

Supplemental Table 1. All 601 Measured Human Colostral Whey Proteins from Women with and without Gestational Diabetes Mellitus

Accession is the Uniprot database identifier (<http://www.uniprot.org/>). Molecular weight, MW, in kilodaltons, kDa. Normalized total spectra values are reported as the mean \pm standard deviation of normalized total spectra. Rankings are based on the absolute values of the orthogonal signal corrected partial least squares discriminant analysis model loadings on the latent variable 1.

				Normalized Total Spectra		Total Spectra		% Sequence Coverage		Number of Unique Peptides		
Protein	Accession	MW	non-GDM	GDM	Median	Range	Median	Range	Median	Range	Rank	
1	14-3-3 protein beta/alpha	P31946	28 kDa	3.22 ± 1.7	1.24 ± 1.3	3	(0, 9)	7	(0, 25)	0	(0, 3)	
2	14-3-3 protein epsilon	P62258	29 kDa	0.843 ± 0.98	0.795 ± 1.3	1	(0, 5)	4	(0, 17)	0	(0, 3)	
3	14-3-3 protein gamma	P61981	28 kDa	0.245 ± 0.85	0 ± 0	2	(0, 5)	4	(0, 23)	0	(0, 2)	
4	14-3-3 protein sigma	P31947	28 kDa	0.599 ± 0.92	0.726 ± 1.5	2	(0, 6)	5	(0, 17)	0	(0, 2)	
5	14-3-3 protein theta	P27348	28 kDa	0.593 ± 1.5	0 ± 0	2	(0, 7)	7	(0, 25)	0	(0, 2)	
6	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase eta-1	Q4KWH8	189 kDa	0.481 ± 0.66	1.18 ± 0.91	0	(0, 3)	0	(0, 1)	0	(0, 2)	
7	40S ribosomal protein S12	P25398	15 kDa	0.248 ± 0.33	0 ± 0	0	(0, 3)	0	(0, 14)	0	(0, 2)	
8	40S ribosomal protein S28	P62857	8 kDa	0.511 ± 0.42	0.2 ± 0.49	0	(0, 2)	0	(0, 30)	0	(0, 2)	
9	45 kDa calcium-binding protein	Q9BRK5	42 kDa	10.3 ± 4.7	5.17 ± 5.7	7	(0, 20)	18	(0, 42)	5	(0, 11)	
10	60S acidic ribosomal protein P2	P05387	12 kDa	0.41 ± 0.57	0.104 ± 0.25	0	(0, 2)	0	(0, 39)	0	(0, 2)	
11	78 kDa glucose-regulated protein	P11021	72 kDa	3.24 ± 1.8	1.38 ± 2.6	2	(0, 10)	4	(0, 13)	1	(0, 6)	
12	A disintegrin and metalloproteinase with thrombospondin motifs 1	Q9UHI8	105 kDa	0.224 ± 0.57	0.35 ± 0.61	0	(0, 3)	0	(0, 3)	0	(0, 2)	
13	A disintegrin and metalloproteinase with thrombospondin motifs 9	Q9P2N4	216 kDa	0.195 ± 0.29	0.279 ± 0.5	0	(0, 2)	0	(0, 2)	0	(0, 2)	
14	Acid sphingomyelinase-like phosphodiesterase 3b	Q92485	51 kDa	0.0927 ± 0.22	0.566 ± 0.63	0	(0, 3)	0	(0, 8)	0	(0, 3)	
15	Actin, alpha cardiac muscle 1	P68032	42 kDa	13.9 ± 6.3	9.92 ± 8.1	13	(3, 38)	24	(6, 30)	0	(0, 0)	
16	Actin, aortic smooth muscle	P62736	42 kDa	12.5 ± 6	6.36 ± 6.6	12	(3, 34)	23	(6, 29)	0	(0, 0)	

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Protein	Accession	MW	non-GDM	GDM	Median	Range	Median	Range	Median	Range	Rank	
17	Actin, cytoplasmic 1	P60709	42 kDa	18.5 ± 8.4	14.1 ± 7.1	16	(3, 56)	30	(9, 60)	0	(0, 1)	
18	Actin, cytoplasmic 2	P63261	42 kDa	18.8 ± 8.7	13.9 ± 7	16	(3, 57)	31	(9, 60)	0	(0, 1)	
19	Acyl-CoA-binding protein	P07108	10 kDa	0.0812 ± 0.19	0.165 ± 0.27	0	(0, 4)	0	(0, 63)	0	(0, 4)	
20	Afamin	P43652	69 kDa	0.373 ± 0.58	0.519 ± 0.8	0	(0, 3)	0	(0, 4)	0	(0, 2)	
21	Aggrin	O00468	217 kDa	0.163 ± 0.39	2 ± 2.3	0	(0, 7)	0	(0, 3)	0	(0, 6)	
22	A-kinase anchor protein 9	Q99996	454 kDa	0.509 ± 0.37	0.92 ± 0.69	1	(0, 2)	0	(0, 1)	0	(0, 1)	
23	Allograft inflammatory factor 1-like	Q9BQI0	17 kDa	0.251 ± 0.59	0.072 ± 0.18	0	(0, 3)	0	(0, 17)	0	(0, 3)	
24	Alpha-1-acid glycoprotein 1	P02763	24 kDa	23.3 ± 6.3	20.2 ± 7.2	21.5	(7, 51)	37	(12, 45)	6	(2, 8)	
25	Alpha-1-acid glycoprotein 2	P19652	24 kDa	9.31 ± 2.9	11.7 ± 5.7	9.5	(1, 28)	26	(4, 41)	3	(0, 5)	
26	Alpha-1-antichymotrypsin	P01011	48 kDa	61.3 ± 34	89.2 ± 49	58	(14, 166)	42	(22, 53)	18	(8, 28)	
27	Alpha-1-antitrypsin	P01009	47 kDa	80.8 ± 20	99.8 ± 48	79.5	(36, 213)	56	(35, 66)	26.5	(13, 41)	
28	Alpha-1B-glycoprotein	P04217	54 kDa	10.4 ± 3.7	7.88 ± 3.8	8.5	(3, 20)	19	(2, 35)	7	(3, 12)	
29	Alpha-2-antiplasmin	P08697	55 kDa	1.16 ± 0.78	0.515 ± 0.66	1	(0, 4)	3	(0, 7)	1	(0, 2)	
30	Alpha-2-HS-glycoprotein	P02765	39 kDa	20.1 ± 8.6	9.36 ± 4.4	17	(3, 33)	27	(0, 51)	8	(3, 12)	8
31	Alpha-2-macroglobulin	P01023	163 kDa	0.16 ± 0.45	0 ± 0	0	(0, 4)	0	(0, 4)	0	(0, 4)	
32	Alpha-actinin-1	P12814	103 kDa	0.069 ± 0.24	0.79 ± 1.5	0	(0, 5)	0	(0, 4)	0	(0, 0)	

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33	Alpha-actinin-4	O43707	105 kDa	0.192 ± 0.3	0.857 ± 1.6	0	(0, 6)	0	(0, 5)	0	(0, 1)	
34	Alpha-amylase 1	P04745	58 kDa	2.97 ± 2.7	1.11 ± 1.9	2	(0, 16)	4	(0, 28)	2	(0, 12)	
35	Alpha-enolase	P06733	47 kDa	5.88 ± 3.6	1.94 ± 1.8	4	(0, 15)	9	(0, 33)	3.5	(0, 11)	
36	Alpha-lactalbumin	P00709	16 kDa	910 ± 220	725 ± 220	839.5	(479, 1565)	83	(66, 87)	44	(27, 56)	
37	Alpha-S1-casein	P47710	22 kDa	620 ± 220	399 ± 320	554	(118, 961)	88	(74, 91)	57.5	(26, 72)	
38	Aminopeptidase N	P15144	110 kDa	0.0627 ± 0.22	0.556 ± 1.1	0	(0, 5)	0	(0, 4)	0	(0, 4)	
39	Amyloid beta A4 protein	P05067	87 kDa	13.3 ± 4.2	8.2 ± 4.4	11	(3, 27)	11	(3, 22)	7.5	(2, 16)	10
40	Amyloid-like protein 2	Q06481	87 kDa	0.45 ± 0.52	0 ± 0	1	(0, 2)	1	(0, 4)	0	(0, 1)	
41	Angiopietin-related protein 4	Q9BY76	45 kDa	3.66 ± 5.8	1.87 ± 2.9	1.5	(0, 29)	3	(0, 33)	1	(0, 13)	
42	Angiotensinogen	P01019	53 kDa	2.26 ± 1.7	1.31 ± 2.4	1	(0, 8)	2	(0, 20)	1	(0, 7)	
43	Ankyrin repeat domain-containing protein 32	Q9BQI6	121 kDa	0.913 ± 1.8	0.128 ± 0.2	0	(0, 5)	0	(0, 1)	0	(0, 2)	
44	Antileukoproteinase	P03973	14 kDa	0 ± 0	0.721 ± 1.2	0	(0, 4)	0	(0, 18)	0	(0, 2)	
45	Antithrombin-III	P01008	53 kDa	2.87 ± 1	3.38 ± 4.2	2	(0, 13)	4	(0, 23)	2	(0, 10)	
46	Apolipoprotein A-I	P02647	31 kDa	38.2 ± 13	16.8 ± 14	32.5	(0, 88)	57	(0, 70)	14.5	(0, 21)	1
47	Apolipoprotein A-II	P02652	11 kDa	3.11 ± 2	1.6 ± 1.9	2	(0, 11)	15	(0, 41)	2	(0, 4)	
48	Apolipoprotein A-IV	P06727	45 kDa	2.52 ± 3.4	0.482 ± 0.71	1	(0, 13)	0	(0, 27)	1	(0, 10)	

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49	Apolipoprotein B-100	P04114	516 kDa	1.07 ± 2.8	0.29 ± 0.71	0	(0, 15)	0	(0, 2)	0	(0, 9)	
50	Apolipoprotein D	P05090	21 kDa	17.1 ± 12	48.1 ± 20	25.5	(0, 65)	38	(0, 42)	7.5	(0, 9)	17
51	Apolipoprotein E	P02649	36 kDa	9.81 ± 5.3	3.21 ± 3	9	(0, 28)	27	(0, 56)	7.5	(0, 16)	7
52	Attractin	O75882	159 kDa	0.064 ± 0.22	1.3 ± 1.8	0	(0, 7)	0	(0, 6)	0	(0, 7)	
53	Azurocidin	P20160	27 kDa	0.199 ± 0.46	0.337 ± 0.83	0	(0, 3)	0	(0, 11)	0	(0, 3)	
54	Basement membrane-specific heparan sulfate proteoglycan core protein	P98160	469 kDa	0.303 ± 0.58	0.682 ± 1.3	0	(0, 5)	0	(0, 1)	0	(0, 4)	
55	BEN domain-containing protein 3	Q5T5X7	94 kDa	0.89 ± 1.2	0.637 ± 0.71	0	(0, 3)	0	(0, 3)	0	(0, 2)	
56	Beta-1,4-galactosyltransferase 1	P15291	44 kDa	29.7 ± 13	16.5 ± 7.9	23	(7, 69)	35	(10, 52)	9.5	(3, 14)	
57	Beta-2-glycoprotein 1	P02749	38 kDa	6.02 ± 2.4	4.48 ± 2.1	5.5	(1, 11)	22	(3, 39)	5	(1, 8)	
58	Beta-2-microglobulin	P61769	14 kDa	43.7 ± 13	25.3 ± 11	35.5	(14, 85)	56	(48, 66)	12	(6, 16)	
59	Beta-actin-like protein 2	Q562R1	42 kDa	5.3 ± 2.8	4.05 ± 3.2	5	(0, 13)	11	(0, 17)	0	(0, 0)	
60	Beta-casein	P05814	25 kDa	1440 ± 620	617 ± 610	1229.5	(73, 1985)	88	(73, 92)	96	(20, 137)	
61	Bile salt-activated lipase	P19835	79 kDa	86.8 ± 41	43.1 ± 39	68.5	(8, 204)	34	(7, 43)	26	(6, 45)	
62	Biotinidase	P43251	61 kDa	0.164 ± 0.31	0.196 ± 0.33	0	(0, 2)	0	(0, 5)	0	(0, 2)	
63	Brain-specific angiogenesis inhibitor 1	O14514	174 kDa	0.199 ± 0.58	0.325 ± 0.59	0	(0, 4)	0	(0, 1)	0	(0, 2)	
64	BRCA1-associated RING domain protein 1	Q99728	87 kDa	0.0353 ± 0.12	0.134 ± 0.33	0	(0, 2)	0	(0, 2)	0	(0, 2)	

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65	Butyrophilin subfamily 1 member A1	Q13410	59 kDa	53 ± 18	32.9 ± 28	50.5	(4, 67)	28	(3, 39)	16.5	(4, 21)	
66	C4b-binding protein alpha chain	P04003	67 kDa	3.18 ± 4.1	8.66 ± 9.9	3	(0, 28)	5	(0, 31)	2	(0, 16)	
67	C4b-binding protein beta chain	P20851	28 kDa	0.537 ± 0.81	0.904 ± 1.3	0	(0, 5)	0	(0, 18)	0	(0, 4)	
68	Calcium and integrin-binding protein 1	Q99828	22 kDa	2.29 ± 1.3	1.77 ± 0.81	2	(0, 6)	8	(0, 27)	1	(0, 5)	
69	Calmodulin	P62158	17 kDa	8.47 ± 5.5	4.65 ± 2.2	7	(0, 17)	32	(0, 43)	3	(0, 5)	
70	Calmodulin-like protein 5	Q9NZT1	16 kDa	0.312 ± 0.86	0.662 ± 0.98	0	(0, 3)	0	(0, 15)	0	(0, 2)	
71	Calreticulin	P27797	48 kDa	2.51 ± 2.4	1.15 ± 1.4	2	(0, 9)	4	(0, 24)	2	(0, 7)	23
72	Calumenin	O43852	37 kDa	1.78 ± 2.2	1.84 ± 2.2	1	(0, 11)	3	(0, 22)	1	(0, 7)	
73	Canalicular multispecific organic anion transporter 1	Q92887	174 kDa	0.218 ± 0.28	0.429 ± 0.4	0	(0, 2)	0	(0, 1)	0	(0, 1)	
74	Carbonic anhydrase 6	P23280	35 kDa	17.4 ± 6.7	11.6 ± 6.2	14	(2, 31)	25	(6, 43)	6	(2, 9)	
75	Cathelicidin antimicrobial peptide	P49913	19 kDa	0.064 ± 0.22	0.622 ± 0.71	0	(0, 2)	0	(0, 14)	0	(0, 2)	
76	Cathepsin B	P07858	38 kDa	1.75 ± 1.4	1.98 ± 1.5	1.5	(0, 6)	4	(0, 15)	1.5	(0, 5)	
77	Cathepsin D	P07339	45 kDa	1.7 ± 2.8	2.69 ± 2.4	0.5	(0, 12)	1	(0, 25)	0.5	(0, 8)	
78	Cathepsin G	P08311	29 kDa	0.171 ± 0.48	0.128 ± 0.2	0	(0, 4)	0	(0, 14)	0	(0, 3)	
79	Cathepsin S	P25774	37 kDa	0.221 ± 0.53	0.341 ± 0.65	0	(0, 3)	0	(0, 10)	0	(0, 3)	
80	C-C motif chemokine 28	Q9NRJ3	14 kDa	0.636 ± 0.87	0.269 ± 0.49	0	(0, 4)	0	(0, 23)	0	(0, 2)	

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81	CCR4-NOT transcription complex subunit 1	A5YKK6	267 kDa	0 ± 0	0.22 ± 0.54	0	(0, 2)	0	(0, 1)	0	(0, 2)	
82	CD59 glycoprotein	P13987	14 kDa	5.5 ± 1.2	5.92 ± 1	6	(0, 9)	29	(0, 36)	3	(0, 6)	
83	CD63 antigen	P08962	26 kDa	1.18 ± 0.8	0.808 ± 0.92	1	(0, 3)	3	(0, 8)	1	(0, 2)	
84	CD81 antigen	P60033	26 kDa	0.332 ± 0.4	0.331 ± 0.81	0	(0, 2)	0	(0, 15)	0	(0, 2)	
85	CD9 antigen	P21926	25 kDa	0.618 ± 0.7	0.203 ± 0.5	0	(0, 2)	0	(0, 7)	0	(0, 2)	
86	Cell division control protein 42 homolog	P60953	21 kDa	0.78 ± 1.4	0.072 ± 0.18	0	(0, 4)	0	(0, 11)	0	(0, 2)	
87	Cell division cycle 5-like protein	Q99459	92 kDa	1.47 ± 0.89	0.607 ± 0.45	1	(0, 3)	1	(0, 3)	1	(0, 2)	18
88	Cell growth regulator with EF hand domain protein 1	Q99674	32 kDa	2 ± 0.86	1.54 ± 1.8	2	(0, 5)	6	(0, 17)	1	(0, 4)	
89	Cellular retinoic acid-binding protein 2	P29373	16 kDa	0.137 ± 0.35	0.0684 ± 0.17	0	(0, 2)	0	(0, 12)	0	(0, 2)	
90	Ceruloplasmin	P00450	122 kDa	4.32 ± 6.6	15.7 ± 16	3	(0, 46)	4	(0, 30)	3	(0, 25)	
91	Chitinase-3-like protein 1	P36222	43 kDa	1.45 ± 2.2	3.86 ± 7.6	1	(0, 16)	3	(0, 32)	1	(0, 9)	
92	Chitinase-3-like protein 2	Q15782	44 kDa	0.0353 ± 0.12	0 ± 0	0	(0, 1)	0	(0, 7)	0	(0, 1)	
93	Chloride intracellular channel protein 1	O00299	27 kDa	0.493 ± 0.6	0 ± 0	0	(0, 2)	0	(0, 12)	0	(0, 2)	
94	Chordin-like protein 2	Q6WN34	47 kDa	71.8 ± 29	35.9 ± 32	66	(5, 98)	34	(11, 45)	13	(4, 22)	
95	Cluster of 14-3-3 protein zeta/delta	P63104	28 kDa	6.23 ± 3.3	2.11 ± 1.8	5	(0, 17)	16	(0, 39)	4	(0, 14)	24
96	Cluster of Cofilin-1	P23528	19 kDa	5.29 ± 3.1	1.83 ± 1.9	4	(0, 14)	24	(0, 52)	3	(0, 7)	

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97	Cluster of Eukaryotic translation initiation factor 5A-1	P63241	17 kDa	0.517 ± 1	0.0684 ± 0.17	0	(0, 3)	0	(0, 12)	0	(0, 2)
98	Cluster of Frizzled-2	Q14332	64 kDa	0.195 ± 0.44	0.675 ± 0.56	0	(0, 2)	0	(0, 3)	0	(0, 1)
99	Cluster of Gamma-glutamyltranspeptidase 1	P19440	61 kDa	2.28 ± 2.2	2.94 ± 0.87	2	(0, 9)	3	(0, 14)	2	(0, 7)
100	Cluster of Haptoglobin	P00738	45 kDa	37.6 ± 12	30.8 ± 23	36	(9, 82)	42	(18, 60)	18	(7, 27)
101	Cluster of Heat shock cognate 71 kDa protein	P11142	71 kDa	3.14 ± 1.7	0.787 ± 0.8	2	(0, 9)	3	(0, 12)	1	(0, 5)
102	Cluster of Heat shock protein HSP 90-alpha	P07900	85 kDa	0.564 ± 0.77	0 ± 0	0	(0, 10)	0	(0, 11)	0	(0, 8)
103	Cluster of Hemoglobin subunit epsilon	P02100	16 kDa	0.0921 ± 0.32	0 ± 0	0	(0, 2)	0	(0, 13)	0	(0, 1)
104	Cluster of Heterogeneous nuclear ribonucleoprotein A1	P09651	39 kDa	0.304 ± 0.76	0.309 ± 0.76	0	(0, 4)	0	(0, 10)	0	(0, 3)
105	Cluster of Histone H1.2	P16403	21 kDa	0 ± 0	0.185 ± 0.45	0	(0, 2)	0	(0, 11)	0	(0, 1)
106	Cluster of Histone H2A type 1-C	Q93077	14 kDa	1.16 ± 2.4	1.01 ± 1.4	0	(0, 12)	0	(0, 27)	0	(0, 3)
107	Cluster of Histone H2B type 1-L	Q99880	14 kDa	2.05 ± 3.3	4 ± 7.1	1	(0, 25)	6	(0, 46)	1	(0, 6)
108	Cluster of Histone H3.1t	Q16695	16 kDa	0.475 ± 1.2	0.595 ± 1.2	0	(0, 5)	0	(0, 17)	0	(0, 3)
109	Cluster of HLA class I histocompatibility antigen, Cw-7 alpha chain	P10321	41 kDa	1.34 ± 1.8	1.19 ± 1.1	1	(0, 7)	2	(0, 15)	1	(0, 5)
110	Cluster of HLA class II histocompatibility antigen, DRB1-4 beta chain	P13760	30 kDa	2.37 ± 5.2	0.34 ± 0.67	0	(0, 21)	0	(0, 31)	0	(0, 12)
111	Cluster of Ig heavy chain V-I region Mot	P06326	14 kDa	8.51 ± 3.5	9.51 ± 1.4	8	(3, 15)	14	(10, 21)	1	(1, 3)
112	Cluster of Ig heavy chain V-III region VH26	P01764	13 kDa	10.1 ± 8.1	19.2 ± 9.9	10.5	(1, 42)	29	(10, 47)	2	(1, 7)

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113	Cluster of Ig kappa chain V-I region WEA	P01610	12 kDa	27.1 ± 14	37.5 ± 16	28	(5, 68)	38	(27, 47)	6	(0, 15)	
114	Cluster of Ig kappa chain V-III region Ti	P01622	12 kDa	28.4 ± 18	47.7 ± 20	27.5	(7, 92)	58	(38, 77)	4	(1, 18)	
115	Cluster of Ig lambda chain V-II region BUR	P01708	12 kDa	6.05 ± 3.1	12.4 ± 9.4	6	(1, 29)	17	(7, 61)	2	(1, 12)	
116	Cluster of Immunoglobulin lambda-like polypeptide 5	B9A064	23 kDa	201 ± 59	265 ± 42	195	(79, 470)	89	(51, 96)	21	(8, 38)	
117	Cluster of Keratin, type I cuticular Ha6	O76013	52 kDa	1.65 ± 3.2	5 ± 12	1	(0, 41)	2	(0, 30)	0	(0, 21)	
118	Cluster of Keratin, type I cytoskeletal 10	P13645	59 kDa	54.9 ± 21	54.9 ± 22	55	(20, 109)	38	(21, 48)	17.5	(9, 26)	
119	Cluster of Keratin, type I cytoskeletal 13	P13646	50 kDa	3.53 ± 5.4	4.21 ± 5.1	5	(0, 22)	4	(0, 9)	0	(0, 1)	
120	Cluster of Keratin, type I cytoskeletal 17	Q04695	48 kDa	4.07 ± 4.1	5.01 ± 4.7	5	(0, 19)	6	(0, 16)	0	(0, 1)	
121	Cluster of Keratin, type II cytoskeletal 2 epidermal	P35908	65 kDa	52 ± 24	70 ± 38	56.5	(10, 143)	46	(15, 65)	27.5	(6, 59)	
122	Cluster of L-lactate dehydrogenase B chain	P07195	37 kDa	0.134 ± 0.25	0 ± 0	0	(0, 3)	0	(0, 11)	0	(0, 3)	
123	Cluster of Peptidyl-prolyl cis-trans isomerase A	P62937	18 kDa	4.52 ± 2.4	1.84 ± 1.7	3	(0, 9)	15	(0, 40)	2	(0, 6)	
124	Cluster of Plastin-2	P13796	70 kDa	0.172 ± 0.6	0.131 ± 0.2	0	(0, 3)	0	(0, 10)	0	(0, 3)	
125	Cluster of POTE ankyrin domain family member F	A5A3E0	121 kDa	20.7 ± 9.7	14.7 ± 7.7	17	(4, 63)	32	(10, 60)	11	(3, 19)	27
126	Cluster of Pregnancy-specific beta-1-glycoprotein 9	Q00887	48 kDa	0.243 ± 0.38	0.2 ± 0.49	0	(0, 1)	0	(0, 5)	0	(0, 1)	
127	Cluster of Pyruvate kinase isozymes M1/M2	P14618	58 kDa	0.252 ± 0.63	0.124 ± 0.3	0	(0, 3)	0	(0, 8)	0	(0, 3)	
128	Cluster of Ras-related protein Rab-8A	P61006	24 kDa	0.254 ± 0.51	0 ± 0	0	(0, 4)	0	(0, 12)	0	(0, 3)	

				Normalized Total Spectra		Total Spectra		% Sequence Coverage		Number of Unique Peptides		
Protein	Accession	MW	non-GDM	GDM	Median	Range	Median	Range	Median	Range	Rank	
129	Cluster of Serum albumin	P02768	69 kDa	238 ± 69	374 ± 200	233	(75, 887)	76	(57, 83)	58	(32, 106)	
130	Cluster of Transforming protein RhoA	P61586	22 kDa	1.33 ± 1.6	0.419 ± 0.52	1	(0, 5)	0	(0, 23)	1	(0, 5)	
131	Cluster of Tropomyosin alpha-4 chain	P67936	29 kDa	1.31 ± 1.4	0.634 ± 1.1	1	(0, 5)	3	(0, 11)	1	(0, 4)	
132	Cluster of Tyrosine-protein phosphatase non-receptor type substrate 1	P78324	55 kDa	0.173 ± 0.27	0.522 ± 0.86	0	(0, 4)	0	(0, 10)	0	(0, 4)	
133	Cluster of Ubiquitin-60S ribosomal protein L40	P62987	15 kDa	7.63 ± 6	3.68 ± 2.6	7	(0, 22)	14	(0, 34)	2	(0, 4)	
134	Clusterin	P10909	52 kDa	250 ± 66	166 ± 96	194	(79, 455)	51	(38, 61)	29	(19, 40)	
135	Clusterin-like protein 1	Q15846	54 kDa	0.149 ± 0.52	0 ± 0	0	(0, 2)	0	(0, 5)	0	(0, 2)	
136	Cofilin-2	Q9Y281	19 kDa	0.118 ± 0.41	0 ± 0	2	(0, 5)	7	(0, 21)	0	(0, 0)	
137	Collagen alpha-1(IV) chain	P02462	161 kDa	0.42 ± 0.72	0 ± 0	0	(0, 2)	0	(0, 2)	0	(0, 2)	
138	Collagen alpha-1(VI) chain	P12109	109 kDa	0 ± 0	0.0677 ± 0.17	0	(0, 1)	0	(0, 2)	0	(0, 1)	
139	Collagen alpha-2(VI) chain	P12110	109 kDa	0.0964 ± 0.33	0 ± 0	0	(0, 2)	0	(0, 2)	0	(0, 2)	
140	Complement C1q tumor necrosis factor-related protein 1	Q9BXJ1	32 kDa	0.391 ± 0.46	0.2 ± 0.49	0	(0, 2)	0	(0, 8)	0	(0, 2)	
141	Complement C1r subcomponent	P00736	80 kDa	0.0396 ± 0.14	0 ± 0	0	(0, 1)	0	(0, 5)	0	(0, 0)	
142	Complement C1r subcomponent-like protein	Q9NZP8	53 kDa	3.45 ± 1.1	2.33 ± 1.3	3	(0, 8)	7	(0, 24)	2	(0, 7)	14
143	Complement C1s subcomponent	P09871	77 kDa	0 ± 0	0.122 ± 0.3	0	(0, 2)	0	(0, 6)	0	(0, 2)	
144	Complement C3	P01024	187 kDa	82.1 ± 46	92 ± 55	73.5	(22, 242)	28	(11, 54)	42	(16, 90)	

			Normalized Total Spectra		Total Spectra		% Sequence Coverage		Number of Unique Peptides		
Protein	Accession	MW	non-GDM	GDM	Median	Range	Median	Range	Median	Range	Rank
145	Complement C4-A	P0C0L4	193 kDa	27.7 ± 22	36.4 ± 26	28	(2, 102)	14	(1, 36)	1	(0, 4)
146	Complement C4-B	P0C0L5	193 kDa	27.1 ± 22	35.8 ± 27	27.5	(2, 101)	14	(1, 37)	1	(0, 3)
147	Complement component C7	P10643	94 kDa	0.159 ± 0.29	0.785 ± 0.66	0	(0, 2)	0	(0, 2)	0	(0, 2)
148	Complement decay-accelerating factor	P08174	41 kDa	0.0854 ± 0.2	0.597 ± 0.76	0	(0, 3)	0	(0, 6)	0	(0, 3)
149	Complement factor B	P00751	86 kDa	2.1 ± 1.8	2.38 ± 3.9	2	(0, 16)	3	(0, 20)	2	(0, 13)
150	Complement factor I	P05156	66 kDa	3.61 ± 2.6	3.14 ± 2.3	3	(0, 12)	4	(0, 16)	3	(0, 8)
151	Corticosteroid-binding globulin	P08185	45 kDa	0.13 ± 0.45	1.05 ± 1.7	0	(0, 6)	0	(0, 10)	0	(0, 3)
152	C-type lectin domain family 11 member A	Q9Y240	36 kDa	14.8 ± 8.7	12.2 ± 6.9	10.5	(0, 31)	28	(0, 42)	8	(0, 12)
153	Cubilin	O60494	399 kDa	0.145 ± 0.34	0 ± 0	0	(0, 2)	0	(0, 1)	0	(0, 2)
154	Cyclin-I2	Q6ZMN8	41 kDa	0.146 ± 0.28	0.209 ± 0.51	0	(0, 2)	0	(0, 6)	0	(0, 2)
155	Cystatin-B	P04080	11 kDa	0.0654 ± 0.23	0.104 ± 0.25	0	(0, 2)	0	(0, 25)	0	(0, 2)
156	Cystatin-C	P01034	16 kDa	11.2 ± 3.2	11 ± 6.2	10	(3, 30)	39	(23, 54)	5	(3, 8)
157	Cysteine-rich motor neuron 1 protein	Q9NZV1	114 kDa	0.681 ± 1.1	0.3 ± 0.36	0	(0, 4)	0	(0, 3)	0	(0, 3)
158	Cytosolic non-specific dipeptidase	Q96KP4	53 kDa	0.108 ± 0.25	0 ± 0	0	(0, 3)	0	(0, 9)	0	(0, 3)
159	Dedicator of cytokinesis protein 4	Q8N110	225 kDa	0.45 ± 0.7	0.824 ± 1.3	0	(0, 4)	0	(0, 1)	0	(0, 2)
160	Deleted in malignant brain tumors 1 protein	Q9UGM3	261 kDa	0.135 ± 0.27	1.52 ± 1.3	0	(0, 4)	0	(0, 1)	0	(0, 2)

				Normalized Total Spectra		Total Spectra		% Sequence Coverage		Number of Unique Peptides		
Protein	Accession	MW	non-GDM	GDM	Median	Range	Median	Range	Median	Range	Rank	
161	Dermcidin	P81605	11 kDa	1.96 ± 1.1	1.91 ± 0.67	2	(0, 5)	10	(0, 41)	1.5	(0, 3)	
162	Desmocollin-2	Q02487	100 kDa	2.03 ± 1.6	0.831 ± 0.78	1	(0, 6)	1	(0, 4)	1	(0, 3)	
163	Desmoplakin	P15924	332 kDa	0.101 ± 0.35	0.513 ± 0.84	0	(0, 3)	0	(0, 2)	0	(0, 3)	
164	Dipeptidyl peptidase 1	P53634	52 kDa	2.15 ± 2.5	1.17 ± 1	1	(0, 10)	3	(0, 13)	1	(0, 7)	
165	Disintegrin and metalloproteinase domain-containing protein 10	O14672	84 kDa	0.263 ± 0.49	0.2 ± 0.49	0	(0, 3)	0	(0, 5)	0	(0, 3)	
166	Disintegrin and metalloproteinase domain-containing protein 15	Q13444	93 kDa	0.181 ± 0.35	0.0684 ± 0.17	0	(0, 2)	0	(0, 3)	0	(0, 2)	
167	DNA polymerase delta catalytic subunit	P28340	124 kDa	0.128 ± 0.31	0 ± 0	0	(0, 2)	0	(0, 2)	0	(0, 1)	
168	DNA repair protein RAD50	Q92878	154 kDa	0.142 ± 0.36	0 ± 0	0	(0, 2)	0	(0, 1)	0	(0, 2)	
169	Dynein heavy chain 10, axonemal	Q8IVF4	515 kDa	0.176 ± 0.26	0.144 ± 0.35	0	(0, 3)	0	(0, 1)	0	(0, 2)	
170	Dynein heavy chain 14, axonemal	Q0VDD8	400 kDa	0.642 ± 0.63	1 ± 0.66	1	(0, 3)	0	(0, 1)	1	(0, 2)	
171	Dystonin	Q03001	861 kDa	6.76 ± 2.8	3.54 ± 2.3	5	(0, 17)	0	(0, 0)	1	(0, 2)	4
172	Dystroglycan	Q14118	97 kDa	7.58 ± 5	2.41 ± 2.8	6	(0, 15)	6	(0, 16)	4	(0, 10)	
173	E3 ubiquitin-protein ligase HERC2	O95714	527 kDa	0.0648 ± 0.22	0 ± 0	0	(0, 2)	0	(0, 0)	0	(0, 2)	
174	EGF-containing fibulin-like extracellular matrix protein 1	Q12805	55 kDa	0.84 ± 1.4	2.44 ± 3.3	0	(0, 8)	0	(0, 20)	0	(0, 7)	
175	Elongation factor 1-alpha 1	P68104	50 kDa	1.25 ± 1.1	0.482 ± 0.9	1	(0, 9)	2	(0, 18)	0	(0, 2)	
176	Elongation factor 1-alpha 2	Q05639	50 kDa	0.62 ± 0.83	0.482 ± 0.9	1	(0, 6)	2	(0, 10)	0	(0, 0)	

			Normalized Total Spectra		Total Spectra		% Sequence Coverage		Number of Unique Peptides			
Protein	Accession	MW	non-GDM	GDM	Median	Range	Median	Range	Median	Range	Rank	
177	Elongation factor 2	P13639	95 kDa	0.101 ± 0.35	0 ± 0	0	(0, 3)	0	(0, 4)	0	(0, 3)	
178	Endoglin	P17813	71 kDa	0.0726 ± 0.17	0.231 ± 0.37	0	(0, 1)	0	(0, 4)	0	(0, 1)	
179	Ephrin-A1	P20827	24 kDa	2.26 ± 2.9	1.6 ± 1.4	1	(0, 11)	4	(0, 24)	1	(0, 6)	
180	Epididymal secretory protein E1	P61916	17 kDa	1.39 ± 2.3	0.559 ± 0.73	0	(0, 11)	0	(0, 44)	0	(0, 6)	
181	Erythrocyte band 7 integral membrane protein	P27105	32 kDa	0.522 ± 1	0.384 ± 0.49	0	(0, 4)	0	(0, 10)	0	(0, 3)	
182	Extracellular sulfatase Sulf-2	Q8IWU5	100 kDa	0.243 ± 0.51	0 ± 0	0	(0, 2)	0	(0, 3)	0	(0, 2)	
183	Extracellular superoxide dismutase [Cu-Zn]	P08294	26 kDa	0.487 ± 0.57	0.711 ± 0.76	0	(0, 3)	0	(0, 12)	0	(0, 2)	
184	Ezrin	P15311	69 kDa	1 ± 1.5	0.0672 ± 0.16	0	(0, 5)	0	(0, 8)	0	(0, 3)	
185	Fatty acid synthase	P49327	273 kDa	1.93 ± 2.4	0.221 ± 0.54	0	(0, 80)	0	(0, 31)	0	(0, 55)	19
186	Fatty acid-binding protein, epidermal	Q01469	15 kDa	0.841 ± 0.81	1.65 ± 1.2	1	(0, 6)	7	(0, 29)	1	(0, 5)	
187	Fatty acid-binding protein, heart	P05413	15 kDa	24.8 ± 12	12.2 ± 12	21.5	(1, 45)	53	(0, 73)	7	(1, 12)	
188	Ferritin heavy chain	P02794	21 kDa	6.05 ± 4.5	3.48 ± 1.8	5	(0, 13)	21	(0, 54)	4	(0, 8)	
189	Fibrinogen alpha chain	P02671	95 kDa	4.01 ± 3.3	2.49 ± 2.9	3.5	(0, 18)	4	(0, 17)	2.5	(0, 11)	
190	Fibrinogen beta chain	P02675	56 kDa	3.91 ± 6.3	2.26 ± 2.2	1	(0, 28)	3	(0, 41)	1	(0, 15)	
191	Fibrinogen gamma chain	P02679	52 kDa	1.96 ± 3.1	2.21 ± 2.1	1.5	(0, 18)	2	(0, 29)	1	(0, 11)	
192	Fibronectin	P02751	263 kDa	0.537 ± 0.89	0.152 ± 0.24	0	(0, 5)	0	(0, 2)	0	(0, 5)	

				Normalized Total Spectra		Total Spectra		% Sequence Coverage		Number of Unique Peptides		
Protein	Accession	MW	non-GDM	GDM	Median	Range	Median	Range	Median	Range	Rank	
193	Fibrous sheath-interacting protein 2	Q5CZC0	781 kDa	0.0705 ± 0.24	0 ± 0	0	(0, 2)	0	(0, 0)	0	(0, 2)	
194	Filaggrin	P20930	435 kDa	0.782 ± 0.88	9.29 ± 15	1	(0, 54)	0	(0, 11)	1	(0, 35)	
195	Filaggrin-2	Q5D862	248 kDa	0.344 ± 0.56	1.51 ± 3.5	0	(0, 12)	0	(0, 4)	0	(0, 7)	
196	Folate receptor alpha	P15328	30 kDa	2.05 ± 0.83	1.89 ± 0.54	2	(0, 6)	9	(0, 25)	2	(0, 5)	
197	Follistatin-related protein 1	Q12841	35 kDa	24.1 ± 11	16.4 ± 7.7	19	(6, 47)	30	(12, 45)	9	(4, 13)	
198	Frizzled-1	Q9UP38	71 kDa	0.262 ± 0.47	0.408 ± 0.35	0	(0, 2)	0	(0, 3)	0	(0, 1)	
199	G protein-regulated inducer of neurite outgrowth 1	Q7Z2K8	102 kDa	0.6 ± 1.2	1.69 ± 1.9	0	(0, 6)	0	(0, 2)	0	(0, 2)	
200	Galectin-1	P09382	15 kDa	0.0692 ± 0.24	0.51 ± 0.82	0	(0, 3)	0	(0, 30)	0	(0, 3)	
201	Galectin-3-binding protein	Q08380	65 kDa	46.5 ± 10	46.7 ± 12	39.5	(19, 92)	32	(22, 41)	16	(9, 25)	
202	Gamma-glutamyltranspeptidase 2	P36268	62 kDa	1.27 ± 1.7	2.03 ± 0.96	2	(0, 6)	3	(0, 8)	0	(0, 0)	
203	Gamma-interferon-inducible lysosomal thiol reductase	P13284	28 kDa	0 ± 0	0.203 ± 0.5	0	(0, 3)	0	(0, 13)	0	(0, 3)	
204	Ganglioside GM2 activator	P17900	21 kDa	1.75 ± 1.2	1.33 ± 1.4	1	(0, 6)	6	(0, 28)	1	(0, 5)	
205	Gelsolin	P06396	86 kDa	1.23 ± 1.8	3.12 ± 2.6	1	(0, 9)	1	(0, 16)	1	(0, 9)	
206	Glutaredoxin-1	P35754	12 kDa	0.106 ± 0.37	0 ± 0	0	(0, 3)	0	(0, 21)	0	(0, 2)	
207	Glyceraldehyde-3-phosphate dehydrogenase	P04406	36 kDa	2.22 ± 4	0.293 ± 0.48	0.5	(0, 18)	1	(0, 42)	0	(0, 10)	
208	Glyceraldehyde-3-phosphate dehydrogenase, testis-specific	O14556	45 kDa	0.506 ± 1.2	0 ± 0	0	(0, 5)	0	(0, 7)	0	(0, 1)	

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Protein	Accession	MW	non-GDM	GDM	Median	Range	Median	Range	Median	Range	Rank	
209	Golgi membrane protein 1	Q8NBJ4	45 kDa	11.5 ± 4.6	4.35 ± 5.2	8.5	(0, 24)	14	(0, 33)	5	(0, 12)	25
210	Golgi-associated plant pathogenesis-related protein 1	Q9H4G4	17 kDa	1.53 ± 1.2	0.823 ± 1.3	1	(0, 4)	8	(0, 22)	1	(0, 3)	
211	G-protein coupled receptor 126	Q86SQ4	137 kDa	1.84 ± 0.89	2.14 ± 1.8	2	(0, 8)	2	(0, 7)	2	(0, 6)	
212	G-protein coupled receptor 56	Q9Y653	78 kDa	0.544 ± 0.61	0.205 ± 0.5	0	(0, 3)	0	(0, 3)	0	(0, 2)	
213	G-protein coupled receptor family C group 5 member B	Q9NZH0	45 kDa	1.26 ± 1.2	1.09 ± 1.4	1	(0, 3)	2	(0, 8)	1	(0, 3)	
214	Granulins	P28799	64 kDa	0.612 ± 1.7	0.968 ± 0.94	0	(0, 7)	0	(0, 12)	0	(0, 6)	
215	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12	Q9UBI6	8 kDa	0.501 ± 0.65	0.251 ± 0.39	0	(0, 2)	0	(0, 25)	0	(0, 2)	
216	Haptoglobin-related protein	P00739	39 kDa	8.15 ± 11	10.6 ± 17	20	(1, 52)	21	(3, 34)	0	(0, 0)	
217	HEAT repeat-containing protein 1	Q9H583	242 kDa	0.226 ± 0.31	0.281 ± 0.69	0	(0, 2)	0	(0, 1)	0	(0, 2)	
218	Heat shock 70 kDa protein 1-like	P34931	70 kDa	0.621 ± 1	0.135 ± 0.21	1	(0, 4)	2	(0, 6)	0	(0, 2)	
219	Heat shock protein HSP 90-beta	P08238	83 kDa	0.256 ± 0.52	0 ± 0	0	(0, 3)	0	(0, 5)	0	(0, 1)	
220	Heat shock-related 70 kDa protein 2	P54652	70 kDa	0.158 ± 0.43	0.063 ± 0.15	1	(0, 5)	2	(0, 4)	0	(0, 0)	
221	Hemoglobin subunit alpha	P69905	15 kDa	0.317 ± 0.54	0 ± 0	0	(0, 5)	0	(0, 30)	0	(0, 3)	
222	Hemoglobin subunit beta	P68871	16 kDa	0.731 ± 1.3	0.072 ± 0.18	0	(0, 8)	0	(0, 54)	0	(0, 5)	
223	Hemoglobin subunit gamma-1	P69891	16 kDa	0.0921 ± 0.32	0 ± 0	0	(0, 2)	0	(0, 13)	0	(0, 0)	
224	Hemopexin	P02790	52 kDa	10.4 ± 6.5	10.6 ± 5.2	10.5	(2, 27)	17	(4, 38)	6	(2, 13)	

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Protein	Accession	MW	non-GDM	GDM	Median	Range	Median	Range	Median	Range	Rank
225	Heterogeneous nuclear ribonucleoproteins A2/B1	P22626	37 kDa	0.238 ± 0.49	0.309 ± 0.76	0	(0, 3)	0	(0, 6)	0	(0, 1)
226	Histidine-rich glycoprotein	P04196	60 kDa	0.0632 ± 0.22	1.18 ± 2.9	0	(0, 11)	0	(0, 9)	0	(0, 4)
227	Histone H1.3	P16402	22 kDa	0 ± 0	0.185 ± 0.45	0	(0, 2)	0	(0, 10)	0	(0, 0)
228	Histone H2A type 2-C	Q16777	14 kDa	0.993 ± 2.5	0.93 ± 1.4	0	(0, 12)	0	(0, 27)	0	(0, 0)
229	Histone H2A.Z	P0C0S5	14 kDa	0.886 ± 1.9	0.723 ± 1.2	0	(0, 9)	0	(0, 13)	0	(0, 0)
230	Histone H2B type 1-D	P58876	14 kDa	0.896 ± 3.1	2.98 ± 7.3	1	(0, 25)	6	(0, 46)	0	(0, 0)
231	Histone H2B type 1-J	P06899	14 kDa	1.68 ± 2.9	3.74 ± 6.9	1	(0, 24)	6	(0, 39)	0	(0, 0)
232	Histone H2B type 1-M	Q99879	14 kDa	1.33 ± 3.2	3.56 ± 7.1	1	(0, 25)	6	(0, 46)	0	(0, 0)
233	Histone H2B type 1-N	Q99877	14 kDa	1.85 ± 3.4	3.87 ± 7.2	1	(0, 25)	6	(0, 46)	0	(0, 0)
234	Histone H3.3	P84243	15 kDa	0.346 ± 1.2	0.498 ± 1.2	0	(0, 5)	0	(0, 17)	0	(0, 0)
235	Histone H4	P62805	11 kDa	0.547 ± 1.5	1.47 ± 3.1	0	(0, 11)	0	(0, 51)	0	(0, 5)
236	HLA class I histocompatibility antigen, A-2 alpha chain	P01892	41 kDa	0.206 ± 0.71	0 ± 0	0	(0, 3)	0	(0, 9)	0	(0, 0)
237	HLA class I histocompatibility antigen, A-33 alpha chain	P16190	41 kDa	0.0822 ± 0.28	0 ± 0	0	(0, 2)	0	(0, 9)	0	(0, 0)
238	HLA class I histocompatibility antigen, B-39 alpha chain	P30475	40 kDa	0.165 ± 0.57	0.22 ± 0.54	1	(0, 4)	2	(0, 11)	0	(0, 1)
239	HLA class I histocompatibility antigen, Cw-4 alpha chain	P30504	41 kDa	0.234 ± 0.6	0.648 ± 1.1	1	(0, 4)	2	(0, 6)	0	(0, 0)
240	HLA class II histocompatibility antigen gamma chain	P04233	34 kDa	8.1 ± 5.3	3.41 ± 5.1	4.5	(0, 25)	10	(0, 16)	3	(0, 4)

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Protein	Accession	MW	non-GDM	GDM	Median	Range	Median	Range	Median	Range	Rank	
241	HLA class II histocompatibility antigen, DP alpha 1 chain	P20036	29 kDa	0.078 ± 0.27	0 ± 0	0	(0, 2)	0	(0, 7)	0	(0, 2)	
242	HLA class II histocompatibility antigen, DQ beta 1 chain	P01920	30 kDa	0.118 ± 0.41	0 ± 0	0	(0, 2)	0	(0, 8)	0	(0, 2)	
243	HLA class II histocompatibility antigen, DR alpha chain	P01903	29 kDa	1.01 ± 2.3	0.609 ± 0.94	0	(0, 9)	0	(0, 30)	0	(0, 5)	
244	HLA class II histocompatibility antigen, DR beta 5 chain	Q30154	30 kDa	0.782 ± 2.6	0 ± 0	0	(0, 10)	0	(0, 25)	0	(0, 1)	
245	HLA class II histocompatibility antigen, DRB1-1 beta chain	P04229	30 kDa	1.12 ± 2.9	0 ± 0	0	(0, 11)	0	(0, 27)	0	(0, 1)	
246	HLA class II histocompatibility antigen, DRB1-13 beta chain	Q5Y7A7	30 kDa	1.11 ± 2.5	0 ± 0	0	(0, 11)	0	(0, 23)	0	(0, 1)	
247	HLA class II histocompatibility antigen, DRB1-8 beta chain	Q30134	30 kDa	0.722 ± 2.2	0 ± 0	0	(0, 9)	0	(0, 23)	0	(0, 1)	
248	Hornerin	Q86YZ3	282 kDa	3.88 ± 3.3	6.92 ± 4.8	5	(0, 17)	1	(0, 4)	2	(0, 6)	
249	Hyaluronan and proteoglycan link protein 3	Q96S86	41 kDa	5.48 ± 3.4	2.4 ± 1.3	3	(0, 16)	8	(0, 34)	3	(0, 9)	
250	Hypoxia up-regulated protein 1	Q9Y4L1	111 kDa	0.438 ± 0.58	0.072 ± 0.18	0	(0, 2)	0	(0, 2)	0	(0, 1)	
251	Ig alpha-1 chain C region	P01876	38 kDa	463 ± 300	795 ± 280	407	(129, 1805)	76	(67, 94)	17	(9, 39)	
252	Ig alpha-2 chain C region	P01877	37 kDa	392 ± 210	698 ± 250	366.5	(93, 1438)	70	(57, 84)	15.5	(4, 32)	
253	Ig delta chain C region	P01880	42 kDa	0.352 ± 1.2	0 ± 0	0	(0, 6)	0	(0, 18)	0	(0, 5)	
254	Ig gamma-1 chain C region	P01857	36 kDa	12.1 ± 8.6	25.4 ± 16	10.5	(3, 63)	32	(9, 61)	3	(1, 7)	
255	Ig gamma-2 chain C region	P01859	36 kDa	4.54 ± 3.8	10.2 ± 7.5	4	(1, 25)	13	(2, 42)	1	(0, 4)	
256	Ig gamma-3 chain C region	P01860	41 kDa	7.47 ± 5.6	15.7 ± 9.8	6.5	(2, 38)	13	(4, 35)	0	(0, 4)	

			Normalized Total Spectra		Total Spectra		% Sequence Coverage		Number of Unique Peptides			
Protein	Accession	MW	non-GDM	GDM	Median	Range	Median	Range	Median	Range	Rank	
257	Ig gamma-4 chain C region	P01861	36 kDa	4.32 ± 5.6	11.4 ± 8.2	4	(1, 31)	13	(2, 38)	0	(0, 2)	
258	Ig heavy chain V-I region EU	P01742	12 kDa	8.03 ± 3.1	8.41 ± 1.8	7	(3, 14)	10	(10, 21)	0	(0, 1)	
259	Ig heavy chain V-I region HG3	P01743	13 kDa	3.52 ± 2.7	4.29 ± 2.7	2.5	(0, 13)	9	(0, 31)	1	(0, 2)	
260	Ig heavy chain V-I region SIE	P01761	14 kDa	1.43 ± 3.9	3.06 ± 3.7	7	(3, 14)	10	(10, 17)	0	(0, 0)	
261	Ig heavy chain V-I region V35	P23083	13 kDa	3.17 ± 2.7	4.36 ± 3.6	2	(0, 14)	10	(0, 49)	1.5	(0, 4)	
262	Ig heavy chain V-I region WOL	P01760	14 kDa	0.788 ± 1.7	1.53 ± 1.7	0	(0, 8)	0	(0, 18)	0	(0, 2)	
263	Ig heavy chain V-II region ARH-77	P06331	16 kDa	1.15 ± 1.7	2.04 ± 1.6	0	(0, 9)	0	(0, 22)	0	(0, 2)	2
264	Ig heavy chain V-II region NEWM	P01825	13 kDa	0.52 ± 0.94	0.611 ± 1.1	0	(0, 7)	0	(0, 25)	0	(0, 1)	
265	Ig heavy chain V-II region OU	P01814	14 kDa	0.998 ± 1.5	2.03 ± 1.6	0	(0, 7)	0	(0, 18)	0	(0, 3)	
266	Ig heavy chain V-II region SESS	P04438	16 kDa	0.838 ± 1.1	1.83 ± 1.4	0	(0, 4)	0	(0, 20)	0	(0, 1)	
267	Ig heavy chain V-II region WAH	P01824	14 kDa	0.126 ± 0.44	0.631 ± 0.7	0	(0, 4)	0	(0, 21)	0	(0, 3)	
268	Ig heavy chain V-III region BRO	P01766	13 kDa	13.2 ± 6.1	19.8 ± 6.8	11.5	(2, 33)	25	(25, 38)	0	(0, 1)	
269	Ig heavy chain V-III region BUR	P01773	13 kDa	0.672 ± 1.6	0.986 ± 1	0	(0, 9)	0	(0, 23)	0	(0, 4)	
270	Ig heavy chain V-III region BUT	P01767	12 kDa	3.91 ± 1.8	5.32 ± 1.8	3	(1, 11)	21	(10, 44)	0.5	(0, 3)	
271	Ig heavy chain V-III region CAM	P01768	14 kDa	1.76 ± 2.9	4.43 ± 4.8	0	(0, 18)	0	(0, 43)	0	(0, 3)	
272	Ig heavy chain V-III region DOB	P01782	13 kDa	0.128 ± 0.44	0.24 ± 0.59	0	(0, 3)	0	(0, 20)	0	(0, 1)	

			Normalized Total Spectra		Total Spectra		% Sequence Coverage		Number of Unique Peptides		
Protein	Accession	MW	non-GDM	GDM	Median	Range	Median	Range	Median	Range	Rank
273	Ig heavy chain V-III region GA	P01769	13 kDa	0.205 ± 0.6	0.59 ± 1	0	(0, 6)	0	(0, 25)	0	(0, 2)
274	Ig heavy chain V-III region GAL	P01781	13 kDa	4.08 ± 4	7.8 ± 4.5	3	(0, 15)	31	(0, 52)	2	(0, 5)
275	Ig heavy chain V-III region GAR	P80419	13 kDa	0.392 ± 0.56	0.625 ± 0.75	0	(0, 3)	0	(0, 25)	0	(0, 2)
276	Ig heavy chain V-III region HIL	P01771	14 kDa	1.2 ± 1.6	1.88 ± 1.1	1	(0, 7)	9	(0, 40)	1	(0, 5)
277	Ig heavy chain V-III region JON	P01780	13 kDa	0.43 ± 0.92	1.64 ± 1.5	0	(0, 7)	0	(0, 25)	0	(0, 3)
278	Ig heavy chain V-III region KOL	P01772	14 kDa	3.83 ± 2.3	5.24 ± 3.2	3	(0, 14)	13	(0, 21)	1	(0, 2)
279	Ig heavy chain V-III region NIE	P01770	13 kDa	0.768 ± 1	1.05 ± 1.1	0	(0, 4)	5	(0, 35)	0	(0, 2)
280	Ig heavy chain V-III region POM	P01774	13 kDa	1.75 ± 5.1	9.98 ± 8.6	5	(0, 28)	16	(0, 32)	0	(0, 1)
281	Ig heavy chain V-III region TEI	P01777	13 kDa	9.36 ± 6.5	16.7 ± 6.7	10	(1, 29)	16	(16, 24)	0	(0, 1)
282	Ig heavy chain V-III region TIL	P01765	12 kDa	7.71 ± 6.3	15.5 ± 7.4	8.5	(1, 32)	26	(10, 26)	0	(0, 0)
283	Ig heavy chain V-III region TRO	P01762	13 kDa	5.95 ± 3.5	8.71 ± 3	5	(0, 21)	16	(0, 37)	1	(0, 3)
284	Ig heavy chain V-III region TUR	P01779	12 kDa	4.67 ± 5.8	11.1 ± 8.6	6	(0, 29)	25	(0, 35)	0	(0, 1)
285	Ig heavy chain V-III region WAS	P01776	13 kDa	4.84 ± 5.1	11.7 ± 7.2	5	(0, 28)	16	(0, 33)	0	(0, 1)
286	Ig heavy chain V-III region WEA	P01763	12 kDa	1.69 ± 2.3	3.59 ± 2.3	2.5	(1, 10)	10	(10, 44)	0	(0, 2)
287	Ig kappa chain C region	P01834	12 kDa	363 ± 180	585 ± 270	296.5	(94, 1060)	80	(78, 93)	16	(8, 31)
288	Ig kappa chain V-I region AG	P01593	12 kDa	3.08 ± 8.3	7.55 ± 8.6	16.5	(3, 38)	32	(17, 32)	0	(0, 0)

			Normalized Total Spectra		Total Spectra		% Sequence Coverage		Number of Unique Peptides		
Protein	Accession	MW	non-GDM	GDM	Median	Range	Median	Range	Median	Range	Rank
289	Ig kappa chain V-I region AU	P01594	12 kDa	14.1 ± 11	21 ± 9.1	16.5	(3, 39)	32	(17, 47)	1	(0, 3)
290	Ig kappa chain V-I region BAN	P04430	12 kDa	1.03 ± 2.4	6.2 ± 5.3	0	(0, 18)	0	(0, 47)	0	(0, 4)
291	Ig kappa chain V-I region CAR	P01596	12 kDa	8.33 ± 6.9	20.4 ± 10	9	(1, 46)	26	(17, 55)	0	(0, 3)
292	Ig kappa chain V-I region Daudi	P04432	14 kDa	0.736 ± 2.5	0.612 ± 1.5	0	(0, 10)	0	(0, 33)	0	(0, 2)
293	Ig kappa chain V-I region DEE	P01597	12 kDa	7.31 ± 8.6	20.4 ± 18	1	(0, 45)	10	(0, 47)	1	(0, 4)
294	Ig kappa chain V-I region EU	P01598	12 kDa	9.88 ± 7	21.1 ± 11	10	(1, 45)	36	(17, 49)	1	(0, 3)
295	Ig kappa chain V-I region Gal	P01599	12 kDa	14.4 ± 10	22.4 ± 7.4	17.5	(4, 41)	28	(17, 44)	1	(0, 5)
296	Ig kappa chain V-I region Hau	P01600	12 kDa	7.36 ± 10	17 ± 11	16	(3, 35)	24	(17, 44)	0	(0, 1)
297	Ig kappa chain V-I region HK101 (Fragment)	P01601	13 kDa	1.09 ± 3.8	3.2 ± 4.4	0	(0, 18)	0	(0, 44)	0	(0, 5)
298	Ig kappa chain V-I region HK102 (Fragment)	P01602	13 kDa	2.69 ± 3.7	6.77 ± 7.8	0	(0, 25)	0	(0, 53)	0	(0, 2)
299	Ig kappa chain V-I region Ka	P01603	12 kDa	0 ± 0	1.57 ± 2.4	0	(0, 9)	0	(0, 43)	0	(0, 3)
300	Ig kappa chain V-I region Kue	P01604	12 kDa	1.16 ± 1.4	2.79 ± 1.8	1	(0, 6)	10	(0, 38)	0	(0, 2)
301	Ig kappa chain V-I region Lay	P01605	12 kDa	0.996 ± 2.1	1.55 ± 1.6	1	(1, 7)	8	(8, 32)	0	(0, 2)
302	Ig kappa chain V-I region Mev	P01612	12 kDa	2.51 ± 3.8	7.3 ± 4.3	2	(0, 15)	17	(0, 50)	1	(0, 3)
303	Ig kappa chain V-I region Ni	P01613	12 kDa	6.02 ± 4.5	7.55 ± 2.3	5	(0, 21)	30	(0, 30)	1	(0, 2)
304	Ig kappa chain V-I region OU	P01606	12 kDa	0.218 ± 0.52	0.746 ± 1.8	0	(0, 7)	0	(0, 44)	0	(0, 2)

			Normalized Total Spectra		Total Spectra		% Sequence Coverage		Number of Unique Peptides		
Protein	Accession	MW	non-GDM	GDM	Median	Range	Median	Range	Median	Range	Rank
305	Ig kappa chain V-I region Rei	P01607	12 kDa	8.81 ± 12	4.45 ± 11	15	(3, 36)	24	(17, 42)	0	(0, 2)
306	Ig kappa chain V-I region Roy	P01608	12 kDa	15.5 ± 8.3	23.7 ± 8.5	17	(4, 39)	32	(17, 43)	1	(0, 3)
307	Ig kappa chain V-I region Scw	P01609	12 kDa	6.58 ± 10	14.4 ± 11	14.5	(3, 37)	17	(17, 35)	0	(0, 1)
308	Ig kappa chain V-I region Walker	P04431	14 kDa	1.36 ± 3.2	3.59 ± 4.2	0	(0, 15)	0	(0, 47)	0	(0, 5)
309	Ig kappa chain V-I region WAT	P80362	12 kDa	10 ± 11	17 ± 12	15	(3, 36)	17	(17, 43)	0	(0, 1)
310	Ig kappa chain V-I region Wes	P01611	12 kDa	3.74 ± 3	6.06 ± 5.3	3	(0, 17)	20	(0, 48)	1	(0, 3)
311	Ig kappa chain V-II region Cum	P01614	13 kDa	3.5 ± 1.8	6.26 ± 2.9	3	(1, 12)	27	(11, 54)	0	(0, 2)
312	Ig kappa chain V-II region FR	P01615	13 kDa	0.786 ± 1.8	2.81 ± 2.3	0	(0, 9)	0	(0, 27)	0	(0, 2)
313	Ig kappa chain V-II region GM607 (Fragment)	P06309	13 kDa	0.846 ± 1.6	2.08 ± 1	3	(1, 6)	24	(11, 33)	0	(0, 1)
314	Ig kappa chain V-II region MIL	P01616	12 kDa	0.421 ± 1	0.183 ± 0.45	0	(0, 5)	0	(0, 30)	0	(0, 1)
315	Ig kappa chain V-II region RPMI 6410	P06310	15 kDa	2.69 ± 2.1	5.43 ± 2.7	3	(1, 13)	28	(10, 47)	1	(0, 3)
316	Ig kappa chain V-II region TEW	P01617	12 kDa	6.27 ± 3.1	8.66 ± 2.7	5	(2, 19)	33	(12, 43)	1	(0, 2)
317	Ig kappa chain V-III region B6	P01619	12 kDa	5.29 ± 6.1	15.6 ± 6	5.5	(0, 30)	26	(0, 66)	1	(0, 4)
318	Ig kappa chain V-III region CLL	P04207	14 kDa	5.26 ± 4.1	11.2 ± 5.6	4	(1, 23)	21	(7, 55)	1	(0, 6)
319	Ig kappa chain V-III region GOL	P04206	12 kDa	21.8 ± 14	38.3 ± 16	22	(5, 76)	50	(31, 77)	0	(0, 4)
320	Ig kappa chain V-III region HAH	P18135	14 kDa	10.2 ± 11	25.4 ± 15	11	(3, 55)	45	(19, 77)	0	(0, 1)

			Normalized Total Spectra		Total Spectra		% Sequence Coverage		Number of Unique Peptides		
Protein	Accession	MW	non-GDM	GDM	Median	Range	Median	Range	Median	Range	Rank
321	Ig kappa chain V-III region HIC	P18136	14 kDa	7.24 ± 12	22.4 ± 20	11	(3, 55)	48	(19, 64)	0	(0, 1)
322	Ig kappa chain V-III region IARC/BL41	P06311	14 kDa	1.05 ± 1.6	4.24 ± 3.3	0	(0, 11)	0	(0, 39)	0	(0, 5)
323	Ig kappa chain V-III region NG9 (Fragment)	P01621	11 kDa	4.21 ± 7.1	12.3 ± 7.9	6.5	(1, 28)	48	(9, 73)	0	(0, 1)
324	Ig kappa chain V-III region POM	P01624	12 kDa	1.11 ± 2.1	0.881 ± 2.2	2	(1, 13)	8	(8, 31)	0	(0, 1)
325	Ig kappa chain V-III region SIE	P01620	12 kDa	23.7 ± 15	41.3 ± 17	25	(6, 83)	55	(38, 66)	0	(0, 2)
326	Ig kappa chain V-III region VG (Fragment)	P04433	13 kDa	6.73 ± 6.2	9.66 ± 8.4	2.5	(0, 33)	18	(0, 56)	1	(0, 5)
327	Ig kappa chain V-III region VH (Fragment)	P04434	13 kDa	4.17 ± 3.3	8.51 ± 4	3.5	(1, 18)	23	(8, 41)	1	(0, 3)
328	Ig kappa chain V-III region WOL	P01623	12 kDa	23.3 ± 14	38.6 ± 15	23	(6, 74)	46	(38, 66)	0	(0, 2)
329	Ig kappa chain V-IV region JI	P06313	15 kDa	7.26 ± 1.9	11.5 ± 3.9	7	(1, 20)	27	(7, 49)	0	(0, 2)
330	Ig kappa chain V-IV region Len	P01625	13 kDa	8.33 ± 2.7	15.2 ± 6	8	(1, 30)	32	(8, 48)	1	(0, 3)
331	Ig kappa chain V-IV region STH (Fragment)	P83593	12 kDa	2.39 ± 1.2	4.59 ± 1.5	3	(0, 10)	19	(0, 28)	0	(0, 2)
332	Ig lambda chain V region 4A	P04211	12 kDa	3.91 ± 1.7	4.96 ± 2.4	3	(0, 12)	14	(0, 31)	2	(0, 5)
333	Ig lambda chain V-I region BL2	P06316	14 kDa	8.89 ± 6.3	16.3 ± 2.6	11	(0, 25)	19	(0, 31)	0	(0, 4)
334	Ig lambda chain V-I region EPS	P06888	11 kDa	5.3 ± 7	12.8 ± 4.2	8	(0, 22)	17	(0, 45)	0	(0, 2)
335	Ig lambda chain V-I region HA	P01700	12 kDa	5.96 ± 3.6	9.44 ± 5.7	5	(1, 24)	35	(12, 61)	1	(0, 4)
336	Ig lambda chain V-I region NEW	P01701	11 kDa	12.1 ± 9.4	19.7 ± 5.2	11	(0, 40)	24	(0, 75)	1	(0, 6)

			Normalized Total Spectra		Total Spectra		% Sequence Coverage		Number of Unique Peptides			
Protein	Accession	MW	non-GDM	GDM	Median	Range	Median	Range	Median	Range	Rank	
337	Ig lambda chain V-I region NEWM	P01703	11 kDa	6.99 ± 4.1	11.4 ± 5.7	5.5	(2, 26)	27	(17, 42)	2	(1, 5)	
338	Ig lambda chain V-I region NIG-64	P01702	11 kDa	7.94 ± 7	15.5 ± 5	10	(0, 27)	23	(0, 32)	0	(0, 2)	
339	Ig lambda chain V-I region VOR	P01699	12 kDa	6.19 ± 4.8	10.1 ± 4.7	5	(0, 25)	23	(0, 36)	1	(0, 2)	15
340	Ig lambda chain V-I region WAH	P04208	12 kDa	18 ± 9.5	25 ± 6.5	15.5	(4, 57)	38	(22, 42)	1	(0, 3)	
341	Ig lambda chain V-II region BO	P01710	12 kDa	0.0324 ± 0.11	0 ± 0	0	(0, 3)	0	(0, 19)	0	(0, 2)	
342	Ig lambda chain V-II region BOH	P01706	12 kDa	1.71 ± 1.1	5.57 ± 3.9	3	(0, 15)	7	(0, 61)	0	(0, 3)	
343	Ig lambda chain V-II region MGC	P01709	12 kDa	1.02 ± 1.9	2.65 ± 4.1	0	(0, 16)	0	(0, 14)	0	(0, 2)	
344	Ig lambda chain V-II region NIG-58	P01713	11 kDa	0.21 ± 0.73	0 ± 0	3	(0, 14)	7	(0, 16)	0	(0, 0)	
345	Ig lambda chain V-II region NIG-84	P04209	12 kDa	0.531 ± 1.6	0.631 ± 1.4	0	(0, 8)	0	(0, 47)	0	(0, 4)	
346	Ig lambda chain V-II region TRO	P01707	12 kDa	3.66 ± 3	8.66 ± 8	5	(0, 22)	14	(0, 51)	0	(0, 1)	
347	Ig lambda chain V-II region WIN	P01712	12 kDa	0 ± 0	0.978 ± 2.4	0	(0, 16)	0	(0, 16)	0	(0, 1)	
348	Ig lambda chain V-III region LOI	P80748	12 kDa	14.3 ± 6.5	20.7 ± 7.1	14	(3, 37)	30	(15, 63)	4	(2, 8)	
349	Ig lambda chain V-III region SH	P01714	11 kDa	9.37 ± 6.5	15.2 ± 4.3	8.5	(0, 32)	42	(0, 65)	3	(0, 7)	
350	Ig lambda chain V-IV region Bau	P01715	11 kDa	8.71 ± 7.1	17.9 ± 4.3	12	(0, 29)	15	(0, 28)	2	(0, 4)	
351	Ig lambda chain V-IV region Hil	P01717	12 kDa	7.47 ± 4	12.4 ± 3.2	7.5	(1, 26)	28	(18, 46)	3	(1, 6)	
352	Ig lambda chain V-IV region MOL	P06889	11 kDa	0.649 ± 1.1	2.59 ± 2.3	0	(0, 6)	0	(0, 37)	0	(0, 2)	

			Normalized Total Spectra		Total Spectra		% Sequence Coverage		Number of Unique Peptides		
Protein	Accession	MW	non-GDM	GDM	Median	Range	Median	Range	Median	Range	Rank
353	Ig lambda chain V-IV region X	P01716	11 kDa	0.082 ± 0.28	0 ± 0	0	(0, 2)	0	(0, 31)	0	(0, 2)
354	Ig lambda chain V-V region DEL	P01719	11 kDa	2.1 ± 4.4	4.38 ± 4.5	0	(0, 19)	0	(0, 65)	0	(0, 7)
355	Ig lambda chain V-VI region AR	P01721	12 kDa	0.158 ± 0.55	0 ± 0	0	(0, 5)	0	(0, 27)	0	(0, 1)
356	Ig lambda chain V-VI region EB4	P06319	14 kDa	0.516 ± 0.83	0.33 ± 0.81	0	(0, 6)	0	(0, 40)	0	(0, 2)
357	Ig lambda chain V-VI region NIG-48	P01722	12 kDa	0 ± 0	0.371 ± 0.91	0	(0, 3)	0	(0, 23)	0	(0, 2)
358	Ig lambda chain V-VI region SUT	P06317	12 kDa	3.08 ± 3.6	3.43 ± 3.3	2	(0, 13)	6	(0, 35)	1.5	(0, 3)
359	Ig lambda chain V-VI region WLT	P06318	12 kDa	0.128 ± 0.3	0.33 ± 0.81	0	(0, 3)	0	(0, 25)	0	(0, 1)
360	Ig lambda-1 chain C regions	P0CG04	11 kDa	112 ± 52	165 ± 25	111.5	(33, 338)	69	(51, 96)	0	(0, 1)
361	Ig lambda-2 chain C regions	P0CG05	11 kDa	142 ± 49	193 ± 34	142.5	(52, 359)	82	(51, 96)	0	(0, 2)
362	Ig lambda-3 chain C regions	P0CG06	11 kDa	145 ± 50	197 ± 34	146.5	(52, 361)	87	(51, 96)	2	(0, 4)
363	Ig lambda-6 chain C region	P0CF74	11 kDa	110 ± 47	149 ± 21	113.5	(46, 321)	49	(32, 70)	0	(0, 1)
364	Ig lambda-7 chain C region	A0M8Q6	11 kDa	97 ± 37	124 ± 21	94	(44, 270)	49	(32, 74)	1	(0, 3)
365	Ig mu chain C region	P01871	49 kDa	60.3 ± 37	88.3 ± 48	60	(7, 157)	38	(14, 49)	7	(2, 11)
366	Ig mu heavy chain disease protein	P04220	43 kDa	33.9 ± 22	55.3 ± 32	31.5	(3, 102)	31	(10, 44)	1	(0, 6)
367	IgGFc-binding protein	Q9Y6R7	572 kDa	1.68 ± 4.4	0.377 ± 0.74	0	(0, 21)	0	(0, 3)	0	(0, 14)
368	Immunoglobulin J chain	P01591	18 kDa	138 ± 120	248 ± 140	105.5	(47, 757)	66	(42, 76)	10.5	(6, 26)

				Normalized Total Spectra		Total Spectra		% Sequence Coverage		Number of Unique Peptides		
Protein	Accession	MW	non-GDM	GDM	Median	Range	Median	Range	Median	Range	Rank	
369	Immunoglobulin lambda-like polypeptide 1	P15814	23 kDa	1.69 ± 2	2.98 ± 2.1	1	(0, 9)	7	(0, 23)	1	(0, 4)	
370	Insulin-like growth factor-binding protein 2	P18065	35 kDa	12.8 ± 10	1.96 ± 2.6	9	(0, 28)	18	(0, 45)	5.5	(0, 13)	
371	Integrin beta-like protein 1	O95965	54 kDa	0.372 ± 0.84	0.14 ± 0.34	0	(0, 4)	0	(0, 9)	0	(0, 4)	
372	Inter-alpha-trypsin inhibitor heavy chain H4	Q14624	103 kDa	0.526 ± 1.1	0.171 ± 0.27	0	(0, 5)	0	(0, 4)	0	(0, 4)	
373	IST1 homolog	P53990	40 kDa	0.048 ± 0.17	0 ± 0	0	(0, 2)	0	(0, 6)	0	(0, 2)	
374	Junction plakoglobin	P14923	82 kDa	0 ± 0	0.911 ± 1.8	0	(0, 7)	0	(0, 8)	0	(0, 5)	
375	Kallikrein-11	Q9UBX7	31 kDa	0 ± 0	0.4 ± 0.81	0	(0, 3)	0	(0, 6)	0	(0, 2)	
376	Kallikrein-6	Q92876	27 kDa	2.94 ± 2.3	2.25 ± 1.7	2	(0, 9)	10	(0, 39)	2	(0, 7)	
377	Kappa-casein	P07498	20 kDa	391 ± 130	193 ± 180	346.5	(24, 570)	55	(34, 60)	30	(8, 49)	
378	Keratin, type I cuticular Ha1	Q15323	47 kDa	0.082 ± 0.28	2.17 ± 5.3	1	(0, 18)	2	(0, 15)	0	(0, 0)	
379	Keratin, type I cuticular Ha2	Q14532	50 kDa	0.594 ± 1.6	1.4 ± 3	1	(0, 11)	2	(0, 4)	0	(0, 0)	
380	Keratin, type I cuticular Ha3-II	Q14525	46 kDa	0.703 ± 1.7	2.36 ± 5.8	1	(0, 20)	2	(0, 16)	0	(0, 2)	
381	Keratin, type I cuticular Ha4	O76011	49 kDa	0 ± 0	2.05 ± 5	0	(0, 18)	0	(0, 9)	0	(0, 0)	
382	Keratin, type I cuticular Ha5	Q92764	50 kDa	0 ± 0	0.498 ± 1.2	1	(0, 11)	2	(0, 7)	0	(0, 1)	
383	Keratin, type I cuticular Ha7	O76014	50 kDa	0 ± 0	0.745 ± 1.8	1	(0, 11)	2	(0, 4)	0	(0, 0)	
384	Keratin, type I cytoskeletal 14	P02533	52 kDa	12.5 ± 8.5	8.73 ± 8.6	12.5	(4, 39)	9	(2, 24)	0	(0, 3)	

			Normalized Total Spectra		Total Spectra		% Sequence Coverage		Number of Unique Peptides		
Protein	Accession	MW	non-GDM	GDM	Median	Range	Median	Range	Median	Range	Rank
385	Keratin, type I cytoskeletal 15	P19012	49 kDa	4.11 ± 5.1	3.33 ± 3.7	5	(0, 19)	5	(0, 10)	0	(0, 1)
386	Keratin, type I cytoskeletal 16	P08779	51 kDa	13.6 ± 7.7	10.2 ± 5.7	12	(4, 40)	7	(2, 24)	0	(0, 5)
387	Keratin, type I cytoskeletal 19	P08727	44 kDa	2.53 ± 4.9	2.85 ± 3.4	4.5	(0, 18)	5	(0, 11)	0	(0, 1)
388	Keratin, type I cytoskeletal 20	P35900	48 kDa	0 ± 0	0.493 ± 1.2	0	(0, 6)	0	(0, 4)	0	(0, 0)
389	Keratin, type I cytoskeletal 24	Q2M2I5	55 kDa	1.62 ± 1.8	2.05 ± 2.1	4	(0, 18)	2	(0, 3)	0	(0, 0)
390	Keratin, type I cytoskeletal 28	Q7Z3Y7	51 kDa	0.815 ± 2.8	0 ± 0	12.5	(3, 39)	4	(3, 7)	0	(0, 1)
391	Keratin, type I cytoskeletal 9	P35527	62 kDa	25.1 ± 8.4	34.2 ± 17	31	(7, 61)	34	(7, 58)	14	(3, 24)
392	Keratin, type II cuticular Hb1	Q14533	55 kDa	0.348 ± 1	2.23 ± 5.5	0	(0, 20)	0	(0, 16)	0	(0, 1)
393	Keratin, type II cuticular Hb2	Q9NSB4	57 kDa	0 ± 0	0.93 ± 2.3	0	(0, 8)	0	(0, 5)	0	(0, 0)
394	Keratin, type II cytoskeletal 1	P04264	66 kDa	59.6 ± 17	75 ± 31	63.5	(20, 145)	42	(17, 54)	21	(7, 30)
395	Keratin, type II cytoskeletal 1b	Q7Z794	62 kDa	0.68 ± 0.92	2.04 ± 3.4	3	(1, 11)	3	(2, 7)	0	(0, 1)
396	Keratin, type II cytoskeletal 2 oral	Q01546	66 kDa	0 ± 0	0.44 ± 1.1	10	(0, 19)	4	(0, 7)	0	(0, 0)
397	Keratin, type II cytoskeletal 3	P12035	64 kDa	0.834 ± 1.7	2.12 ± 2.5	6	(0, 15)	3	(0, 7)	0	(0, 1)
398	Keratin, type II cytoskeletal 4	P19013	57 kDa	0.069 ± 0.24	0.454 ± 0.71	3	(0, 9)	2	(0, 5)	0	(0, 0)
399	Keratin, type II cytoskeletal 5	P13647	62 kDa	8.65 ± 4	17.6 ± 12	10	(2, 42)	10	(3, 29)	3	(0, 12)
400	Keratin, type II cytoskeletal 6A	P02538	60 kDa	4.3 ± 6.3	11.3 ± 13	11	(0, 36)	9	(0, 25)	0	(0, 1)

			Normalized Total Spectra		Total Spectra		% Sequence Coverage		Number of Unique Peptides			
Protein	Accession	MW	non-GDM	GDM	Median	Range	Median	Range	Median	Range	Rank	
401	Keratin, type II cytoskeletal 6C	P48668	60 kDa	5.6 ± 5.8	12.9 ± 12	11	(0, 36)	9	(0, 27)	0	(0, 1)	
402	Keratin, type II cytoskeletal 7	P08729	51 kDa	0.161 ± 0.35	0.434 ± 1.1	0	(0, 4)	0	(0, 7)	0	(0, 1)	
403	Keratin, type II cytoskeletal 71	Q3SY84	57 kDa	0 ± 0	0.32 ± 0.78	0	(0, 4)	0	(0, 4)	0	(0, 0)	
404	Keratin, type II cytoskeletal 72	Q14CN4	56 kDa	0.143 ± 0.36	0.84 ± 1.1	0	(0, 4)	0	(0, 4)	0	(0, 1)	
405	Keratin, type II cytoskeletal 73	Q86Y46	59 kDa	0 ± 0	0.508 ± 0.83	0	(0, 5)	0	(0, 6)	0	(0, 0)	
406	Keratin, type II cytoskeletal 74	Q7RTS7	58 kDa	0 ± 0	0.0672 ± 0.16	0	(0, 6)	0	(0, 5)	0	(0, 0)	
407	Keratin, type II cytoskeletal 75	O95678	60 kDa	1.29 ± 2	3.7 ± 5.8	3	(0, 18)	4	(0, 10)	0	(0, 2)	
408	Keratin, type II cytoskeletal 79	Q5XKE5	58 kDa	0.0601 ± 0.21	0 ± 0	3	(0, 16)	4	(0, 12)	0	(0, 0)	
409	Keratin, type II cytoskeletal 8	P05787	54 kDa	0.192 ± 0.67	1.44 ± 2.7	4.5	(0, 18)	2	(0, 7)	0	(0, 1)	
410	Kin of IRRE-like protein 3	Q8IZU9	85 kDa	0.24 ± 0.41	0.898 ± 1.1	0	(0, 4)	0	(0, 2)	0	(0, 2)	
411	Kininogen-1	P01042	72 kDa	8.05 ± 3	4.35 ± 2	7	(1, 11)	10	(2, 18)	5	(1, 10)	13
412	Kunitz-type protease inhibitor 1	O43278	58 kDa	2.25 ± 1.4	1.4 ± 0.94	2	(0, 6)	3	(0, 9)	2	(0, 5)	
413	Lactadherin	Q08431	43 kDa	38.3 ± 18	38.9 ± 13	32	(14, 100)	48	(30, 71)	15	(9, 28)	
414	Lactoperoxidase	P22079	80 kDa	0.553 ± 1.1	0 ± 0	0	(0, 4)	0	(0, 6)	0	(0, 4)	
415	Lactotransferrin	P02788	78 kDa	1050 ± 250	973 ± 310	1049	(562, 1817)	81	(75, 88)	104	(73, 134)	
416	Laminin subunit beta-4	A4D0S4	194 kDa	0.0632 ± 0.22	0.0677 ± 0.17	0	(0, 2)	0	(0, 1)	0	(0, 2)	

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Protein	Accession	MW	non-GDM	GDM	Median	Range	Median	Range	Median	Range	Rank
417	Latent-transforming growth factor beta-binding protein 1	Q14766	187 kDa	0.515 ± 0.58	0.69 ± 0.56	1	(0, 3)	1	(0, 2)	1	(0, 2)
418	Latent-transforming growth factor beta-binding protein 3	Q9NS15	139 kDa	0.0977 ± 0.34	0 ± 0	0	(0, 2)	0	(0, 2)	0	(0, 2)
419	Leucine-rich alpha-2-glycoprotein	P02750	38 kDa	72.7 ± 15	58.9 ± 26	67	(31, 104)	46	(32, 52)	13	(9, 16)
420	Leucine-rich repeat transmembrane neuronal protein 2	O43300	59 kDa	0.102 ± 0.26	0 ± 0	0	(0, 2)	0	(0, 3)	0	(0, 2)
421	Leucine-rich repeat-containing protein 15	Q8TF66	64 kDa	0 ± 0	0.435 ± 1.1	0	(0, 4)	0	(0, 4)	0	(0, 3)
422	LIM and SH3 domain protein 1	Q14847	30 kDa	0.352 ± 0.93	0.0684 ± 0.17	0	(0, 5)	0	(0, 13)	0	(0, 4)
423	Lipolysis-stimulated lipoprotein receptor	Q86X29	71 kDa	1.41 ± 1.2	0.986 ± 1.3	1	(0, 7)	2	(0, 8)	1	(0, 4)
424	Lipoprotein lipase	P06858	53 kDa	31.6 ± 14	20.2 ± 21	28.5	(0, 74)	33	(0, 43)	12	(0, 22)
425	Long-chain-fatty-acid--CoA ligase 4	O60488	79 kDa	0.144 ± 0.5	0.136 ± 0.21	0	(0, 3)	0	(0, 4)	0	(0, 2)
426	Ly6/PLAUR domain-containing protein 3	O95274	36 kDa	0.991 ± 1.1	1.61 ± 1.5	1	(0, 5)	4	(0, 15)	1	(0, 4)
427	Lymphocyte antigen 6D	Q14210	13 kDa	0.667 ± 1.2	0.62 ± 1	0	(0, 5)	0	(0, 23)	0	(0, 3)
428	Lysosomal alpha-glucosidase	P10253	105 kDa	0.425 ± 0.71	0.337 ± 0.54	0	(0, 3)	0	(0, 3)	0	(0, 2)
429	Lysosome-associated membrane glycoprotein 2	P13473	45 kDa	0.676 ± 1.3	1.22 ± 1.1	0	(0, 5)	0	(0, 7)	0	(0, 3)
430	Lysozyme C	P61626	17 kDa	5.98 ± 5.6	7.32 ± 5.5	5	(0, 30)	29	(0, 49)	3	(0, 9)
431	Macrophage colony-stimulating factor 1	P09603	60 kDa	1.17 ± 1.5	0.269 ± 0.66	0	(0, 5)	0	(0, 5)	0	(0, 2)
432	Macrophage mannose receptor 1	P22897	166 kDa	7.45 ± 8.2	2.93 ± 4.6	6	(0, 93)	4	(0, 35)	5.5	(0, 47)

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433	Macrophage migration inhibitory factor	P14174	12 kDa	0.833 ± 0.58	0.267 ± 0.49	0.5	(0, 2)	0	(0, 17)	0.5	(0, 2)	22
434	Macrophage-capping protein	P40121	38 kDa	0.0705 ± 0.24	0.252 ± 0.45	0	(0, 2)	0	(0, 7)	0	(0, 2)	
435	Mammaglobin-A	Q13296	10 kDa	1.11 ± 1.8	4.58 ± 2.7	1	(0, 12)	9	(0, 23)	1	(0, 2)	
436	MARCKS-related protein	P49006	20 kDa	1.43 ± 1.3	0.702 ± 0.78	1	(0, 3)	7	(0, 14)	1	(0, 2)	
437	Matrilin-3	O15232	53 kDa	5.07 ± 3.1	2.77 ± 4.5	3.5	(0, 14)	7	(0, 27)	3	(0, 10)	
438	Matrilysin	P09237	30 kDa	0.0802 ± 0.28	0.185 ± 0.45	0	(0, 2)	0	(0, 6)	0	(0, 1)	
439	Matrix Gla protein	P08493	12 kDa	0.244 ± 0.46	0.445 ± 0.53	0	(0, 2)	0	(0, 19)	0	(0, 2)	
440	Melanotransferrin	P08582	80 kDa	0 ± 0	0.601 ± 1.3	0	(0, 5)	0	(0, 9)	0	(0, 5)	
441	Metalloproteinase inhibitor 1	P01033	23 kDa	2.98 ± 2.3	2.61 ± 3.5	3	(0, 11)	13	(0, 52)	2.5	(0, 9)	
442	Microfibrillar-associated protein 2	P55001	21 kDa	3.36 ± 1.8	2.18 ± 2	2.5	(0, 9)	5	(0, 15)	1.5	(0, 4)	
443	Moesin	P26038	68 kDa	0.529 ± 0.79	0.0672 ± 0.16	0	(0, 3)	0	(0, 5)	0	(0, 2)	
444	Monocyte differentiation antigen CD14	P08571	40 kDa	45.3 ± 13	33.8 ± 27	40	(4, 75)	49	(9, 62)	14	(3, 16)	
445	Msx2-interacting protein	Q96T58	402 kDa	0.535 ± 0.55	0.376 ± 0.33	0	(0, 2)	0	(0, 1)	0	(0, 2)	
446	Mucin-1	P15941	122 kDa	18.3 ± 5.1	11.8 ± 4.5	16	(8, 30)	5	(2, 7)	5	(3, 7)	11
447	Mucin-16	Q8WXI7	2353 kDa	0 ± 0	0.674 ± 1.7	0	(0, 5)	0	(0, 0)	0	(0, 5)	
448	Mucin-4	Q99102	232 kDa	4.6 ± 3.4	2.33 ± 1.5	3	(0, 12)	1	(0, 6)	3	(0, 9)	

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449	Mucin-5B	Q9HC84	596 kDa	0.864 ± 2.9	6.91 ± 10	0	(0, 36)	0	(0, 5)	0	(0, 20)
450	Mucin-6	Q6W4X9	257 kDa	0 ± 0	1.25 ± 1.7	0	(0, 5)	0	(0, 2)	0	(0, 4)
451	Mucin-like protein 1	Q96DR8	9 kDa	4.89 ± 4.5	5.48 ± 3.4	5	(0, 12)	10	(0, 18)	1	(0, 2)
452	Multiple coagulation factor deficiency protein 2	Q8NI22	16 kDa	0 ± 0	0.144 ± 0.35	0	(0, 2)	0	(0, 23)	0	(0, 2)
453	Myeloperoxidase	P05164	84 kDa	0.945 ± 2.6	2.04 ± 2.8	0	(0, 14)	0	(0, 16)	0	(0, 9)
454	Myosin light chain 6B	P14649	23 kDa	0.384 ± 0.43	0.304 ± 0.74	0	(0, 2)	0	(0, 10)	0	(0, 1)
455	Myosin light polypeptide 6	P60660	17 kDa	1.07 ± 0.97	0.537 ± 0.97	1	(0, 4)	6	(0, 25)	0	(0, 2)
456	Myosin-9	P35579	227 kDa	0.141 ± 0.36	0.197 ± 0.34	0	(0, 3)	0	(0, 2)	0	(0, 3)
457	Myristoylated alanine-rich C-kinase substrate	P29966	32 kDa	4.52 ± 4.5	0.594 ± 1.2	2	(0, 14)	7	(0, 31)	2	(0, 7)
458	N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase	P20933	37 kDa	0.134 ± 0.36	0.391 ± 0.69	0	(0, 3)	0	(0, 7)	0	(0, 2)
459	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	O94760	31 kDa	0.14 ± 0.26	0 ± 0	0	(0, 2)	0	(0, 7)	0	(0, 2)
460	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	O14745	39 kDa	7.1 ± 5.4	1.18 ± 1	3	(0, 14)	9	(0, 37)	3	(0, 10)
461	Nephronectin	Q6UXI9	62 kDa	0.829 ± 1.1	0.209 ± 0.51	0	(0, 4)	0	(0, 9)	0	(0, 4)
462	Neuroendocrine secretory protein 55	O95467	28 kDa	0 ± 0	0.702 ± 1.7	0	(0, 5)	0	(0, 11)	0	(0, 3)
463	Neuropilin-1	O14786	103 kDa	0.101 ± 0.25	1.23 ± 2.6	0	(0, 9)	0	(0, 12)	0	(0, 8)
464	Neuroserpin	Q99574	46 kDa	1.01 ± 1.1	1.56 ± 1.3	1	(0, 4)	2	(0, 10)	1	(0, 4)

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Protein	Accession	MW	non-GDM	GDM	Median	Range	Median	Range	Median	Range	Rank
465	Neutral alpha-glucosidase AB	Q14697	107 kDa	2.14 ± 1.8	0.725 ± 1.2	1	(0, 8)	2	(0, 8)	1	(0, 7)
466	Neutrophil defensin 1	P59665	10 kDa	4.57 ± 1.5	6.74 ± 1.9	4.5	(0, 11)	19	(0, 19)	0	(0, 0)
467	Neutrophil defensin 3	P59666	10 kDa	4.57 ± 1.5	6.74 ± 1.9	4.5	(0, 11)	19	(0, 19)	0	(0, 0)
468	Neutrophil elastase	P08246	29 kDa	0.719 ± 2.3	0.0612 ± 0.15	0	(0, 11)	0	(0, 23)	0	(0, 5)
469	Nuclear receptor coactivator 2	Q15596	159 kDa	0 ± 0	0.36 ± 0.44	0	(0, 2)	0	(0, 1)	0	(0, 2)
470	Nuclease-sensitive element-binding protein 1	P67809	36 kDa	0.159 ± 0.33	0 ± 0	0	(0, 3)	0	(0, 12)	0	(0, 2)
471	Nucleobindin-1	Q02818	54 kDa	26.7 ± 11	11.6 ± 13	21	(0, 43)	37	(0, 59)	14	(0, 22)
472	Nucleobindin-2	P80303	50 kDa	18.5 ± 12	7.89 ± 11	12.5	(0, 39)	24	(0, 50)	8	(0, 16)
473	Nucleotide exchange factor SIL1	Q9H173	52 kDa	2.2 ± 1.6	0.866 ± 0.99	2	(0, 4)	4	(0, 11)	2	(0, 3)
474	Olfactomedin-4	Q6UX06	57 kDa	2.67 ± 4.3	4.08 ± 5	0	(0, 20)	0	(0, 24)	0	(0, 12)
475	Olfactomedin-like protein 3	Q9NRN5	46 kDa	0.0458 ± 0.16	0 ± 0	0	(0, 1)	0	(0, 7)	0	(0, 1)
476	Osteopontin	P10451	35 kDa	89.4 ± 50	65.6 ± 67	84	(6, 176)	43	(13, 63)	16	(4, 27)
477	Parathyroid hormone-related protein	P12272	20 kDa	0.0667 ± 0.23	0 ± 0	0	(0, 4)	0	(0, 24)	0	(0, 3)
478	Peptidyl-prolyl cis-trans isomerase B	P23284	24 kDa	1.57 ± 2	1.55 ± 2.4	1	(0, 12)	4	(0, 30)	1	(0, 7)
479	Peptidyl-prolyl cis-trans isomerase C	P45877	23 kDa	1.44 ± 1.3	0.622 ± 1.1	1	(0, 5)	6	(0, 15)	1	(0, 3)
480	Perilipin-2	Q99541	48 kDa	5.92 ± 5.7	1.34 ± 1.5	3	(0, 22)	7	(0, 40)	3	(0, 12)

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481	Perilipin-3	O60664	47 kDa	3.65 ± 6.8	0.346 ± 0.85	1	(0, 23)	3	(0, 45)	1	(0, 13)
482	Peroxiredoxin-1	Q06830	22 kDa	2.77 ± 2	2.38 ± 1.3	2	(0, 8)	11	(0, 38)	1	(0, 5)
483	Peroxiredoxin-2	P32119	22 kDa	1.95 ± 1.7	0.228 ± 0.36	1	(0, 5)	4	(0, 24)	0	(0, 4)
484	Peroxiredoxin-4	Q13162	31 kDa	0 ± 0	0.715 ± 1	0	(0, 4)	0	(0, 11)	0	(0, 0)
485	Peroxiredoxin-5, mitochondrial	P30044	22 kDa	0.146 ± 0.34	0 ± 0	0	(0, 2)	0	(0, 9)	0	(0, 2)
486	Phosphatidylethanolamine-binding protein 1	P30086	21 kDa	1.95 ± 1.4	0.707 ± 1.1	1	(0, 6)	8	(0, 32)	1	(0, 5)
487	Phosphatidylethanolamine-binding protein 4	Q96S96	26 kDa	0.19 ± 0.32	0.233 ± 0.37	0	(0, 2)	0	(0, 7)	0	(0, 2)
488	Plasma protease C1 inhibitor	P05155	55 kDa	0.947 ± 0.84	0.845 ± 1.1	1	(0, 6)	2	(0, 12)	1	(0, 5)
489	Plasminogen	P00747	91 kDa	7.41 ± 5.7	8.25 ± 4.9	7	(0, 25)	7	(0, 27)	5	(0, 17)
490	Plasminogen activator inhibitor 1 RNA-binding protein	Q8NC51	45 kDa	0.233 ± 0.38	0.0684 ± 0.17	0	(0, 3)	0	(0, 9)	0	(0, 3)
491	Platelet glycoprotein 4	P16671	53 kDa	5.84 ± 3	3.2 ± 1.4	4	(1, 11)	8	(0, 22)	3.5	(1, 8)
492	Platelet-derived growth factor C	Q9NRA1	39 kDa	0.123 ± 0.43	0 ± 0	0	(0, 1)	0	(0, 5)	0	(0, 1)
493	Podocalyxin	O00592	59 kDa	5.18 ± 1.8	3.86 ± 2.1	4.5	(0, 8)	6	(0, 10)	3	(0, 6)
494	Podocalyxin-like protein 2	Q9NZ53	65 kDa	0.326 ± 0.53	0.433 ± 0.67	0	(0, 2)	0	(0, 7)	0	(0, 2)
495	Poliovirus receptor	P15151	45 kDa	0.199 ± 0.47	0.14 ± 0.34	0	(0, 2)	0	(0, 6)	0	(0, 2)
496	Polymeric immunoglobulin receptor	P01833	83 kDa	897 ± 170	1050 ± 240	947	(349, 1564)	55	(49, 61)	70.5	(54, 101)

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Protein	Accession	MW	non-GDM	GDM	Median	Range	Median	Range	Median	Range	Rank	
497	POTE ankyrin domain family member E	Q6S8J3	121 kDa	7.03 ± 3.2	5.34 ± 3.6	6.5	(1, 21)	4	(1, 7)	0	(0, 0)	
498	POTE ankyrin domain family member I	P0CG38	121 kDa	5.87 ± 2.9	4.76 ± 2.4	6	(0, 18)	3	(0, 5)	0	(0, 1)	
499	POTE ankyrin domain family member J	P0CG39	117 kDa	0.255 ± 0.88	1.13 ± 2	3	(0, 11)	2	(0, 3)	0	(0, 0)	
500	Pregnancy-specific beta-1-glycoprotein 1	P11464	47 kDa	0.243 ± 0.38	0.2 ± 0.49	0	(0, 1)	0	(0, 5)	0	(0, 1)	
501	Pre-miRNA 5'-monophosphate methyltransferase	Q7Z5W3	33 kDa	0.0678 ± 0.23	0 ± 0	0	(0, 2)	0	(0, 7)	0	(0, 2)	
502	Proactivator polypeptide	P07602	58 kDa	56.2 ± 30	47.2 ± 32	44.5	(12, 114)	42	(14, 60)	20	(8, 33)	
503	Probable ATP-dependent RNA helicase DDX46	Q7L014	117 kDa	0.261 ± 0.41	0.304 ± 0.74	0	(0, 2)	0	(0, 2)	0	(0, 2)	
504	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	Q02809	84 kDa	0.241 ± 0.84	0 ± 0	0	(0, 4)	0	(0, 4)	0	(0, 2)	
505	Pro-epidermal growth factor	P01133	134 kDa	0.775 ± 0.68	1.18 ± 1.2	1	(0, 4)	1	(0, 5)	1	(0, 3)	
506	Profilin-1	P07737	15 kDa	2.59 ± 2.6	0.704 ± 1.2	1	(0, 12)	11	(0, 46)	1	(0, 5)	
507	Prolactin-inducible protein	P12273	17 kDa	25 ± 8.9	34.3 ± 10	26	(4, 60)	58	(29, 66)	8	(3, 14)	
508	Prominin-1	O43490	97 kDa	0.198 ± 0.49	0.742 ± 1.8	0	(0, 6)	0	(0, 8)	0	(0, 5)	
509	Prostasin	Q16651	36 kDa	4.59 ± 2	7.95 ± 4.2	5	(0, 21)	13	(0, 32)	3	(0, 8)	6
510	Proteasome activator complex subunit 1	Q06323	29 kDa	0.15 ± 0.41	0 ± 0	0	(0, 2)	0	(0, 8)	0	(0, 2)	
511	Protein AHNAK2	Q8IVF2	617 kDa	0.0958 ± 0.24	0.207 ± 0.51	0	(0, 2)	0	(0, 0)	0	(0, 2)	
512	Protein AMBP	P02760	39 kDa	2.48 ± 1.9	1.85 ± 1.4	2	(0, 10)	6	(0, 22)	2	(0, 4)	

			Normalized Total Spectra		Total Spectra		% Sequence Coverage		Number of Unique Peptides			
Protein	Accession	MW	non-GDM	GDM	Median	Range	Median	Range	Median	Range	Rank	
513	Protein CutA	O60888	19 kDa	2.25 ± 1.3	1.62 ± 1.5	2	(0, 6)	8	(0, 23)	1	(0, 2)	
514	Protein disulfide-isomerase	P07237	57 kDa	1.36 ± 1.7	0.275 ± 0.51	0	(0, 7)	0	(0, 18)	0	(0, 6)	21
515	Protein disulfide-isomerase A3	P30101	57 kDa	0.203 ± 0.39	0 ± 0	0	(0, 2)	0	(0, 5)	0	(0, 2)	
516	Protein DJ-1	Q99497	20 kDa	1.08 ± 0.79	0.0965 ± 0.24	0	(0, 3)	0	(0, 12)	0	(0, 3)	3
517	Protein FAM3B	P58499	26 kDa	2.77 ± 1.6	0.876 ± 1.3	2	(0, 6)	7	(0, 29)	2	(0, 6)	5
518	Protein OS-9	Q13438	76 kDa	3.83 ± 2.6	0.938 ± 1.6	2	(0, 10)	3	(0, 14)	2	(0, 9)	
519	Protein S100-A1	P23297	11 kDa	1.72 ± 1.4	0.635 ± 0.67	1	(0, 4)	19	(0, 38)	1	(0, 2)	
520	Protein S100-A11	P31949	12 kDa	0.608 ± 0.73	1.61 ± 1.6	1	(0, 7)	9	(0, 28)	1	(0, 3)	
521	Protein S100-A12	P80511	11 kDa	0.129 ± 0.34	0.461 ± 0.82	0	(0, 3)	0	(0, 10)	0	(0, 2)	
522	Protein S100-A4	P26447	12 kDa	0.138 ± 0.48	0.063 ± 0.15	0	(0, 2)	0	(0, 17)	0	(0, 2)	
523	Protein S100-A6	P06703	10 kDa	0.524 ± 0.86	1.17 ± 1	1	(0, 4)	8	(0, 24)	0.5	(0, 2)	
524	Protein S100-A8	P05109	11 kDa	2.93 ± 3.7	6.03 ± 4.3	3	(0, 18)	28	(0, 67)	3	(0, 8)	
525	Protein S100-A9	P06702	13 kDa	3.85 ± 3.6	12.4 ± 9.2	4	(0, 36)	42	(0, 90)	3	(0, 11)	
526	Protein S100-P	P25815	10 kDa	0.199 ± 0.36	0.615 ± 0.69	0	(0, 2)	0	(0, 24)	0	(0, 2)	
527	Prothrombin	P00734	70 kDa	1.74 ± 1.6	0.656 ± 0.49	1	(0, 6)	2	(0, 12)	1	(0, 5)	
528	Putative beta-actin-like protein 3	Q9BYX7	42 kDa	1.89 ± 2	2.21 ± 1.9	3	(0, 10)	7	(0, 13)	0	(0, 0)	

				Normalized Total Spectra		Total Spectra		% Sequence Coverage		Number of Unique Peptides		
Protein	Accession	MW	non-GDM	GDM	Median	Range	Median	Range	Median	Range	Rank	
529	Putative heat shock protein HSP 90-beta 2	Q58FF8	44 kDa	0.0705 ± 0.24	0 ± 0	0	(0, 2)	0	(0, 6)	0	(0, 0)	
530	Putative V-set and immunoglobulin domain-containing-like protein IGHV4OR15-8	A6NJ16	14 kDa	0.49 ± 0.5	0.557 ± 0.49	0	(0, 2)	0	(0, 12)	0	(0, 2)	
531	Putative zinc-alpha-2-glycoprotein-like 1	A8MT79	23 kDa	10.2 ± 6.7	17.6 ± 4.9	15	(7, 30)	23	(13, 30)	0	(0, 1)	
532	Rab GDP dissociation inhibitor beta	P50395	51 kDa	0.149 ± 0.52	0 ± 0	0	(0, 2)	0	(0, 4)	0	(0, 1)	
533	Radixin	P35241	69 kDa	0.336 ± 0.6	0 ± 0	0	(0, 4)	0	(0, 7)	0	(0, 2)	
534	Ras-related protein Rab-13	P51153	23 kDa	0.0474 ± 0.16	0 ± 0	0	(0, 4)	0	(0, 10)	0	(0, 2)	
535	Ras-related protein Rap-1b-like protein	A6NIZ1	21 kDa	0.128 ± 0.34	0 ± 0	0	(0, 2)	0	(0, 10)	0	(0, 1)	
536	Reticulocalbin-1	Q15293	39 kDa	0.148 ± 0.28	0 ± 0	0	(0, 4)	0	(0, 10)	0	(0, 2)	
537	Retinol-binding protein 4	P02753	23 kDa	0.17 ± 0.35	0.568 ± 1	0	(0, 4)	0	(0, 14)	0	(0, 3)	
538	Ribonuclease pancreatic	P07998	18 kDa	1.12 ± 0.77	1.02 ± 0.89	1	(0, 4)	4	(0, 26)	1	(0, 3)	
539	Ribonuclease T2	O00584	29 kDa	3.32 ± 2.2	3.57 ± 2.6	3	(0, 10)	12	(0, 30)	3	(0, 7)	
540	RNA polymerase II-associated protein 1	Q9BWH6	153 kDa	0.0648 ± 0.22	0.0849 ± 0.21	0	(0, 2)	0	(0, 1)	0	(0, 2)	
541	Sclerostin domain-containing protein 1	Q6X4U4	23 kDa	1.58 ± 1.8	0.381 ± 0.68	1	(0, 6)	0	(0, 21)	1	(0, 4)	
542	Secreted frizzled-related protein 1	Q8N474	35 kDa	0.4 ± 0.6	0.858 ± 0.84	0	(0, 4)	0	(0, 8)	0	(0, 2)	
543	Secretoglobin family 1D member 2	O95969	10 kDa	0.316 ± 0.5	2.41 ± 3.4	0	(0, 12)	0	(0, 32)	0	(0, 3)	
544	Secretoglobin family 3A member 1	Q96QR1	10 kDa	0.235 ± 0.46	0.879 ± 1.4	0	(0, 5)	0	(0, 62)	0	(0, 2)	

				Normalized Total Spectra		Total Spectra		% Sequence Coverage		Number of Unique Peptides		
Protein	Accession	MW	non-GDM	GDM	Median	Range	Median	Range	Median	Range	Rank	
545	Selenium-binding protein 1	Q13228	52 kDa	2.4 ± 1.9	0.783 ± 0.76	1	(0, 8)	2	(0, 14)	1	(0, 6)	
546	Selenoprotein P	P49908	43 kDa	4.46 ± 2.2	2.07 ± 1.8	3.5	(0, 9)	5	(0, 15)	2	(0, 6)	9
547	Serotransferrin	P02787	77 kDa	82.5 ± 18	105 ± 42	83	(35, 232)	50	(33, 69)	30	(20, 59)	
548	Serum amyloid A-1 protein	P0DJ18	14 kDa	0.365 ± 0.61	0.193 ± 0.47	0	(0, 2)	0	(0, 21)	0	(0, 2)	
549	SH3 domain-binding glutamic acid-rich-like protein 3	Q9H299	10 kDa	0.52 ± 0.56	0.261 ± 0.48	0	(0, 2)	0	(0, 27)	0	(0, 2)	
550	Signal-regulatory protein beta-1 isoform 3	Q5TFQ8	43 kDa	0 ± 0	0.336 ± 0.82	0	(0, 4)	0	(0, 10)	0	(0, 0)	
551	Soluble calcium-activated nucleotidase 1	Q8WVQ1	45 kDa	0.242 ± 0.5	0.281 ± 0.34	0	(0, 3)	0	(0, 6)	0	(0, 3)	
552	SPARC-like protein 1	Q14515	75 kDa	10.1 ± 11	5.21 ± 4.7	5	(0, 36)	8	(0, 35)	4	(0, 20)	
553	Sulfhydryl oxidase 1	O00391	83 kDa	6.45 ± 5.1	3.11 ± 3.7	5	(0, 22)	9	(0, 25)	4	(0, 13)	
554	Suppressor of tumorigenicity 14 protein	Q9Y5Y6	95 kDa	0.956 ± 1.3	0.711 ± 0.81	1	(0, 3)	1	(0, 4)	1	(0, 2)	
555	Suprabasin	Q6UWP8	61 kDa	0.989 ± 1	0.938 ± 0.84	1	(0, 4)	3	(0, 8)	1	(0, 3)	
556	Synaptosomal-associated protein 23	O00161	23 kDa	0.828 ± 1.2	0 ± 0	0	(0, 4)	0	(0, 21)	0	(0, 4)	
557	Syndecan-2	P34741	22 kDa	0.524 ± 0.96	0 ± 0	0	(0, 4)	0	(0, 7)	0	(0, 3)	
558	Syntaxin-3	Q13277	33 kDa	0.224 ± 0.48	0 ± 0	0	(0, 3)	0	(0, 10)	0	(0, 3)	
559	Syntenin-1	O00560	32 kDa	2.01 ± 1.6	1.7 ± 1.1	2	(0, 8)	3	(0, 28)	1	(0, 5)	
560	Targeting protein for Xk1p2	Q9ULW0	86 kDa	0.202 ± 0.51	0.553 ± 0.49	0	(0, 2)	0	(0, 3)	0	(0, 2)	

				Normalized Total Spectra		Total Spectra		% Sequence Coverage		Number of Unique Peptides		
Protein	Accession	MW	non-GDM	GDM	Median	Range	Median	Range	Median	Range	Rank	
561	Tenascin	P24821	241 kDa	352 ± 87	427 ± 96	336.5	(104, 720)	52	(29, 60)	98	(53, 160)	16
562	Tetraspanin-6	O43657	28 kDa	0.456 ± 0.61	0.251 ± 0.39	0	(0, 2)	0	(0, 9)	0	(0, 2)	
563	Thioredoxin	P10599	12 kDa	2.65 ± 1.6	1.93 ± 0.99	2	(0, 5)	21	(0, 40)	2	(0, 4)	
564	Thrombospondin-1	P07996	129 kDa	18.2 ± 9.3	33.9 ± 15	19.5	(0, 63)	17	(0, 39)	13.5	(0, 27)	
565	Thrombospondin-2	P35442	130 kDa	0.853 ± 1.2	0.877 ± 0.94	1	(0, 4)	1	(0, 2)	0	(0, 1)	
566	Thrombospondin-3	P49746	104 kDa	0.0956 ± 0.33	0 ± 0	0	(0, 2)	0	(0, 2)	0	(0, 1)	
567	Titin	Q8WZ42	3816 kDa	1.04 ± 1.5	3.7 ± 3.6	5	(0, 9)	0	(0, 0)	1	(0, 3)	
568	Transcobalamin-1	P20061	48 kDa	1.12 ± 1.7	3 ± 4.8	0	(0, 11)	0	(0, 23)	0	(0, 8)	
569	Transforming growth factor beta receptor type 3	Q03167	94 kDa	0 ± 0	0.0677 ± 0.17	0	(0, 1)	0	(0, 4)	0	(0, 1)	
570	Trans-Golgi network integral membrane protein 2	O43493	51 kDa	0.487 ± 0.82	0.309 ± 0.53	0	(0, 3)	0	(0, 6)	0	(0, 2)	
571	Transketolase	P29401	68 kDa	0.174 ± 0.6	0 ± 0	0	(0, 3)	0	(0, 5)	0	(0, 2)	
572	Translationally-controlled tumor protein	P13693	20 kDa	0.669 ± 1	0.2 ± 0.34	0	(0, 3)	0	(0, 15)	0	(0, 3)	
573	Transmembrane protein 132A	Q24JP5	110 kDa	0.38 ± 0.59	0.208 ± 0.35	0	(0, 3)	0	(0, 5)	0	(0, 2)	
574	Transmembrane protein 201	Q5SNT2	72 kDa	0.758 ± 0.66	1.27 ± 1.2	1	(0, 4)	1	(0, 8)	1	(0, 3)	20
575	Transthyretin	P02766	16 kDa	17.1 ± 4.1	11.2 ± 3.3	15.5	(6, 28)	42	(18, 50)	7	(3, 12)	12
576	Trefoil factor 1	P04155	9 kDa	0 ± 0	1.03 ± 1.4	0	(0, 4)	0	(0, 44)	0	(0, 3)	

			Normalized Total Spectra		Total Spectra		% Sequence Coverage		Number of Unique Peptides			
Protein	Accession	MW	non-GDM	GDM	Median	Range	Median	Range	Median	Range	Rank	
577	Trefoil factor 3	Q07654	9 kDa	0.14 ± 0.48	1.1 ± 1.4	0	(0, 4)	0	(0, 50)	0	(0, 3)	
578	Triosephosphate isomerase	P60174	31 kDa	2.77 ± 2.3	1.06 ± 0.8	1.5	(0, 10)	5	(0, 39)	1	(0, 8)	26
579	Tropomyosin alpha-3 chain	P06753	33 kDa	1.04 ± 1.2	0.634 ± 1.1	0.5	(0, 5)	2	(0, 11)	0	(0, 1)	
580	Tropomyosin beta chain	P07951	33 kDa	0.147 ± 0.28	0.248 ± 0.61	0	(0, 2)	0	(0, 6)	0	(0, 0)	
581	Trypsin-1	P07477	27 kDa	3.07 ± 2.9	2.17 ± 2.2	2.5	(0, 7)	8	(0, 8)	2	(0, 4)	
582	Tubulointerstitial nephritis antigen-like	Q9GZM7	52 kDa	0.133 ± 0.31	0.265 ± 0.49	0	(0, 2)	0	(0, 5)	0	(0, 2)	
583	Tumor necrosis factor ligand superfamily member 13	O75888	27 kDa	0.6 ± 0.54	0.265 ± 0.33	0	(0, 3)	0	(0, 8)	0	(0, 2)	
584	Tumor necrosis factor receptor superfamily member 11B	O00300	46 kDa	1.82 ± 2.2	0.43 ± 0.67	0	(0, 8)	0	(0, 26)	0	(0, 7)	
585	Ubiquitin-40S ribosomal protein S27a	P62979	18 kDa	7.59 ± 6.1	3.68 ± 2.6	7	(0, 22)	12	(0, 28)	0	(0, 0)	
586	Uncharacterized protein KIAA1958	Q8N8K9	79 kDa	0.206 ± 0.4	0.0672 ± 0.16	0	(0, 2)	0	(0, 2)	0	(0, 2)	
587	UPF0415 protein C7orf25	Q9BPX7	46 kDa	4.39 ± 2.8	5.3 ± 2.8	5	(0, 12)	2	(0, 3)	1	(0, 3)	
588	Vascular cell adhesion protein 1	P19320	81 kDa	0.269 ± 0.79	0 ± 0	0	(0, 5)	0	(0, 7)	0	(0, 5)	
589	VEGF co-regulated chemokine 1	Q6UXB2	14 kDa	0.205 ± 0.55	0.193 ± 0.47	0	(0, 3)	0	(0, 17)	0	(0, 2)	
590	Vimentin	P08670	54 kDa	0.0678 ± 0.23	0.928 ± 2.3	0	(0, 9)	0	(0, 17)	0	(0, 7)	
591	Vitamin D-binding protein	P02774	53 kDa	15.3 ± 6.5	19.5 ± 11	13.5	(2, 42)	28	(3, 53)	11	(2, 21)	
592	Vitronectin	P04004	54 kDa	10.3 ± 5.2	8.81 ± 4.1	8.5	(2, 25)	14	(1, 29)	6	(1, 11)	

			Normalized Total Spectra		Total Spectra		% Sequence Coverage		Number of Unique Peptides		
Protein	Accession	MW	non-GDM	GDM	Median	Range	Median	Range	Median	Range	Rank
593	Voltage-dependent L-type calcium channel subunit alpha-1F	O60840	221 kDa	1.97 ± 3.1	0.446 ± 0.46	0	(0, 13)	0	(0, 1)	0	(0, 2)
594	von Willebrand factor A domain-containing protein 1	Q6PCB0	47 kDa	4.39 ± 3	2.95 ± 2.5	3.5	(0, 14)	7	(0, 27)	3	(0, 8)
595	V-type proton ATPase subunit S1	Q15904	52 kDa	0.257 ± 0.33	0.0684 ± 0.17	0	(0, 2)	0	(0, 6)	0	(0, 2)
596	WAP four-disulfide core domain protein 2	Q14508	13 kDa	0.0663 ± 0.15	1.22 ± 1.6	0	(0, 5)	0	(0, 31)	0	(0, 2)
597	Xanthine dehydrogenase/oxidase	P47989	146 kDa	46.4 ± 32	18.1 ± 27	35	(0, 108)	21	(0, 42)	23	(0, 47)
598	Zinc finger protein 318	Q5VUA4	251 kDa	0.187 ± 0.31	0.252 ± 0.45	0	(0, 3)	0	(0, 1)	0	(0, 2)
599	Zinc finger protein 518A	Q6AHZ1	167 kDa	0 ± 0	0.17 ± 0.42	0	(0, 2)	0	(0, 1)	0	(0, 2)
600	Zinc-alpha-2-glycoprotein	P25311	34 kDa	83.2 ± 20	109 ± 26	79.5	(41, 194)	60	(48, 71)	16	(11, 27)
601	Zymogen granule protein 16 homolog B	Q96DA0	23 kDa	1.33 ± 1.4	1.76 ± 1.5	1	(0, 7)	4	(0, 22)	1	(0, 5)

Supplemental Table 2. Validation of orthogonal signal corrected partial least squares discriminant analysis model and selected proteins

	Q^2 ^a	AUC ^b	Sensitivity ^c	Specificity ^d
Selected model (27) ^e	0.770 ± 0.063 ^{f,g}	0.791 ± 0.14 ^{f,g}	0.723 ± 0.24 ^{f,g}	0.860 ± 0.23 ^{f,g}
Permuted model (27) ^h	0.060 ± 0.65	0.475 ± 0.21	0.449 ± 0.24	0.500 ± 0.34
Excluded model (233) ⁱ	0.076 ± 0.42 ^{f,g}	0.370 ± 0.19 ^{f,g}	0.425 ± 0.22 ^{f,g}	0.315 ± 0.29 ^{f,g}
Permuted model (233) ^h	0.302 ± 0.27	0.508 ± 0.23	0.513 ± 0.26	0.504 ± 0.37

^a Cross-validated model fit, mean ± stdev.

^b Area under the receiver operator characteristic curve, mean ± stdev.

^c True positive or recall rate, mean ± stdev.

^d True negative rate, mean ± stdev.

^e Model including only the selected features (number of proteins).

^f Differences between the selected and permuted (null distribution) models, P < 0.05.

^g Differences between the selected and excluded models, P < 0.05.

^h Model based on permuted class labels (number of proteins).

ⁱ Model excluding the selected features (number of proteins).