Entry	Gene Name	Peptide	UTERINE FLUIDS			M1 CERVICAL SAMPLES			M3 CERVICAL SAMPLES		
			Fold Change	FDR	AUC	Fold Change	FDR	AUC	Fold Change	FDR	AUC
P00338	LDHA	LVIITAGAR	7.127	0.000	0.9575	1.486	0.114	0.758	1.572	0.034	0.748
P06733	ENO1	YISPDQLADLYK	5.091	0.000	0.9477	1.209	0.210	0.690	1.690	0.016	0.814
P00338	LDHA	VTLTSEEEAR	6.183	0.000	0.9444	1.471	0.114	0.758	1.502	0.041	0.735
P06733	ENO1	TIAPALVSK	4.753	0.000	0.9379	1.322	0.154	0.716	1.561	0.018	0.791
P14618	PKM	NTGIICTIGPASR	5.405	0.000	0.9346	1.317	0.211	0.680	1.374	0.019	0.781
P42574	CASP3	SGTDVDAANLR	6.428	0.001	0.9020	1.410	0.251	0.663	1.250	0.059	0.712
P16949	STMN1	SHEAEVLK	4.651	0.001	0.8987	1.491	0.154	0.711	2.318	0.022	0.770
O00299	CLIC1	LAALNPESNTAGLDIFAK	3.373	0.001	0.8922	1.125	0.300	0.627	1.694	0.018	0.801
O00299	CLIC1	NSNPALNDNLEK	3.290	0.001	0.8922	1.244	0.251	0.663	1.422	0.021	0.771
P55060	CSE1L	ANIVHLMLSSPEQIQK	5.637	0.001	0.8922	2.013	0.114	0.765	2.248	0.016	0.827
P55060	CSE1L	LLQTDDEEEAGLLELLK	5.914	0.001	0.8905	2.165	0.095	0.788	2.527	0.016	0.819
P14174	MIF	LLCGLLAER	3.669	0.001	0.8889	1.229	0.269	0.647	1.628	0.018	0.797
P43490	NAMPT	YLLETSGNLDGLEYK	10.476	0.001	0.8889	1.664	0.154	0.711	1.183	0.259	0.627
Q06830	PRDX1	LVQAFQFTDK	5.115	0.001	0.8889	1.344	0.248	0.667	1.565	0.016	0.807
P16949	STMN1	AIEENNNFSK	4.630	0.001	0.8889	1.582	0.154	0.712	2.319	0.021	0.771
Q01469	FABP5	LVVECVMNNVTCTR	2.730	0.001	0.8856	0.376	0.738	0.546	1.104	0.723	0.539
Q01469	FABP5	ELGVGIALR	2.544	0.001	0.8824	0.460	0.765	0.539	1.004	0.974	0.503
O43278	SPINT1	SFVYGGCLGNK	4.416	0.001	0.8824	0.960	0.666	0.559	1.528	0.046	0.729
P43490	NAMPT	YDGHLPIEIK	9.572	0.001	0.8725	1.739	0.114	0.748	1.074	0.324	0.608
P12830	CDH1	VFYSITGQGADTPPVGVFIIER	4.498	0.001	0.8660	0.775	0.619	0.572	1.832	0.018	0.791
O43278	SPINT1	WYYDPTEQICK	4.056	0.001	0.8644	0.755	0.666	0.559	1.527	0.071	0.703
P61604	HSPE1	FLPLFDR	5.020	0.002	0.8529	1.986	0.134	0.725	1.987	0.019	0.781
P35222	CTNNB1	LVQLLVR	4.875	0.002	0.8480	2.034	0.114	0.748	2.129	0.016	0.819
Q06830	PRDX1	ADEGISFR	4.575	0.002	0.8448	1.449	0.210	0.693	1.586	0.016	0.817
P12830	CDH1	NLVQIK	3.738	0.002	0.8382	0.897	0.888	0.516	1.817	0.016	0.814
P62937	PPIA	FEDENFILK	2.830	0.002	0.8366	1.142	0.308	0.624	1.582	0.019	0.784
P60174	TPI1	VVLAYEPVWAIGTGK	3.320	0.003	0.8333	1.268	0.278	0.637	1.664	0.019	0.781
P62937	PPIA	VSFELFADK	3.057	0.003	0.8301	1.178	0.290	0.634	1.835	0.016	0.833
P61604	HSPE1	VLLPEYGGTK	5.448	0.003	0.8268	1.744	0.210	0.683	1.871	0.027	0.758
P40121	CAPG	EGNPEEDLTADK	4.366	0.003	0.8268	1.358	0.308	0.624	1.389	0.065	0.708
P14780	MMP9	SLGPALLLLQK	3.551	0.003	0.8235	0.670	0.475	0.595	0.439	0.270	0.624
P07237	P4HB	ILEFFGLK	3.264	0.004	0.8186	0.913	0.300	0.627	1.249	0.338	0.605
P35222	CTNNB1	LLNDEDQVVVNK	4.478	0.004	0.8137	2.069	0.210	0.683	2.318	0.019	0.784
P40121	CAPG	YQEGGVESAFHK	3.808	0.004	0.8121	1.403	0.270	0.644	1.404	0.027	0.758
P10451	SPP1	ANDESNEHSDVIDSQELSK	8.453	0.004	0.8105	1.961	0.114	0.745	1.404	0.595	0.557
P16070	CD44	TEAADLCK	3.198	0.005	0.8072	1.712	0.131	0.729	1.623	0.034	0.745
P05164	MPO	VVLEGGIDPILR	9.227	0.006	0.8007	1.363	0.702	0.552	1.078	0.347	0.601
P07355	ANXA2	GVDEVTIVNILTNR	8.099	0.006	0.7974	0.682	0.656	0.562	1.347	0.034	0.745
P14780	MMP9	AFALWSAVTPLTFTR	3.671	0.006	0.7974	0.647	0.501	0.588	0.583	0.417	0.588
P05164	MPO	IANVFTNAFR	8.567	0.007	0.7941	1.498	0.656	0.562	0.953	0.590	0.559
P04792	HSPB1	LATQSNEITIPVTFESR	5.090	0.007	0.7908	1.534	0.269	0.650	1.325	0.016	0.824
P60174	TPI1	SNVSDAVAQSTR	3.397	0.007	0.7908	1.369	0.210	0.690	1.510	0.024	0.765
P30041	PRDX6	DFTPVCTTELGR	2.831	0.009	0.7843	1.234	0.300	0.627	1.645	0.034	0.748
P09211	GSTP1	ASCLYGQLPK	2.951	0.009	0.7843	1.274	0.269	0.650	1.293	0.059	0.712
P04792	HSPB1	LFDQAFGLPR	5.632	0.010	0.7778	1.742	0.262	0.660	1.235	0.016	0.810
P04083	ANXA1	GGPGSAVSPYPTFNPSSDVAALHK	6.153	0.011	0.7745	0.622	0.484	0.592	1.265	0.432	0.585

P04083	ANXA1	DITSDTSGDFR	**6.761**	**0.011**	**0.7745**	0.698	0.484	0.592	1.122	0.958	0.507
P09211	GSTP1	TLGLYGK	**2.910**	**0.011**	**0.7745**	1.277	0.269	0.650	1.372	**0.048**	**0.725**
P30041	PRDX6	LSILYPATTGR	**3.283**	**0.014**	**0.7647**	1.326	0.269	0.647	1.434	0.077	0.696
P14174	MIF	VYINYYDMNAANVGWNNSTFA	**8.416**	**0.008**	**0.7598**	1.339	0.210	0.681	1.524	0.053	**0.719**
O43852	CALU	TFDQLTPEESK	**4.042**	**0.016**	**0.7582**	**2.083**	0.128	**0.725**	1.578	0.082	0.691
P07237	P4HB	ALAPEYAK	**2.741**	**0.016**	**0.7582**	0.780	0.777	0.536	1.117	0.573	0.562
Q13938	CAPS	SGDGVVTVDDLR	**3.670**	**0.018**	**0.7549**	**2.351**	0.210	0.681	1.409	0.437	0.583
P22626	HNRNPA2B1	TLETVPLER	**2.214**	**0.020**	**0.7500**	1.412	0.269	0.657	1.536	0.059	**0.712**
P10451	SPP1	AIPVAQDLNAPSDWDSR	**3.958**	**0.021**	**0.7484**	0.851	0.226	0.675	0.580	0.766	0.533
Q13938	CAPS	EAVIAAAFAK	**3.323**	**0.024**	**0.7418**	**2.136**	0.248	0.667	1.631	0.299	0.614
P50454	SERPINH1	GVVEVTHDLQK	**2.413**	**0.026**	**0.7386**	**5.886**	0.062	**0.828**	**3.977**	**0.038**	**0.735**
Q01995	TAGLN	TLMALGSLAVTK	**2.046**	**0.040**	**0.7222**	**3.938**	0.269	0.652	**6.348**	**0.016**	**0.840**
P30086	PEBP1	VLTPTQVK	1.967	**0.040**	**0.7222**	0.766	0.844	0.523	1.392	0.071	**0.703**
P80188	LCN2	VPLQQNFQDNQFQGK	**2.535**	**0.044**	**0.7157**	0.661	0.270	0.644	0.648	0.190	0.647
P30086	PEBP1	LYEQLSGK	1.997	**0.045**	**0.7157**	0.944	0.720	0.549	1.410	0.077	0.696
P50454	SERPINH1	DTQSGSLLFIGR	**2.674**	**0.042**	**0.7157**	**5.425**	0.210	0.662	**4.222**	**0.046**	**0.717**
P05787	KRT8	LSELEAALQR	**12.502**	**0.047**	**0.7124**	**5.547**	0.114	**0.761**	**2.612**	**0.036**	**0.742**
P17931	LGALS3	GNDVAFHFNPR	**2.540**	**0.047**	**0.7124**	1.239	0.300	0.627	1.322	**0.018**	**0.797**
P22626	HNRNPA2B1	GGNFGFGDSR	**2.706**	**0.047**	**0.7108**	1.343	0.278	0.637	1.989	**0.021**	**0.775**
P17931	LGALS3	IALDFQR	**2.606**	0.057	**0.7026**	1.274	0.278	0.641	1.283	**0.018**	**0.794**
P09466	PAEP	VLVEDDEIMQGFIR	0.038	**0.047**	0.6993	0.007	0.248	0.660	0.003	0.054	**0.712**
P07339	CTSD	VGFAEAAR	1.575	0.069	0.6928	1.485	0.270	0.644	1.166	0.100	0.680
P07339	CTSD	VSTLPAITLK	1.598	0.069	0.6928	1.217	0.637	0.569	1.104	0.233	0.634
P80188	LCN2	ELTSELK	**2.045**	0.074	0.6895	0.631	0.278	0.637	0.671	0.233	0.634
Q16658	FSCN1	YLAPSGPSGTLK	1.800	0.084	0.6830	1.463	0.300	0.631	**2.187**	**0.034**	**0.745**
P07355	ANXA2	QDIAFAYQR	**8.887**	0.066	0.6797	0.719	0.827	0.526	1.114	0.097	0.681
Q01995	TAGLN	EFTESQLQEGK	1.881	0.111	0.6699	**5.254**	0.269	0.641	**5.804**	**0.021**	**0.773**
Q16658	FSCN1	FLIVAHDDGR	1.960	0.122	0.6634	1.865	0.154	**0.709**	**2.124**	**0.048**	**0.724**
P05787	KRT8	WSLLQQQK	**13.174**	0.122	0.6634	**6.437**	0.114	**0.742**	**2.400**	**0.048**	**0.725**
P08253	MMP2	VDAAFNWSK	0.727	0.121	0.6634	1.664	0.398	0.608	0.716	0.088	0.688
P15941	MUC1	EGTINVHDVETQFNQYK	1.751	0.131	0.6585	0.899	0.918	0.511	1.682	0.082	0.693
P15941	MUC1	QGGFLGLSNIK	1.785	0.181	0.6405	1.015	0.656	0.565	1.413	0.190	0.647
P09382	LGALS1	LPDGYEFK	1.368	0.181	0.6405	**2.074**	0.114	**0.745**	**2.030**	**0.044**	**0.732**
P14618	PKM	APIIAVTR	1.926	0.181	0.6405	**4.230**	0.269	0.654	1.492	0.212	0.641
P00441	SOD1	AVCVLK	1.631	0.181	0.6405	0.936	0.827	0.526	1.384	0.091	0.686
P00441	SOD1	TLVVHEK	1.620	0.190	0.6373	0.888	0.702	0.552	1.382	0.114	0.673
P09382	LGALS1	SFVLNLGK	1.249	0.365	0.5980	**2.018**	0.131	**0.729**	**2.099**	**0.026**	**0.761**
P01833	PIGR	GGCITLISSEGYVSSK	1.127	0.468	0.5801	0.265	0.210	0.683	0.661	0.290	0.618
Q14508	WFDC2	VSCVTPNF	0.900	0.611	0.5588	0.514	0.656	0.562	0.519	0.096	0.683
P15328	FOLR1	FNWNHCGEMAPACK	0.362	0.628	0.5556	0.557	0.765	0.539	0.530	0.282	0.621
P09603	CSF1	TFYETPLQLLEK	0.917	0.678	0.5458	1.302	0.777	0.533	1.330	0.290	0.614
P01833	PIGR	VYTVDLGR	1.152	0.739	0.5392	0.547	0.475	0.595	0.673	0.311	0.611
P08670	VIM	ILLAELEQLK	0.994	0.757	0.5359	1.189	0.269	0.647	1.485	0.075	0.699
P15328	FOLR1	TELLNVCMNAK	0.399	0.759	0.5343	0.591	0.974	0.503	0.605	0.347	0.601
P16035	TIMP2	EVDSGNDIYGNPIK	0.876	0.805	0.5278	0.563	0.278	0.637	0.660	0.077	0.696
P08670	VIM	ISLPLPNFSSLNLR	0.965	0.861	0.5196	**2.646**	0.095	**0.804**	**2.722**	**0.019**	**0.784**
O75556	SCGB2A1	TINSDISIPEYK	**2.476**	0.930	0.5098	0.188	0.827	0.526	0.134	0.835	0.523
Q14508	WFDC2	EGSCPQVNINFPQLGLCR	1.118	0.961	0.5049	0.517	0.765	0.539	0.529	0.299	0.614