

Table S1 Differentially expressed peptides in the amniotic fluid

Sequence	Entry name	Start position	End position	Log FC	P value
DGAKGDAGPAGPKGEPGSPGENGAP	COL1A1	274	298	7.3801	0.0250
MCLQEEFQCLNHRCSVAVQRCDGVD	LRP10	139	163	7.3753	0.0000
GPPGEPGPPG	COL5A2	1212	1221	6.6793	0.0081
EPPQSPWDRVKD	APOA1	26	37	6.5004	0.0000
MYHRYWEEYSKGADYMDCLYRYLNT	CUL2	86	110	6.2338	0.0092
FHCLEYFKSFNFNTLLGEEWKQPES	C4orf33	165	189	6.0869	0.0031
RSSASAAPSQAEPACPPRQACGGGG	ORAI3	212	236	5.9765	0.0178
EGSALGKQL	APOA1	58	66	5.8323	0.0001
SPGSAPGSTPGSAPGSAPGSAPGS	TMEM271	166	189	5.7544	0.0072
IEQKSNEEGSEEKGPVEVREY	SFN	65	84	5.7215	0.0000
TGETVTGSGTQTQAGATQT	CRNN	223	241	5.7089	0.0000
NDEDPVVVTK	JUP	152	161	5.6968	0.0000
IENEEQEYVQTVK	ANXA1	14	26	5.6352	0.0000
GESDLDLEDGGEDAQSFQQEVIP	SCN10A	1002	1026	5.6274	0.0000
ISHELDSASSEVN	SPP1	302	314	5.5951	0.0015
AAEVQAGNENEPREADKSHPEQRE	SLC9A3R1	125	149	5.5799	0.0120
ENDPVLGPDGKTHGNK	SPINK5	178	193	5.2090	0.0090
GPPGEPGPP	COL5A2	1212	1220	4.9676	0.0122
SNEEGSEEKGPVEVREY	SFN	69	84	4.9368	0.0000
TPPPQLQQQVK	SPRR3	11	22	4.8344	0.0060
ATVQQLLEGRW	FABP5	2	11	4.8231	0.0002
STRSPYLFSCGEDKQVKCWDLEYNK	PLRG1	255	279	4.7794	0.0000
KSMSCYVLSNVLDYNTIEVSDQVD	VPS35	434	458	4.7180	0.0206
HLEHPEQQDQGLK	IVL	509	521	4.6164	0.0020
QPPPQEIFVPTTK	SPRR3	26	38	4.4513	0.0036
SVGEAGPEGPPGEPGPPGP	COL5A2	1204	1222	4.2287	0.0200
GPPDVPDH	ITIH4	674	681	4.2117	0.0142
WDDIEFELLTWEDEGDFGDPWSRIP	MAGED1	707	731	4.1511	0.0176
VPPPPMEPDHP	PGAM4	121	131	4.0564	0.0016
EGPEVDVNLPK	AHNAK	765	775	4.0458	0.0002
TATTSLASPFVTTACHTLCPDHPPS	ANKRD33	310	334	3.7785	0.0096
GPSTPGVLSNC	ATG9B	749	759	3.7475	0.0371
NLEKETEGL	APOA1	98	106	3.7456	0.0009
FVELGTQPATQ	APOA2	90	100	3.6645	0.0014
GASRQCLSTVECYNATTNEWYIAE	KLHL2	457	481	3.5280	0.0173
STHCQDINECAMPVCRHGDCLNPNP	LTBP3	350	374	3.5259	0.0121
NEEQEYVQTVK	ANXA1	16	26	3.5208	0.0047
STVTPGPAQQ	SPRR3	155	164	3.5105	0.0308
DSELGERPPEDNQSFQYDHEAFLGK	RCN1	42	66	3.4879	0.0061
TPPPQLQQQV	SPRR3	11	21	3.4780	0.0070
HIWTWKRDERYFFQGNQYWRYSK	MMP21	399	423	3.4627	0.0451
HQTGETVTGSGTQTQAGATQT	CRNN	221	241	3.4308	0.0001
GPPGEPGPPGPPGPP	COL5A2	1212	1226	3.3846	0.0291
IGDSWEKYVHGVRVYQCYCYGRGIGE	FN1	572	596	3.3161	0.0000
FIENEEQEYVQTVK	ANXA1	13	26	3.3017	0.0034
SPPPPPPPG	MICAL3	1458	1466	3.2933	0.0324
ELQEKLSPGGEEM	APOA1	160	172	3.2232	0.0002
DVPPPPMEPDHP	PGAM4	120	131	3.2022	0.0012
QRHEEPKTTITDEFEQGTIYFDYEK	CNOT3	707	731	3.1374	0.0020
GPPDVPDHA	ITIH4	674	682	3.0776	0.0143
PEPAKSAPAP	H2BC9	2	11	3.0583	0.0070
SPPPPPPP	FHDC1	57	64	3.0177	0.0243
QPPPQEIFVPTT	SPRR3	26	37	2.9379	0.0055
SSGNAKIGHAPNPF	PRDX1	2	15	2.9278	0.0239
DQSRVNLGPIT	UMOD	594	605	2.9148	0.0466
LPPFPDHV	MFAP2	26	33	2.9012	0.0140
IFSSDLYDHWVSMVMDQGNDEEKINT	ARHGAP20	445	469	2.8955	0.0188
EDENFILK	PPIA	84	91	2.8858	0.0303
PSPDWTSSSRENQHPNLLGGAGEPP	PRR15	48	72	2.8171	0.0420
TEVAQELTEL	RNF135	132	141	2.8121	0.0125
PEEEEFHEVEEYFEEGEFHEVEEFI	TTN	11305	11329	2.7670	0.0051
VGDEDFVHL	CSTB	59	67	2.7054	0.0211
PPPQEIFVPTTK	SPRR3	27	38	2.5783	0.0085
EEHPVLLTEAPLNPK	ACTG1	99	113	2.5046	0.0001
DDPIEKVIEG	SBSN	26	35	2.4573	0.0060
ASGVAVSDGVK	CFL1	2	13	2.4143	0.0022
GSQTQTQAGATQTEQDSSHQTG	CRNN	229	251	2.2824	0.0098
DESQVAERLT	CLU	328	338	2.2376	0.0010
YFSYEHFYIYCKFWELDTDHLYI	PPP2R3A	894	918	2.1812	0.0380
DPPPPPLP	LFNG	27	34	2.1589	0.0400
GPPGPTGPPG	COL3A1	618	627	2.1496	0.0145
GPPGEPGPPG	COL5A2	1212	1222	2.0952	0.0247
PPPPPPPPPP	RAPH1	629	640	2.0206	0.0473
PAPPPPPPPP	FHDC1	32	41	1.9542	0.0380
SQHTLPTL	IVL	2	11	1.8637	0.0404
RLTEVDVYDEEININLREESDWHY	GREB1	1368	1392	1.7204	0.0376
KDCGKGFWMWSDLSQHQVHTGDKP	ZNF662	335	359	1.7146	0.0185
QYDRDKYWNFRDDYFRNWNPNKP	SPOCK1	50	74	1.6003	0.0275
SHELDSASSEVN	SPP1	303	314	1.5127	0.0003
GPEGPPGEPGPPGPP	COL5A2	1209	1223	1.4887	0.0387
ENEEQEYVQTVK	ANXA1	15	26	1.3979	0.0330
SKSESPKEPEQL	HNRNPA1	2	13	0.8636	0.0443
KADDLITSRQQYSSDHSSSHSPHGSH	INO80D	805	829	0.8593	0.0440
PDDMGSEPKRTLPRFKGNFTMEKF	ZFX4	1465	1489	0.7736	0.0138
AAPPSPAWEPEPEAGLEPEREPGP	KLF13	115	139	-0.6074	0.0326
LGDNSEDADIEIQDCNCGITVHEGC	PHF14	326	350	-0.6101	0.0132
PSTPPNSPMQTP	TRAK1	779	790	-0.8260	0.0398
MLKFLAKGEVPGKSCDEPMDSTMD	ATE1	97	121	-1.0029	0.0461
DDEDEDVEGDEDDDEVSEEEEEFL	ANP32B	194	218	-1.0114	0.0064
WDRERYWRECERDYQDDTLELYNRE	YLPM1	1221	1245	-1.0627	0.0004
MRCPEDEYAGYGYSHYHQYQDGYQ	CCDC80	911	935	-1.1012	0.0165
NCDMDCSLFESCHETSECLELAMEI	MDFIC2	159	183	-1.3034	0.0446
CHGTQCGFCTPGMVMSIYTLRNP	AOX1	109	133	-1.3522	0.0478
HLWPDGSLGDWKSFSCHCYWGAGP	HYAL3	380	404	-1.3770	0.0068
SVASQGFSTCGHYAMSTVSNAAYP	SEC24B	170	194	-1.3858	0.0393
DGEAGAQQPPG	COL1A1	613	624	-1.3893	0.0195
FYYDYNFINFHEDLSYGPSEEPDL	ADAMTS7	1063	1087	-1.4111	0.0375
EDEEMKTDSD	CHD1	244	254	-1.5439	0.0271
LSHEEEDDEEEEEEEEEEEEEEE	MYT1	255	279	-1.6184	0.0490
DFRYCEYTEWDLQFKNYQLFDYMN	MAN2A1	426	450	-1.6625	0.0454
TLNEDEEWKCDQDMEDDGRDAAPP	AXIN1	240	264	-1.8047	0.0416
QYSYRCDYNDGCGDSEAGCLFRD	LRP2	2755	2779	-1.9507	0.0116
TSENDQLLFCDDCRGYHMYCLNP	DPF3	324	348	-1.9799	0.0209
TSSVPQETRTQHLYQSNENSSSSI	SETD5	796	820	-1.9832	0.0076
TSGCGSAGGCGSVSCGNANFSGSV	CAAP1	40	64	-2.1196	0.0299
SVQQQTSEMIPSEEEEEDEEEEEE	TUT7	833	857	-2.1212	0.0153
SDCPSGAWGKHNDHEEDVGLTCTG	SSC5D	849	873	-2.1763	0.0497
WHRNSHNSADNEFYFRYPSQDVHA	RHBG	45	69	-2.3336	0.0360
CTTCGQHYHGMCLDIAPTPLKRW	KMT2C	359	383	-2.4920	0.0096
PEDPLVAEEYADAFDSYCEESDEE	NEK11	469	493	-2.6608	0.0084
FYCKEIEEDYSLAPGDTYIPPHG	DNAH3	3754	3778	-2.6821	0.0460
IQEEGEEEEEEEEEEEEEEEEEE	DCAF8L2	120	144	-2.7199	0.0275
DGLQRHSDEEEDDEEEEEEEEEEE	ZBTB47	270	294	-2.9176	0.0359
SGLSSTGSEVHQEDICSNSRDSPP	PROX1	114	138	-2.9762	0.0454
ELERPPGNE	FGA	260	268	-3.3192	0.0447
DDELAEYDLDKYDEEGDPAETLGE	PWP1	89	113	-3.4865	0.0034
SIDSNDSDDDVDDTDDSHQS	SPP1	102	120	-3.5241	0.0111
RALDSSPEANTEDDKTEEDVMPKPN	TMEM233	12	36	-3.7684	0.0186
PGGLEPKGE	IGFBP4	238	246	-3.8087	0.0423
MYFYLLQGAECCLLAAMAYDRYVA	OR2T10	101	125	-4.2523	0.0222
LGEGPGDTAEEELFLSVHDAVQTA	SLC26A1	663	687	-4.3135	0.0000
DAEDGHGPGEQQ	CFB	246	257	-4.3865	0.0246
IDSNDSDVDDTDDSHQS	SPP1	103	120	-4.5528	0.0044
AGEPGRDGVPGGPMRGMPSGPPGP	COL3A1	521	545	-5.1403	0.0234
PTSPNYTPTSPSYSPSYSPSYSP	POLR2A	1750	1774	-5.4640	0.0087
NDSDDVDDTDDSHQS	SPP1	106	120	-5.5633	0.0075
SNSDDVDDTDDSHQS	SPP1	105	120	-5.5729	0.0051
DDVDDTDDSHQS	SPP1	109	120	-6.1833	0.0033
PGDLGAPGPGA	COL1A1	664	675	-7.5101	0.0237
DGQPGAKGEPGDAGAK	COL1A1	820	835	-7.6401	0.0114

FC, fold change.