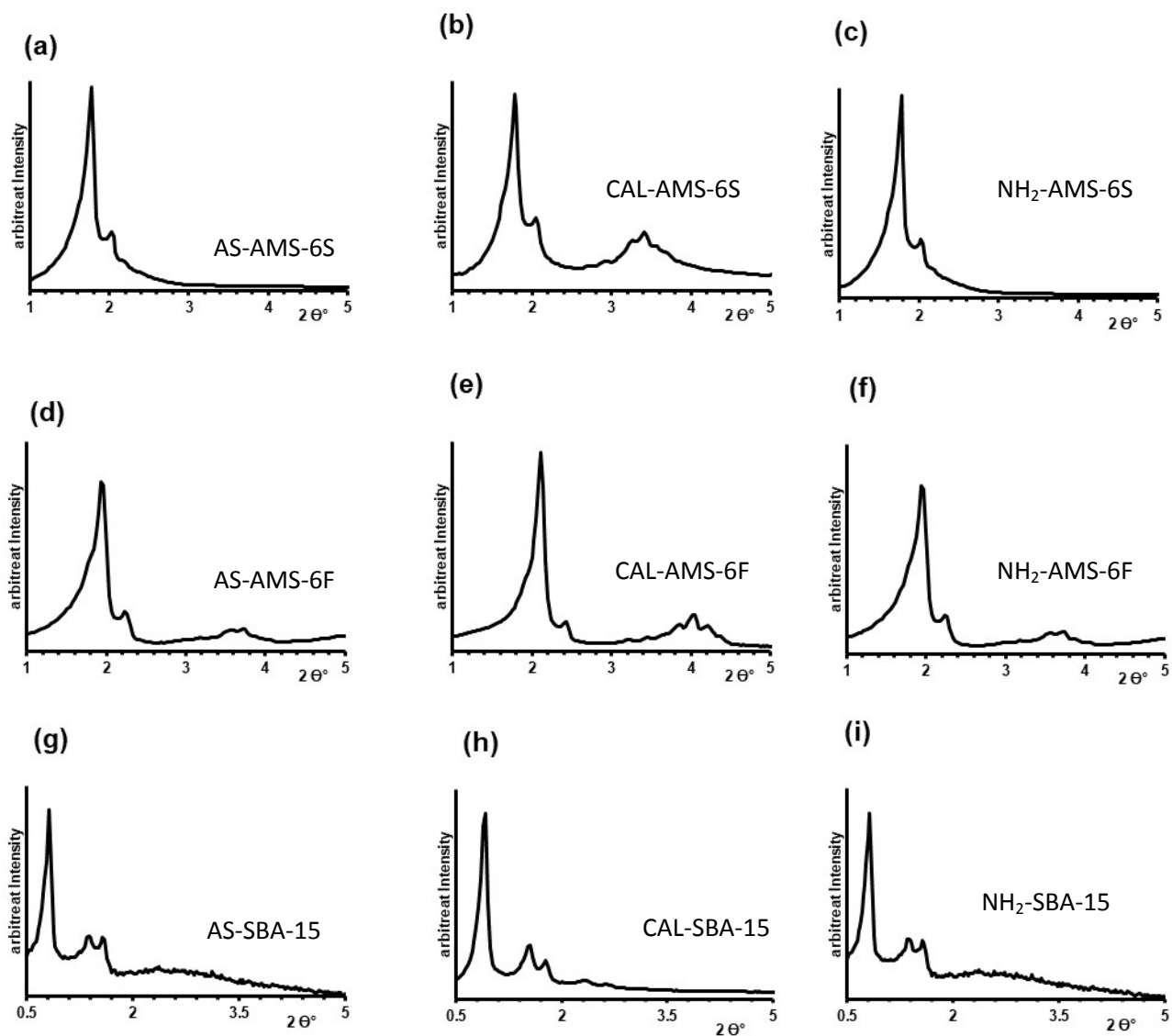


Fig. S2 Representative SEM images of lyophilised samples of the soft corona of calcined MSPs (a) AMS-6F-T₁₀, (b) SBA-15T₃₀, and (c) AMS-6ST₁₂₀, showing agglomeration and a surface protein coating. TEM images of lyophilised samples of the hard corona of (e) AMS-6FT₁₂₀, (f) SBA-15T₃₀ and (g) AMS-6ST₁₂₀, showing significant contrast surrounding individual particles, except for AMS-6S which shows a homogenous thin layer surrounding the particle. Scale bars equal 200 nm. Images are representative of all incubation time points.

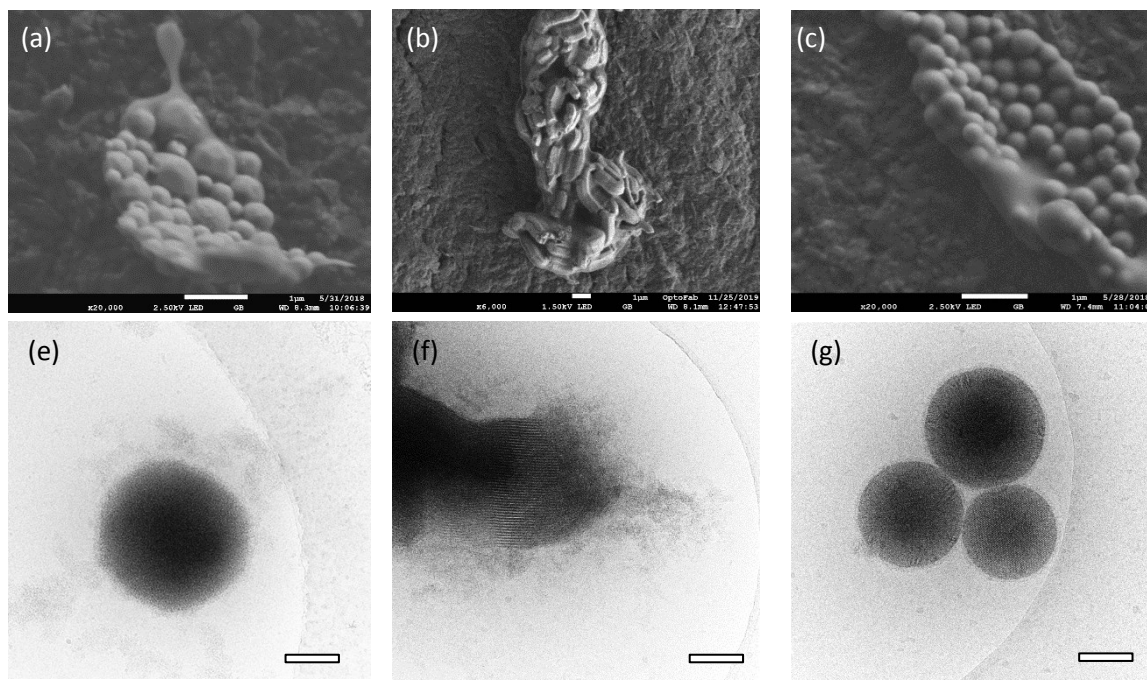


Fig. S3 Comparison of protein adsorption profiles on as synthesised (AS) and calcined (CAL) MSPs after protein corona formation for 10 min (T₁₀) and three times washing cycle in water by Coomassie stained protein SDS-PAGE gel.

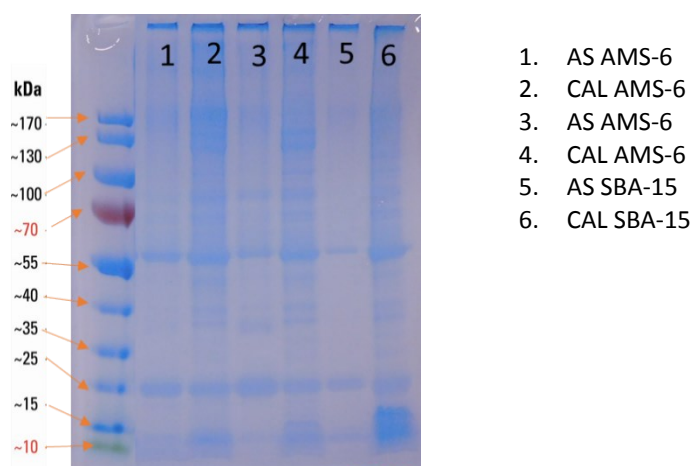


Fig. S4 Venn diagram displaying the number of unique and common proteins identified in the formed hard coronas of AS and CAL-MSPs after incubation at T_{10} in BS, and their respective overlaps.

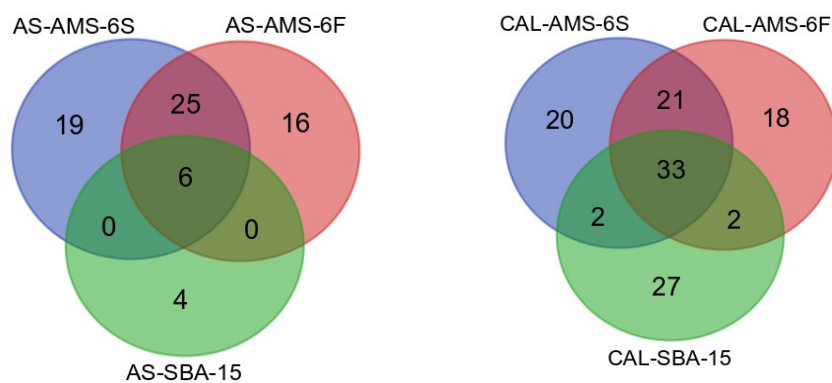


Fig. S5 Comparison of protein adsorption profiles of MSPs at different incubations times in BS, by Coomassie stained protein SDS-PAGE gels recorded after a third washing cycle (experimental triplicates are shown).

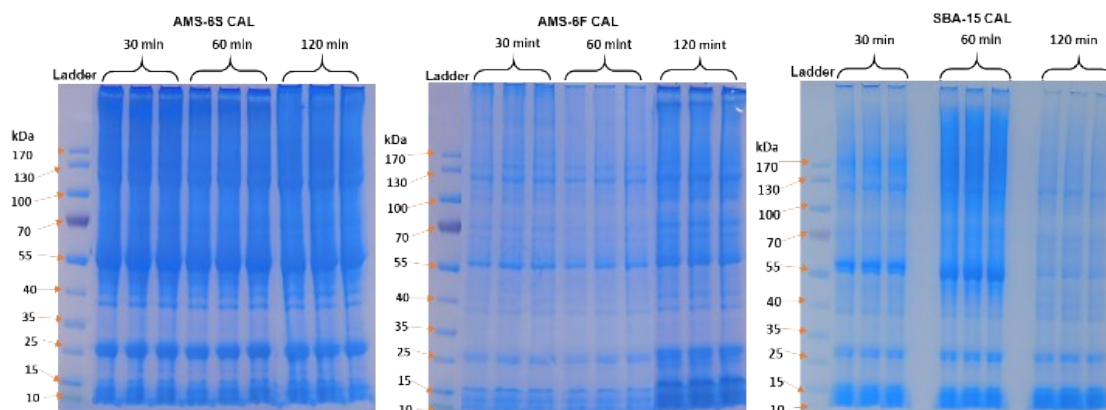


Fig. S6 (a) Total number of proteins adsorbed onto calcined MSPs as a function of incubation time in FBS. (b) Classification of top 30 identified corona proteins according to their molecular mass for CAL-AMS-6S, CAL-AMS-F and CAL-SBA-15 as a function of incubation time.

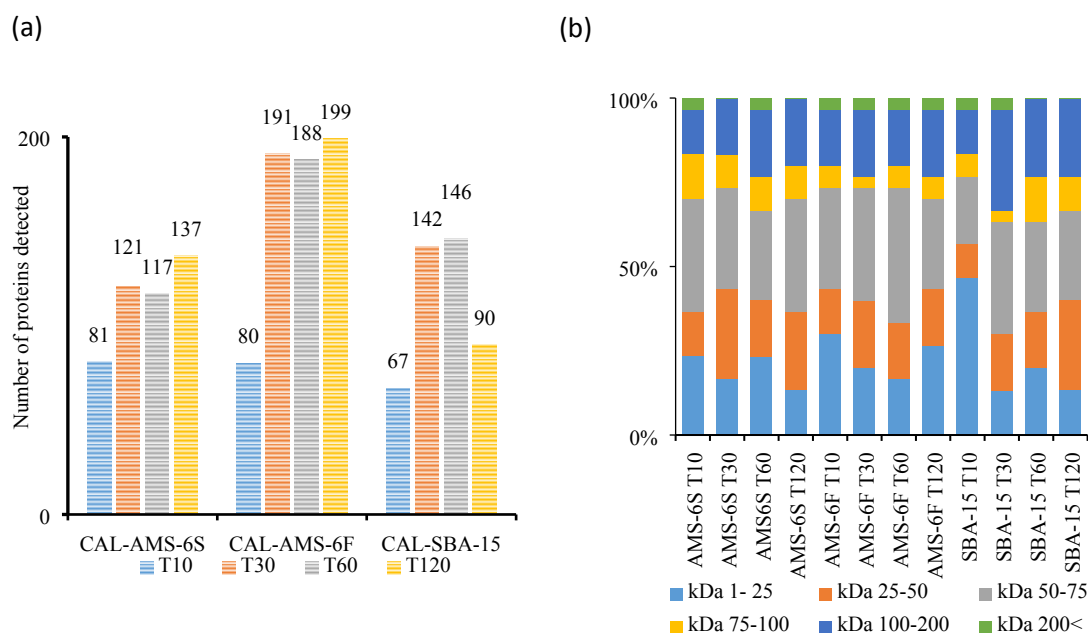
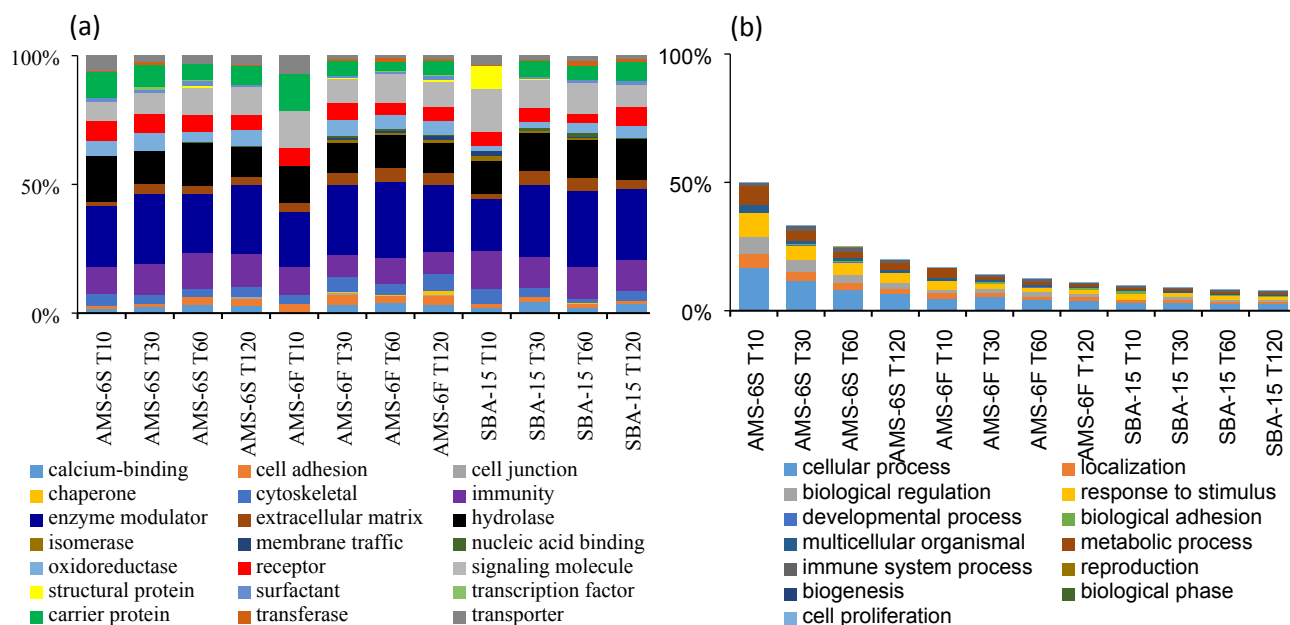
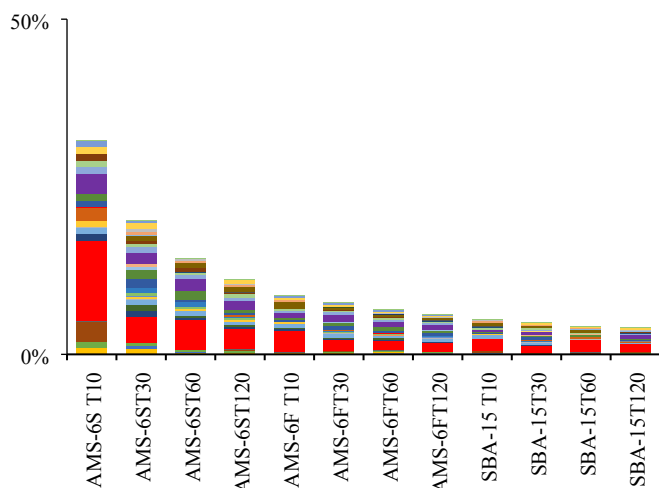


Fig. S7 Bioinformatics classification of the specific hard corona of calcined MSPs incubated at different times in BS based on (a) protein class, (b) biological process, (c) molecular pathway and (d) function.

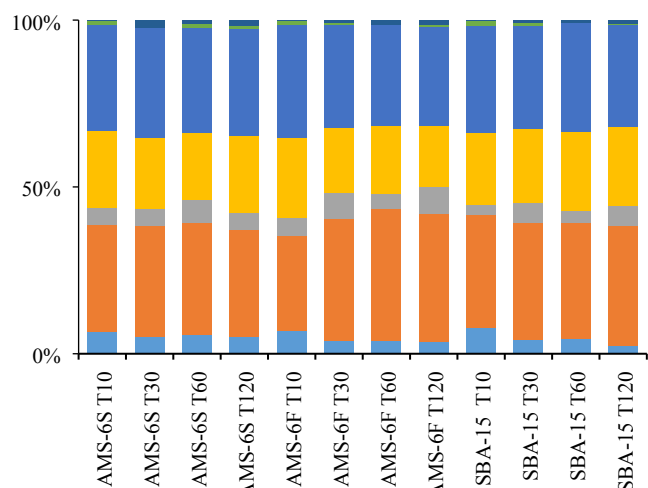


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(c)



(d)



- Adenine and hypoxanthine salvage
- Adrenaline and noradrenaline biosynthesis
- Alzheimer disease-amyloid secretase
- Alzheimer disease-presenilin
- Angiogenesis
- Angiotensin II-stimulated signaling through G proteins and beta-arrestin
- Apoptosis signaling pathway
- Axon guidance mediated by netrin
- B cell activation
- Blood coagulation
- Cadherin signaling
- CCKR signaling map
- Cytoskeletal regulation by Rho GTPase
- Dopamine receptor mediated signaling
- EGF receptor signaling pathway
- FAS signaling pathway
- FGF signaling
- Fructose galactose metabolism
- Glycolysis
- Gonadotropin-releasing hormone receptor
- Heterotrimeric G-protein signaling pathway-Gi alpha and Gs alpha mediated
- Heterotrimeric G-protein signaling pathway-Gq alpha and Go alpha mediated
- Huntington disease
- Inflammation mediated by chemokine and cytokine signaling
- Insulin/IGF pathway-mitogen activated protein kinase kinase/MAP kinase cascade
- Insulin/IGF pathway-protein kinase B signaling cascade
- Integrin signalling
- Nicotine pharmacodynamics
- Nicotinic acetylcholine receptor signaling
- p53 pathway
- Parkinson disease
- Phenylethylamine degradation
- PI3 kinase pathway
- Plasminogen activating cascade
- Proline biosynthesis
- Purine metabolism
- Pyruvate metabolism
- T cell activation
- Toll receptor signaling
- Vitamin D metabolism
- Wnt signaling pathway
- Xanthine and guanine salvage

- molecular transducer
- binding
- structural molecule
- molecular function regulator
- catalytic activity
- transporter
- transcription regulator

Fig. S8 The composition of the most abundant proteins as determined by LC-MS of the hard protein corona of amine functionalised NH₂-MSPs as a function of incubation time at 30 and 120 mins. in BS.

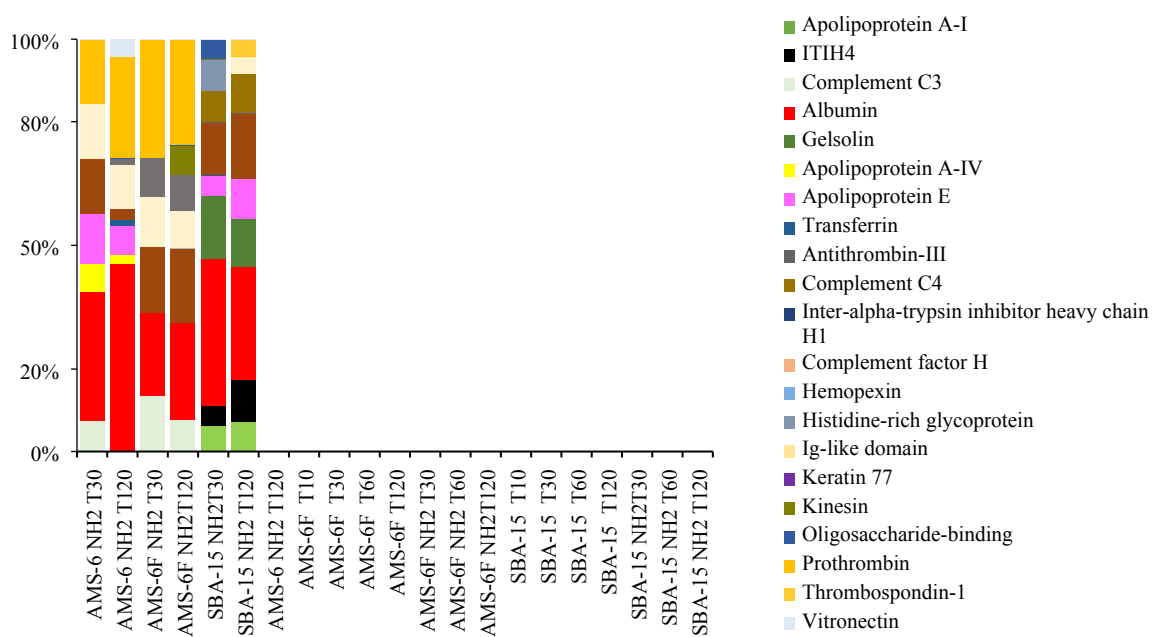


Table S1. Composition of the top 30 proteins of the hard corona of MSPs in this work and their relative abundance, after different incubation times in BS.

AS-AMS-6ST ₁₀				
Accession Number	Entry name	Mass	%RPA	SD
P15497	Apolipoprotein A-I	30.28	33.44	2.36
A0A140T897	Serum albumin	69.32	17.68	1.94
Q2UVX4	Complement C3	187.25	9.12	0.77
P00735	Prothrombin	70.51	5.08	0.56
F1N3Q7	Apolipoprotein A4	52.29	4.13	0.33
Q7SIH1	Alpha-2-macroglobulin	167.58	3.85	0.18
Q29443	Transferrin	77.75	3.36	0.20
P35541	Serum amyloid A	14.52	2.85	0.50
F1MMD7	Inter-alpha-trypsin inhibitor H4	101.51	2.41	0.69
P81644	Apolipoprotein A-II	11.20	2.12	0.09
A6QNZ7	Keratin 10	54.85	1.94	0.10
A0A140T881	Apolipoprotein E	37.42	1.69	0.14
P19035	Apolipoprotein C-III	10.69	1.54	1.10
Q148H7	Cytokeratin-79	57.72	1.49	0.08
P02070	Hemoglobin subunit beta	15.95	1.09	0.32
F1MSZ6	Serpin family C member 1	48.86	1.03	0.05
P01966	Hemoglobin subunit alpha	15.18	0.94	0.13
G3X6K8	Haptoglobin	41.98	0.89	0.07
G8JKW7	Serpin A3-7	46.58	0.77	0.10
Q3ZBS7	Vitronectin	53.58	0.71	0.07
F1MMP5	Inter-alpha-trypsin inhibitor eavy chain H1	101.24	0.42	0.02
Q32L76	Serum amyloid A-4	14.69	0.41	0.09
Q2KJF1	Alpha-1B-glycoprotein	53.55	0.39	0.08
A5PJE3	Fibrinogen alpha chain	67.00	0.38	0.08
Q5GN72	Alpha-1-acid glycoprotein	23.16	0.34	0.02
Q3SZV7	Hemopexin	52.21	0.30	0.21
F1N1I6	Gelsolin	92.08	0.24	0.03
F1MMK9	Kinesin family member 12	53.00	0.18	0.00
Q5E9B1	L-lactate dehydrogenase B chain	36.72	0.17	0.12
A6QPP2	SERPIND1 protein	55.21	0.12	0.09

CAL-AMS-6ST ₁₀				
Accession Number	Entry name	Mass	%RPA	SD
P15497	Apolipoprotein A-I	30.28	18.32	1.42
F1MMD7	Inter-alpha-trypsin inhibitor H4	101.51	13.70	1.42
Q2UVX4	Complement C3	187.25	10.09	0.92
A0A140T897	Serum albumin	69.32	8.27	0.24
F1N1I6	Gelsolin	92.08	6.89	0.30

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P35541	Serum amyloid A	14.52	5.35	0.74
F1N3Q7	Apolipoprotein A4	52.29	3.84	0.27
AOA140T881	Apolipoprotein E	37.42	3.62	0.15
Q29443	Transferrin	77.75	3.09	0.20
Q7SIH1	Alpha-2-macroglobulin	167.58	2.86	0.24
P00735	Prothrombin	70.51	1.96	0.08
P02070	Hemoglobin subunit beta	15.95	1.60	0.05
P01966	Hemoglobin subunit alpha	15.18	1.53	0.12
P19035	Apolipoprotein C-III	10.69	1.38	0.07
AOA140T8C8	Kininogen-1	68.97	1.36	0.39
F1N0I3	Coagulation factor V	239.55	1.29	0.13
A5PJE3	Fibrinogen alpha chain	67.00	1.16	0.02
Q28085	Complement factor H	140.37	0.98	0.06
A6QNZ7	Keratin 10	54.85	0.90	0.05
F1MSZ6	Serpin family C member 1	48.86	0.89	0.08
A5PJT7	ECM1 protein	57.64	0.76	0.05
P81644	Apolipoprotein A-II	11.20	0.61	0.09
Q3SZV7	Hemopexin	52.21	0.59	0.03
Q148H7	(ytokeratin-79	57.72	0.58	0.07
E1BJF9	Serum amyloid A protein	19.64	0.55	0.04
F1N3A1	Thrombospondin-1	129.39	0.53	0.08
E1B726	Plasminogen	91.24	0.47	0.01
Q2KJF1	Alpha-1B-glycoprotein	53.55	0.45	0.07
P12763	Alpha-2-HS-glycoprotein	38.42	0.38	0.05
E1BIK4	C-X-C motif chemokine	12.60	0.38	0.28

CAL-AMS-6ST ₃₀				
Accession Number	Entry name	Mass	%RPA	SD
P02769	Serum albumin	69.32	22.34	1.23
P15497	Apolipoprotein A-I	30.28	15.33	0.57
Q2UVX4	Complement C3	187.25	8.95	0.49
Q7SIH1	Alpha-2-macroglobulin	167.57	8.05	0.33
F1MMD7	Inter-alpha-trypsin inhibitor H4	101.53	3.46	0.01
Q3SZV7	Hemopexin	52.21	3.43	0.25
G5E604	Ig-like domain-containing protein	11.06	3.11	0.15
Q28085	Complement factor H	140.37	2.74	0.05
F1N3Q7	Apolipoprotein A-IV	42.99	2.72	0.47
AOA140T881	Apolipoprotein E	36.04	2.49	0.23
F1MLW7	Ig-like domain-containing protein	24.40	1.78	0.13
F1N1I6	Gelsolin	85.69	1.62	0.15
P06868	Plasminogen	91.22	1.45	0.03
Q29443	Transferrin	75.83	1.38	0.03
Q8SPP7	Peptidoglycan recognition protein 1	21.06	1.36	0.05

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Q2KIT0	Protein HP-20 homolog	20.65	1.12	0.35
P00735	Prothrombin	70.51	1.11	0.06
F1N3A1	Thrombospondin-1	129.39	1.10	0.04
F1MSZ6	Antithrombin-III	52.44	0.94	0.09
Q2KIS7	Tetranectin	22.14	0.86	0.12
A5PJE3	Fibrinogen alpha chain	67.00	0.81	0.05
P12763	Alpha-2-HS-glycoprotein	38.42	0.79	0.16
P81187	Complement factor B	85.41	0.67	0.07
AOA140T843	Beta-2-glycoprotein 1	38.25	0.61	0.16
Q2KJF1	Alpha-1B-glycoprotein	53.55	0.60	0.05
Q3MHN2	Complement component C9	62.00	0.60	0.04
G3MYU2	Keratin 77	66.02	0.59	0.06
E1BJF9	Serum amyloid A protein	14.60	0.56	0.05
P02070	Hemoglobin subunit beta	15.95	0.50	0.02
P19035	Apolipoprotein C-III	10.69	0.48	0.05

CAL-AMS-6ST ₆₀				
Accession Number	Entry name	Mass	%RPA	SD
P02769	Serum albumin	69.32	22.55	0.95
P15497	Apolipoprotein A-I	30.28	15.61	0.79
Q2UVX4	Complement C3	187.25	7.86	0.74
Q7SIH1	Alpha-2-macroglobulin	167.57	7.67	0.29
F1N3Q7	Apolipoprotein A-IV	42.99	4.22	0.28
G5E604	Ig-like domain-containing protein	11.06	3.59	0.35
Q28085	Complement factor H (H factor 1)	140.37	3.37	0.28
Q3SZV7	Hemopexin	52.21	3.09	0.17
F1MMD7	Inter-alpha-trypsin inhibitor H4	101.53	2.92	0.41
F1N1I6	Gelsolin	85.69	2.44	0.18
F1N3A1	Thrombospondin-1	129.39	1.87	0.09
Q8SPP7	Peptidoglycan recognition protein 1	21.06	1.71	0.14
AOA140T881	Apolipoprotein E	36.04	1.71	0.26
Q2KIS7	Tetranectin	22.14	1.52	0.08
P06868	Plasminogen	91.22	1.26	0.06
P00735	Prothrombin	70.51	1.13	0.01
Q2KIT0	Protein HP-20 homolog	20.65	1.03	0.30
F1MSZ6	Antithrombin-III	52.44	0.91	0.05
Q3ZBS7	Vitronectin	53.58	0.88	0.27
AOA140T843	Beta-2-glycoprotein 1	38.25	0.85	0.29
Q29443	Transferrin	75.83	0.85	0.10
E1BJF9	Serum amyloid A protein	14.60	0.81	0.03
F1MLW7	Embryo-specific fibronectin 1 transcript	24.40	0.79	0.06
B8Y9S9	Fibrinogen alpha chain	262.42	0.72	0.04
A5PJE3	Complement factor B	67.00	0.69	0.04

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P81187	Alpha-1B-glycoprotein	85.41	0.69	0.08
Q2KJF1	Ig-like domain-containing protein	53.55	0.61	0.06
G5E5V1	Alpha-2-HS-glycoprotein	14.48	0.47	0.07
P12763	Ceruloplasmin	38.42	0.46	0.04
F1N076	Keratin 77	123.81	0.43	0.02

CAL-AMS-6ST ₁₂₀				
Accession Number	Entry name	Mass	%RPA	SD
P15497	Apolipoprotein A-I	30.28	19.94	0.86
P02769	Serum albumin	69.32	19.33	0.84
Q2UVX4	Complement C3	187.25	8.98	0.07
Q7SIH1	Alpha-2-macroglobulin	167.57	7.17	0.38
F1MMD7	Inter-alpha-trypsin inhibitor heavy chain H4	101.53	4.14	0.56
Q3SZV7	Hemopexin	52.21	3.43	0.09
F1N3Q7	Apolipoprotein A-IV	42.99	2.91	0.22
Q28085	Complement factor H	140.37	2.89	0.01
G5E604	Ig-like domain-containing protein	11.06	2.56	0.03
AOA140T881	Apolipoprotein E	36.04	1.94	0.02
F1N1I6	Gelsolin	85.69	1.79	0.10
F1N3A1	Thrombospondin-1	129.39	1.54	0.15
Q2KIT0	Protein HP-20 homolog	20.65	1.53	0.15
F1MLW7	Antithrombin-III	24.40	1.42	0.07
F1MSZ6	Transferrin	52.44	1.11	0.08
Q29443	Plasminogen	75.83	1.08	0.06
P06868	Prothrombin	91.22	1.06	0.01
P00735	Tetranectin	70.51	1.05	0.04
E1BH06	Peptidoglycan recognition protein 1	192.76	0.86	0.05
Q8SPP7	Alpha-2-HS-glycoprotein	21.06	0.81	0.02
P12763	Fibrinogen alpha chain	38.42	0.81	0.07
A5PJE3	Serum amyloid A protein	67.00	0.79	0.05
E1BJF9	Complement factor B	14.60	0.75	0.01
P81187	Beta-2-glycoprotein 1	85.41	0.70	0.02
AOA140T843	Keratin 77	38.25	0.65	0.25
G3MYU2	Alpha-1B-glycoprotein	66.02	0.61	0.03
Q2KJF1	Vitronectin	53.55	0.54	0.01
Q3ZBS7	Hemoglobin subunit beta	53.58	0.52	0.11
P02070	Complement component C9	15.95	0.51	0.02

NH ₂ -AMS-6S T ₃₀				
Accession Number	Entry name	Mass	%RPA	SD
P02769	Serum albumin	69.32	25.68	0.83
P00735	Prothrombin	70.51	12.77	0.55

Q7SIH1	Alpha-2-macroglobulin	167.58	10.95	0.86
A0A140T881	Apolipoprotein E	36.04	9.83	0.23
Q2UVX4	Complement C3	187.25	6.05	0.41
F1N3Q7	Apolipoprotein A-IV	42.99	5.59	0.29
F1MMD7	Inter-alpha-trypsin inhibitor heavy chain H4	101.53	2.35	0.24
F1MSZ6	Antithrombin-III	52.44	2.14	0.05
Q3ZBS7	Vitronectin	53.58	2.12	0.55
G3X6K8	Haptoglobin	44.87	2.06	0.09
F1MMK9	Protein AMBP	39.29	1.88	0.38
P15497	Apolipoprotein A-I	30.28	1.88	0.09
F1MNV4	Inter-alpha-trypsin inhibitor heavy chain H2	106.16	1.62	0.06
Q29443	Transferrin	77.75	1.60	0.05
F1MMP5	Inter-alpha-trypsin inhibitor heavy chain H1	101.24	1.49	0.10
F1MKS5	Histidine-rich glycoprotein	60.74	1.20	0.02
Q2KJF1	Alpha-1B-glycoprotein	53.55	0.99	0.05
Q3SYR8	Immunoglobulin J chain	17.86	0.97	0.09
A0A140T8C8	Kininogen-1	68.97	0.91	0.03
Q28085	Complement factor H	140.37	0.83	0.02
Q3SZV7	Hemopexin	52.21	0.71	0.08
Q3MHN2	Complement component C9	62.00	0.42	0.05
P81947	Tubulin alpha-1B chain	50.15	0.41	0.01
F1N6W9	Collagen type XVIII alpha 1 chain	153.88	0.41	0.04
F1N076	Ceruloplasmin	123.81	0.35	0.03
P00745	Vitamin K-dependent protein C	51.41	0.35	0.03
G5E5K5	Serglycin	16.49	0.34	0.11
F1MD73	Uncharacterized protein	190.10	0.33	0.00
P80012	von Willebrand factor (vWF) (Fragment)	102.60	0.28	0.01
F1MYN5	Fibulin-1	77.49	0.27	0.02

NH₂-AMS-6ST₆₀				
Accession Number	Entry name	Mass	%RPA	SD
P02769	Serum albumin	69.32	31.77	0.45
P00735	Prothrombin	70.51	26.99	0.38
A0A140T881	Apolipoprotein E	36.04	8.11	0.25
Q7SIH1	Alpha-2-macroglobulin	167.58	4.69	0.50
Q3ZBS7	Vitronectin	53.58	4.15	0.53
Q2UVX4	Complement C3	187.25	3.90	0.26
F1N3Q7	Apolipoprotein A-IV	42.99	3.54	0.17
F1MMK9	Protein AMBP	39.29	2.51	0.26
F1MSZ6	Antithrombin-III	52.44	2.26	0.22
F1MNV4	Inter-alpha-trypsin inhibitor heavy chain H2	106.16	1.90	0.10

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F1MMP5	Inter-alpha-trypsin inhibitor heavy chain H1	101.24	1.37	0.07
Q29443	Transferrin	77.75	1.34	0.05
Q2KJF1	Alpha-1B-glycoprotein	53.55	1.11	0.18
P15497	Apolipoprotein A-I	30.28	1.10	0.06
F1MMD7	Inter-alpha-trypsin inhibitor heavy chain H4	101.53	0.99	0.10
Q3SZV7	Hemopexin	52.21	0.63	0.46
P00741	Coagulation factor IX	52.05	0.62	0.05
P81947	Tubulin alpha-1B chain	50.15	0.41	0.05
P00744	Vitamin K-dependent protein Z	43.11	0.41	0.09
Q3SYW7	SPARC like 1	74.93	0.29	0.01
F1N3A1	Thrombospondin-1	129.39	0.27	0.38
F1N6W9	Collagen type XVIII alpha 1 chain	153.88	0.21	0.09
P00745	Vitamin K-dependent protein C	51.41	0.18	0.26
P81948	Tubulin alpha-4A chain	49.92	0.18	0.13
F1MKS5	Histidine-rich glycoprotein	60.74	0.16	0.18
A6QPP2	SERPIND1 protein	55.21	0.16	0.11
G5E513	Uncharacterized protein	49.97	0.11	0.08
P80012	von Willebrand factor	102.60	0.10	0.10
E1BNI8	5'-nucleotidase domain containing 2	64.32	0.09	0.13
A5PJ69	SERPINA10 protein	51.99	0.09	0.13

NH₂-AMS-6ST₁₂₀				
Accession Number	Entry name	Mass	%RPA	SD
P02769	Serum albumin	69.32	45.22	1.36
P00735	Prothrombin	70.51	24.54	1.92
A0A140T881	Apolipoprotein E	36.04	6.84	0.90
Q3ZBS7	Vitronectin	53.58	4.11	0.29
Q7SIH1	Alpha-2-macroglobulin	167.58	2.56	1.95
F1N3Q7	Apolipoprotein A-IV	42.99	2.23	0.09
F1MNMW4	Inter-alpha-trypsin inhibitor heavy chain H2	106.16	1.68	0.17
Q29443	Transferrin	77.75	1.64	0.18
F1MMP5	Inter-alpha-trypsin inhibitor heavy chain H1	101.24	1.58	0.11
F1MMD7	Inter-alpha-trypsin inhibitor heavy chain H4	101.53	1.47	0.53
P15497	Apolipoprotein A-I	30.28	1.45	0.18
Q2UVX4	Complement C3	187.25	1.25	0.16
F1N3A1	Thrombospondin-1	129.39	0.91	1.29
F1MMK9	Protein AMBP	39.29	0.91	1.29
G3NOV0	Uncharacterized protein	35.95	0.81	0.32
Q3SYW7	SPARC like 1	74.93	0.55	0.03
F1MSZ6	Antithrombin-III	52.44	0.43	0.60
G5E5T5	Uncharacterized protein	42.47	0.34	0.24
P81947	Tubulin alpha-1B chain	50.15	0.25	0.18
F1N6W9	Collagen type XVIII alpha 1 chain	153.88	0.24	0.07

F1MD73	Uncharacterized protein	190.10	0.22	0.17
E1BH06	Uncharacterized protein	192.77	0.15	0.21
Q3SZV7	Hemopexin	52.21	0.14	0.20
P80012	von Willebrand factor	102.60	0.14	0.10
Q5KR47-2	Tropomyosin alpha-3 chain	32.82	0.09	0.13
G5E513	Uncharacterized protein	49.97	0.09	0.06
Q2KJF1	Alpha-1B-glycoprotein (Alpha-1-B glycoprotein)	53.55	0.08	0.12
A0A140T8C8	Kininogen-1	68.97	0.06	0.08

AS-AMS-6FT₁₀				
Accession Number	Entry name	Mass	%RPA	SD
P15497	Apolipoprotein A-I	30.28	61.43	4.11
A0A140T897	Serum albumin	69.32	10.79	0.26
Q2UVX4	Complement C3	187.25	5.08	0.06
P00735	Prothrombin	70.51	3.59	0.66
F1N3Q7	Apolipoprotein A4	52.29	2.60	0.21
Q7SIH1	Alpha-2-macroglobulin (Alpha-2-M)	167.58	2.51	0.31
P35541	Serum amyloid A protein (SAA)	12.15	2.04	0.18
Q29443	Serotransferrin (Transferrin)	77.75	1.53	0.06
A6QNZ7	Keratin 10	54.85	1.47	0.08
A0A140T881	Apolipoprotein E	37.42	1.35	0.22
F1MMD7	Inter-alpha-trypsin inhibitor heavy chain H4	101.51	1.24	0.35
Q3ZBS7	Vitronectin	35.95	0.94	0.09
F1MSZ6	Serpin family C member 1	48.86	0.83	0.10
P19035	Apolipoprotein C-III	26.66	0.57	0.06
Q148H7	Keratin	57.72	0.56	0.03
G8JKW7	Serpin A3-7	46.58	0.53	0.10
P01966	Hemoglobin subunit alpha	15.18	0.41	0.07
P02070	Hemoglobin subunit beta	192.80	0.29	0.09
F1N514	CD5L protein	50.21	0.27	0.03
Q2KJF1	Alpha-1B-glycoprotein	53.55	0.25	0.03
P00741	Coagulation factor IX	14.64	0.21	0.01
P81644	Apolipoprotein A-II	11.20	0.21	0.04
G3X6K8	Haptoglobin	41.98	0.20	0.05
Q5E9B1	L-lactate dehydrogenase B chain	14.38	0.17	0.02
E1BIK4	C-X-C motif chemokine	21.49	0.12	0.17
Q5GN72	Alpha-1-acid glycoprotein	23.16	0.12	0.02
Q3SZV7	Hemopexin	52.21	0.09	0.12
A5PJE3	Fibrinogen alpha chain	67.00	0.08	0.06
F1MRD0	Actin	41.85	0.06	0.04
P28800	Alpha-2-antiplasmin	54.71	0.05	0.07

CAL-AMS-6FT ₁₀				
Accession Number	Entry name	Mass	%RPA	SD
P15497	Apolipoprotein A-I	30.28	16.51	0.59
F1MMD7	Inter-alpha-trypsin inhibitor heavy chain H4	101.51	15.58	0.37
Q2UVX4	Complement C3	187.25	12.09	0.74
AOA140T897	Serum albumin	69.32	11.29	0.76
F1N116	Gelsolin	92.08	8.32	0.51
Q7SIH1	Alpha-2-macroglobulin	167.58	3.93	0.16
F1N3Q7	Apolipoprotein A4	52.29	3.89	0.27
AOA140T881	Apolipoprotein E	37.42	2.18	0.04
A6QNZ7	Keratin 10	54.85	1.92	0.07
P35541	Serum amyloid A protein	14.52	1.92	0.27
P81644	Apolipoprotein A-II	11.20	1.77	0.59
Q29443	Transferrin	77.75	1.41	0.10
A5PJE3	Fibrinogen alpha chain	67.00	1.20	0.18
P12763	Alpha-2-HS-glycoprotein	38.42	1.17	0.10
F1N3A1	Thrombospondin-1	129.39	1.10	0.07
F1MSZ6	Serpin family C member 1	48.86	1.06	0.06
P00735	Prothrombin	70.51	1.06	0.04
F1N0I3	Coagulation factor V	239.55	1.00	0.22
Q148H7	Cytokeratin-79	57.72	0.90	0.01
AOA140T8C8	Kininogen-1	68.97	0.89	0.21
Q8SPP7	Peptidoglycan recognition protein 1	21.06	0.79	0.23
P19035	Apolipoprotein C-III	10.69	0.73	0.09
Q3SZV7	Hemopexin	52.21	0.71	0.04
E1BIK4	C-X-C motif chemokine	12.60	0.68	0.09
Q2KIS7	Tetranectin	22.14	0.62	0.01
Q2KIU3	Protein HP-25 homolog 2	22.91	0.53	0.08
P02070	Hemoglobin subunit beta	15.95	0.50	0.03
A5PJT7	ECM1 protein	57.64	0.43	0.32
Q28085	Complement factor H	140.37	0.36	0.04
P19660	Cathelicidin-2	20.03	0.35	0.03

CAL-AMS-6FT ₃₀				
Accession Number	Entry name	Mass	%RPA	SD
P02769	ALBU_BOVIN	69.32	11.29	3.18
Q7SIH1	Alpha-2-macroglobulin	167.57	10.01	1.73
P15497	Apolipoprotein A-I	30.28	8.78	0.85
Q2UVX4	Complement factor H	187.25	8.53	0.90
F1N116	Gelsolin	85.69	7.32	0.62
F1MMD7	Inter-alpha-trypsin inhibitor heavy chain H4	101.53	6.97	1.03
Q28085	Complement factor H	140.37	4.59	0.35
G3MYU2	Keratin 77	66.02	3.61	0.56

F1N3A1	Thrombospondin-1	129.39	3.23	0.34
AOA140T881	Apolipoprotein E	36.04	3.10	0.59
G5E604	Ig-like domain-containing protein	11.06	2.78	0.83
F1N3Q7	Apolipoprotein A-IV	42.99	2.35	0.62
F1MSZ6	Antithrombin-III	52.44	1.38	0.39
A6QNZ7	Keratin 10	59.51	1.33	0.31
P00735	Prothrombin	70.51	1.28	0.36
Q8SPP7	Peptidoglycan recognition protein 1	21.06	1.25	0.17
Q3SZV7	Hemopexin	52.21	1.09	0.06
B8Y9S9	Embryo-specific fibronectin 1 transcript variant	262.42	1.05	0.33
A5PJT7	ECM1 protein	57.64	1.03	0.05
F1MLW7	Tetranectin	24.40	1.02	0.10
Q2KIS7	L-lactate dehydrogenase B chain	22.14	0.93	0.06
Q5E9B1	Fibrinogen alpha chain	36.72	0.84	0.02
A5PJE3	Vitronectin	67.00	0.83	0.03
Q3ZBS7	MYO1B protein	53.58	0.72	0.09
A6QLD6	IF rod domain-containing protein	131.83	0.71	0.53
E1B991	Immunoglobulin J chain	65.87	0.68	0.15
Q3SYR8	Plasminogen	17.86	0.67	0.01
F1MW79	Keratin 18	30.88	0.58	0.06
F6S1Q0	Serum amyloid A protein	47.96	0.54	0.39
E1BJF9	Ig-like domain-containing protein	14.60	0.54	0.17

CAL-AMS-6FT₆₀				
Accession Number	Entry name	Mass	%RPA	SD
P02769	Serum albumin	69.32	13.02	1.07
Q7SIH1	Alpha-2-macroglobulin	167.57	10.11	1.57
F1MMD7	Inter-alpha-trypsin inhibitor heavy chain H4	101.53	8.18	3.77
Q2UVX4	Complement C3	187.25	7.90	1.52
F1N1I6	Gelsolin	85.69	7.05	1.67
P15497	Apolipoprotein A-I	30.28	5.93	0.62
G3MYU2	Keratin 77	66.02	5.05	2.04
Q28085	Complement factor H (H factor 1)	140.37	4.38	1.38
F1N3Q7	Apolipoprotein A-IV	42.99	2.77	0.38
AOA140T881	Apolipoprotein E	36.04	2.58	0.56
G5E604	Ig-like domain-containing protein	11.06	2.57	0.51
A6QNZ7	Keratin 10	59.51	1.80	0.71
Q3SZV7	Hemopexin	52.21	1.75	0.14
F1MSZ6	Antithrombin-III	52.44	1.64	0.51
Q5E9B1	L-lactate dehydrogenase B chain	36.72	1.49	0.42
F1N3A1	Thrombospondin-1	129.39	1.48	0.39
A5PJE3	Fibrinogen alpha chain	67.00	1.06	0.18
Q8SPP7	Peptidoglycan recognition protein 1	21.06	1.06	0.58

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A5PJT7	ECM1 protein	57.64	1.03	0.10
P00735	Prothrombin	70.51	1.01	0.50
P06868	Plasminogen	91.22	0.93	0.03
E1B991	IF rod domain-containing protein	65.87	0.89	0.41
Q2KJF1	Alpha-1B-glycoprotein	53.55	0.73	0.15
Q29443	Stransferrin	75.83	0.70	0.26
Q3ZBS7	Vitronectin	53.58	0.62	0.26
Q3SYR8	Immunoglobulin J chain	17.86	0.61	0.08
Q2KIT0	Protein HP-20 homolog	20.65	0.60	0.10
B8Y9S9	Embryo-specific fibronectin 1 transcript variant	262.42	0.59	0.15
E1BJF9	Serum amyloid A protein	14.60	0.58	0.11
F6S1Q0	Keratin 18	47.96	0.56	0.65

CAL-AMS-6FT₁₂₀				
Accession Number	Entry name	Mass	%RPA	SD
P02769	Serum albumin	69.32	11.38	0.73
Q7SIH1	Alpha-2-macroglobulin	167.57	10.83	3.56
P15497	Apolipoprotein A-I	30.28	6.60	0.26
F1N1I6	Gelsolin	85.69	5.48	0.41
Q2UVX4	Complement C3	187.25	5.43	0.43
G5E604	Ig-like domain-containing protein	11.06	4.94	0.29
A0A140T881	Apolipoprotein E	36.04	4.89	0.64
Q28085	Complement factor H (H factor 1)	140.37	4.68	0.30
F1N3Q7	Apolipoprotein A-IV	42.99	4.44	0.60
F1MMD7	Inter-alpha-trypsin inhibitor heavy chain H4	101.53	2.87	1.76
F1MSZ6	Antithrombin-III	52.44	1.80	0.46
A5PJE3	Fibrinogen alpha chain	67.00	1.74	0.06
Q3SZV7	Hemopexin	52.21	1.67	0.07
F1MLW7	L-lactate dehydrogenase B chain	24.40	1.58	0.09
Q5E9B1	Embryo-specific fibronectin 1 transcript variant	36.72	1.51	0.04
B8Y9S9	Peptidoglycan recognition protein 1	262.42	1.34	0.22
Q8SPP7	Keratin 10	21.06	1.20	0.05
A6QNZ7	Vitronectin	59.51	1.12	0.17
E1BJF9	Serum amyloid A protein	14.60	1.09	0.08
A5PJT7	ECM1 protein	57.64	1.05	0.37
P06868	Plasminogen	91.22	0.92	0.01
P13384	Insulin-like growth factor-binding protein 2	34.02	0.91	0.04
F1N3A1	Thrombospondin-1	129.39	0.88	0.09
P00735	Prothrombin	70.51	0.86	0.08
Q3SYR8	Immunoglobulin J chain	17.86	0.78	0.01
E1B991	IF rod domain-containing protein	65.87	0.70	0.16
Q2KIT0	Protein HP-20 homolog	20.65	0.62	0.07

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F1N076	Ceruloplasmin	123.81	0.60	0.06
Q2KIS7	Tetranectin	22.14	0.59	0.06
F1MCF8	Ig-like domain-containing protein	24.54	0.55	0.06

NH₂-AMS-6FT₃₀				
Accession Number	Entry name	Mass	%RPA	SD
P00735	Prothrombin	70.51	19.12	1.87
A0A140T897	Serum albumin	69.32	13.30	0.29
Q7SIH1	Alpha-2-macroglobulin	167.58	10.77	0.29
Q2UVX4	Complement C3	187.25	9.05	0.31
F1MMP5	Inter-alpha-trypsin inhibitor heavy chain H1	101.24	6.70	0.23
F1MNV4	Inter-alpha-trypsin inhibitor heavy chain H2	106.16	6.32	0.14
P15497	Apolipoprotein A-I	30.28	3.74	0.26
F1MMK9	Protein AMBP	39.29	3.62	0.14
A0A140T881	Apolipoprotein E	36.04	3.33	0.08
Q3ZBS7	Vitronectin	53.58	2.26	0.07
Q3Y5Z3	Adiponectin	26.13	2.08	0.02
F1N3Q7	Apolipoprotein A-IV	42.99	1.92	0.05
E1BMJ0	Serpin family G member 1	51.71	1.63	0.07
F1MSZ6	Antithrombin-III	52.44	1.56	0.05
G3X6K8	Haptoglobin	44.87	0.98	0.04
F1MMD7	Inter-alpha-trypsin inhibitor heavy chain H4	101.53	0.98	0.08
Q29443	Transferrin	77.75	0.68	0.03
Q5GN72	Alpha-1-acid glycoprotein	23.16	0.63	0.01
F1N076	Ceruloplasmin	123.81	0.63	0.02
A0A140T8C8	Kininogen-1	68.97	0.61	0.04
B8Y9S9	Fibronectin	262.43	0.55	0.01
Q28107	Coagulation factor V	248.98	0.54	0.04
P81187	Complement factor B	85.37	0.48	0.10
A6QPP2	SERPIND1 protein	55.21	0.45	0.07
Q2KJF1	Alpha-1B-glycoprotein	53.55	0.43	0.04
G5E5K5	Serglycin	16.49	0.38	0.04
F1N3A1	Thrombospondin-1	129.39	0.37	0.03
G3N0V2	Keratin 1	63.15	0.35	0.01
P56652	Inter-alpha-trypsin inhibitor heavy chain H3	99.55	0.33	0.01
F1MNN7	Lipopolysaccharide-binding protein	53.70	0.31	0.03

NH₂-AMS-6FT₆₀				
Accession Number	Entry name	Mass	%RPA	SD
P00735	Prothrombin	70.51	22.57	0.48
A0A140T897	Serum albumin	69.32	17.03	0.20
Q7SIH1	Alpha-2-macroglobulin	167.58	9.08	0.31

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P15497	Apolipoprotein A-I	30.28	6.41	0.89
F1MMP5	Inter-alpha-trypsin inhibitor heavy chain H1	101.24	6.31	0.39
Q2UVX4	Complement C3	187.25	5.68	0.09
F1MNV4	Inter-alpha-trypsin inhibitor heavy chain H2	106.16	5.41	0.42
F1MMK9	Protein AMBP	39.29	4.05	0.12
A0A140T881	Apolipoprotein E	36.04	2.87	0.03
F1N3Q7	Apolipoprotein A-IV	42.99	2.18	0.10
Q3ZBS7	Vitronectin	53.58	1.54	0.08
F1MMD7	Inter-alpha-trypsin inhibitor heavy chain H4	101.53	1.48	0.22
Q3Y5Z3	Adiponectin	26.13	1.39	0.07
F1MSZ6	Antithrombin-III	52.44	1.08	0.03
Q29443	Transferrin	77.75	1.05	0.10
G3X6K8	Haptoglobin	44.87	1.02	0.07
E1BKZ0	Pericentrin	327.24	0.80	1.14
F1N3A1	Thrombospondin-1	129.39	0.65	0.04
Q5GN72	Alpha-1-acid glycoprotein	23.16	0.54	0.04
F1N076	Ceruloplasmin	123.81	0.52	0.02
A0A140T8C8	Kininogen-1	68.97	0.50	0.01
B8Y9S9	Fibronectin	262.43	0.50	0.01
E1BMJ0	Serpin family G member 1	51.71	0.45	0.02
P81187	Complement factor B	85.37	0.41	0.05
P56652	Inter-alpha-inhibitor heavy chain 3	99.55	0.40	0.01
Q2KJF1	Alpha-1B-glycoprotein	53.55	0.38	0.01
Q28107	Coagulation factor V	248.98	0.34	0.04
G3N0V2	Keratin 1	63.15	0.25	0.01
P80012	von Willebrand factor	102.60	0.25	0.02
P07224	Vitamin K-dependent protein S	75.13	0.22	0.02

NH₂-AMS-6FT₁₂₀				
Accession Number	Entry name	Mass	%RPA	SD
P00735	Prothrombin	70.51	17.94	1.13
A0A140T897	Serum albumin	69.32	16.48	0.42
Q7SIH1	Alpha-2-macroglobulin	167.58	12.60	0.64
F1MMP5	Inter-alpha-trypsin inhibitor heavy chain H1	101.24	6.83	0.07
F1MNV4	Inter-alpha-trypsin inhibitor heavy chain H2	106.16	6.14	0.18
Q2UVX4	Complement C3	187.25	5.40	0.18
F1MMK9	Protein AMBP	39.29	4.93	0.25
A0A140T881	Apolipoprotein E	36.04	3.66	0.11
P15497	Apolipoprotein A-I	30.28	3.36	0.20
Q3ZBS7	Vitronectin	53.58	2.61	0.09
Q3Y5Z3	Adiponectin	26.13	2.48	0.28
F1N3Q7	Apolipoprotein A-IV	42.99	1.69	0.08
E1BMJ0	Serpin family G member 1	51.71	1.44	0.03

F1MSZ6	Antithrombin-III	52.44	1.15	0.06
F1MMD7	Inter-alpha-trypsin inhibitor heavy chain H4	101.53	0.97	0.12
Q29443	Transferrin	77.75	0.97	0.04
G3X6K8	Haptoglobin	44.87	0.87	0.04
F1N076	Ceruloplasmin	123.81	0.71	0.03
B8Y9S9	Fibronectin	262.43	0.64	0.05
Q5GN72	Alpha-1-acid glycoprotein	23.16	0.61	0.17
A0A140T8C8	Kininogen-1	68.97	0.54	0.03
P81187	Complement factor B	85.37	0.49	0.07
F1N3A1	Thrombospondin-1	129.39	0.47	0.01
P56652	Inter-alpha-inhibitor heavy chain 3	99.55	0.46	0.01
Q28107	Coagulation factor V	248.98	0.45	0.05
Q2KJF1	Alpha-1B-glycoprotein	53.55	0.42	0.03
Q3SZV7	Hemopexin	52.21	0.32	0.06
A6QPP2	SERPIND1 protein	55.21	0.26	0.02
G3NOV2	Keratin 1	63.15	0.26	0.04
P07224	Vitamin K-dependent protein S	75.13	0.24	0.01

AS-SBA-15T ₁₀				
Accession Number	Entry name	Mass	%RPA	SD
G5E604	Uncharacterized protein	12.94	33.68	10.09
P01045	Kininogen-2	68.71	31.02	5.70
P35541	Serum amyloid A	14.52	15.14	3.10
P15497	Apolipoprotein A-I	30.28	7.75	5.55
P35541	Apolipoprotein C-III	30.28	3.68	1.34
Q3SYR8	Immunoglobulin J chain	17.86	3.25	0.50
Q2UVX4	Complement C3	187.25	2.16	3.05
A0A140T897	Serum albumin	69.32	1.36	1.09
Q7SIH1	Alpha-2-macroglobulin	167.58	0.93	1.32
G5E5T5	Uncharacterized protein	56.04	0.54	0.38
A6QNZ7	Keratin 10	54.85	0.50	0.70

CAL-SBA-15T ₁₀				
Accession Number	Entry name	Mass	%RPA	SD
P15497	Apolipoprotein A-I	30.28	14.59	0.30
G5E604	Ig-like domain-containing protein	12.94	12.53	0.29
A0A140T897	Serum albumin	69.32	9.92	0.08
F1N1I6	Gelsolin	92.08	9.84	0.95
Q2UVX4	Complement C3	187.25	9.43	1.64
P35541	Serum amyloid A	14.52	8.79	0.39
Q7SIH1	Alpha-2-macroglobulin	167.58	4.32	0.34

F1MMD7	Inter-alpha-trypsin inhibitor heavy chain H4	101.51	3.00	0.54
A0A140T881	Apolipoprotein E	37.42	2.95	0.34
A0A140T8C8	Kininogen-1	68.97	2.57	0.22
G3N2D7	Ig-like domain-containing protein	12.15	2.21	0.21
P19035	Apolipoprotein C-III	10.69	2.16	0.18
F1N3A1	Thrombospondin-1	129.39	2.01	0.38
E1BIK4	C-X-C motif chemokine	12.60	1.42	1.07
Q29443	Transferrin	77.75	1.29	0.19
Q8SPP7	Oligosaccharide-binding protein	21.06	1.27	0.43
A5PJE3	Fibrinogen alpha chain	67.00	1.27	0.20
P02070	Hemoglobin subunit beta	15.95	0.92	0.09
F1MSZ6	Antithrombin-III	48.86	0.76	0.57
P81644	Apolipoprotein A-II	11.20	0.64	0.29
P00735	Prothrombin	70.51	0.57	0.40
P19034	Apolipoprotein C-II	11.06	0.51	0.62
P82943	Regakine-1	10.28	0.51	0.03
Q2KJF1	Alpha-1B-glycoprotein	53.55	0.51	0.05
Q3SYR8	Immunoglobulin J chain	17.86	0.50	0.05
F1N0I3	Coagulation factor V	239.55	0.48	0.35
Q2KIS7	Tetranectin	22.14	0.47	0.34
A6QNZ7	Keratin 10	54.85	0.47	0.14
P01035	Cystatin-C	16.27	0.42	0.30
Q5E9F5	Transgelin-2	22.43	0.37	0.13

CAL-SBA-15T ₃₀				
Accession Number	Entry name	Mass	%RPA	SD
F1MMD7	Inter-alpha-trypsin inhibitor heavy chain H4	101.53	16.52	0.51
Q7SIH1	Alpha-2-macroglobulin	167.58	12.33	0.60
F1N1I6	Gelsolin	85.69	10.60	0.73
A0A140T881	Apolipoprotein E	36.04	10.02	0.49
P01030	Complement C4	101.89	7.97	0.84
A0A140T897	Serum albumin	69.32	4.85	0.18
Q28085	Complement factor H	140.37	4.73	0.27
F1MSZ6	Antithrombin-III	52.44	3.63	0.17
F1N3Q7	Apolipoprotein A-IV	42.99	3.34	0.03
Q2UVX4	Complement C3	187.25	2.85	0.15
F1N3A1	Thrombospondin-1	129.39	2.81	0.21
Q8SPP7	Oligosaccharide-binding protein	21.06	2.63	0.13
P15497	Apolipoprotein A-I	30.28	2.15	0.24
A5PJT7	ECM1 protein (Extracellular matrix protein 1)	57.64	1.61	0.17
Q3SZV7	Hemopexin	52.21	1.41	0.05
Q3ZBS7	Vitronectin	53.58	0.93	0.04
F1MKS5	Histidine-rich glycoprotein	60.74	0.68	0.13

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P00735	Prothrombin	70.51	0.64	0.04
P56425	Cathelicidin-7	18.85	0.63	0.02
P13384	Insulin-like growth factor-binding protein 2	34.02	0.56	0.02
F1N6W9	Collagen type XVIII alpha 1 chain	153.88	0.46	0.04
A6QPP2	SERPIND1 protein	55.21	0.45	0.01
Q58DP6	Ribonuclease 4	16.94	0.44	0.14
F1MM32	Sulfhydryl oxidase	63.00	0.43	0.01
Q2KJF1	Alpha-1B-glycoprotein	53.55	0.37	0.02
G3X6K8	Haptoglobin	44.87	0.32	0.04
B8Y9S9	Fibronectin	262.43	0.32	0.01
G3MYM8	Proteoglycan 4	116.92	0.31	0.04
F1MMP5	Inter-alpha-trypsin inhibitor heavy chain H1	101.24	0.27	0.04
F1MLW7	Uncharacterized protein	24.40	0.24	0.02

CAL-SBA-15T ₆₀				
Accession Number	Entry name	Mass	%RPA	SD
A0A140T897	Serum albumin	69.32	17.11	0.25
F1MMD7	Inter-alpha-trypsin inhibitor heavy chain H4	101.53	14.80	0.65
Q7SIH1	Alpha-2-macroglobulin	167.58	12.33	0.20
P01030	Complement C4	101.89	11.09	0.87
F1N1I6	Gelsolin	85.69	7.07	0.55
P15497	Apolipoprotein A-I	30.28	5.16	0.34
Q2UVX4	Complement C3	187.25	3.54	0.12
Q28085	Complement factor H	140.37	3.53	0.22
A0A140T881	Apolipoprotein E	36.04	3.36	0.07
Q2KJF1	Alpha-1B-glycoprotein	53.55	1.58	0.04
F1MSZ6	Antithrombin-III	52.44	1.54	0.11
F1N3A1	Thrombospondin-1	129.39	1.52	0.09
A5PJT7	ECM1 protein	57.64	1.42	0.08
Q3SZV7	Hemopexin	52.21	1.41	0.11
F1N3Q7	Apolipoprotein A-IV	42.99	1.36	0.18
G3X6K8	Haptoglobin	44.87	1.32	0.05
Q8SPP7	Oligosaccharide-binding protein	21.06	1.14	0.27
Q29443	Transferrin	77.75	0.62	0.03
Q3ZBS7	Vitronectin	53.58	0.61	0.10
Q5GN72	Alpha-1-acid glycoprotein	23.16	0.53	0.07
P02070	Hemoglobin subunit beta	15.95	0.45	0.04
Q58DP6	Ribonuclease 4	16.94	0.44	0.08
P00735	Prothrombin	70.51	0.43	0.03
Q3MHN2	Complement component C9	62.00	0.42	0.03
F1MMP5	Inter-alpha-trypsin inhibitor heavy chain H1	101.24	0.36	0.03
P56425	Cathelicidin-7	18.85	0.35	0.03
P81187	Complement factor B	85.37	0.34	0.01

E1B726	Plasminogen	91.24	0.31	0.04
Q2KIT0	Protein HP-20 homolog	20.65	0.30	0.04
A0A140T843	Beta-2-glycoprotein 1	38.25	0.30	0.01

CAL-SBA-15T ₁₂₀				
Accession Number	Entry name	Mass	%RPA	SD
A0A140T897	Serum albumin	69.32	24.15	0.76
F1MMD7	Inter-alpha-trypsin inhibitor heavy chain H4	101.53	16.67	0.63
F1N1I6	Gelsolin	85.69	11.29	0.47
P01030	Complement C4	101.89	10.93	2.26
Q7SIH1	Alpha-2-macroglobulin	167.58	5.13	0.24
Q28085	Complement factor H	140.37	3.90	0.18
Q2UVX4	Complement C3	187.25	3.64	0.19
P15497	Apolipoprotein A-I	30.28	3.25	0.51
A0A140T881	Apolipoprotein E	36.04	2.34	0.37
A5PJT7	ECM1 protein	57.64	1.81	0.05
F1N3A1	Thrombospondin-1	129.39	1.67	0.17
F1N3Q7	Apolipoprotein A-IV	42.99	1.56	0.08
Q3SZV7	Hemopexin	52.21	1.51	0.13
Q8SPP7	Oligosaccharide-binding protein	21.06	1.48	0.19
F1MSZ6	Antithrombin-III	52.44	1.19	0.11
Q3ZBS7	Vitronectin	53.58	0.79	0.00
Q58DP6	Ribonuclease 4	16.94	0.70	0.05
Q2KJF1	Alpha-1B-glycoprotein	53.55	0.68	0.05
Q29443	Transferrin	77.75	0.67	0.12
P56425	Cathelicidin-7	18.85	0.50	0.05
Q3MHN2	Complement component C9	62.00	0.47	0.06
Q3SYR8	Immunoglobulin J chain	17.86	0.34	0.01
G3X6K8	Haptoglobin	44.87	0.33	0.01
F1MMK9	Protein AMBP	39.29	0.28	0.03
A0A140T843	Beta-2-glycoprotein 1	38.25	0.25	0.03
F1MMP5	Inter-alpha-trypsin inhibitor heavy chain H1	101.24	0.24	0.01
P81187	Complement factor B	85.37	0.24	0.01
A6QPP2	SERPIND1 protein	55.21	0.24	0.02
G8JKW7	Uncharacterized protein	46.34	0.21	0.02
P13384	Insulin-like growth factor-binding protein 2	34.02	0.21	0.07

NH ₂ -SBA-15T ₃₀				
Accession Number	Entry name	Mass	%RPA	SD
A0A140T897	Serum albumin	69.32	26.62	0.44
F1N1I6	Gelsolin	85.69	11.49	0.82
Q7SIH1	Alpha-2-macroglobulin	167.58	9.56	1.95

P01030	Complement C4	101.89	5.76	0.21
F1MKS5	Histidine-rich glycoprotein	60.74	5.74	0.22
P15497	Apolipoprotein A-I	30.28	4.61	0.15
A0A140T881	Apolipoprotein E	36.04	3.74	0.13
F1MMD7	Inter-alpha-trypsin inhibitor heavy chain H4	101.53	3.72	0.19
Q8SPP7	Oligosaccharide-binding protein	21.06	3.60	0.05
F1N3Q7	Apolipoprotein A-IV	42.99	2.93	0.15
Q28085	Complement factor H	140.37	2.86	0.14
Q2UVX4	Complement C3	187.25	2.22	0.20
Q29443	Transferrin	77.75	1.65	0.04
F1N3A1	Thrombospondin-1	129.39	1.31	0.05
A5PJT7	ECM1 protein	57.64	1.25	0.03
P81187	Complement factor B	85.37	1.20	0.15
P13384	Insulin-like growth factor-binding protein 2	34.02	0.95	0.02
Q3SZV7	Hemopexin	52.21	0.78	0.02
F1MM32	Sulfhydryl oxidase	63.00	0.71	0.04
P56425	Cathelicidin-7	18.85	0.64	0.01
Q58DP6	Ribonuclease 4	16.94	0.56	0.06
F1MD76	Folliculin interacting protein 2	111.33	0.50	0.41
P23805	Conglutinin	38.00	0.46	0.03
E1BNR0	Apolipoprotein B	515.76	0.46	0.03
E1B726	Plasminogen	91.24	0.41	0.05
F1MUT4	Coagulation factor XI	69.89	0.39	0.01
Q3MHN2	Complement component C9	62.00	0.34	0.13
G5E5V1	Uncharacterized protein	14.48	0.33	0.24
Q3ZBS7	Vitronectin	53.58	0.31	0.02
F1MSZ6	Antithrombin-III	52.44	0.30	0.01

NH ₂ -SBA-15T ₆₀				
Accession Number	Entry name	Mass	%RPA	SD
Q7SIH1	Alpha-2-macroglobulin	167.58	15.82	1.29
A0A140T881	Apolipoprotein E	36.04	9.99	0.57
A0A140T897	Serum albumin	69.32	9.67	0.41
F1N1I6	Gelsolin	85.69	7.34	0.88
P01030	Complement C4	101.89	7.01	0.62
P15497	Apolipoprotein A-I	30.28	6.62	0.65
F1MKS5	Histidine-rich glycoprotein	60.74	4.53	0.08
Q8SPP7	Oligosaccharide-binding protein	21.06	4.49	0.33
Q2UVX4	Complement C3	187.25	3.74	0.50
F1N3Q7	Apolipoprotein A-IV	42.99	3.16	0.16
F1MMD7	Inter-alpha-trypsin inhibitor heavy chain H4	101.53	3.03	0.54
Q28085	Complement factor H	140.37	2.20	0.04

F1N3A1	Thrombospondin-1	129.39	1.72	0.07
Q2KJF1	Alpha-1B-glycoprotein	53.55	1.21	0.04
F1MSZ6	Antithrombin-III	52.44	1.05	0.04
Q58DP6	Ribonuclease 4	16.94	0.93	0.05
P13384	Insulin-like growth factor-binding protein 2	34.02	0.92	0.02
A5PJT7	ECM1 protein	57.64	0.87	0.04
P56425	Cathelicidin-7	18.85	0.84	0.07
F1MMP5	Inter-alpha-trypsin inhibitor heavy chain H1	101.24	0.81	0.00
Q3SZV7	Hemopexin	52.21	0.79	0.02
G3X6K8	Haptoglobin	44.87	0.71	0.03
Q3ZBS7	Vitronectin	53.575	0.695795	0.035756
F1MM32	Sulfhydryl oxidase	62.998	0.594126	0.044537
P00735	Prothrombin	70.506	0.500731	0.008457
Q29437	Serum amine oxidase	84.757	0.470461	0.048305
Q29443	Transferrin	77.753	0.451378	0.016845
E1B726	Plasminogen	91.243	0.448954	0.050071
F1MW79	Uncharacterized protein	30.881	0.447608	0.347964
P02070	Hemoglobin subunit beta	15.954	0.44516	0.027268

NH₂-SBA-15T₁₂₀				
Accession Number	Entry name	Mass	%RPA	SD
A0A140T897	Serum albumin	69.32	20.33	0.54
Q7SIH1	Alpha-2-macroglobulin	167.58	11.74	1.09
F1N1I6	Gelsolin	85.69	8.62	0.70
F1MMD7	Inter-alpha-trypsin inhibitor heavy chain H4	101.53	7.63	0.03
A0A140T881	Apolipoprotein E	36.04	7.34	0.30
P01030	Complement C4	101.89	7.16	0.65
P15497	Apolipoprotein A-I	30.28	5.32	0.30
F1N3A1	Thrombospondin-1	129.39	3.05	0.02
Q28085	Complement factor H	140.37	2.95	0.13
Q2UVX4	Complement C3	187.25	2.42	0.03
Q8SPP7	Oligosaccharide-binding protein	21.06	2.32	0.15
F1MSZ6	Antithrombin-III	52.44	2.12	0.08
F1N3Q7	Apolipoprotein A-IV	42.99	1.91	0.06
F1MKS5	Histidine-rich glycoprotein	60.74	1.88	0.05
P13384	Insulin-like growth factor-binding protein 2	34.02	1.50	0.09
A5PJT7	ECM1 protein	57.64	1.36	0.06
Q29443	Transferrin	77.75	0.80	0.03
Q3SZV7	Hemopexin	52.21	0.72	0.06
E1BKZ0	Pericentrin	327.24	0.71	1.00
Q3ZBS7	Vitronectin	53.58	0.60	0.02
G3X6K8	Haptoglobin	44.87	0.56	0.06
Q58DP6	Ribonuclease 4	16.94	0.54	0.02

P56425	Cathelicidin-7	18.85	0.53	0.03
F1MM32	Sulfhydryl oxidase	63.00	0.40	0.01
P00735	Prothrombin	70.51	0.39	0.01
E1B726	Plasminogen	91.24	0.37	0.01
B8Y9S9	Fibronectin	262.43	0.35	0.02
F1MMK9	Protein AMBP	39.29	0.33	0.01
Q2KJF1	Alpha-1B-glycoprotein	53.55	0.28	0.02
G3MYM8	Proteoglycan 4	116.92	0.25	0.00

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