

			UTERINE FLUIDS			M1 CERVICAL SAMPLES			M3 CERVICAL SAMPLES		
Entry	Gene Name	Peptide	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	NTGIICIGPASR	5.405	0.000	0.9346	1.317	0.211	0.680	1.374	0.019	0.781
P42574	CASP3	SGTDVDAAANLR	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	ANIVHMLMLSSPEIQK	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	LVVECVMNVTCTR	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	YDGHLPPIEK	9.572	0.001	0.8725	1.739	0.114	0.748	1.074	0.324	0.608
P12830	CDH1	VFYSITGQGADTPPVGVFIER	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	VVLAYEPVWAI GTGK	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	GVDEV TIVNLTNR	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	LATQSN EITIPVTFESR	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	LFDQA FGLPR	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