Supplemental Table 1A: In-solution Trypsin Digestion of Albumin

Page 1 of 2

Locus	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Validation Status	Descriptive Name
UniRef100_P02768	**111**	**155**	**65.40%**	**609**	**69367**	**6.3**	**U**	**Serum albumin precursor**

Unique	FileName	XCorr	DeltCN	Conf%	M+H+	CalcM+H+	PPM	TotalIntensity	SpR	SpScore	IonProportion	Redundancy	Sequence
	HW_albumin_solution_2ul.1803.1803.2	2.964337	0.22868688	100	1226.6052	1226.6052	0	4747.18	1	1024.0997	88.9	1	R.FKDLGEENFK.A
	HW_albumin_solution_2ul.1801.1801.3	3.362195	0.20995532	98.8	1226.6068	1226.6052	1.3	6670.396	1	1221.7721	61.1	2	R.FKDLGEENFK.A
	HW_albumin_solution_2ul.1664.1664.2	1.8726445	0.07981005	92.5	951.44275	951.4418	1	4162.803	2	517.1312	85.7	1	K.DLGEENFK.A
	HW_albumin_solution_2ul.3546.3546.3	4.3256063	0.49181017	100	2490.2854	2490.285	0.2	7901.299	1	1733.118	42.5	1	K.ALVLIAFAQYLQQCPFEDHVK.L
	HW_albumin_solution_2ul.2832.2832.3	3.969544	0.3594285	100	2094.0105	2094.0115	-0.5	4750.7236	1	910.52765	48.4	1	L.IAFAQYLQQCPFEDHVK.L
	HW_albumin_solution_2ul.2302.2302.3	4.611546	0.4660937	100	1909.8889	1909.8901	-0.6	6496.818	1	1602.8187	53.6	1	A.FAQYLQQCPFEDHVK.L
	HW_albumin_solution_2ul.1981.1981.3	2.541197	0.25037268	98.6	1762.8237	1762.8218	1.1	3477.6753	1	527.6774	51.9	1	F.AQYLQQCPFEDHVK.L
	HW_albumin_solution_2ul.1986.1986.2	4.097447	0.5074002	100	1762.8237	1762.8218	1.1	8153.0054	1	1300.0657	73.1	1	F.AQYLQQCPFEDHVK.L
	HW_albumin_solution_2ul.1937.1937.3	2.9560215	0.2106946	98.8	1691.7863	1691.7847	0.9	7026.4175	9	796.97076	43.8	1	A.QYLQQCPFEDHVK.L
	HW_albumin_solution_2ul.1832.1832.3	2.991284	0.21186037	98.8	1563.7266	1563.7261	0.3	4817.041	3	447.95047	45.5	1	Q.YLQQCPFEDHVK.L
	HW_albumin_solution_2ul.1609.1609.3	2.487617	0.090366475	86.7	1400.6644	1400.6627	1.2	5542.859	3	840.788	55	1	Y.LQQCPFEDHVK.L
	HW_albumin_solution_2ul.2137.2137.2	3.2148063	0.31350815	100	1149.6146	1149.615	-0.3	4025.5305	1	735.3183	83.3	1	K.LVNEVTEFAK.T
	HW_albumin_solution_2ul.2082.2082.2	2.467391	0.24134119	100	1017.5377	1017.5364	1.3	3888.155	2	345.2962	68.8	2	K.SLHTLFGDK.L
	HW_albumin_solution_2ul.2666.2666.3	4.3088064	0.49855074	100	1932.0371	1932.0372	-0.1	7827.511	1	781.4415	35.9	2	K.SLHTLFGDKLCTVATLR.E
	HW_albumin_solution_2ul.2673.2673.2	3.9913898	0.44234264	100	1932.0393	1932.0372	1.1	7733.5093	1	1252.403	65.6	1	K.SLHTLFGDKLCTVATLR.E
	HW_albumin_solution_2ul.2667.2667.4	2.794369	0.29008695	100	1932.0452	1932.0372	4.1	4813.253	26	802.4909	35.4	1	K.SLHTLFGDKLCTVATLR.E
	HW_albumin_solution_2ul.2093.2093.2	2.2906847	0.07065375	92.6	817.41907	817.4203	-1.5	2100.0615	4	267.93924	91.7	1	L.HTLFGDK.L
	HW_albumin_solution_2ul.1667.1667.2	2.3528037	0.054999065	89.1	933.51965	933.5187	1	3665.4111	5	584.6094	85.7	1	K.LCTVATLR.E
	HW_albumin_solution_2ul.1506.1506.2	2.836682	0.4726653	100	1434.5337	1434.5334	0.2	5962.3916	1	738.0684	68.2	1	R.ETYGEMADCCAK.Q
	HW_albumin_solution_2ul.1502.1502.2	2.6680815	0.30027094	100	1450.5223	1450.5284	-4.2	4648.9897	1	459.81094	68.2	3	R.ETYGEM*ADCCAK.Q
	HW_albumin_solution_2ul.1607.1607.4	3.1689746	0.34207565	100	2636.2312	2636.227	1.6	6089.5815	1	853.2912	30.8	3	K.QEPERNECFLQHKDDNPNLPR.L
	HW_albumin_solution_2ul.1611.1611.3	3.501901	0.3516262	100	2636.2327	2636.227	2.1	7555.4326	1	690.45544	33.8	1	K.QEPERNECFLQHKDDNPNLPR.L
	HW_albumin_solution_2ul.1689.1689.3	4.0112586	0.26957482	100	1996.9296	1996.9294	0.1	7775.9473	1	867.1153	40	1	R.NECFLQHKDDNPNLPR.L
	HW_albumin_solution_2ul.1403.1403.3	2.4204822	0.12461711	91.6	1593.8152	1593.8132	1.2	8501.181	1	1117.9447	47.9	1	C.FLQHKDDNPNLPR.L
	HW_albumin_solution_2ul.1250.1250.2	1.532197	0.07737546	92	940.449	940.4483	0.7	4316.466	17	393.59546	71.4	1	K.DDNPNLPR.L
	HW_albumin_solution_2ul.2218.2218.2	2.251833	0.23656149	100	1057.5706	1057.571	-0.5	4310.022	13	379.185	68.8	2	R.LVRPEVDVM.C
	HW_albumin_solution_2ul.1740.1740.2	2.079543	0.13250382	98.9	1073.5662	1073.5659	0.2	4556.4204	1	413.40955	68.8	1	R.LVRPEVDVM*.C
	HW_albumin_solution_2ul.2142.2142.2	2.1963868	0.24372856	100	1217.6029	1217.6017	1	5697.511	3	524.5784	66.7	1	R.LVRPEVDVMC.T
	HW_albumin_solution_2ul.2195.2195.2	2.6234078	0.3809874	100	1318.6499	1318.6494	0.4	5096.9277	1	526.3355	70	1	R.LVRPEVDVMCT.A
	HW_albumin_solution_2ul.2233.2233.2	2.0299811	0.35573936	100	1389.6876	1389.6865	0.8	6410.5186	4	378.12634	50	1	R.LVRPEVDVMCTA.F
	HW_albumin_solution_2ul.2824.2824.2	2.3745537	0.28996673	100	1536.7561	1536.7549	0.8	4980.934	1	479.91064	62.5	1	R.LVRPEVDVMCTAF.H
	HW_albumin_solution_2ul.2813.2813.4	3.396298	0.34156373	100	2650.2676	2650.264	1.4	7442.9814	1	1211.3481	28.6	1	R.LVRPEVDVMCTAFHDNEETFLK.K
	HW_albumin_solution_2ul.2820.2820.3	6.6656504	0.54603744	100	2650.2686	2650.264	1.8	9130.799	1	1913.8134	41.7	1	R.LVRPEVDVMCTAFHDNEETFLK.K
	HW_albumin_solution_2ul.2425.2425.4	4.069046	0.34660676	100	2666.2588	2666.259	-0.1	5656.795	1	1394.0199	34.9	1	R.LVRPEVDVM*CTAFHDNEETFLK.K
	HW_albumin_solution_2ul.2427.2427.3	4.529199	0.4195239	100	2666.2598	2666.259	0.3	5254.8086	1	843.5697	38.1	1	R.LVRPEVDVM*CTAFHDNEETFLK.K
	HW_albumin_solution_2ul.2699.2699.5	4.254703	0.25865197	98.5	2778.3516	2778.359	-2.6	6322.668	1	1735.253	30.1	2	R.LVRPEVDVMCTAFHDNEETFLKK.Y
	HW_albumin_solution_2ul.2642.2642.4	4.9624496	0.4625469	100	2778.3552	2778.359	-1.3	6106.2437	1	982.3937	29.5	4	R.LVRPEVDVMCTAFHDNEETFLKK.Y
	HW_albumin_solution_2ul.2655.2655.3	8.096066	0.5376766	100	2778.357	2778.359	-0.7	7212.76	1	1471.8956	38.6	2	R.LVRPEVDVMCTAFHDNEETFLKK.Y
	HW_albumin_solution_2ul.2241.2241.5	4.2181144	0.32670984	100	2794.3533	2794.354	-0.3	6316.966	1	1957.389	30.1	2	R.LVRPEVDVM*CTAFHDNEETFLKK.Y
	HW_albumin_solution_2ul.2243.2243.4	3.9681008	0.320346	100	2794.3552	2794.354	0.4	8227.104	1	1277.2821	29.5	1	R.LVRPEVDVM*CTAFHDNEETFLKK.Y
	HW_albumin_solution_2ul.2248.2248.3	5.7319727	0.47546923	100	2794.361	2794.354	2.5	5046.699	1	943.254	40.9	1	R.LVRPEVDVM*CTAFHDNEETFLKK.Y
	HW_albumin_solution_2ul.2069.2069.3	2.9707751	0.30479395	100	1611.7102	1611.7108	-0.4	6289.928	1	764.7734	45.8	1	M.CTAFHDNEETFLK.K
	HW_albumin_solution_2ul.2071.2071.2	3.8313904	0.41743058	100	1611.7134	1611.7108	1.6	7040.707	1	1258.3759	79.2	1	M.CTAFHDNEETFLK.K
	HW_albumin_solution_2ul.1800.1800.4	4.6321497	0.32726157	100	1739.8071	1739.8058	0.8	7538.006	1	1605.0018	44.9	2	M.CTAFHDNEETFLKK.Y
	HW_albumin_solution_2ul.1799.1799.3	4.4481683	0.3917802	100	1739.8086	1739.8058	1.6	5613.8613	1	2076.8813	65.4	1	M.CTAFHDNEETFLKK.Y
	HW_albumin_solution_2ul.1672.1672.3	3.4713478	0.38991645	100	1478.7273	1478.7274	-0.1	5015.13	1	1086.8439	59.1	1	T.AFHDNEETFLKK.Y
	HW_albumin_solution_2ul.1585.1585.3	3.371737	0.28846166	100	1407.6923	1407.6903	1.4	7035.64	1	923.6172	52.5	1	A.FHDNEETFLKK.Y
	HW_albumin_solution_2ul.1914.1914.2	2.7451172	0.31758958	100	1055.5884	1055.5884	0	5437.8687	1	820.634	92.9	1	K.KYLYEIAR.R
	HW_albumin_solution_2ul.2088.2088.2	2.0200577	0.07224437	91.8	927.4934	927.49347	-0.1	2742.8923	1	491.13422	91.7	1	K.YLYEIAR.R
	HW_albumin_solution_2ul.3307.3307.3	3.7126386	0.35097492	100	1898.9949	1898.9952	-0.2	5871.7896	1	1614.7723	53.6	2	R.RHPYFYAPELLFFAK.R
	HW_albumin_solution_2ul.3376.3376.3	4.216502	0.39452216	100	1742.8931	1742.894	-0.6	5617.5747	1	1144.9674	51.9	1	R.HPYFYAPELLFFAK.R
	HW_albumin_solution_2ul.3379.3379.2	3.0086336	0.3108168	100	1742.8942	1742.894	0.1	4992.927	1	781.0558	73.1	1	R.HPYFYAPELLFFAK.R
	HW_albumin_solution_2ul.3435.3435.2	3.5585566	0.36696413	100	1345.7205	1345.7191	1	4241.0303	1	1098.067	90	1	Y.FYAPELLFFAK.R
	HW_albumin_solution_2ul.3226.3226.2	1.7981184	0.10505807	93.9	1198.6505	1198.6506	-0.1	4140.4854	35	231.42725	55.6	1	F.YAPELLFFAK.R
	HW_albumin_solution_2ul.1322.1322.2	2.96991	0.3784671	100	1371.5674	1371.5669	0.4	6967.2607	1	901.0546	68.2	1	K.AAFTECCQAADK.A
	HW_albumin_solution_2ul.1401.1401.2	1.6095868	0.06036349	87	880.4416	880.4411	0.6	2837.621	1	556.5715	92.9	1	K.AEFAEVSK.L
	HW_albumin_solution_2ul.1632.1632.2	5.55906	0.54993397	100	2086.8381	2086.8376	0.2	7847.0083	1	2176.008	78.1	1	K.VHTECCHGDLLECADDR.A
	HW_albumin_solution_2ul.1628.1628.3	5.0914574	0.5107144	100	2086.8386	2086.8376	0.5	5795.9575	1	2048.53	57.8	1	K.VHTECCHGDLLECADDR.A
	HW_albumin_solution_2ul.1626.1626.4	2.630234	0.20624644	97.8	2086.84	2086.8376	1.2	6355.8184	7	1084.3928	31.2	1	K.VHTECCHGDLLECADDR.A
	HW_albumin_solution_2ul.1840.1840.5	2.7789829	0.081093766	85	2585.1218	2585.118	1.5	4414.4355	86	630.75104	24.4	1	K.VHTECCHGDLLECADDRADLAK.Y

Supplemental Table 1A: In-solution Trypsin Digestion of Albumin

Unique	FileName	XCorr	DeltCN	Conf%	M+H+	CalcM+H+	PPM	TotalIntensity	SpR	SpScore	IonProportion	Redundancy	Sequence
	HW_albumin_solution_2ul.1842.1842.3	5.331651	0.38906872	100	2585.122	2585.118	1.6	5282.151	1	1298.8076	46.4	1	K.VHTECCHGDLLECADDRADLAK.Y
	HW_albumin_solution_2ul.1896.1896.4	3.094042	0.3422969	100	2585.1226	2585.118	1.8	6086.6323	1	1063.0278	32.5	2	K.VHTECCHGDLLECADDRADLAK.Y
	HW_albumin_solution_2ul.1278.1278.2	4.018011	0.44601372	100	1443.6425	1443.6421	0.3	6274.22	1	1395.7217	86.4	2	K.YICENQDSISSK.L
	HW_albumin_solution_2ul.1361.1361.3	3.093171	0.078318335	86.9	1546.797	1546.7969	0.1	4718.921	1	670.139	50	1	K.LKECCEKPLLEK.S
	HW_albumin_solution_2ul.1365.1365.4	2.873384	0.08717579	86.4	1546.7985	1546.7969	1	4032.4668	11	756.4725	43.9	1	K.LKECCEKPLLEK.S
	HW_albumin_solution_2ul.2657.2657.3	5.9432554	0.5977904	100	2990.342	2990.3394	0.9	6726.446	1	1668.2933	38.5	2	K.SHCIAEVENDEM*PADLPSLAADFVESK.D
	HW_albumin_solution_2ul.3386.3386.2	2.9139483	0.43118995	100	1639.7853	1639.7825	1.7	6513.8047	1	1330.4319	75	1	K.DVFLGM*FLYEYAR.R
	HW_albumin_solution_2ul.3028.3028.2	3.1280136	0.4383153	100	1262.6221	1262.6238	-1.4	5481.4424	1	1024.6906	83.3	1	F.LGMFLYEYAR.R
	HW_albumin_solution_2ul.2637.2637.2	3.2126021	0.4154666	100	1278.6198	1278.6187	0.9	5869.504	1	1045.5651	83.3	1	F.LGM*FLYEYAR.R
	HW_albumin_solution_2ul.2130.2130.2	2.5823433	0.10617824	94.8	961.47906	961.4778	1.3	2528.572	15	413.7737	91.7	1	M.FLYEYAR.R
	HW_albumin_solution_2ul.2148.2148.2	1.7329617	0.21091871	100	1085.5747	1085.5739	0.8	3781.5479	22	336.6969	68.8	1	R.RHPDYSVVL.L
	HW_albumin_solution_2ul.2604.2604.2	1.8313452	0.38313502	100	1198.658	1198.6578	0.1	3481.8762	142	170.78	55.6	1	R.RHPDYSVVLL.L
	HW_albumin_solution_2ul.2634.2634.2	3.4694753	0.39776242	100	1467.8429	1467.843	-0.1	6235.1167	1	1052.9443	77.3	1	R.RHPDYSVVLLLR.L
	HW_albumin_solution_2ul.2631.2631.3	4.5631557	0.27542645	100	1467.8434	1467.843	0.2	7697.9453	1	2743.5383	70.5	9	R.RHPDYSVVLLLR.L
	HW_albumin_solution_2ul.2830.2830.3	3.0036204	0.07417824	86.3	1311.742	1311.742	0	3891.5605	16	1135.877	55	1	R.HPDYSVVLLLR.L
	HW_albumin_solution_2ul.2829.2829.2	2.6683352	0.31535017	100	1311.7429	1311.742	0.7	2898.938	1	513.3573	85	1	R.HPDYSVVLLLR.L
	HW_albumin_solution_2ul.2916.2916.2	4.876609	0.39640135	100	2045.0978	2045.0953	1.2	4177.666	1	691.16095	62.5	1	K.VFDEFKPLVEEPQNLIK.Q
	HW_albumin_solution_2ul.2968.2968.3	4.6528783	0.28020296	100	2046.0809	2045.0953	-8.7	5368.9165	1	1678.9205	54.7	3	K.VFDEFKPLVEEPQNLIK.Q
	HW_albumin_solution_2ul.2923.2923.2	3.9257767	0.2560172	100	1798.9581	1798.9585	-0.2	4234.6367	1	805.0069	71.4	1	F.DEFKPLVEEPQNLIK.Q
	HW_albumin_solution_2ul.1899.1899.2	2.6381018	0.08789852	94.1	1069.5895	1069.5887	0.7	5015.718	19	700.81805	81.2	1	L.VEEPQNLIK.Q
	HW_albumin_solution_2ul.2695.2695.3	4.4127727	0.17898864	97.8	1657.751	1657.7527	-1	6596.3457	1	1753.5231	56.2	1	K.QNCELFEQLGEYK.F
	HW_albumin_solution_2ul.2690.2690.2	4.421632	0.3984996	100	1657.7513	1657.7527	-0.8	9776.864	1	1582.0292	79.2	1	K.QNCELFEQLGEYK.F
	HW_albumin_solution_2ul.2713.2713.2	3.7679393	0.42430684	100	1415.6488	1415.6511	-1.6	6616.1885	1	1440.265	85	1	N.CELFEQLGEYK.F
	HW_albumin_solution_2ul.2211.2211.2	2.6742282	0.11146339	96.8	960.56323	960.5625	0.8	3738.834	1	948.66907	92.9	1	K.FQNALLVR.Y
	HW_albumin_solution_2ul.2128.2128.3	4.2430067	0.39669675	100	1639.9387	1639.9377	0.6	6351.254	1	1385.5835	53.6	4	K.KVPQVSTPTLVEVSR.N
	HW_albumin_solution_2ul.2270.2270.2	3.104821	0.3925251	100	1511.8423	1511.8428	-0.3	6222.0234	1	1100.973	73.1	1	K.VPQVSTPTLVEVSR.N
	HW_albumin_solution_2ul.2280.2280.3	2.6130528	0.13390395	93.4	1511.8445	1511.8428	1.1	5998.1934	17	638.34216	40.4	1	K.VPQVSTPTLVEVSR.N
	HW_albumin_solution_2ul.2031.2031.2	1.7616935	0.32520884	100	1187.6641	1187.6631	0.8	2831.8188	1	274.34106	65	1	Q.VSTPTLVEVSR.N
	HW_albumin_solution_2ul.1353.1353.2	3.2865224	0.42453146	100	1138.4961	1138.498	-1.7	5443.174	1	1152.99	100	2	K.CCTESLVNR.R
	HW_albumin_solution_2ul.2158.2158.2	2.0978546	0.17247136	100	850.4237	850.424	-0.4	3349.0283	1	534.3517	91.7	1	R.RPCFSAL.E
	HW_albumin_solution_2ul.2409.2409.3	4.2099204	0.23302166	98.6	1910.9338	1910.9318	1.1	5359.68	1	1406.9503	51.7	3	R.RPCFSALEVDETYVPK.E
	HW_albumin_solution_2ul.2464.2464.2	3.4243925	0.32778868	100	1910.9348	1910.9318	1.6	4219.978	1	488.8526	56.7	1	R.RPCFSALEVDETYVPK.E
	HW_albumin_solution_2ul.2677.2677.2	5.4040265	0.47757825	100	1754.8328	1754.8306	1.3	6886.7334	1	1639.9447	75	1	R.PCFSALEVDETYVPK.E
	HW_albumin_solution_2ul.2598.2598.2	4.5106635	0.51412636	100	1657.7748	1657.7778	-1.8	5365.0864	1	1571.151	84.6	1	P.CFSALEVDETYVPK.E
	HW_albumin_solution_2ul.2516.2516.2	3.6007202	0.34236944	100	1497.7472	1497.7472	0	5827.7847	1	1267.998	79.2	1	C.FSALEVDETYVPK.E
	HW_albumin_solution_2ul.2124.2124.2	3.2650943	0.41427872	100	1350.6748	1350.6787	-2.9	4216.3174	1	819.7209	77.3	1	F.SALEVDETYVPK.E
	HW_albumin_solution_2ul.1538.1538.2	1.5655798	0.07337307	91.4	1079.5275	1079.5255	1.8	5328.79	2	403.47586	62.5	1	L.EVDETYVPK.E
	HW_albumin_solution_2ul.1436.1436.2	2.2277646	0.18958707	100	950.4851	950.4829	2.3	5293.629	1	770.82513	85.7	1	E.VDETYVPK.E
	HW_albumin_solution_2ul.3146.3146.2	1.9954126	0.14078605	98.9	1105.4845	1105.4836	0.8	5271.282	3	492.9379	68.8	1	K.EFNAETFTF.H
	HW_albumin_solution_2ul.2842.2842.3	2.547029	0.24338989	98.7	2260.022	2260.0227	-0.3	5893.1606	4	423.86484	30.6	1	K.EFNAETFTFHADICTLSEK.E
	HW_albumin_solution_2ul.1963.1963.2	3.4882343	0.40397063	100	1421.6729	1421.673	-0.1	4480.587	1	775.06024	77.3	1	F.TFHADICTLSEK.E
	HW_albumin_solution_2ul.1961.1961.3	2.6994271	0.23946568	98.7	1421.6731	1421.673	0.1	3289.3123	4	390.85138	47.7	1	F.TFHADICTLSEK.E
	HW_albumin_solution_2ul.2036.2036.2	3.184008	0.1903187	100	1128.7001	1128.6987	1.2	5525.2114	1	1238.0275	88.9	1	K.KQTALVELVK.H
	HW_albumin_solution_2ul.2052.2052.3	3.9878721	0.15343627	97.9	1129.7037	1128.6987	1.5	6073.0283	1	2320.2	72.2	2	K.KQTALVELVK.H
	HW_albumin_solution_2ul.2349.2349.2	1.7907171	0.16960502	100	1000.6057	1000.6037	2	2888.384	10	192.71625	62.5	1	K.QTALVELVK.H
	HW_albumin_solution_2ul.3077.3077.2	2.715766	0.3682056	100	1342.6344	1342.6348	-0.3	8303.357	1	1365.3939	72.7	2	K.AVMDDFAAFVEK.C
	HW_albumin_solution_2ul.3018.3018.3	3.4983838	0.28442022	100	1342.6354	1342.6348	0.5	6307.45	1	1357.185	52.3	1	K.AVMDDFAAFVEK.C
	HW_albumin_solution_2ul.2662.2662.2	3.4996703	0.40673062	100	1358.6301	1358.6296	0.4	5490.0103	1	1224.0044	81.8	3	K.AVM*DDFAAFVEK.C
	HW_albumin_solution_2ul.1110.1110.3	3.37707	0.3070576	100	1627.7274	1627.7268	0.4	6654.568	1	1155.4504	48.1	1	K.ADDKETCFAEEGKK.L
	HW_albumin_solution_2ul.2388.2388.2	2.7769015	0.38038835	100	1141.6937	1141.694	-0.2	5544.2793	2	801.0366	72.7	1	K.KLVAASQAALGL.-
	HW_albumin_solution_2ul.2656.2656.2	3.411539	0.3020191	100	1013.5984	1013.599	-0.6	4138.085	1	1088.1501	85	6	K.LVAASQAALGL.-

Supplemental Table 1B: In-gel Trypsin Digestion of Albumin

Locus	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Validation Status	Descriptive Name
UniRef100_P02768	**87**	**98**	**61.20%**	**609**	**69367**	**6.3**	**U**	**Serum albumin precursor**

Unique	FileName	XCorr	DeltCN	Conf%	M+H+	CalcM+H+	PPM	Total Intensity	SpR	SpScore	Ion Proportion	Redundancy	Sequence
	HW_albumin_ingel.1828.1828.2	3.195374	0.22350986	100	1226.6046	1226.605	-0.5	4375.1436	2	982.3727	88.9	1	R.FKDLGEENFK.A
	HW_albumin_ingel.1827.1827.3	3.601726	0.25260255	100	1226.6068	1226.605	1.3	6973.7915	1	1493.929	66.7	1	R.FKDLGEENFK.A
	HW_albumin_ingel.3526.3526.3	3.888048	0.4945334	100	2490.2893	2490.285	1.8	7395.597	1	1083.962	37.5	1	K.ALVLIAFAQYLQQCPFEDHVK.L
	HW_albumin_ingel.2331.2331.3	3.100106	0.27364296	100	1909.8878	1909.89	-1.2	6807.917	1	596.8859	35.7	1	A.FAQYLQQCPFEDHVK.L
	HW_albumin_ingel.1967.1967.3	3.81344	0.3348917	100	1762.8224	1762.822	0.3	4720.007	1	751.0443	50	1	F.AQYLQQCPFEDHVK.L
	HW_albumin_ingel.2018.2018.2	4.011968	0.40525082	100	1762.8235	1762.822	1	8171.154	1	1317.975	73.1	1	F.AQYLQQCPFEDHVK.L
	HW_albumin_ingel.1847.1847.3	2.916712	0.2490735	100	1563.728	1563.726	1.2	3844.9849	3	472.8723	50	1	Q.YLQQCPFEDHVK.L
	HW_albumin_ingel.1850.1850.2	2.934742	0.36440346	100	1563.7286	1563.726	1.6	7135.106	1	1016.504	77.3	1	Q.YLQQCPFEDHVK.L
	HW_albumin_ingel.1597.1597.3	2.431196	0.12747693	90	1400.6641	1400.663	1	4725.314	1	742.3881	50	1	Y.LQQCPFEDHVK.L
	HW_albumin_ingel.2184.2184.2	3.11425	0.30391964	100	1149.615	1149.615	0	4174.561	1	912.9632	88.9	1	K.LVNEVTEFAK.T
	HW_albumin_ingel.2134.2134.2	2.488415	0.2783482	100	1017.5362	1017.536	-0.2	4174.733	1	615.6977	87.5	1	K.SLHTLFGDK.L
	HW_albumin_ingel.2141.2141.2	2.165842	0.20929633	100	817.4207	817.4203	0.5	2195.4136	40	204.5974	83.3	1	L.HTLFGDK.L
	HW_albumin_ingel.1671.1671.2	2.152193	0.0932617	92.9	933.521	933.5187	2.5	3848.7263	9	485.5061	78.6	1	K.LCTVATLR.E
	HW_albumin_ingel.1491.1491.2	2.67515	0.3554993	100	1434.5356	1434.533	1.5	5757.096	1	577.241	63.6	1	R.ETYGEMADCCAK.Q
	HW_albumin_ingel.1756.1756.4	2.572357	0.17441154	96.5	1996.9291	1996.929	-0.2	7785.059	14	837.9314	32.2	1	R.NECFLQHKDDNPNLPR.L
	HW_albumin_ingel.1758.1758.3	3.784598	0.28460613	100	1996.9304	1996.929	0.5	7186.8745	3	668.0223	35	1	R.NECFLQHKDDNPNLPR.L
	HW_albumin_ingel.1250.1250.2	2.474122	0.23136874	100	940.4495	940.4483	1.3	4846.5723	2	715.6571	85.7	1	K.DDNPNLPR.L
	HW_albumin_ingel.2254.2254.2	2.299861	0.31693488	100	1057.571	1057.571	0	3962.3643	26	346.038	68.8	1	R.LVRPEVDVM.C
	HW_albumin_ingel.2264.2264.2	1.973856	0.21186288	100	1073.5634	1073.566	-2.4	4747.0864	2	448.308	68.8	2	R.LVRPEVDVM*.C
	HW_albumin_ingel.2853.2853.4	3.990938	0.33303034	100	2650.2632	2650.264	-0.3	6800.2827	1	1381.639	31.7	1	R.LVRPEVDVMCTAFHDNEETFLK.K
	HW_albumin_ingel.2459.2459.4	4.01811	0.34179372	100	2666.2617	2666.259	1	7271.2817	1	1840.857	34.1	1	R.LVRPEVDVM*CTAFHDNEETFLK.K
	HW_albumin_ingel.2461.2461.3	5.000168	0.44582936	100	2666.2664	2666.259	2.7	5030.5986	1	755.0065	38.1	1	R.LVRPEVDVM*CTAFHDNEETFLK.K
	HW_albumin_ingel.2291.2291.5	3.273131	0.23890413	100	2794.355	2794.354	0.3	7298.337	1	2174.347	30.7	1	R.LVRPEVDVM*CTAFHDNEETFLKK.Y
	HW_albumin_ingel.2111.2111.3	3.352645	0.33987102	100	1611.7119	1611.711	0.7	7270.038	1	964.2156	47.9	1	M.CTAFHDNEETFLK.K
	HW_albumin_ingel.2113.2113.2	4.118394	0.47510475	100	1611.7137	1611.711	1.8	7674.277	1	1623.834	83.3	1	M.CTAFHDNEETFLK.K
	HW_albumin_ingel.1820.1820.4	2.667563	0.270682	100	1739.8037	1739.806	-1.2	6802.7397	9	802.9227	35.9	1	M.CTAFHDNEETFLKK.Y
	HW_albumin_ingel.1822.1822.3	4.289485	0.37139758	100	1739.806	1739.806	0.1	5423.4263	2	964.9941	50	1	M.CTAFHDNEETFLKK.Y
	HW_albumin_ingel.2073.2073.3	3.49156	0.27912343	100	1451.6797	1451.68	-0.3	3928.2449	2	580.4204	50	1	C.TAFHDNEETFLK.K
	HW_albumin_ingel.2000.2000.3	2.720895	0.09914117	87.1	1350.6332	1350.632	0.5	6432.6934	1	1105.832	55	1	T.AFHDNEETFLK.K
	HW_albumin_ingel.1938.1938.2	2.416112	0.23377377	100	1055.5894	1055.588	0.9	4591.4863	2	770.7638	92.9	1	K.KYLYEIAR.R
	HW_albumin_ingel.1941.1941.3	2.334354	0.05881789	83.3	1055.5901	1055.588	1.6	5895.1357	11	1417.698	67.9	1	K.KYLYEIAR.R
	HW_albumin_ingel.2137.2137.2	1.980887	0.07943472	89.7	927.49335	927.4935	-0.1	2514.3035	1	585.9912	100	1	K.YLYEIAR.R
	HW_albumin_ingel.3101.3101.2	1.737622	0.12233841	89.5	1249.625	1249.625	-0.2	4352.3345	8	292.039	61.1	1	R.HPYFYAPELL.F
	HW_albumin_ingel.3362.3362.2	2.642471	0.30180916	100	1742.8948	1742.894	0.4	5326.0273	1	452.7645	61.5	1	R.HPYFYAPELLFFAK.R
	HW_albumin_ingel.3360.3360.3	3.994936	0.30482507	100	1742.8949	1742.894	0.5	5477.0596	1	1565.207	59.6	1	R.HPYFYAPELLFFAK.R
	HW_albumin_ingel.3417.3417.2	3.198204	0.3813407	100	1345.7181	1345.719	-0.7	3866.8743	1	822.6211	85	1	Y.FYAPELLFFAK.R
	HW_albumin_ingel.1322.1322.2	3.148876	0.32590523	100	1371.5682	1371.567	1	7116.636	1	1247.536	77.3	1	K.AAFTECCQAADK.A
	HW_albumin_ingel.1641.1641.2	5.825736	0.56229305	100	2086.8386	2086.838	0.5	7228.4653	1	1948.754	75	1	K.VHTECCHGDLLECADDR.A
	HW_albumin_ingel.1634.1634.3	4.711394	0.45090497	100	2086.839	2086.838	0.7	6260.4146	1	1886.218	56.2	1	K.VHTECCHGDLLECADDR.A
	HW_albumin_ingel.1878.1878.4	2.812541	0.19885124	100	2585.1174	2585.118	-0.2	5995.12	1	871.9154	29.4	1	K.VHTECCHGDLLECADDRADLAK.Y
	HW_albumin_ingel.1714.1714.3	3.678075	0.24001396	100	1460.5867	1460.589	-1.8	8823.521	2	1373.829	47.7	1	C.CHGDLLECADDR.A
	HW_albumin_ingel.1358.1358.4	3.602763	0.21027146	100	1546.7987	1546.797	1.2	4551.957	24	748.3292	43.9	1	K.LKECCEKPLLEK.S
	HW_albumin_ingel.1355.1355.3	2.855812	0.12447747	93.2	1546.7999	1546.797	2	4233.9873	1	767.4023	56.8	1	K.LKECCEKPLLEK.S
	HW_albumin_ingel.3084.3084.3	4.815466	0.46708152	100	2990.347	2990.339	2.5	6273.3267	1	1038.072	33.7	1	K.SHCIAEVENDEM*PADLPSLAADFVESK.D
	HW_albumin_ingel.1861.1861.2	2.452503	0.24078827	100	979.51044	979.5095	1	3317.2195	1	642.1246	87.5	1	S.LAADFVESK.D
	HW_albumin_ingel.3371.3371.2	3.830437	0.4100951	100	1639.7839	1639.783	0.9	6194.449	1	1268.483	75	1	K.DVFLGM*FLYEYAR.R
	HW_albumin_ingel.3027.3027.2	2.893848	0.29028767	100	1262.6226	1262.624	-1	6210.2114	1	1079.842	83.3	1	F.LGMFLYEYAR.R
	HW_albumin_ingel.2661.2661.2	3.215031	0.3711634	100	1278.6201	1278.619	1.1	6974.609	1	1237.518	83.3	1	F.LGM*FLYEYAR.R
	HW_albumin_ingel.2191.2191.2	1.689824	0.07784775	82.7	1085.5748	1085.574	0.9	4443.681	141	200.3381	56.2	1	R.RHPDYSVVL.L
	HW_albumin_ingel.2627.2627.2	1.859918	0.28898978	100	1198.6593	1198.658	1.2	3520.74	118	194.3828	61.1	1	R.RHPDYSVVLL.L
	HW_albumin_ingel.2675.2675.3	4.486714	0.34723297	100	1467.8446	1467.843	1.1	6849.311	1	2083.454	61.4	4	R.RHPDYSVVLLLR.L
	HW_albumin_ingel.2849.2849.2	2.447961	0.19862558	100	1311.7417	1311.742	-0.2	2901.1257	1	415.4913	80	1	R.HPDYSVVLLLR.L
	HW_albumin_ingel.1375.1375.2	1.6254	0.06338324	79	984.48926	984.4884	0.9	3822.305	82	231.5754	64.3	1	K.TYETTLEK.C
	HW_albumin_ingel.2952.2952.3	4.920148	0.33634114	100	2045.0952	2045.095	-0.1	5283.4824	1	1502.447	53.1	3	K.VFDEFKPLVEEPQNLIK.Q
	HW_albumin_ingel.2936.2936.2	4.859949	0.38767204	100	2045.0952	2045.095	-0.1	4051.5522	1	725.2506	65.6	1	K.VFDEFKPLVEEPQNLIK.Q
	HW_albumin_ingel.2376.2376.2	3.153668	0.21503672	100	1279.7261	1279.726	0.4	5911.4995	1	1062.498	80	1	K.PLVEEPQNLIK.Q
	HW_albumin_ingel.2718.2718.3	4.090893	0.2852637	100	1657.7498	1657.753	-1.8	6303.5537	1	1726.599	58.3	1	K.QNCELFEQLGEYK.F
	HW_albumin_ingel.2726.2726.2	3.951184	0.45615003	100	1657.7516	1657.753	-0.7	8309.814	1	1546.135	83.3	1	K.QNCELFEQLGEYK.F
	HW_albumin_ingel.2247.2247.2	2.599475	0.12478186	100	960.5618	960.5625	-0.7	3908.653	1	944.342	92.9	1	K.FQNALLVR.Y
	HW_albumin_ingel.2147.2147.2	3.008884	0.4628193	100	1639.9381	1639.938	0.2	5259.692	1	815.8173	71.4	1	K.KVPQVSTPTLVEVSR.N
	HW_albumin_ingel.2174.2174.3	4.419632	0.3558125	100	1639.9385	1639.938	0.4	6417.2163	1	1626.698	55.4	2	K.KVPQVSTPTLVEVSR.N
	HW_albumin_ingel.2296.2296.2	3.183777	0.35221773	100	1511.8423	1511.843	-0.3	6552.968	1	1245.684	73.1	1	K.VPQVSTPTLVEVSR.N
	HW_albumin_ingel.2309.2309.3	3.38503	0.17824994	100	1511.843	1511.843	0.2	5752.0225	3	914.4763	48.1	1	K.VPQVSTPTLVEVSR.N
	HW_albumin_ingel.2070.2070.2	1.901035	0.28767008	100	1187.6648	1187.663	1.4	3875.4897	17	229.2334	55	1	Q.VSTPTLVEVSR.N
	HW_albumin_ingel.1344.1344.2	2.593584	0.3089433	100	1138.502	1138.498	3.4	4834.0195	1	824.0143	87.5	1	K.CCTESLVNR.R

Supplemental Table 1B: In-gel Trypsin Digestion of Albumin

Unique	FileName	XCorr	DeltCN	Conf%	M+H+	CalcM+H+	PPM	Total Intensity	SpR	SpScore	Ion Proportion	Redundancy	Sequence
	HW_albumin_ingel.2441.2441.3	4.328799	0.18458492	100	1910.9298	1910.932	-1	6489.877	1	1394.873	48.3	2	R.RPCFSALEVDETYVPK.E
	HW_albumin_ingel.2499.2499.2	3.71266	0.399026	100	1910.9343	1910.932	1.3	4154.804	1	554.1569	60	1	R.RPCFSALEVDETYVPK.E
	HW_albumin_ingel.2701.2701.2	4.975519	0.4077169	100	1754.8296	1754.831	-0.6	7421.5967	1	2031.949	78.6	1	R.PCFSALEVDETYVPK.E
	HW_albumin_ingel.2624.2624.2	5.126413	0.5156089	100	1657.7783	1657.778	0.3	7675.737	1	2369.636	88.5	1	P.CFSALEVDETYVPK.E
	HW_albumin_ingel.2546.2546.2	2.61321	0.274817	100	1497.7455	1497.747	-1.1	6101.4683	1	701.0837	62.5	1	C.FSALEVDETYVPK.E
	HW_albumin_ingel.2170.2170.2	3.285255	0.39768	100	1350.677	1350.679	-1.3	4614.092	1	1100.801	81.8	1	F.SALEVDETYVPK.E
	HW_albumin_ingel.2092.2092.2	3.390339	0.44159952	100	1263.6472	1263.647	0.4	5449.9907	1	1163.003	85	1	S.ALEVDETYVPK.E
	HW_albumin_ingel.1535.1535.2	1.429138	0.07878503	75.2	1079.5272	1079.526	1.6	5239.8594	2	450.412	68.8	1	L.EVDETYVPK.E
	HW_albumin_ingel.1991.1991.3	2.765443	0.26645625	100	1421.6713	1421.673	-1.2	3303.696	1	531.5095	54.5	1	F.TFHADICTLSEK.E
	HW_albumin_ingel.1992.1992.2	3.476648	0.3113829	100	1421.6714	1421.673	-1.1	4765.049	1	780.9825	77.3	1	F.TFHADICTLSEK.E
	HW_albumin_ingel.1519.1519.2	2.458278	0.17449565	100	1036.4989	1036.498	0.9	6268.234	1	998.0046	87.5	1	H.ADICTLSEK.E
	HW_albumin_ingel.2079.2079.3	4.202961	0.1711264	100	1128.6995	1128.699	0.6	5452.9937	1	1932.836	69.4	1	K.KQTALVELVK.H
	HW_albumin_ingel.2077.2077.2	2.934923	0.19794779	100	1128.6997	1128.699	0.9	6545.442	1	1362.631	88.9	1	K.KQTALVELVK.H
	HW_albumin_ingel.2380.2380.2	1.878065	0.1839423	100	1000.605	1000.604	1.3	2539.8218	6	198.108	62.5	1	K.QTALVELVK.H
	HW_albumin_ingel.3023.3023.3	3.429937	0.3577629	100	1342.6342	1342.635	-0.5	5099.706	2	825.087	50	1	K.AVMDDFAAFVEK.C
	HW_albumin_ingel.3016.3016.2	3.087749	0.40915823	100	1342.6349	1342.635	0.1	7508.874	1	1357.754	77.3	1	K.AVMDDFAAFVEK.C
	HW_albumin_ingel.2681.2681.2	3.693497	0.45882687	100	1358.6315	1358.63	1.3	5151.047	1	1200.954	81.8	1	K.AVM*DDFAAFVEK.C
	HW_albumin_ingel.1255.1255.3	2.990874	0.21738847	100	1499.6354	1499.632	2.3	7555.23	2	760.0784	39.6	1	K.ADDKETCFAEEGK.K
	HW_albumin_ingel.1116.1116.3	3.965989	0.27723253	100	1627.7275	1627.727	0.4	6775.8027	1	1229.704	50	1	K.ADDKETCFAEEGKK.L
	HW_albumin_ingel.1635.1635.2	2.502197	0.13911812	100	1028.6101	1028.61	0.2	4984.948	1	747.5302	80	1	K.KLVAASQAALG.L
	HW_albumin_ingel.2422.2422.2	3.054059	0.3679473	100	1141.6946	1141.694	0.5	8186.997	1	970.5601	68.2	1	K.KLVAASQAALGL.-
	HW_albumin_ingel.2944.2944.2	3.259211	0.3979762	100	1013.5994	1013.599	0.4	5289.295	1	1238.493	85	4	K.LVAASQAALGL.-

Supplemental Table 1C: In-solution Trypsin Digestion of Human Peroxiredoxin

Page 1 of 1

Locus	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Validation Status	Descriptive Name
UniRef100_P30041	59	67	71.00%	224	25035	6.4	U	Peroxiredoxin-6

Unique	FileName	XCorr	DeltCN	Conf%	M+H+	CalcM+H+	PPM	TotalIntensity	SpR	SpScore	IonProportion	Redundancy	Sequence
*	HW_prdx6_solution_2ul.2798.2798.3	5.582833	0.4349409	100	2098.0923	2098.0928	-0.2	6952.1484	1	1969.9989	48.8	1	M.PGGLLLGDVAPNFEANTTVGR.I
*	HW_prdx6_solution_2ul.3011.3011.2	5.8465714	0.467526	100	2098.0955	2098.0928	1.3	5358.448	1	1790.7196	72.5	4	M.PGGLLLGDVAPNFEANTTVGR.I
*	HW_prdx6_solution_2ul.2777.2777.2	3.0521605	0.321106	100	2001.0377	2001.04	-1.2	4838.5884	1	484.396	44.7	1	P.GGLLLGDVAPNFEANTTVGR.I
	HW_prdx6_solution_2ul.2026.2026.2	3.031743	0.39103734	100	1395.6586	1395.6573	0.9	5188.9624	1	1030.53	81.8	1	R.DFTPVCTTELGR.A
	HW_prdx6_solution_2ul.1436.1436.2	3.1318989	0.3146254	100	1133.5605	1133.562	-1.3	6342.317	1	1219.0784	88.9	1	F.TPVCTTELGR.A
	HW_prdx6_solution_2ul.2036.2036.2	2.8093657	0.253182	100	1032.5122	1032.5143	-2	3713.754	1	658.12256	87.5	1	T.PVCTTELGR.A
	HW_prdx6_solution_2ul.2694.2694.3	3.3167627	0.4212828	100	1897.0061	1897.0066	-0.3	3296.2537	1	433.93732	40.6	2	K.LIALSIDSVEDHLAWSK.D
	HW_prdx6_solution_2ul.2909.2909.2	4.7664332	0.50809556	100	1897.0079	1897.0066	0.7	8127.4727	1	2002.7839	75	1	K.LIALSIDSVEDHLAWSK.D
	HW_prdx6_solution_2ul.2918.2918.2	4.785393	0.55929303	100	1670.8364	1670.8384	-1.2	8868.535	1	2513.061	78.6	1	I.ALSIDSVEDHLAWSK.D
	HW_prdx6_solution_2ul.2097.2097.2	3.560043	0.40098503	100	1486.7191	1486.7173	1.2	7477.2344	1	1146.7124	70.8	1	L.SIDSVEDHLAWSK.D
*	HW_prdx6_solution_2ul.1427.1427.2	3.7912881	0.39525515	100	1582.6699	1582.6691	0.5	7950.417	1	1471.745	75	1	K.DINAYNCEEPTEK.L
*	HW_prdx6_solution_2ul.2745.2745.4	4.5071096	0.49965283	100	2649.2463	2649.2502	-1.5	7730.957	1	1542.7925	32.5	1	K.DINAYNCEEPTEKLPFPIIDDR.N
*	HW_prdx6_solution_2ul.2744.2744.2	4.653697	0.47685143	100	2649.2488	2649.2502	-0.6	7052.847	1	912.7466	50	1	K.DINAYNCEEPTEKLPFPIIDDR.N
*	HW_prdx6_solution_2ul.2737.2737.3	5.227366	0.3798251	100	2649.2493	2649.2502	-0.4	7067.038	1	890.04596	36.9	1	K.DINAYNCEEPTEKLPFPIIDDR.N
*	HW_prdx6_solution_2ul.2531.2531.4	3.528313	0.5087141	100	2919.389	2919.3943	-1.8	5590.344	1	1226.4492	32.6	1	K.DINAYNCEEPTEKLPFPIIDDRNR.E
*	HW_prdx6_solution_2ul.2535.2535.3	5.074903	0.44480744	100	2919.3914	2919.3943	-1	8185.947	1	728.90405	29.3	1	K.DINAYNCEEPTEKLPFPIIDDRNR.E
*	HW_prdx6_solution_2ul.2646.2646.3	3.9826078	0.40559065	100	2421.1438	2421.1392	1.9	6497.0317	1	748.53503	36.8	1	I.NAYNCEEPTEKLPFPIIDDR.N
*	HW_prdx6_solution_2ul.2637.2637.3	3.1953828	0.18197902	100	2307.0977	2307.0962	0.6	5063.5435	2	621.2997	37.5	1	N.AYNCEEPTEKLPFPIIDDR.N
*	HW_prdx6_solution_2ul.2594.2594.3	4.5837684	0.300836	100	2072.9966	2072.9958	0.4	8392.732	1	2351.538	51.6	1	Y.NCEEPTEKLPFPIIDDR.N
*	HW_prdx6_solution_2ul.2602.2602.3	4.0262275	0.27747664	100	1958.9514	1958.9529	-0.7	9004.811	1	2210.7754	51.7	1	N.CEEPTEKLPFPIIDDR.N
*	HW_prdx6_solution_2ul.2666.2666.2	2.9430783	0.24693479	100	1085.5995	1085.599	0.4	4511.425	1	831.6141	87.5	1	K.LPFPIIDDR.N
*	HW_prdx6_solution_2ul.2380.2380.2	2.9320648	0.1188765	100	1355.7433	1355.743	0.2	8027.19	8	616.4015	70	1	K.LPFPIIDDRNR.E
*	HW_prdx6_solution_2ul.2935.2935.3	4.586973	0.39112246	100	2171.1367	2171.1377	-0.4	6995.338	1	1229.7389	44.4	2	R.NRELAILLGM*LDPAEKDEK.G
*	HW_prdx6_solution_2ul.2828.2828.4	3.06278	0.11296012	96.6	2171.1384	2171.1377	0.3	4183.18	1	1002.6448	32.4	1	R.NRELAILLGM*LDPAEKDEK.G
*	HW_prdx6_solution_2ul.2962.2962.2	4.3527565	0.42664376	100	1528.8295	1528.8291	0.2	6587.6816	1	1732.5051	80.8	1	R.ELAILLGM*LDPAEK.D
*	HW_prdx6_solution_2ul.3145.3145.3	2.5992348	0.33748564	100	1884.9999	1884.9987	0.6	4325.35	18	300.39316	32.8	1	R.ELAILLGMLDPAEKDEK.G
*	HW_prdx6_solution_2ul.3146.3146.2	4.0542235	0.3922292	100	1885.0006	1884.9987	1	5588.296	1	869.6163	62.5	1	R.ELAILLGMLDPAEKDEK.G
*	HW_prdx6_solution_2ul.2763.2763.2	4.1938057	0.4240159	100	1900.9933	1900.9937	-0.2	5289.639	1	985.89	65.6	1	R.ELAILLGM*LDPAEKDEK.G
*	HW_prdx6_solution_2ul.2623.2623.3	3.4407802	0.2848031	100	2629.3596	2629.3574	0.8	6378.8804	1	828.8817	34.8	1	R.ELAILLGM*LDPAEKDEKGM*PVTAR.V
*	HW_prdx6_solution_2ul.2464.2464.2	2.5594628	0.29631895	100	1007.55396	1007.556	-2.1	3668.4102	1	492.16934	75	1	R.VVFVFGPDK.K
*	HW_prdx6_solution_2ul.2164.2164.2	3.02127	0.2818917	100	1135.6515	1135.651	0.4	7944.196	2	1049.2275	77.8	2	R.VVFVFGPDKK.L
*	HW_prdx6_solution_2ul.2162.2162.3	2.0444694	0.11839359	90.3	1135.6519	1135.651	0.8	2481.4321	97	195.03374	41.7	1	R.VVFVFGPDKK.L
*	HW_prdx6_solution_2ul.2171.2171.2	2.5750978	0.122053355	100	937.515	937.51416	0.9	3322.539	5	554.7545	85.7	1	V.FVFGPDKK.L
	HW_prdx6_solution_2ul.2387.2387.3	2.5997255	0.14940952	96.2	1432.852	1432.8522	-0.1	5318.0605	3	720.9278	45.8	2	K.LKLSILYPATTGR.N
	HW_prdx6_solution_2ul.2393.2393.2	3.510875	0.35137665	100	1432.8525	1432.8522	0.3	6392.6562	1	1457.6239	79.2	1	K.LKLSILYPATTGR.N
	HW_prdx6_solution_2ul.2222.2222.2	2.6794975	0.1774521	100	1191.6731	1191.6732	-0.1	3846.154	1	795.4918	90	1	K.LSILYPATTGR.N
*	HW_prdx6_solution_2ul.2340.2340.2	3.06156	0.451004	100	1200.7201	1200.7198	0.2	6337.76	1	1303.8054	85	1	R.VVISLQLTAEK.R
*	HW_prdx6_solution_2ul.2245.2245.3	2.3619063	0.1324463	96.7	1356.8209	1356.8209	0	2078.5881	2	289.18118	50	1	R.VVISLQLTAEKR.V
*	HW_prdx6_solution_2ul.2136.2136.2	3.2544332	0.3397183	100	1356.822	1356.8209	0.8	7731.9927	1	1285.821	77.3	1	R.VVISLQLTAEKR.V
*	HW_prdx6_solution_2ul.1647.1647.2	1.8142079	0.05257072	83.3	1071.5936	1071.5946	-0.9	3559.0115	3	384.11737	75	1	K.RVATPVDWK.D
*	HW_prdx6_solution_2ul.2579.2579.4	3.027311	0.17923357	97.9	2882.4563	2882.4604	-1.4	5952.561	2	1057.2302	26.7	1	K.RVATPVDWKDGDSVMVLPTIPEEEAK.K
*	HW_prdx6_solution_2ul.2342.2342.4	3.3025835	0.26362735	100	2898.452	2898.4553	-1.2	5535.8706	1	745.55676	25.3	1	K.RVATPVDWKDGDSVM*VLPTIPEEEAK.K
*	HW_prdx6_solution_2ul.2346.2346.3	4.5903497	0.479409	100	2898.4573	2898.4553	0.7	7987.5215	1	1010.94116	32	1	K.RVATPVDWKDGDSVM*VLPTIPEEEAK.K
	HW_prdx6_solution_2ul.1810.1810.2	1.6602572	0.15851438	95.2	915.49396	915.49347	0.5	2154.6208	2	196.76176	64.3	1	R.VATPVDWK.D
*	HW_prdx6_solution_2ul.1800.1800.2	1.9760635	0.17008641	98.3	1202.571	1202.5688	1.8	4053.9915	1	367.60007	65	1	R.VATPVDWKDGD.S
*	HW_prdx6_solution_2ul.2690.2690.3	4.015083	0.24231273	100	2726.363	2726.3594	1.3	3815.267	1	814.09845	35.4	1	R.VATPVDWKDGDSVMVLPTIPEEEAK.K
*	HW_prdx6_solution_2ul.2462.2462.2	3.6868012	0.36464432	100	2742.3506	2742.3542	-1.3	6791.7393	1	466.90378	35.4	1	R.VATPVDWKDGDSVM*VLPTIPEEEAK.K
*	HW_prdx6_solution_2ul.2450.2450.3	4.375925	0.40638041	100	2742.3555	2742.3542	0.4	4546.623	1	760.065	35.4	2	R.VATPVDWKDGDSVM*VLPTIPEEEAK.K
*	HW_prdx6_solution_2ul.2569.2569.3	4.657038	0.18469498	100	2854.4534	2854.4543	-0.3	4731.517	2	679.40295	32	1	R.VATPVDWKDGDSVMVLPTIPEEEAKK.L
*	HW_prdx6_solution_2ul.2562.2562.4	2.8224058	0.27757517	100	2854.4556	2854.4543	0.4	6108.2915	9	611.21185	25.3	1	R.VATPVDWKDGDSVMVLPTIPEEEAKK.L
*	HW_prdx6_solution_2ul.2326.2326.4	2.7562056	0.21754883	100	2870.453	2870.4492	1.3	6318.655	2	672.65753	23.3	1	R.VATPVDWKDGDSVM*VLPTIPEEEAKK.L
*	HW_prdx6_solution_2ul.2329.2329.3	4.6175957	0.3698624	100	2870.4539	2870.4492	1.6	5243.035	1	845.1717	34	1	R.VATPVDWKDGDSVM*VLPTIPEEEAKK.L
*	HW_prdx6_solution_2ul.2642.2642.3	2.4858563	0.17424487	96.1	2259.0823	2259.085	-1.2	7376.9004	14	577.0798	27.6	1	V.DWKDGDSVMVLPTIPEEEAK.K
*	HW_prdx6_solution_2ul.2366.2366.3	3.901131	0.2922142	100	2275.079	2275.0798	-0.3	4309.345	2	527.9756	39.5	1	V.DWKDGDSVM*VLPTIPEEEAK.K
*	HW_prdx6_solution_2ul.2072.2072.3	3.3986382	0.11083239	96.3	1973.9745	1973.9736	0.4	7090.7114	15	840.7916	38.2	1	W.KDGDSVM*VLPTIPEEEAK.K
*	HW_prdx6_solution_2ul.2547.2547.2	2.805653	0.30437532	100	1829.8848	1829.8837	0.6	4532.4785	1	1084.6783	59.4	1	K.DGDSVMVLPTIPEEEAK.K
*	HW_prdx6_solution_2ul.2250.2250.2	2.6786969	0.24284749	100	1845.8795	1845.8787	0.5	3472.51	1	592.12946	56.2	1	K.DGDSVM*VLPTIPEEEAK.K
*	HW_prdx6_solution_2ul.2359.2359.2	2.8319387	0.21411669	100	1957.9805	1957.9786	0.9	4665.012	2	536.09454	52.9	1	K.DGDSVMVLPTIPEEEAKK.L
*	HW_prdx6_solution_2ul.1898.1898.2	1.5963054	0.09237718	78.4	1225.6682	1225.6675	0.6	3277.3699	18	146.40868	55	1	M.VLPTIPEEEAK.K

Supplemental Table 1D: In-gel Trypsin Digestion of Peroxiredoxin

Page 1 of 1

Locus	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Validation Status	Descriptive Name
UniRef100_P30041	**26**	**30**	**58.50%**	**224**	**25035**	**6.4**	**U**	**Peroxiredoxin-6**

Unique	FileName	XCorr	DeltCN	Conf%	M+H+	CalcM+H+	PPM	TotalIntensity	SpR	SpScore	IonProportion	Redundancy	Sequence
*	HW_prdx6_ingel.2806.2806.2	5.4406962	0.50325656	100	2098.0928	2098.0928	0	6057.979	1	1385.4852	62.5	1	M.PGGLLLGDVAPNFEANTTVGR.I
	HW_prdx6_ingel.2041.2041.2	2.6949937	0.3433119	100	1395.657	1395.6573	-0.3	5017.8535	1	696.4977	72.7	1	R.DFTPVCTTELGR.A
	HW_prdx6_ingel.1440.1440.2	2.4755917	0.24168955	100	1133.5621	1133.562	0.1	6311.538	1	811.87317	77.8	1	F.TPVCTTELGR.A
	HW_prdx6_ingel.2052.2052.2	2.420361	0.2603636	100	1032.5115	1032.5143	-2.7	4155.2305	1	710.5934	87.5	1	T.PVCTTELGR.A
	HW_prdx6_ingel.2112.2112.2	3.946819	0.3375166	100	1486.7184	1486.7173	0.7	7429.004	1	1084.1296	70.8	1	L.SIDSVEDHLAWSK.D
*	HW_prdx6_ingel.2647.2647.2	2.9024022	0.32657748	100	1085.5988	1085.599	-0.2	4222.849	1	674.5351	87.5	2	K.LPFPIIDDR.N
*	HW_prdx6_ingel.2693.2693.2	2.3976548	0.27637	100	972.51385	972.5149	-1.1	2639.781	1	513.03174	92.9	1	L.PFPIIDDR.N
*	HW_prdx6_ingel.3257.3257.2	4.366693	0.4652653	100	1512.8348	1512.8342	0.4	7049.775	1	2190.2131	84.6	1	R.ELAILLGMLDPAEK.D
*	HW_prdx6_ingel.2941.2941.2	3.9588184	0.4250944	100	1528.8297	1528.8291	0.4	7074.6626	1	1761.6349	80.8	1	R.ELAILLGM*LDPAEK.D
*	HW_prdx6_ingel.3119.3119.2	4.3386636	0.37489492	100	1884.9987	1884.9987	0	6153.7666	1	969.17566	62.5	1	R.ELAILLGMLDPAEKDEK.G
*	HW_prdx6_ingel.2773.2773.3	1.9541205	0.18443905	95	1900.9937	1900.9937	0	3482.6726	4	275.28787	28.1	1	R.ELAILLGM*LDPAEKDEK.G
*	HW_prdx6_ingel.2780.2780.2	3.422839	0.4266424	100	1900.9948	1900.9937	0.6	6053.143	1	1086.4194	68.8	1	R.ELAILLGM*LDPAEKDEK.G
*	HW_prdx6_ingel.2622.2622.2	2.6592464	0.36167628	100	1007.55566	1007.556	-0.4	3255.644	1	563.1671	81.2	2	R.VVFVFGPDK.K
*	HW_prdx6_ingel.2225.2225.2	2.8131833	0.35813257	100	1135.6449	1135.651	-5.4	9051.081	1	1090.9932	77.8	2	R.VVFVFGPDKK.L
*	HW_prdx6_ingel.2187.2187.3	2.6138153	0.18091847	94.4	1135.6515	1135.651	0.4	2287.831	33	213.65257	44.4	2	R.VVFVFGPDKK.L
*	HW_prdx6_ingel.2197.2197.2	2.7668595	0.17373241	97.6	937.513	937.51416	-1.2	3540.645	1	882.0224	100	1	V.FVFGPDKK.L
	HW_prdx6_ingel.2251.2251.2	2.711092	0.18270572	97.5	1191.6731	1191.6732	-0.1	4249.0757	1	767.91376	85	1	K.LSILYPATTGR.N
	HW_prdx6_ingel.1798.1798.2	1.7642941	0.10875584	90.6	1078.5892	1078.5891	0.1	3791.2483	2	389.21008	61.1	1	L.SILYPATTGR.N
*	HW_prdx6_ingel.2373.2373.2	3.685001	0.4388103	100	1200.7205	1200.7198	0.5	5376.652	1	1254.3407	90	1	R.VVISLQLTAEK.R
*	HW_prdx6_ingel.2153.2153.3	1.8797381	0.2665552	100	1356.8201	1356.8209	-0.6	2289.36	5	222.36255	40.9	1	R.VVISLQLTAEKR.V
	HW_prdx6_ingel.1725.1725.2	1.5222356	0.20795907	97.4	915.49426	915.49347	0.9	1766.5867	6	145.66875	57.1	1	R.VATPVDWK.D
*	HW_prdx6_ingel.2287.2287.3	3.090005	0.19050543	94.1	1845.8768	1845.8787	-1	6952.3057	48	628.2926	35.9	1	K.DGDSVM*VLPTIPEEEAK.K
*	HW_prdx6_ingel.2280.2280.2	2.6879783	0.35039103	100	1845.8805	1845.8787	1	4028.6746	1	504.74347	53.1	1	K.DGDSVM*VLPTIPEEEAK.K
*	HW_prdx6_ingel.2387.2387.3	2.953678	0.33355847	100	1957.9791	1957.9786	0.2	4142.9062	1	853.871	42.6	1	K.DGDSVMVLPTIPEEEAKK.L
*	HW_prdx6_ingel.2393.2393.2	2.8093052	0.19436955	97.2	1957.9824	1957.9786	1.9	4371.357	3	352.98523	44.1	1	K.DGDSVMVLPTIPEEEAKK.L
*	HW_prdx6_ingel.2089.2089.3	3.5935159	0.3351299	100	1973.9755	1973.9736	0.9	5902.955	1	1666.801	50	1	K.DGDSVM*VLPTIPEEEAKK.L

Supplemental Table 2A: Protein Groups Identified in the Human Serum Proteome Analysis

The data was searched with 1.1Da precursor tolerance and partial tryptic boundary, as indicated in "Methods."
The search results were filtered using the "default" filter: 10 ppm, full tryptic boundary, and ΔCn >=0.05
Only proteins with two or more peptides are listed. The global non-redundant peptide FDR for this dataset is 0.12%. Protein FDR is 0.9%
Protein Groups are separated by horizontal lines.

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q13784	44	1025	83.20%	244	28158	5.5	APOA4 protein
UniRef100_Q53F31	63	1925	78.50%	474	52951	5.5	Vitamin D-binding protein variant
UniRef100_Q6GTG1	61	1872	78.10%	474	52937	5.5	Group-specific component
UniRef100_P02647	50	550	75.70%	267	30778	5.8	Apolipoprotein A-I precursor (Apo-AI) (ApoA-I) [Contains: Apolipoprotein A-I(1-242)]
UniRef100_Q2TAZ5	63	1357	75.10%	449	51034	7.1	Complement factor H
UniRef100_P02753	26	791	74.10%	201	23010	6.1	Plasma retinol-binding protein precursor (PRBP) (RBP) [Contains: Plasma retinol-binding protein(1-182); Plasma retinol-binding protein(1-181); Plasma retinol-binding protein(1-179); Plasma retinol- binding protein(1-176)]
UniRef100_Q5VY30	26	791	74.90%	199	22944	6.1	Retinol binding protein 4, plasma
UniRef100_P02790	49	3337	72.30%	462	51676	7	Hemopexin precursor
UniRef100_P06727	62	1167	72.20%	396	45399	5.4	Apolipoprotein A-IV precursor
UniRef100_P02649	43	289	69.40%	317	36154	5.7	Apolipoprotein E precursor
UniRef100_P68871	12	46	68.70%	147	15998	7.3	Hemoglobin subunit beta
UniRef100_Q549N7	12	46	68.70%	147	16051	7.7	Mutant beta-globin
UniRef100_Q2TU87	35	1845	67.90%	287	32821	6	Growth-inhibiting protein 25
UniRef100_P04003	58	1272	67.30%	597	67033	7.3	C4b-binding protein alpha chain precursor
UniRef100_P02749	43	917	67.00%	345	38298	8	Beta-2-glycoprotein 1 precursor (Beta-2-glycoprotein I) (Apolipoprotein H) (Apo-H) (B2GPI) (Beta(2)GPI)
UniRef100_UPI0000161B15	43	917	67.00%	345	38312	8	apolipoprotein H precursor
UniRef100_P00734	84	1545	66.70%	622	70037	5.9	Prothrombin precursor (EC 3.4.21.5) (Coagulation factor II) [Contains: Activation peptide fragment 1; Activation peptide fragment 2; Thrombin light chain; Thrombin heavy chain]
UniRef100_Q53H04	84	1545	66.70%	622	70064	5.9	Coagulation factor II variant
UniRef100_Q4QZ40	84	1545	66.70%	622	69965	6	Prothrombin
UniRef100_P02768	75	859	66.30%	609	69367	6.3	Serum albumin precursor
UniRef100_P07360	24	357	65.80%	202	22277	8.3	Complement component C8 gamma chain precursor
UniRef100_Q14CU0	24	357	65.80%	202	22219	8.6	Complement component 8, gamma polypeptide
UniRef100_Q14CT8	24	357	65.80%	202	22196	8.6	Complement component 8, gamma polypeptide
UniRef100_Q68CK1	55	708	65.50%	576	62128	7.4	Peptidoglycan recognition protein L
UniRef100_Q27I61	137	1803	64.40%	1676	188304	6.5	Complement component 5
UniRef100_P37802	12	27	63.80%	199	22391	8.2	Transgelin-2
UniRef100_UPI000013D3E3	12	27	57.70%	220	24454	8.2	Transgelin-2 (SM22-alpha homolog).
UniRef100_P08603	126	2984	63.70%	1231	139070	6.6	Complement factor H precursor
UniRef100_Q96PD5	55	666	63.50%	576	62217	7.5	N-acetylmuramoyl-L-alanine amidase precursor
UniRef100_UPI0000D820D0	446	2977	63.40%	4563	515537	7	apolipoprotein B precursor
UniRef100_P02766	5	14	63.30%	147	15887	5.7	Transthyretin precursor
UniRef100_P69905	9	32	62.00%	142	15258	8.7	Hemoglobin subunit alpha
UniRef100_Q53F97	9	32	62.00%	142	15281	8.7	Alpha 2 globin variant
UniRef100_P02652	8	51	62.00%	100	11175	6.6	Apolipoprotein A-II precursor (Apo-AII) (ApoA-II) [Contains: Apolipoprotein A-II(1-76)]
UniRef100_Q96KN2	34	141	61.90%	507	56692	5.3	Beta-Ala-His dipeptidase precursor
UniRef100_O95445	20	72	61.70%	188	21253	6	Apolipoprotein M
UniRef100_P43652	55	583	61.40%	599	69069	5.9	Afamin precursor
UniRef100_P29622	35	263	60.70%	427	48542	7.8	Kallistatin precursor

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_UPI000020AD55	96	2103	60.40%	914	101241	6.7	Transmembrane protein 110.
UniRef100_Q14624-2	97	2123	60.40%	914	101209	6.7	Isoform 2 of Q14624
UniRef100_P10643	63	406	60.40%	843	93518	6.5	Complement component C7 precursor
UniRef100_UPI000013D400	63	406	60.40%	843	93500	6.4	Complement component C7 precursor.
UniRef100_Q59HB3	130	966	60.10%	1615	183578	6.8	Apolipoprotein B variant
UniRef100_UPI0000367804	35	220	59.50%	639	65433	8	keratin 2
UniRef100_P01008	76	1139	59.50%	464	52602	6.7	Antithrombin-III precursor
UniRef100_P00751	78	1779	58.90%	764	85533	7.1	Complement factor B precursor (EC 3.4.21.47) (C3/C5 convertase) (Properdin factor B) (Glycine-rich beta glycoprotein) (GBG) (PBF2) [Contains: Complement factor B Ba fragment; Complement factor B Bb fragment]
UniRef100_Q53HP3	57	325	58.60%	752	83284	7.4	Complement component 2 variant
UniRef100_P06681	58	329	58.60%	752	83268	7.4	Complement C2 precursor (EC 3.4.21.43) (C3/C5 convertase) [Contains: Complement C2b fragment; Complement C2a fragment]
UniRef100_P02656	10	217	58.60%	99	10852	5.4	Apolipoprotein C-III precursor
UniRef100_P11226	16	82	58.10%	248	26144	5.5	Mannose-binding protein C precursor
UniRef100_Q4VB13	16	82	58.10%	248	26090	5.3	Mannose-binding lectin (Protein C) 2, soluble
UniRef100_Q4VB12	16	82	58.10%	248	26202	5.3	Mannose-binding lectin (Protein C) 2, soluble
UniRef100_Q6MZS0	93	1570	57.60%	1255	137248	5.4	Hypothetical protein DKFZp686O22169
UniRef100_UPI000013E305	17	115	57.40%	202	22537	5.7	Tetranectin precursor (TN) (C-type lectin domain family 3 member B) (Plasminogen kringle 4-binding protein).
UniRef100_P02655	15	200	57.40%	101	11284	4.7	Apolipoprotein C-II precursor
UniRef100_P00736	43	390	57.30%	705	80174	6.3	Complement C1r subcomponent precursor (EC 3.4.21.41) (Complement component 1, r subcomponent) [Contains: Complement C1r subcomponent heavy chain; Complement C1r subcomponent light chain]
UniRef100_UPI0000001C2B	43	390	57.30%	705	80200	6.3	complement component 1, r subcomponent
UniRef100_P00746	20	65	57.30%	253	27004	7.9	Complement factor D precursor
UniRef100_Q8WZB4	20	65	57.30%	253	27033	7.7	Adipsin/complement factor D precursor
UniRef100_Q6FHW3	20	65	63.60%	228	24423	7.2	DF protein
UniRef100_O75636	22	194	56.90%	299	32903	6.7	Ficolin-3 precursor
UniRef100_P35542	12	81	56.90%	130	14807	9.2	Serum amyloid A-4 protein precursor
UniRef100_UPI000013D6C3	96	2115	56.80%	930	103357	7	inter-alpha (globulin) inhibitor H4
UniRef100_Q14624	97	2135	56.80%	930	103325	7	Inter-alpha-trypsin inhibitor heavy chain H4 precursor (ITI heavy chain H4) (Inter-alpha-inhibitor heavy chain 4) (Inter-alpha-trypsin inhibitor family heavy chain-related protein) (IHRP) (Plasma kallikrein sensitive glycoprotein 120) (PK-120) (GP120) [Contains: 70 kDa inter-alpha-trypsin inhibitor heavy chain H4; 35 kDa inter-alpha- trypsin inhibitor heavy chain H4]
UniRef100_P04278	17	57	56.70%	402	43779	6.7	Sex hormone-binding globulin precursor
UniRef100_P25311	36	476	56.60%	295	33872	5.9	Zinc-alpha-2-glycoprotein precursor
UniRef100_Q8N4N0	36	476	56.00%	298	34259	6.1	Alpha-2-glycoprotein 1, zinc-binding
UniRef100_P05160	43	222	56.30%	661	75511	6.4	Coagulation factor XIII B chain precursor
UniRef100_P01042-2	46	1103	56.20%	427	47883	6.7	Isoform LMW of P01042
UniRef100_Q6PAU9	46	1103	56.20%	427	47901	6.7	Kininogen 1
UniRef100_Q53EQ0	46	1103	56.20%	427	47853	6.7	Kininogen 1 variant
UniRef100_UPI0000111E76	12	204	56.10%	214	23481	5.1	HUMANIZED ANTIBODY HFE7A, LIGHT CHAIN
UniRef100_UPI0000111056	12	205	55.80%	215	23281	6	IGM-KAPPA COLD AGGLUTININ (LIGHT CHAIN)
UniRef100_UPI000057D03C	13	205	55.30%	215	23472	7.1	F105 LIGHT CHAIN
UniRef100_UPI00003677FC	176	2634	55.10%	2296	252819	5.9	fibronectin 1 isoform 5 preproprotein
UniRef100_P06396	65	890	54.50%	782	85697	6.3	Gelsolin precursor

Supplemental Table 2A: Protein Groups Identified in the Human Serum Proteome Analysis

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q7Z4X5	6	13	54.30%	151	17190	5.2	Proline-rich acidic protein
UniRef100_Q96NZ9	6	13	54.30%	151	17227	5.4	Proline-rich acidic protein
UniRef100_Q8NCS2	6	13	55.00%	149	16925	5.1	PRAP1 protein
UniRef100_Q6N0A6	169	2380	54.20%	2296	252760	6	Hypothetical protein DKFZp686M04163
UniRef100_UPI0000110F9C	14	208	54.20%	212	23248	8	IGG1-KAPPA 3D6 FAB (LIGHT CHAIN)
UniRef100_P01033	10	32	54.10%	207	23171	8.1	Metalloproteinase inhibitor 1 precursor
UniRef100_P02775	14	324	53.90%	128	13894	8.8	Platelet basic protein precursor (PBP) (Small inducible cytokine B7) (CXCL7) (Leukocyte-derived growth factor) (LDGF) (Macrophage-derived growth factor) (MDGF) [Contains: Connective tissue-activating peptide III (CTAP-III) (Low-affinity platelet factor IV) (LA-PF4); TC-2; Connective tissue-activating peptide III(1-81) (CTAP-III(1-81)); Beta- thromboglobulin (Beta-TG); Neutrophil-activating peptide 2(74) (NAP- 2(74)); Neutrophil-activating peptide 2(73) (NAP-2(73)); Neutrophil-activating peptide 2 (NAP-2); TC-1; Neutrophil-activating peptide 2(1- 66) (NAP-2(1-66)); Neutrophil-activating peptide 2(1-63) (NAP-2(1- 63))]
UniRef100_Q8N355	12	88	53.40%	234	24793	6.4	IGL@ protein
UniRef100_P07996	70	325	53.20%	1170	129383	4.9	Thrombospondin-1 precursor
UniRef100_Q59E99	70	325	50.80%	1225	134849	5	Thrombospondin 1 variant
UniRef100_P60709	22	71	53.10%	375	41737	5.5	Actin, cytoplasmic 1
UniRef100_Q96HG5	22	71	54.10%	368	41005	5.8	Actin, beta
UniRef100_Q53GK6	22	71	53.10%	375	41723	5.5	Beta actin variant
UniRef100_Q53G99	22	71	53.10%	375	41765	5.6	Beta actin variant
UniRef100_Q53G76	22	71	53.10%	375	41721	5.5	Beta actin variant
UniRef100_P63261	22	71	53.10%	375	41793	5.5	Actin, cytoplasmic 2
UniRef100_UPI000011073A	14	208	52.80%	214	23409	7.2	PROTEIN (ANTIBODY (LIGHT CHAIN))
UniRef100_P05156	55	677	52.70%	583	65720	7.5	Complement factor I precursor (EC 3.4.21.45) (C3B/C4B inactivator) [Contains: Complement factor I heavy chain; Complement factor I light chain]
UniRef100_UPI0000D615A9	55	677	52.70%	583	65750	7.5	Complement factor I precursor (EC 3.4.21.45) (C3B/C4B inactivator) [Contains: Complement factor I heavy chain; Complement factor I light chain].
UniRef100_P08185	20	155	52.60%	405	45141	6	Corticosteroid-binding globulin precursor
UniRef100_UPI00001BB2AE	20	155	52.60%	405	45125	6	corticosteroid binding globulin precursor
UniRef100_P00915	18	64	52.10%	261	28870	7.1	Carbonic anhydrase 1
UniRef100_Q68DP9	161	2444	52.00%	2267	249357	5.6	Hypothetical protein DKFZp686K08164
UniRef100_P03952	38	265	51.30%	638	71370	8.2	Plasma kallikrein precursor (EC 3.4.21.34) (Plasma prekallikrein) (Kininogenin) (Fletcher factor) [Contains: Plasma kallikrein heavy chain; Plasma kallikrein light chain]
UniRef100_UPI0000D615EA	38	265	51.00%	641	71726	8.3	Plasma kallikrein precursor (EC 3.4.21.34) (Plasma prekallikrein) (Kininogenin) (Fletcher factor) [Contains: Plasma kallikrein heavy chain; Plasma kallikrein light chain].
UniRef100_Q4W5C3	38	265	51.30%	638	71343	8.2	Hypothetical protein KLKB1
UniRef100_P01011	44	2147	51.10%	423	47651	5.5	Alpha-1-antichymotrypsin precursor (ACT) [Contains: Alpha-1- antichymotrypsin His-Pro-less]
UniRef100_P02760	41	631	51.10%	352	38999	6.2	AMBP protein precursor [Contains: Alpha-1-microglobulin (Protein HC) (Complex-forming glycoprotein heterogeneous in charge) (Alpha-1 microglycoprotein); Inter-alpha-trypsin inhibitor light chain (ITI-LC) (Bikunin) (HI-30)]
UniRef100_UPI000013D401	55	390	51.00%	934	104786	6.8	Complement component C6 precursor.
UniRef100_P35527	32	155	50.70%	623	62129	5.3	Keratin, type I cytoskeletal 9
UniRef100_UPI00001AE6F7	32	155	50.70%	623	62064	5.2	keratin 9
UniRef100_UPI000014D030	94	2620	50.40%	911	101402	6.8	inter-alpha (globulin) inhibitor H1
UniRef100_P05546	43	616	50.30%	499	57071	6.9	Heparin cofactor 2 precursor
UniRef100_Q8IVC0	43	616	50.30%	499	56957	6.8	Serpin peptidase inhibitor, clade D (Heparin cofactor), member 1

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_UPI000034ECF8	20	38	50.30%	348	39030	7.1	haptoglobin-related protein
UniRef100_P02748	31	451	49.40%	559	63173	5.6	Complement component C9 precursor [Contains: Complement component C9a; Complement component C9b]
UniRef100_P19827	88	2562	49.30%	911	101389	6.8	Inter-alpha-trypsin inhibitor heavy chain H1 precursor
UniRef100_P06702	9	57	49.10%	114	13242	6.1	Protein S100-A9
UniRef100_P07358	39	431	48.90%	591	67047	8.1	Complement component C8 beta chain precursor
UniRef100_UPI000013C9B2	39	431	48.90%	591	66948	8.1	complement component 8, beta polypeptide preproprotein
UniRef100_P08697	34	355	48.90%	491	54566	6.3	Alpha-2-antiplasmin precursor
UniRef100_Q8N5U7	34	355	48.90%	491	54594	6.3	SERPINF2 protein
UniRef100_P05543	30	226	48.90%	415	46325	6.3	Thyroxine-binding globulin precursor
UniRef100_P23528	7	10	48.80%	166	18502	8.1	Cofilin-1
UniRef100_UPI0000DBEF3C	7	10	35.80%	226	24041	7.9	Cofilin-1 (Cofilin, non-muscle isoform) (18 kDa phosphoprotein) (p18).
UniRef100_P04264	31	292	48.60%	644	66018	8.1	Keratin, type II cytoskeletal 1
UniRef100_UPI000013CD4D	31	292	48.60%	644	66039	8.1	keratin 1
UniRef100_P02750	20	204	48.10%	347	38178	7	Leucine-rich alpha-2-glycoprotein precursor
UniRef100_Q68CK4	20	213	48.10%	347	38168	7	Leucine-rich alpha-2-glycoprotein
UniRef100_P02765	22	1300	48.00%	367	39325	5.7	Alpha-2-HS-glycoprotein precursor (Fetuin-A) (Alpha-2-Z-globulin) (Ba- alpha-2-glycoprotein) [Contains: Alpha-2-HS-glycoprotein chain A; Alpha-2-HS-glycoprotein chain B]
UniRef100_UPI000013D9D0	22	1300	48.00%	367	39341	5.7	Alpha-2-HS-glycoprotein precursor (Fetuin-A) (Alpha-2-Z-globulin) (Ba- alpha-2-glycoprotein) [Contains: Alpha-2-HS-glycoprotein chain A; Alpha-2-HS-glycoprotein chain B].
UniRef100_Q6B0J6	17	100	47.90%	355	39731	5.2	Paraoxonase 1
UniRef100_P07357	35	294	47.80%	584	65163	6.5	Complement component C8 alpha chain precursor
UniRef100_UPI00001AEB07	35	294	47.80%	584	65063	6.6	Complement component C8 alpha chain precursor (Complement component 8 subunit alpha).
UniRef100_O00391	34	101	47.70%	747	82578	8.9	Sulfhydryl oxidase 1 precursor
UniRef100_A2RUI4	35	294	47.60%	584	65163	6.6	Complement component 8, alpha polypeptide
UniRef100_Q8IZ60	21	82	47.60%	540	60734	6.7	Extracellular matrix protein 1
UniRef100_UPI0000043C2E	21	82	47.60%	540	60704	6.7	extracellular matrix protein 1 isoform 1 precursor
UniRef100_P07225	43	375	47.30%	676	75123	5.7	Vitamin K-dependent protein S precursor
UniRef100_UPI000014279E	43	375	47.30%	676	75073	5.7	protein S (alpha)
UniRef100_P09871	43	290	46.90%	688	76685	5	Complement C1s subcomponent precursor (EC 3.4.21.42) (C1 esterase) [Contains: Complement C1s subcomponent heavy chain; Complement C1s subcomponent light chain]
UniRef100_P36955	29	323	46.70%	418	46342	6.4	Pigment epithelium-derived factor precursor
UniRef100_P01024	84	361	46.20%	1663	187147	6.4	Complement C3 precursor [Contains: Complement C3 beta chain; Complement C3 alpha chain; C3a anaphylatoxin; Complement C3b alpha' chain; Complement C3c alpha' chain fragment 1; Complement C3dg fragment; Complement C3g fragment; Complement C3d fragment; Complement C3f fragment; Complement C3c alpha' chain fragment 2]
UniRef100_O43866	12	40	45.50%	347	38088	5.5	CD5 antigen-like precursor
UniRef100_P04004	39	898	45.20%	478	54306	5.8	Vitronectin precursor (Serum-spreading factor) (S-protein) (V75) [Contains: Vitronectin V65 subunit; Vitronectin V10 subunit; Somatomedin B]
UniRef100_P09486	17	61	45.20%	303	34632	4.8	SPARC precursor
UniRef100_Q0KKI6	11	202	45.20%	219	24030	8.1	Immunoblobulin light chain
UniRef100_Q8TCD0	11	202	41.40%	239	26235	8.1	Hypothetical protein
UniRef100_Q6PIH6	11	202	41.20%	240	26234	6.8	IGKV1-5 protein
UniRef100_Q9UGM5	16	110	44.80%	382	42055	6.8	Fetuin-B precursor
UniRef100_UPI0000D61BC2	16	110	44.50%	384	42282	7.2	Fetuin-B precursor (Gugu) (IRL685) (16G2).
UniRef100_P13645	33	244	44.40%	593	59519	5.2	Keratin, type I cytoskeletal 10
UniRef100_UPI0000456AA0	33	244	47.50%	554	56562	5.2	Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10).

Supplemental Table 2A: Protein Groups Identified in the Human Serum Proteome Analysis

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_UPI000013D842	33	244	45.00%	584	58827	5.2	Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10).
UniRef100_UPI00000718F2	33	244	45.00%	584	58827	5.2	keratin 10
UniRef100_P00338	15	28	44.00%	332	36689	8.3	L-lactate dehydrogenase A chain
UniRef100_Q6GMV8	11	83	44.00%	234	24910	6.7	Hypothetical protein
UniRef100_P80108	35	83	43.80%	840	92336	6.4	Phosphatidylinositol-glycan-specific phospholipase D precursor
UniRef100_Q14520	29	177	43.60%	560	62672	6.5	Hyaluronan-binding protein 2 precursor (EC 3.4.21.-) (Plasma hyaluronan-binding protein) (Hepatocyte growth factor activator-like protein) (Factor VII-activating protease) (Factor seven-activating protease) (FSAP) [Contains: Hyaluronan-binding protein 2 50 kDa heavy chain; Hyaluronan-binding protein 2 50 kDa heavy chain alternate form; Hyaluronan-binding protein 2 27 kDa light chain; Hyaluronan-binding protein 2 27 kDa light chain alternate form]
UniRef100_Q96IY4	19	125	43.50%	423	48412	7.7	Carboxypeptidase B2 precursor
UniRef100_UPI000013C764	19	125	43.50%	423	48424	7.7	Carboxypeptidase B2 precursor (EC 3.4.17.20) (Carboxypeptidase U) (CPU) (Thrombin-activable fibrinolysis inhibitor) (TAFI) (Plasma carboxypeptidase B) (pCPB).
UniRef100_P00748	38	288	43.40%	615	67818	7.7	Coagulation factor XII precursor (EC 3.4.21.38) (Hageman factor) (HAF) [Contains: Coagulation factor XIIa heavy chain; Beta-factor XIIa part 1; Beta-factor XIIa part 2; Coagulation factor XIIa light chain]
UniRef100_Q8IZZ5	38	288	43.40%	615	67735	7.7	Coagulation factor XII-Mie
UniRef100_Q06033	49	313	43.30%	885	99121	5.9	Inter-alpha-trypsin inhibitor heavy chain H3 precursor
UniRef100_P35858	30	284	43.30%	605	66035	6.8	Insulin-like growth factor-binding protein complex acid labile chain precursor
UniRef100_Q8TAY0	30	284	43.30%	605	66067	6.8	Insulin-like growth factor binding protein, acid labile subunit
UniRef100_Q59EP2	28	566	43.20%	491	53778	6.4	Angiotensinogen variant
UniRef100_Q86U78	28	566	43.70%	485	53114	6.3	Angiotensinogen (Serine (Or cysteine) proteinase inhibitor, clade A (Alpha-1 antiproteinase, antitrypsin), member 8)
UniRef100_UPI000050D08C	11	200	43.20%	220	24185	6.5	IGG Light chain
UniRef100_Q96JD0	3	8	43.10%	116	12294	5	Amyloid lambda 6 light chain variable region SAR
UniRef100_P01042	55	1174	42.40%	644	71957	6.8	Kininogen-1 precursor (Alpha-2-thiol proteinase inhibitor) [Contains: Kininogen-1 heavy chain; Bradykinin (Kallidin I); Lysyl-bradykinin (Kallidin II); Kininogen-1 light chain; Low molecular weight growth- promoting factor]
UniRef100_Q8NEJ1	11	83	42.40%	236	25024	7.7	Hypothetical protein
UniRef100_P13796	22	37	42.30%	627	70289	5.3	Plastin-2
UniRef100_Q5TBN4	22	37	42.30%	627	70289	5.4	Lymphocyte cytosolic protein 1
UniRef100_P19823	63	1535	42.20%	946	106436	6.9	Inter-alpha-trypsin inhibitor heavy chain H2 precursor
UniRef100_Q5T986	63	1535	42.20%	946	106463	6.9	Inter-alpha (Globulin) inhibitor H2
UniRef100_P04217	30	1042	41.80%	495	54273	5.9	Alpha-1B-glycoprotein precursor
UniRef100_Q5TFM6	16	219	41.50%	330	37651	7.4	Complement factor H-related 1
UniRef100_Q6P491	11	202	41.40%	239	26246	8.3	IGKV2-24 protein
UniRef100_Q9P1C5	45	708	41.30%	494	55367	6.4	PRO2769
UniRef100_P04196	39	753	41.10%	525	59578	7.5	Histidine-rich glycoprotein precursor
UniRef100_UPI00002398DE	9	183	41.00%	212	23072	7.2	Fab 48d light chain
UniRef100_A0A5E4	11	83	40.90%	235	24747	5.9	Hypothetical protein
UniRef100_P55056	10	117	40.90%	127	14553	8.9	Apolipoprotein C-IV precursor
UniRef100_Q53YY8	10	117	40.90%	127	14537	8.9	Apolipoprotein C-IV
UniRef100_P51884	19	263	40.80%	338	38429	6.6	Lumican precursor
UniRef100_P00918	9	19	40.80%	260	29246	7.4	Carbonic anhydrase 2
UniRef100_Q9UNU2	12	55	40.70%	354	38138	8.5	Complement protein C4B frameshift mutant
UniRef100_UPI00001B1414	9	183	40.70%	214	23341	6.9	ANTIBODY 2F5 (LIGHT CHAIN)

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P26927	21	38	40.60%	711	80380	7.7	Hepatocyte growth factor-like protein precursor (Macrophage stimulatory protein) (MSP) (Macrophage-stimulating protein) [Contains: Hepatocyte growth factor-like protein alpha chain; Hepatocyte growth factor-like protein beta chain]
UniRef100_UPI0000457108	21	38	40.70%	710	80205	7.7	Hepatocyte growth factor-like protein precursor (Macrophage stimulatory protein) (MSP) (Macrophage-stimulating protein) [Contains: Hepatocyte growth factor-like protein alpha chain; Hepatocyte growth factor-like protein beta chain].
UniRef100_Q6GTN4	21	38	40.60%	711	80320	7.7	Macrophage stimulating 1
UniRef100_Q53GN8	21	38	40.60%	711	80350	7.7	Macrophage stimulating 1 (Hepatocyte growth factor-like) variant
UniRef100_Q569I9	9	145	40.60%	234	25390	6.7	IGKC protein
UniRef100_P23142	25	100	40.50%	703	77261	5.3	Fibulin-1 precursor
UniRef100_UPI00001C1A97	25	100	40.50%	703	77242	5.3	fibulin 1 isoform D
UniRef100_P17936	13	115	40.20%	291	31674	8.7	Insulin-like growth factor-binding protein 3 precursor
UniRef100_UPI0000D61C3C	13	115	42.10%	278	30640	8.5	Insulin-like growth factor-binding protein 3 precursor (IGFBP-3) (IBP- 3) (IGF-binding protein 3).
UniRef100_UPI00004F8E1F	13	115	39.40%	297	32223	8.6	insulin-like growth factor binding protein 3 isoform a precursor
UniRef100_P22792	25	214	40.00%	545	60615	6	Carboxypeptidase N subunit 2 precursor
UniRef100_UPI00005989D1	25	214	40.00%	545	60585	6.1	PREDICTED: similar to Carboxypeptidase N subunit 2 precursor (Carboxypeptidase N polypeptide 2) (Carboxypeptidase N 83 kDa chain) (Carboxypeptidase N regulatory subunit) (Carboxypeptidase N large subunit)
UniRef100_P02792	7	23	40.00%	175	20020	5.8	Ferritin light chain
UniRef100_Q8WU07	7	23	40.00%	175	20062	5.8	Ferritin, light polypeptide
UniRef100_Q6IBT7	7	23	40.00%	175	19992	5.8	Ferritin
UniRef100_Q5FWG0	24	196	39.90%	489	53711	6.3	IGHM protein
UniRef100_P20851	18	94	39.70%	252	28357	5.1	C4b-binding protein beta chain precursor
UniRef100_P20851-2	18	94	39.80%	251	28286	5.1	Isoform 2 of P20851
UniRef100_Q6NS95	10	45	39.70%	234	25148	6.7	IGL@ protein
UniRef100_P01620	3	7	39.40%	109	11775	8.5	Ig kappa chain V-III region SIE
UniRef100_Q9UL78	3	7	39.40%	109	11646	8.3	Myosin-reactive immunoglobulin light chain variable region
UniRef100_P01623	3	7	39.40%	109	11746	8.9	Ig kappa chain V-III region WOL
UniRef100_P04180	12	53	39.30%	440	49578	6.1	Phosphatidylcholine-sterol acyltransferase precursor
UniRef100_Q96RS4	24	134	39.10%	728	81860	5.1	Complement factor MASP-3
UniRef100_UPI00006C2065	136	459	39.00%	2813	309290	5.5	von Willebrand factor preproprotein
UniRef100_Q92820	13	32	39.00%	318	35964	7.1	Gamma-glutamyl hydrolase precursor
UniRef100_P36980	13	112	38.90%	270	30651	6.4	Complement factor H-related protein 2 precursor
UniRef100_P36980-2	13	112	43.20%	243	27897	6.9	Isoform Short of P36980
UniRef100_P05109	5	31	38.70%	93	10834	7	Protein S100-A8
UniRef100_P05155	43	900	38.60%	500	55154	6.5	Plasma protease C1 inhibitor precursor
UniRef100_P04275	135	458	38.40%	2813	309296	5.5	von Willebrand factor precursor (vWF) [Contains: von Willebrand antigen 2 (von Willebrand antigen II)]
UniRef100_P10909	38	375	38.30%	449	52495	6.3	Clusterin precursor (Complement-associated protein SP-40,40) (Complement cytolysis inhibitor) (CLI) (NA1/NA2) (Apolipoprotein J) (Apo-J) (Testosterone-repressed prostate message 2) (TRPM-2) [Contains: Clusterin beta chain (ApoJalpha) (Complement cytolysis inhibitor a chain); Clusterin alpha chain (ApoJbeta) (Complement cytolysis inhibitor b chain)]
UniRef100_Q68DR3	23	419	38.10%	312	35124	7.7	Hypothetical protein DKFZp779H1622
UniRef100_P02743	14	174	37.70%	223	25387	6.5	Serum amyloid P-component precursor (SAP) (9.5S alpha-1-glycoprotein) [Contains: Serum amyloid P-component(1-203)]

Supplemental Table 2A: Protein Groups Identified in the Human Serum Proteome Analysis

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P00740	17	134	37.30%	461	51778	5.5	Coagulation factor IX precursor (EC 3.4.21.22) (Christmas factor) (Plasma thromboplastin component) (PTC) [Contains: Coagulation factor IXa light chain; Coagulation factor IXa heavy chain]
UniRef100_P16035	8	16	37.30%	220	24399	7.5	Metalloproteinase inhibitor 2 precursor
UniRef100_UPI0000DD8474	8	16	30.60%	268	29068	6.6	PREDICTED: similar to Metalloproteinase inhibitor 2 precursor (TIMP-2) (Tissue inhibitor of metalloproteinases 2) (CSC-21K)
UniRef100_P00738	19	41	37.20%	406	45205	6.6	Haptoglobin precursor [Contains: Haptoglobin alpha chain; Haptoglobin beta chain]
UniRef100_P15169	23	134	37.10%	458	52286	7.3	Carboxypeptidase N catalytic chain precursor
UniRef100_P06276	21	145	37.00%	602	68418	7.4	Cholinesterase precursor
UniRef100_P01625	5	11	36.80%	114	12640	7.9	Ig kappa chain V-IV region Len
UniRef100_UPI0000112A1D	5	11	36.80%	114	12625	7.9	IMMUNOGLOBULIN LIGHT CHAIN VARIABLE DOMAIN
UniRef100_O75882-2	55	297	36.60%	1272	141429	7	Isoform 2 of O75882
UniRef100_O75882-3	55	297	38.90%	1198	133701	7	Isoform 3 of O75882
UniRef100_Q08380	24	104	36.40%	585	65331	5.3	Galectin-3-binding protein precursor
UniRef100_P08571	17	85	36.30%	375	40076	6.2	Monocyte differentiation antigen CD14 precursor (Myeloid cell-specific leucine-rich glycoprotein) [Contains: Monocyte differentiation antigen CD14, urinary form; Monocyte differentiation antigen CD14, membrane- bound form]
UniRef100_P25774	8	18	36.30%	331	37496	8.3	Cathepsin S precursor
UniRef100_Q6FHS5	8	18	36.30%	331	37526	8.2	CTSS protein
UniRef100_P41222	7	16	36.30%	190	21029	7.8	Prostaglandin-H2 D-isomerase precursor
UniRef100_Q5SQ09	7	16	32.50%	212	22836	9.9	Prostaglandin D2 synthase 21kDa
UniRef100_Q2NL86	19	71	36.10%	757	82861	4.6	Cartilage oligomeric matrix protein
UniRef100_Q9UL83	3	6	36.10%	108	11834	8.7	Myosin-reactive immunoglobulin light chain variable region
UniRef100_Q9UK55	19	92	35.80%	444	50707	8.3	Protein Z-dependent protease inhibitor precursor
UniRef100_P07737	5	13	35.70%	140	15054	8.3	Profilin-1
UniRef100_P02776	4	24	35.60%	101	10845	8.6	Platelet factor 4 precursor
UniRef100_Q9UC64	4	24	66.70%	54	6033	10	PF 4-derived endothelial cell growth inhibitor PEAK II
UniRef100_P00742	20	165	35.50%	488	54732	5.9	Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor) (Stuart- Prower factor) [Contains: Factor X light chain; Factor X heavy chain; Activated factor Xa heavy chain]
UniRef100_P04406	8	17	35.50%	335	36053	8.5	Glyceraldehyde-3-phosphate dehydrogenase
UniRef100_UPI0000161FB8	24	137	35.30%	699	79247	5.5	mannan-binding lectin serine protease 1 isoform 1 precursor
UniRef100_P61769	4	12	35.30%	119	13715	6.5	Beta-2-microglobulin precursor [Contains: Beta-2-microglobulin variant pI 5.3]
UniRef100_Q6IAT8	4	12	35.30%	119	13697	6.5	B2M protein
UniRef100_P01023	40	118	35.10%	1474	163277	6.4	Alpha-2-macroglobulin precursor
UniRef100_UPI0000155718	40	118	35.10%	1474	163291	6.4	alpha-2-macroglobulin precursor
UniRef100_UPI000013DFEA	16	46	34.70%	398	43974	5.8	apolipoprotein L1 isoform a precursor
UniRef100_UPI0000167BCC	16	46	33.30%	414	45919	6.3	apolipoprotein L1 isoform b precursor
UniRef100_P07195	15	31	34.40%	334	36639	6.1	L-lactate dehydrogenase B chain
UniRef100_P24592	6	17	34.20%	240	25322	7.8	Insulin-like growth factor-binding protein 6 precursor
UniRef100_P30043	7	17	34.00%	206	22119	7.6	Flavin reductase
UniRef100_UPI000013D3F5	7	17	33.20%	211	22594	7.6	Flavin reductase (EC 1.5.1.30) (FR) (NADPH-dependent diaphorase) (NADPH-flavin reductase) (FLR) (Biliverdin reductase B) (EC 1.3.1.24) (BVR-B) (Biliverdin-IX beta-reductase) (Green heme-binding protein) (GHBP).
UniRef100_P05090	7	52	33.90%	189	21276	5.1	Apolipoprotein D precursor
UniRef100_P63104	8	19	33.10%	245	27745	4.8	14-3-3 protein zeta/delta
UniRef100_P60174	5	7	32.90%	249	26669	6.9	Triosephosphate isomerase
UniRef100_Q53HE2	5	7	32.90%	249	26713	7.4	Triosephosphate isomerase 1 variant

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_A2NB45	2	5	32.70%	113	12388	8.5	Cold agglutinin FS-1 L-chain
UniRef100_UPI0000518FE7	2	5	30.30%	122	13446	7.6	ANTI EGFR ANTIBODY FV REGION
UniRef100_P01617	2	5	32.70%	113	12316	6	Ig kappa chain V-II region TEW
UniRef100_P02533	13	42	32.60%	472	51622	5.2	Keratin, type I cytoskeletal 14
UniRef100_UPI00001AE5AA	13	42	32.60%	472	51561	5.2	Keratin, type I cytoskeletal 14 (Cytokeratin-14) (CK-14) (Keratin-14) (K14).
UniRef100_P22891	15	62	32.50%	400	44744	6	Vitamin K-dependent protein Z precursor
UniRef100_UPI0000D61AAE	15	62	30.70%	424	47285	6.1	Vitamin K-dependent protein Z precursor.
UniRef100_Q5JVF5	15	62	30.80%	422	47053	6	Protein Z, vitamin K-dependent plasma glycoprotein
UniRef100_P06732	10	15	32.30%	381	43101	7.3	Creatine kinase M-type
UniRef100_P22352	13	96	32.30%	226	25505	8	Glutathione peroxidase 3 precursor
UniRef100_UPI0000161B50	13	96	32.30%	226	25402	8.1	plasma glutathione peroxidase 3 precursor
UniRef100_Q2M1W7	17	80	32.20%	655	70648	7.2	HGF activator, preproprotein
UniRef100_Q6PI81	14	33	32.00%	478	52667	7.6	IGHM protein
UniRef100_P04070	21	81	31.90%	461	52071	6.3	Vitamin K-dependent protein C precursor (EC 3.4.21.69) (Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV) [Contains: Vitamin K-dependent protein C light chain; Vitamin K-dependent protein C heavy chain; Activation peptide]
UniRef100_P23142-4	18	90	31.80%	683	74462	5.3	Isoform C of P23142
UniRef100_Q6GMY2	24	196	31.80%	606	66185	6.9	IGHM protein
UniRef100_P27918	14	81	30.90%	469	51276	7.9	Properdin precursor
UniRef100_UPI000016A184	14	81	31.90%	454	49667	7.9	Properdin precursor (Factor P).
UniRef100_P15531	4	4	30.30%	152	17149	6.2	Nucleoside diphosphate kinase A
UniRef100_UPI0000E11DA6	4	4	30.30%	152	17119	6.2	Nucleoside diphosphate kinase A
UniRef100_P22392	4	4	30.30%	152	17298	8.4	Nucleoside diphosphate kinase B
UniRef100_Q14019	2	4	30.30%	142	15945	5.7	Coactosin-like protein
UniRef100_P01034	5	32	30.10%	146	15799	8.8	Cystatin-C precursor
UniRef100_Q5EVA1	4	8	30.00%	227	25734	6.1	Cousin-of-RKIP 1 protein
UniRef100_Q96S96	4	8	30.00%	227	25733	6.5	PEBP family protein precursor
UniRef100_P05154	16	109	29.80%	406	45702	9.3	Plasma serine protease inhibitor precursor
UniRef100_UPI0000F51D3A	16	109	30.60%	395	44471	8.7	Plasma serine protease inhibitor
UniRef100_UPI000013E52C	16	109	29.80%	406	45675	9.3	Plasma serine protease inhibitor precursor (PCI) (Protein C inhibitor) (Serpin A5) (Plasminogen activator inhibitor 3) (PAI-3) (PAI3) (Acrosomal serine protease inhibitor).
UniRef100_Q15848	6	15	29.50%	244	26414	5.7	Adiponectin precursor
UniRef100_Q5TAB2	12	30	28.60%	637	69707	5.3	Cartilage acidic protein 1
UniRef100_Q9NQ79	12	30	27.50%	661	71421	5.1	Cartilage acidic protein 1 precursor
UniRef100_Q6Q788	7	7	28.40%	366	41213	6.4	Apolipoprotein A-V precursor
UniRef100_Q96PQ8	15	36	28.10%	679	75553	7	Factor VII active site mutant immunoconjugate
UniRef100_P18065	7	10	28.00%	328	35138	7.5	Insulin-like growth factor-binding protein 2 precursor
UniRef100_UPI000013C98D	7	10	28.30%	325	34814	7.5	Insulin-like growth factor-binding protein 2 precursor (IGFBP-2) (IBP- 2) (IGF-binding protein 2).
UniRef100_Q9H4G4	3	6	27.90%	154	17218	9.4	Golgi-associated plant pathogenesis-related protein 1
UniRef100_P15144	21	32	27.70%	967	109539	5.5	Aminopeptidase N
UniRef100_UPI000004ECB0	21	32	27.70%	967	109511	5.4	membrane alanine aminopeptidase precursor
UniRef100_Q59E93	21	32	27.40%	977	110593	5.5	Membrane alanine aminopeptidase variant
UniRef100_P43251	21	107	27.70%	523	58913	5.8	Biotinidase precursor
UniRef100_A1L4H1	2	5	27.50%	91	9906	4.7	Hypothetical LOC284297
UniRef100_Q13103	9	30	27.00%	211	24338	8.3	Secreted phosphoprotein 24 precursor
IPITrypsinPIG	16	2115	26.80%	231	24409	7.2	TRYP_PIG
gi|12345|prg	16	2115	27.80%	223	23476	7.9	Promega sequencing grade modified trypsin

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P08294	8	14	26.70%	240	25851	6.6	Extracellular superoxide dismutase [Cu-Zn] precursor
UniRef100_P78417	7	10	26.60%	241	27566	6.6	Glutathione transferase omega-1
UniRef100_P02654	8	69	26.50%	83	9332	8.5	Apolipoprotein C-I precursor
UniRef100_P55058	10	36	26.40%	493	54739	7	Phospholipid transfer protein precursor
UniRef100_P55058-2	10	36	29.50%	441	49272	6.6	Isoform 2 of P55058
UniRef100_P01591	4	9	26.30%	137	15594	4.7	Immunoglobulin J chain
UniRef100_P00450	19	26	26.20%	1065	122205	5.7	Ceruloplasmin precursor
UniRef100_UPI0000F0A4E8	19	26	26.20%	1065	122194	5.8	CERULOPLASMIN
UniRef100_UPI000045718B	19	26	26.20%	1065	122219	5.7	Ceruloplasmin precursor (EC 1.16.3.1) (Ferroxidase).
UniRef100_P62937	5	13	26.10%	165	18012	7.8	Peptidyl-prolyl cis-trans isomerase A
UniRef100_O00533	22	43	26.00%	1208	135027	5.8	Neural cell adhesion molecule L1-like protein precursor
UniRef100_UPI000013CF0F	22	43	25.70%	1224	136698	5.8	cell adhesion molecule with homology to L1CAM precursor
UniRef100_O00533-2	22	43	25.70%	1224	136654	5.8	Isoform 2 of O00533
UniRef100_UPI000013E857	2	2	25.90%	116	12593	5.2	Immunoglobulin Kappa light chain V gene segment
UniRef100_P61916	3	7	25.80%	151	16570	7.7	Epididymal secretory protein E1 precursor
UniRef100_Q53HV6	3	7	25.80%	151	16584	7.7	Niemann-Pick disease, type C2 variant
UniRef100_P54108	6	27	25.70%	245	27630	7.8	Cysteine-rich secretory protein 3 precursor
UniRef100_Q53FA9	6	27	25.70%	245	27658	7.8	Cysteine-rich secretory protein 3 variant
UniRef100_Q3MJ82	6	27	25.70%	245	27640	7.8	Cysteine-rich secretory protein 3
UniRef100_P01344	5	46	25.60%	180	20140	9.3	Insulin-like growth factor II precursor (IGF-II) (Somatomedin A) [Contains: Insulin-like growth factor II Ala-25 Del]
UniRef100_UPI0000456460	5	46	25.10%	183	20423	9.4	Insulin-like growth factor II precursor (IGF-II) (Somatomedin A) [Contains: Insulin-like growth factor II Ala-25 Del].
UniRef100_P01344-2	5	46	25.10%	183	20477	9.5	Isoform 2 of P01344
UniRef100_UPI000011236E	4	13	25.20%	222	23655	8.5	chimera of Fab2C4: "humanized" murine monoclo
UniRef100_P13647	15	50	24.90%	590	62378	7.8	Keratin, type II cytoskeletal 5
UniRef100_Q9UL85	3	6	24.80%	109	11761	8.5	Myosin-reactive immunoglobulin kappa chain variable region
UniRef100_P32119	7	23	24.70%	198	21892	6	Peroxiredoxin-2
UniRef100_UPI0000456C19	7	23	33.10%	148	16102	6.6	Peroxiredoxin-2 (EC 1.11.1.15) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1) (Thiol-specific antioxidant protein) (TSA) (PRP) (Natural killer cell-enhancing factor B) (NKEF-B).
UniRef100_Q658S4	3	4	24.60%	122	13425	8.9	Hypothetical protein DKFZp666N164
UniRef100_Q9NS71	3	4	16.20%	185	20331	5.9	Gastrokine-1 precursor
UniRef100_Q05DH5	9	10	24.50%	331	37581	9.1	EXTL2 protein
UniRef100_Q9UBQ6	9	10	24.50%	330	37466	8.9	Exostosin-like 2
UniRef100_Q8N8F1	9	10	24.60%	329	37395	8.9	CDNA FLJ39595 fis, clone SKNSH2001931, highly similar to Exostoses
UniRef100_Q49A43	9	10	24.50%	330	37470	8.9	Exostoses (Multiple)-like 2
UniRef100_P19652	4	5	24.40%	201	23603	5.1	Alpha-1-acid glycoprotein 2 precursor
UniRef100_Q6IB74	4	5	24.40%	201	23615	5.1	ORM2 protein
UniRef100_Q16270	4	12	24.10%	282	29130	7.9	Insulin-like growth factor-binding protein 7 precursor
UniRef100_P02741	7	27	24.10%	224	25039	5.6	C-reactive protein precursor [Contains: C-reactive protein(1-205)]
UniRef100_Q53GX9	12	58	24.00%	487	53541	7.3	Complement C1r-like protein
UniRef100_P02538	13	46	23.90%	564	60045	8	Keratin, type II cytoskeletal 6A
UniRef100_P09172	9	16	23.70%	603	67613	6.3	Dopamine beta-hydroxylase precursor
UniRef100_UPI0000E5D219	9	16	23.20%	617	69065	6.4	dopamine beta-hydroxylase precursor
UniRef100_P08779	9	37	23.50%	473	51268	5	Keratin, type I cytoskeletal 16
UniRef100_A1IGE4	8	30	23.50%	247	26390	5.2	Collectin kidney I

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q9BWP8	8	30	21.40%	271	28665	5.4	Collectin sub-family member 11
UniRef100_Q7Z6N1	8	30	21.60%	268	29006	5.8	Collectin sub-family member 11
UniRef100_Q5CZ85	8	30	26.10%	222	23773	4.9	Hypothetical protein DKFZp686N1868
UniRef100_A1IGE6	8	30	26.00%	223	24041	4.9	Collectin kidney I
UniRef100_A1IGE5	8	30	23.50%	247	26317	5	Collectin kidney I
UniRef100_Q86UD1	5	13	23.40%	273	30688	6.8	Protein OAF homolog
UniRef100_P67936	5	7	23.40%	248	28522	4.7	Tropomyosin alpha-4 chain
UniRef100_Q28520	22	142	23.10%	649	72402	5.5	Vitamin K-dependent protein S precursor
UniRef100_A0N5G5	2	6	22.90%	118	12766	9	Rheumatoid factor D5 light chain
UniRef100_P02671	14	35	22.50%	866	94973	6	Fibrinogen alpha chain precursor [Contains: Fibrinopeptide A]
UniRef100_P01860	5	12	22.40%	290	32331	7.6	Ig gamma-3 chain C region
UniRef100_P07339	7	8	22.30%	412	44552	6.5	Cathepsin D precursor (EC 3.4.23.5) [Contains: Cathepsin D light chain; Cathepsin D heavy chain]
UniRef100_A2VDJ4	5	8	22.30%	292	32959	6.8	C14orf109 protein
UniRef100_Q9UJJ9	5	8	21.30%	305	33974	6.9	N-acetylglucosamine-1-phosphotransferase subunit gamma precursor
UniRef100_P13591	14	28	21.50%	848	93361	4.9	Neural cell adhesion molecule 1, 140 kDa isoform precursor
UniRef100_UPI0000E445E3	14	28	21.20%	858	94574	4.9	neural cell adhesion molecule 1 isoform 2
UniRef100_Q86X47	14	28	21.20%	858	94601	4.9	Neural cell adhesion molecule 1
UniRef100_Q59FL7	14	28	22.60%	807	89176	5.4	Neural cell adhesion molecule 1, 120 kDa isoform variant
UniRef100_P13592	14	28	23.90%	761	83770	4.9	Neural cell adhesion molecule 1, 120 kDa isoform precursor
UniRef100_P01859	7	34	21.50%	326	35885	7.6	Ig gamma-2 chain C region
UniRef100_UPI0000F30363	7	34	21.50%	326	35943	7.6	Immunoglobulin heavy chain C gene segment
UniRef100_Q6P6C4	7	34	15.10%	465	51325	7	Hypothetical protein
UniRef100_Q15828	2	6	21.50%	149	16511	8.1	Cystatin-M precursor
UniRef100_Q6IBD2	2	6	21.50%	149	16493	8.1	CST6 protein
UniRef100_P0C0S8	3	4	21.50%	130	14091	10.9	Histone H2A type 1
UniRef100_UPI000013C8E5	3	4	18.10%	155	16610	10.2	H2A histone family, member J isoform 2
UniRef100_Q9BTM1	3	4	21.70%	129	14019	10.9	H2A histone family, member J
UniRef100_Q99878	3	4	21.90%	128	13936	10.9	Histone H2A type 1-J
UniRef100_Q96KK5	3	4	21.90%	128	13906	10.9	Histone H2A type 1-H
UniRef100_Q6FI13	3	4	21.50%	130	14095	10.9	Histone H2A type 2-A
UniRef100_Q16777	3	4	21.70%	129	13988	10.9	Histone H2A type 2-C
UniRef100_P20671	3	4	21.50%	130	14107	10.9	Histone H2A type 1-D
UniRef100_Q10588	5	7	21.40%	318	35724	7.8	ADP-ribosyl cyclase 2 precursor
UniRef100_UPI000066D9E4	5	7	20.40%	333	37482	8	ADP-ribosyl cyclase 2 precursor (EC 3.2.2.5) (Cyclic ADP-ribose hydrolase 2) (cADPr hydrolase 2) (Bone marrow stromal antigen 1) (BST- 1) (CD157 antigen).
UniRef100_UPI0000126AFB	5	7	21.40%	318	35738	7.8	bone marrow stromal cell antigen 1 precursor
UniRef100_Q1XII0	5	7	26.20%	260	29326	6.8	Bone marrow stromal cell antigen 1 nirs variant 1
UniRef100_P60900	4	4	21.10%	246	27399	6.7	Proteasome subunit alpha type 6
UniRef100_P04075	4	7	20.90%	364	39420	8.1	Fructose-bisphosphate aldolase A
UniRef100_Q9UNN8	4	8	20.60%	238	26671	7.2	Endothelial protein C receptor precursor
UniRef100_Q9UNW1	6	18	20.50%	487	55051	7.8	Multiple inositol polyphosphate phosphatase 1 precursor (EC 3.1.3.62) (Inositol (1,3,4,5)-tetrakisphosphate 3-phosphatase) (Ins(1,3,4,5)P(4) 3-phosphatase)
UniRef100_Q12805	7	18	20.30%	493	54641	5.1	EGF-containing fibulin-like extracellular matrix protein 1 precursor
UniRef100_UPI000013EF28	7	18	21.30%	470	52066	5.2	EGF-containing fibulin-like extracellular matrix protein 1 precursor (Fibulin-3) (FIBL-3) (Fibrillin-like protein) (Extracellular protein S1-5).
UniRef100_Q12805-4	7	18	20.30%	492	54554	5.1	Isoform 4 of Q12805

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q12805-3	7	18	20.30%	492	54584	5.1	Isoform 3 of Q12805
UniRef100_UPI00001125A4	7	23	20.30%	428	46852	8.9	IGG1 MCG INTACT ANTIBODY (HEAVY CHAIN)
UniRef100_A2NU35	6	20	19.90%	377	41287	7.9	C gamma 3
UniRef100_UPI0000F30357	6	20	21.60%	347	38111	8.1	Immunoglobulin heavy chain C gene segment
UniRef100_UPI0000F30356	6	20	20.70%	362	39720	8	Immunoglobulin heavy chain C gene segment
UniRef100_UPI0000F30355	6	20	16.80%	446	49135	6.9	Immunoglobulin heavy chain C gene segment
UniRef100_UPI0000E59B66	6	20	19.90%	377	41329	7.9	Immunoglobulin heavy chain C gene segment
UniRef100_Q8NF17	6	20	14.70%	509	56111	7.6	FLJ00385 protein
UniRef100_Q8N4Y9	6	20	14.40%	521	57156	7.7	IGHG3 protein
UniRef100_Q6N030	6	20	14.50%	518	57020	8.1	Hypothetical protein DKFZp686I15212
UniRef100_Q5EBM2	6	20	14.50%	519	56813	6.9	Hypothetical protein
UniRef100_P05451	3	8	19.90%	166	18731	5.9	Lithostathine 1 alpha precursor
UniRef100_P02787	12	21	19.60%	698	77050	7.1	Serotransferrin precursor
UniRef100_UPI000013D5A6	12	21	19.60%	698	77064	7.1	Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal- binding globulin).
UniRef100_Q53H26	12	21	19.60%	698	77080	7	Transferrin variant
UniRef100_Q06AH7	12	21	19.60%	698	76960	7.2	Transferrin
UniRef100_UPI000013D168	21	44	19.20%	1482	163862	6.4	Pregnancy zone protein precursor.
UniRef100_P62258	5	11	19.20%	255	29174	4.7	14-3-3 protein epsilon
UniRef100_Q4VJB6	5	11	21.00%	233	26504	4.9	14-3-3 protein epsilon isoform transcript variant 1
UniRef100_Q3SXP2	2	3	19.20%	151	16104	5.1	VMO1 protein
UniRef100_Q7Z5L0	2	3	14.40%	202	21534	5.1	Vitelline membrane outer layer protein 1 homolog precursor
UniRef100_UPI000013CD50	11	56	19.10%	564	60067	8	keratin 6B
UniRef100_P01343	4	18	19.00%	153	17026	9.1	Insulin-like growth factor IA precursor
UniRef100_Q14620	4	18	21.20%	137	15177	9.3	Insulin-like growth factor I precursor
UniRef100_Q13429	4	18	20.90%	139	15611	9.6	Insulin-like growth factor-I
UniRef100_P16545	4	18	19.00%	153	17010	9.1	Insulin-like growth factor I precursor
UniRef100_P05019	4	18	14.90%	195	21841	9.7	Insulin-like growth factor IB precursor
UniRef100_Q92954-3	28	101	18.90%	1311	141106	9.4	Isoform C of Q92954
UniRef100_P62736	10	39	18.80%	377	42009	5.4	Actin, aortic smooth muscle
UniRef100_Q13707	10	39	21.50%	330	36807	5.3	ACTA2 protein
UniRef100_P68133	10	39	18.80%	377	42051	5.4	Actin, alpha skeletal muscle
UniRef100_P68032	10	39	18.80%	377	42019	5.4	Actin, alpha cardiac muscle 1
UniRef100_P63267	10	39	18.90%	376	41877	5.5	Actin, gamma-enteric smooth muscle
UniRef100_P02144	3	6	18.80%	154	17184	7.7	Myoglobin
UniRef100_P13987	3	7	18.80%	128	14177	6.5	CD59 glycoprotein precursor
UniRef100_Q9UBR2	4	6	18.20%	303	33868	7.1	Cathepsin Z precursor
UniRef100_P80188	3	7	18.20%	198	22588	8.9	Neutrophil gelatinase-associated lipocalin precursor
UniRef100_UPI0000D61913	3	7	18.00%	200	22902	8.9	Neutrophil gelatinase-associated lipocalin precursor (NGAL) (p25) (25 kDa alpha-2-microglobulin-related subunit of MMP-9) (Lipocalin-2) (Oncogene 24p3).
UniRef100_Q6FGL5	3	7	18.20%	198	22562	8.9	LCN2 protein
UniRef100_Q5SYV9	3	7	18.00%	200	22788	8.5	Lipocalin 2
UniRef100_Q92954-6	30	100	18.10%	1361	146467	9.5	Isoform F of Q92954
UniRef100_P12955	8	11	18.10%	493	54548	6	Xaa-Pro dipeptidase
UniRef100_P02735	2	14	18.00%	122	13532	6.8	Serum amyloid A protein precursor (SAA) [Contains: Amyloid protein A (Amyloid fibril protein AA); Serum amyloid protein A(2-104); Serum amyloid protein A(3-104); Serum amyloid protein A(2-103); Serum amyloid protein A(2-102); Serum amyloid protein A(4-101)]

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_UPI000013F119	2	14	18.00%	122	13546	6.8	Serum amyloid A protein precursor (SAA) [Contains: Amyloid protein A (Amyloid fibril protein AA); Serum amyloid protein A(2-104); Serum amyloid protein A(3-104); Serum amyloid protein A(2-103); Serum amyloid protein A(2-102); Serum amyloid protein A(4-101
UniRef100_Q6FG67	2	14	18.00%	122	13532	6.8	Amyloid protein A
UniRef100_P12259	42	162	17.80%	2224	251669	6	Coagulation factor V precursor (Activated protein C cofactor) [Contains: Coagulation factor V heavy chain; Coagulation factor V light chain]
UniRef100_UPI0000D6203D	42	162	17.80%	2230	252304	6	Coagulation factor V precursor (Activated protein C cofactor) [Contains: Coagulation factor V heavy chain; Coagulation factor V light chain].
UniRef100_UPI000016A8CE	42	162	17.80%	2224	251701	6	coagulation factor V precursor
UniRef100_Q5R347	42	162	17.80%	2224	251673	6	Coagulation factor V
UniRef100_Q5R346	42	162	17.80%	2229	252206	6	Coagulation factor V
UniRef100_P07451	3	4	17.70%	260	29557	7.3	Carbonic anhydrase 3
UniRef100_P49913	5	14	17.60%	170	19301	9.4	Cathelicidin antimicrobial peptide precursor (18 kDa cationic antimicrobial protein) (CAP-18) (hCAP-18) [Contains: Antibacterial protein FALL-39 (FALL-39 peptide antibiotic); Antibacterial protein LL-37]
UniRef100_A2VCL0	2	2	17.60%	102	11377	11.4	HIST2H4B protein
UniRef100_Q8MTV8	2	2	17.50%	103	11314	11	Histone H4
UniRef100_Q6NWP7	2	2	17.50%	103	11339	11.4	HIST1H4I protein
UniRef100_Q6FGB8	2	2	17.50%	103	11393	11.4	Histone H4
UniRef100_Q6B823	2	2	41.90%	43	4916	10.9	Histone H4
UniRef100_P62805	2	2	17.50%	103	11367	11.4	Histone H4
UniRef100_Q4LE82	21	76	17.50%	1751	193445	7	C4A variant protein
UniRef100_O00187	11	50	17.50%	686	75733	5.8	Mannan-binding lectin serine protease 2 precursor (EC 3.4.21.104) (Mannose-binding protein-associated serine protease 2) (MASP-2) (MBL- associated serine protease 2) [Contains: Mannan-binding lectin serine protease 2 A chain; Mannan-binding lectin serine protease 2 B chain]
UniRef100_UPI0000161FB9	11	50	17.50%	686	75702	5.6	mannan-binding lectin serine protease 2 isoform 1 precursor
UniRef100_P13598	5	9	17.50%	275	30654	7.4	Intercellular adhesion molecule 2 precursor
UniRef100_UPI0000046822	5	9	17.50%	275	30653	7.7	intercellular adhesion molecule 2 precursor
UniRef100_P24593	5	11	17.30%	272	30570	8.2	Insulin-like growth factor-binding protein 5 precursor
UniRef100_Q9Y5C1	6	7	17.20%	460	53638	6.7	Angiopoietin-related protein 3 precursor
UniRef100_A2BHY4	21	84	16.90%	1744	192796	7.3	Complement component C4B (Childo blood group) (Complement component C4B (Childo blood group) 2)
UniRef100_Q6U2E9	21	84	16.90%	1744	192750	7.3	C4B1
UniRef100_P14151	5	33	16.70%	372	42187	6.6	L-selectin precursor
UniRef100_Q8WW79	5	33	16.50%	375	42413	6.6	SELL protein
UniRef100_Q53TX4	4	5	16.70%	377	41968	6.7	Hypothetical protein NIF3L1
UniRef100_Q9GZT8	4	5	18.00%	350	38984	6.4	NIF3-like protein 1
UniRef100_Q658J0	4	5	19.00%	332	37029	6.5	Hypothetical protein DKFZp762L015
UniRef100_P15151-2	3	4	16.70%	372	40125	6	Isoform Beta of P15151
UniRef100_Q5SZQ2	11	27	16.60%	692	74286	6.6	Proprotein convertase subtilisin/kexin type 9
UniRef100_Q8NBP7	11	27	16.60%	692	74372	6.5	Proprotein convertase subtilisin/kexin type 9 precursor
UniRef100_Q6EMK4	10	24	16.60%	673	71713	7.4	Vasorin precursor
UniRef100_O15511	2	3	16.60%	151	16320	5.7	Actin-related protein 2/3 complex subunit 5
UniRef100_UPI000023F825	3	11	16.50%	231	24741	8.3	Fab 447-52D, heavy chain
UniRef100_P27105	3	4	16.30%	288	31731	7.9	Erythrocyte band 7 integral membrane protein
UniRef100_P49908	6	34	16.00%	381	42705	7.7	Selenoprotein P precursor

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_UPI00001C1D4A	6	34	16.00%	381	41673	7.9	selenoprotein P precursor
UniRef100_A2A2F9	4	4	15.90%	408	45295	5.7	Chromosome 20 open reading frame 3
UniRef100_UPI0000456F75	4	4	15.60%	416	46528	6.2	Adipocyte plasma membrane-associated protein (BSCv protein).
UniRef100_Q9HDC9	4	4	15.60%	416	46480	6.2	Adipocyte plasma membrane-associated protein
UniRef100_P22692	6	13	15.90%	258	27934	7.2	Insulin-like growth factor-binding protein 4 precursor
UniRef100_Q5U012	6	13	15.90%	258	28006	7	Insulin-like growth factor binding protein 4
UniRef100_P33151	11	23	15.70%	784	87516	5.4	Cadherin-5 precursor
UniRef100_UPI000016B272	11	23	15.70%	784	87528	5.4	Cadherin-5 precursor (Vascular endothelial-cadherin) (VE-cadherin) (7B4 antigen) (CD144 antigen).
UniRef100_Q59EA3	11	23	15.20%	807	89924	5.5	Cadherin 5, type 2 preproprotein variant
UniRef100_P20933	3	6	15.60%	346	37194	6.3	N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase precursor (EC 3.5.1.26) (Glycosylasparaginase) (Aspartylglucosaminidase) (N4-(N- acetyl-beta-glucosaminyl)-L-asparagine amidase) (AGA) [Contains: Glycosylasparaginase alpha chain; Glycosylasparaginase beta chain]
UniRef100_UPI000013D53C	3	6	15.60%	346	37208	6.3	N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase precursor (EC 3.5.1.26) (Glycosylasparaginase) (Aspartylglucosaminidase) (N4-(N- acetyl-beta-glucosaminyl)-L-asparagine amidase) (AGA) [Contains: Glycosylasparaginase alpha chain; Glycosylasparaginase beta c
UniRef100_P0C0L5	19	75	15.50%	1744	192792	7.2	Complement C4-B precursor (Basic complement C4) [Contains: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-B; C4d-B; Complement C4 gamma chain]
UniRef100_P02763	3	5	15.40%	201	23512	5	Alpha-1-acid glycoprotein 1 precursor
UniRef100_Q5T539	3	5	15.40%	201	23540	5.1	Orosomucoid 1
UniRef100_P30041	3	7	15.20%	224	25035	6.4	Peroxiredoxin-6
UniRef100_Q15485	4	7	15.00%	313	34019	6.5	Ficolin-2 precursor
UniRef100_UPI00001415AE	4	7	17.10%	275	30228	6.3	ficolin 2 isoform b precursor
UniRef100_Q6IS69	4	7	15.00%	313	34001	6.8	Ficolin (Collagen/fibrinogen domain containing lectin) 2
UniRef100_P05121	4	7	14.90%	402	45060	7.2	Plasminogen activator inhibitor 1 precursor
UniRef100_O43852	3	4	14.90%	315	37107	4.6	Calumenin precursor
UniRef100_O43852-2	3	4	14.90%	315	37135	4.6	Isoform 2 of O43852
UniRef100_P15151-3	4	6	14.80%	364	39305	6.2	Isoform Gamma of P15151
UniRef100_P20774	4	10	14.80%	298	33922	5.6	Mimecan precursor
UniRef100_UPI0000F2ADE0	4	10	13.90%	316	36096	6.8	osteoglycin preproprotein isoform 1
UniRef100_Q7Z532	4	10	14.80%	298	33922	5.5	Osteoglycin OG
UniRef100_Q5TBF5	4	10	16.40%	268	30456	8.3	Osteoglycin
UniRef100_Q01469	2	2	14.80%	135	15164	7	Fatty acid-binding protein, epidermal
UniRef100_UPI00001AFB9F	2	2	14.80%	135	15271	7	PREDICTED: similar to Fatty acid-binding protein, epidermal (E-FABP) (Psoriasis-associated fatty acid-binding protein homolog) (PA-FABP)
UniRef100_P43121	6	11	14.70%	646	71608	5.8	Cell surface glycoprotein MUC18 precursor
UniRef100_P05062	4	7	14.60%	364	39473	7.9	Fructose-bisphosphate aldolase B
UniRef100_Q8NHT3	4	7	16.80%	316	34751	8.2	ALDOB protein
gi|21689593|gb|AAM68133.1	2	3	14.50%	138	14722	5.2	rubber elongation factor [Hevea brasiliensis]
UniRef100_P11021	7	11	14.10%	654	72333	5.2	78 kDa glucose-regulated protein precursor (GRP 78) (Heat shock 70 kDa protein 5) (Immunoglobulin heavy chain-binding protein) (BiP) (Endoplasmic reticulum lumenal Ca(2+)-binding protein grp78)
UniRef100_P20029	7	11	14.00%	655	72422	5.2	78 kDa glucose-regulated protein precursor

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q99969	4	9	14.10%	163	18618	9.1	Retinoic acid receptor responder protein 2 precursor
UniRef100_P35443	8	23	14.00%	961	105869	4.7	Thrombospondin-4 precursor
UniRef100_Q13822	9	10	14.00%	863	99004	7.4	Ectonucleotide pyrophosphatase/phosphodiesterase family member 2 precursor
UniRef100_UPI000013D05C	9	10	14.00%	863	98994	7.4	autotaxin isoform 2 preproprotein
UniRef100_UPI000013C57A	9	10	13.20%	915	105201	8.2	autotaxin isoform 1 preproprotein
UniRef100_Q13822-2	9	10	13.20%	915	105211	8.2	Isoform 2 of Q13822
UniRef100_O95497	4	9	14.00%	513	57012	5.6	Pantetheinase precursor
UniRef100_UPI0000138A3D	4	9	14.00%	513	57024	5.6	vanin 1 precursor
UniRef100_P11597	6	16	13.80%	493	54756	6.1	Cholesteryl ester transfer protein precursor
UniRef100_Q53YZ1	6	16	13.80%	493	54770	6.1	Cholesteryl ester transfer protein, plasma
UniRef100_P09972	2	4	13.70%	364	39456	6.9	Fructose-bisphosphate aldolase C
UniRef100_Q7Z7M0	21	25	13.50%	2386	254570	6.9	Multiple epidermal growth factor-like domains 8
UniRef100_Q16853	9	10	13.50%	763	84622	6.5	Membrane copper amine oxidase
UniRef100_P24387	3	4	13.40%	322	36144	6.5	Corticotropin-releasing factor-binding protein precursor
UniRef100_Q53F32	3	4	13.40%	322	36145	6.4	Corticotropin releasing hormone binding protein variant
UniRef100_Q04917	4	8	13.40%	246	28219	4.8	14-3-3 protein eta
UniRef100_O14818	3	4	13.30%	248	27887	8.5	Proteasome subunit alpha type 7
UniRef100_Q05DH1	3	4	13.90%	238	26714	8.9	Hypothetical protein
UniRef100_O14818-2	3	4	18.50%	178	20193	8.5	Isoform 2 of O14818
UniRef100_P20618	2	2	13.30%	241	26489	8.1	Proteasome subunit beta type 1 precursor
UniRef100_Q59GN1	2	2	16.30%	196	21274	8.7	Proteasome beta 1 subunit variant
UniRef100_Q53FT8	2	2	13.30%	241	26491	8.1	Proteasome beta 1 subunit variant
UniRef100_P27348	4	8	13.10%	245	27764	4.8	14-3-3 protein theta
UniRef100_P68254-2	4	8	13.20%	243	27701	4.9	Isoform 2 of P68254
UniRef100_P04179	2	5	13.10%	222	24722	8.3	Superoxide dismutase [Mn], mitochondrial precursor
UniRef100_UPI000020D3E0	2	5	15.80%	183	20724	8.3	manganese superoxide dismutase isoform B precursor
UniRef100_UPI000006D275	2	5	13.10%	222	24750	8.3	manganese superoxide dismutase isoform A precursor
UniRef100_P59998	2	3	13.10%	168	19667	8.4	Actin-related protein 2/3 complex subunit 4
UniRef100_UPI0000D61ABF	2	3	14.10%	156	17071	8.5	Tubulin--tyrosine ligase-like protein 3 (HOTTL).
UniRef100_UPI00005E7FE3	2	3	13.20%	167	19488	8.4	Tubulin--tyrosine ligase-like protein 3 (HOTTL).
UniRef100_Q9H7Z5	2	3	14.10%	156	16968	8.8	CDNA FLJ14048 fis, clone HEMBA1006650, weakly similar to ARP2/3 COMPLEX 20 KD SUBUNIT
UniRef100_Q01459	3	4	13.00%	385	43760	6.6	Di-N-acetylchitobiase precursor
UniRef100_P61981	4	8	13.00%	247	28303	4.9	14-3-3 protein gamma
UniRef100_O43505	2	2	12.80%	415	47119	7.2	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase
UniRef100_P16930	4	6	12.60%	419	46374	6.9	Fumarylacetoacetase
UniRef100_P61224	2	6	12.50%	184	20825	5.8	Ras-related protein Rap-1b precursor
UniRef100_Q5U0C3	2	6	12.50%	184	20953	6.6	RAP1A, member of RAS oncogene family
UniRef100_P62834	2	6	12.50%	184	20987	6.6	Ras-related protein Rap-1A precursor
UniRef100_P18428	5	21	12.30%	481	53384	6.7	Lipopolysaccharide-binding protein precursor
UniRef100_Q8TCF0	5	21	12.40%	477	52934	6.8	LBP protein
UniRef100_P25789	2	3	12.30%	261	29484	7.7	Proteasome subunit alpha type 4
UniRef100_Q7Z474	2	3	13.50%	237	26576	7.3	PSMA4 protein
UniRef100_A4D2D2	4	9	12.00%	449	47958	7.4	Procollagen C-endopeptidase enhancer
UniRef100_UPI0000161B54	4	9	12.00%	449	47946	7.4	procollagen C-endopeptidase enhancer
UniRef100_Q15113	4	9	12.00%	449	47973	7.4	Procollagen C-endopeptidase enhancer 1 precursor

Supplemental Table 2A: Protein Groups Identified in the Human Serum Proteome Analysis

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P07359	9	16	11.80%	626	68955	6.7	Platelet glycoprotein Ib alpha chain precursor (Glycoprotein Ibalpha) (GP-Ib alpha) (GPIbA) (GPIb-alpha) (Antigen CD42b-alpha) (CD42b antigen) [Contains: Glycocalicin]
UniRef100_UPI0000D622AC	9	16	11.80%	627	68967	6.7	Platelet glycoprotein Ib alpha chain precursor (Glycoprotein Ibalpha) (GP-Ib alpha) (GPIbA) (GPIb-alpha) (Antigen CD42b-alpha) (CD42b antigen) [Contains: Glycocalicin].
UniRef100_P40197	3	7	11.80%	560	60959	9.6	Platelet glycoprotein V precursor
UniRef100_P04745	4	5	11.70%	511	57768	6.9	Salivary alpha-amylase precursor
UniRef100_UPI00006C1E8E	4	5	16.40%	366	41567	7.8	PREDICTED: similar to Salivary alpha-amylase precursor (1,4-alpha-D-glucan glucanohydrolase)
UniRef100_Q6NSB3	4	5	12.10%	495	56211	8.6	AMY1A protein
UniRef100_UPI000013D4D9	10	11	11.50%	1247	136377	5.3	nidogen 1 precursor
UniRef100_Q15582	7	12	11.30%	683	74681	7.7	Transforming growth factor-beta-induced protein ig-h3 precursor
UniRef100_UPI000045734C	7	12	11.30%	682	74591	7.3	Transforming growth factor-beta-induced protein ig-h3 precursor (Beta ig-h3) (Kerato-epithelin) (RGD-containing collagen-associated protein) (RGD-CAP).
UniRef100_P13727	2	3	11.30%	222	25232	6.7	Bone-marrow proteoglycan precursor (BMPG) (Proteoglycan 2) [Contains: Eosinophil granule major basic protein (EMBP) (MBP) (Pregnancy- associated major basic protein)]
UniRef100_UPI000013CF50	2	3	11.30%	222	25206	6.8	proteoglycan 2 preproprotein
UniRef100_P33908	6	11	11.20%	653	72969	6.5	Mannosyl-oligosaccharide 1,2-alpha-mannosidase IA (EC 3.2.1.113) (Processing alpha-1,2-mannosidase IA) (Alpha-1,2-mannosidase IA) (Mannosidase alpha class 1A member 1) (Man(9)-alpha-mannosidase)
UniRef100_UPI0000D614C3	6	11	10.80%	676	75373	6.3	Mannosyl-oligosaccharide 1,2-alpha-mannosidase IA (EC 3.2.1.113) (Processing alpha-1,2-mannosidase IA) (Alpha-1,2-mannosidase IA) (Mannosidase alpha class 1A member 1) (Man(9)-alpha-mannosidase) (Man9-mannosidase).
UniRef100_Q02985	6	83	10.90%	330	37323	7.5	Complement factor H-related protein 3 precursor
UniRef100_P07307	2	2	10.90%	311	35191	6.4	Asialoglycoprotein receptor 2
UniRef100_UPI0000D622B1	2	2	10.90%	313	35489	6.2	Asialoglycoprotein receptor 2 (ASGP-R 2) (ASGPR 2) (Hepatic lectin H2).
UniRef100_UPI00002007B9	2	2	10.90%	311	35092	6.3	Asialoglycoprotein receptor 2 (ASGP-R 2) (ASGPR 2) (Hepatic lectin H2).
UniRef100_Q7Z4G9	2	2	11.10%	306	34655	6.3	HBxAg-binding protein
UniRef100_P07307-3	2	2	11.80%	287	32550	5.8	Isoform 3 of P07307
UniRef100_P07307-2	2	2	11.60%	292	33087	5.9	Isoform 2 of P07307
UniRef100_P19320	6	7	10.70%	739	81276	5.2	Vascular cell adhesion protein 1 precursor
UniRef100_UPI000059D017	6	7	11.70%	677	74347	5.2	Vascular cell adhesion protein 1 precursor (V-CAM 1) (CD106 antigen) (INCAM-100).
UniRef100_UPI000013EA49	6	7	12.20%	647	71255	5.2	vascular cell adhesion molecule 1 isoform b precursor
UniRef100_Q53FL7	6	7	10.70%	739	81264	5.2	Vascular cell adhesion molecule 1 isoform a variant
UniRef100_P19320-2	6	7	12.20%	646	71184	5.2	Isoform 2 of P19320
UniRef100_P05067	7	14	10.50%	770	86943	4.8	Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer disease amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease nexin-II) (PN-II) (APPI) (PreA4) [Contains: Soluble APP-alpha (S-APP- alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59)) (AICD-59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57) (Amyloid intracellular domain 57) (AID(57)) (AICD-57); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain 50) (AID(50)) (AICD-50); C31]
UniRef100_Q6GSC0	7	14	10.80%	751	84819	4.8	Amyloid beta (A4) protein
UniRef100_P05067-9	7	14	10.80%	752	85040	4.8	Isoform L
UniRef100_P05067-7	7	14	11.10%	733	82916	4.8	Isoform L
UniRef100_P07738	2	3	10.40%	259	30005	6.5	Bisphosphoglycerate mutase

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q9UHG3	3	3	10.30%	505	56640	6.2	Prenylcysteine oxidase precursor
UniRef100_UPI000013D518	3	3	10.30%	505	56700	6.2	prenylcysteine oxidase 1
UniRef100_P01009	3	4	10.30%	418	46737	5.6	Alpha-1-antitrypsin precursor
UniRef100_Q86U18	3	4	11.60%	370	41448	5.3	Full-length cDNA clone CS0DM003YH14 of Fetal liver of Homo sapiens
UniRef100_Q0PVP5	3	4	10.30%	418	46606	5.7	Alpha-1 antitrypsin variant
UniRef100_Q86YW5	2	11	10.30%	311	32679	6.1	Trem-like transcript 1 protein precursor
UniRef100_Q86YW5-2	2	11	16.10%	199	21323	5.1	Isoform 2 of Q86YW5
UniRef100_P06753-3	2	3	10.10%	247	28955	4.8	Isoform 3 of P06753
UniRef100_UPI0000D61FFA	2	3	10.10%	247	28839	4.8	Tropomyosin alpha-3 chain (Tropomyosin-3) (Tropomyosin gamma) (hTM5).
UniRef100_UPI0000D61FF9	2	3	10.10%	248	28916	4.8	Tropomyosin alpha-3 chain (Tropomyosin-3) (Tropomyosin gamma) (hTM5).
UniRef100_UPI0000D619EC	2	3	10.80%	232	27125	4.7	UPI0000D619EC UniRef100 entry
UniRef100_UPI000020489E	2	3	10.10%	248	29079	4.8	Tropomyosin alpha-3 chain (Tropomyosin-3) (Tropomyosin gamma) (hTM5).
UniRef100_Q6QA25	2	3	10.10%	248	29033	4.8	Tropomyosin 3
UniRef100_Q5VU72	2	3	10.10%	247	28793	4.8	Tropomyosin 3
UniRef100_Q5VU66	2	3	10.10%	248	28870	4.8	Tropomyosin 3
UniRef100_Q5VU59	2	3	10.80%	232	27175	4.8	Tropomyosin 3
UniRef100_Q5VU58	2	3	10.10%	248	28922	4.8	Tropomyosin 3
UniRef100_Q5HYB6	2	3	10.80%	232	27176	4.7	Hypothetical protein DKFZp686J1372
UniRef100_Q2QD06	2	3	10.10%	247	28823	4.8	RcTPM3
UniRef100_P28074	2	3	10.10%	208	22897	8.5	Proteasome subunit beta type 5 precursor
UniRef100_Q7Z3B5	2	3	7.90%	266	28810	6.5	Hypothetical protein DKFZp686I0180
UniRef100_P00488	5	9	10.00%	732	83267	6.1	Coagulation factor XIII A chain precursor
UniRef100_UPI000013D585	5	9	10.00%	732	83268	6	coagulation factor XIII A1 subunit precursor
UniRef100_Q59HA7	5	9	9.60%	757	85956	6.2	Coagulation factor XIII A chain variant
UniRef100_Q5DVJ7	5	8	9.90%	578	65337	4.9	Complement factor H-related protein 4A precursor
UniRef100_UPI0000D6206A	5	8	9.90%	578	65351	4.9	Complement factor H-related protein 4 precursor (FHR-4).
UniRef100_Q6UXB8	4	6	9.90%	463	49471	5.4	Peptidase inhibitor 16
UniRef100_Q8TCB8	4	6	11.30%	408	44375	5.5	PI16 protein
UniRef100_Q8NBK0	4	6	9.90%	463	49367	5.5	CDNA PSEC0164 fis, clone PLACE1010482, weakly similar to GLIOMA PATHOGENESIS-RELATED PROTEIN
UniRef100_Q8IYL8	4	6	9.90%	463	49467	5.4	Peptidase inhibitor 16
UniRef100_Q6ZVG9	4	6	17.00%	270	29670	5.7	CDNA FLJ42598 fis, clone BRACE3010397
UniRef100_P61204	2	3	9.90%	181	20601	7.4	ADP-ribosylation factor 3
UniRef100_P84077	2	3	9.90%	181	20697	6.8	ADP-ribosylation factor 1
UniRef100_Q86VB7	7	8	9.60%	1156	125437	5.9	Scavenger receptor cysteine-rich type 1 protein M130 precursor (CD163 antigen) (Hemoglobin scavenger receptor) [Contains: Soluble CD163 (sCD163)]
UniRef100_UPI00004565CC	7	8	9.60%	1156	125451	5.9	Scavenger receptor cysteine-rich type 1 protein M130 precursor (CD163 antigen) (Hemoglobin scavenger receptor) [Contains: Soluble CD163 (sCD163)].
UniRef100_Q86VB7-4	7	8	9.60%	1154	124944	6.2	Isoform 4 of Q86VB7
UniRef100_Q86VB7-3	7	8	9.90%	1121	121595	6.1	Isoform 3 of Q86VB7
UniRef100_Q86VB7-2	7	8	9.60%	1161	125968	6.1	Isoform 2 of Q86VB7
UniRef100_Q4LE33	19	28	9.50%	2233	244402	4.9	TNC variant protein
UniRef100_Q12860	6	8	9.50%	1018	113320	5.9	Contactin-1 precursor
UniRef100_Q12860-2	6	8	9.60%	1007	111867	5.8	Isoform 2 of Q12860
UniRef100_P11717	17	30	9.10%	2491	274274	5.9	Cation-independent mannose-6-phosphate receptor precursor

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_UPI0000072478	17	30	9.10%	2491	274373	5.9	Cation-independent mannose-6-phosphate receptor precursor (CI Man-6-P receptor) (CI-MPR) (M6PR) (Insulin-like growth factor 2 receptor) (Insulin-like growth factor II receptor) (IGF-II receptor) (M6P/IGF2 receptor) (M6P/IGF2R) (300 kDa mannose 6-phosphate
UniRef100_O14786	5	5	8.90%	923	103120	5.9	Neuropilin-1 precursor
UniRef100_UPI00004045CF	5	5	12.80%	641	72094	6.8	Neuropilin-1 precursor (Vascular endothelial cell growth factor 165 receptor) (CD304 antigen).
UniRef100_Q9H2E1	5	5	11.60%	704	79002	5.9	Neuropilin-1 soluble isoform 11
UniRef100_Q96I90	5	5	13.50%	609	68348	6.2	Neuropilin 1
UniRef100_Q71SW6	5	5	12.80%	641	72066	6.8	Muscle type neuropilin 1
UniRef100_Q6X907	5	5	9.10%	906	101291	6.1	Neuropilin-1
UniRef100_Q68DN3	5	5	8.90%	923	103085	5.9	Hypothetical protein DKFZp781F1414
UniRef100_Q5T7F3	5	5	8.90%	923	103134	5.9	Neuropilin 1
UniRef100_Q5T7F2	5	5	12.70%	644	71935	5.6	Neuropilin 1
UniRef100_Q5T7F1	5	5	13.50%	609	68376	6.2	Neuropilin 1
UniRef100_Q5T7F0	5	5	11.60%	704	79030	5.9	Neuropilin 1
UniRef100_O14786-2	5	5	12.70%	644	71907	5.6	Isoform 2 of O14786
UniRef100_Q96MH4	3	11	8.80%	388	43649	6.4	CDNA FLJ32377 fis, clone SKMUS1000014, highly similar to Polyubiquitin 9
UniRef100_UPI0000D6227D	3	11	8.80%	388	43667	6.4	Ubiquitin.
UniRef100_UPI0000D6227C	3	11	8.80%	388	43677	6.4	Ubiquitin.
UniRef100_UPI0000D6227B	3	11	8.80%	388	43645	6.4	Ubiquitin.
UniRef100_Q13790	3	19	8.80%	308	33463	5.5	Apolipoprotein F precursor
UniRef100_UPI0000456625	3	19	8.30%	326	35481	5.8	Apolipoprotein F precursor (Apo-F) (Lipid transfer inhibitor protein) (LTIP).
UniRef100_Q6YHK3	8	12	8.70%	1445	161688	5.8	CD109 antigen precursor
UniRef100_Q6YHK3-4	8	12	8.80%	1428	159695	5.8	Isoform 4 of Q6YHK3
UniRef100_P18206	8	9	8.70%	1134	123799	5.7	Vinculin
UniRef100_P18206-2	8	9	9.30%	1066	116722	6.1	Isoform 1 of P18206
UniRef100_O00299	2	3	8.70%	241	26923	5.2	Chloride intracellular channel protein 1
UniRef100_UPI00004702FA	2	3	13.20%	159	17767	4.8	Chloride intracellular channel protein 1 (Nuclear chloride ion channel 27) (NCC27) (Chloride channel ABP) (Regulatory nuclear chloride ion channel protein) (hRNCC).
UniRef100_Q53FB0	2	3	8.70%	241	27015	5.2	Chloride intracellular channel 1 variant
UniRef100_A2VDG3	4	7	8.60%	454	49964	6.8	KRT76 protein
UniRef100_Q59HE0	4	7	5.40%	725	80116	6.6	Colony stimulating factor 1 receptor variant
UniRef100_P07333	4	7	4.00%	972	107984	6.4	Macrophage colony-stimulating factor 1 receptor precursor
UniRef100_Q96CX2	2	3	8.60%	325	35701	5.6	BTB/POZ domain-containing protein KCTD12
UniRef100_Q7Z528	2	5	8.60%	266	30425	5.2	E3-16
UniRef100_Q9Y287	2	5	8.60%	266	30338	5.1	Integral membrane protein 2B (Transmembrane protein BRI) [Contains: ABri/ADan amyloid peptide]
UniRef100_Q9NX12	2	5	8.60%	266	30312	5.2	CDNA FLJ20496 fis, clone KAT08729
UniRef100_Q96B24	2	5	8.60%	266	30368	5.1	Integral membrane protein 2B
UniRef100_O75015	2	3	8.60%	233	26216	6.7	Low affinity immunoglobulin gamma Fc region receptor III-B precursor
UniRef100_UPI000066D8C5	2	3	7.40%	269	29884	6.9	Low affinity immunoglobulin gamma Fc region receptor III-B precursor (IgG Fc receptor III-1) (Fc-gamma RIII-beta) (Fc-gamma RIIIb) (FcRIIIb) (Fc-gamma RIII) (FcRIII) (FcR-10) (CD16b antigen).
UniRef100_Q9UPY7	2	3	8.60%	233	26215	7.2	Fc-gamma receptor IIIb
UniRef100_UPI000013CBF6	4	40	8.50%	458	49588	5	Keratin, type I cytoskeletal 13 (Cytokeratin-13) (CK-13) (Keratin-13) (K13).
UniRef100_UPI0000E4FB5A	4	40	8.50%	458	49558	5	keratin 13 isoform a
UniRef100_UPI0000E4FB59	4	40	9.30%	420	45837	4.9	keratin 13 isoform b
UniRef100_UPI000013F0CC	4	40	9.30%	420	45867	4.9	Keratin, type I cytoskeletal 13 (Cytokeratin-13) (CK-13) (Keratin-13) (K13).

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P54289	6	7	8.40%	1091	123183	5.2	Dihydropyridine-sensitive L-type calcium channel subunits alpha- 2/delta precursor [Contains: L-type calcium channel subunit alpha-2; L-type calcium channel subunit delta]
UniRef100_UPI0000D61C7B	6	7	8.60%	1071	121188	5.4	Dihydropyridine-sensitive L-type calcium channel subunits alpha- 2/delta precursor [Contains: L-type calcium channel subunit alpha-2; L-type calcium channel subunit delta].
UniRef100_Q9UIU0	6	7	8.30%	1110	125308	5.4	Dihydropyridine receptor alpha 2 subunit
UniRef100_Q17R45	6	7	8.40%	1091	123183	5.2	Calcium channel, voltage-dependent, alpha 2/delta subunit 1
UniRef100_P55290	4	8	8.30%	713	78287	5	Cadherin-13 precursor
UniRef100_P08253	3	6	8.30%	660	73882	5.5	72 kDa type IV collagenase precursor
UniRef100_Q12913	7	9	8.20%	1337	145927	5.6	Receptor-type tyrosine-protein phosphatase eta precursor
UniRef100_UPI00004564C8	7	9	8.20%	1337	145941	5.6	Receptor-type tyrosine-protein phosphatase eta precursor (EC 3.1.3.48) (Protein-tyrosine phosphatase eta) (R-PTP-eta) (HPTP eta) (Protein- tyrosine phosphatase receptor type J) (Density-enhanced phosphatase 1) (DEP-1) (CD148 antigen).
UniRef100_Q6P4H4	7	9	20.40%	539	57190	5.6	PTPRJ protein
UniRef100_P54802	3	3	8.20%	743	82167	6.5	Alpha-N-acetylglucosaminidase precursor (EC 3.2.1.50) (N-acetyl-alpha- glucosaminidase) (NAG) [Contains: Alpha-N-acetylglucosaminidase 82 kDa form; Alpha-N-acetylglucosaminidase 77 kDa form]
UniRef100_UPI0000D62335	3	3	14.60%	419	47120	7.5	Alpha-N-acetylglucosaminidase precursor (EC 3.2.1.50) (N-acetyl-alpha- glucosaminidase) (NAG) [Contains: Alpha-N-acetylglucosaminidase 82 kDa form; Alpha-N-acetylglucosaminidase 77 kDa form].
UniRef100_UPI000013C885	3	3	8.20%	743	82266	6.6	alpha-N-acetylglucosaminidase precursor
UniRef100_Q59FD0	3	3	13.60%	449	50312	6.7	Huntingtin interacting protein-1-related
UniRef100_Q14769	3	3	9.50%	639	72028	6.4	Alpha-N-acetylglucosaminidase
UniRef100_P04040	3	5	8.20%	527	59756	7.4	Catalase
UniRef100_P10124	2	5	8.20%	158	17624	4.8	Secretory granule proteoglycan core protein precursor
UniRef100_Q5VW06	2	5	8.20%	158	17652	5	Proteoglycan 1, secretory granule
UniRef100_P55103	3	5	8.00%	352	38238	7.1	Inhibin beta C chain precursor
UniRef100_Q6P179	5	6	7.70%	915	105526	6.8	LRAP protein
UniRef100_Q9HBX2	5	6	7.30%	960	110462	6.7	Aminopeptidase
UniRef100_Q7Z5K1	5	6	7.30%	960	110447	6.7	Leukocyte-derived arginine aminopeptidase long form variant
UniRef100_Q13740	2	3	7.70%	583	65102	6.3	CD166 antigen precursor
UniRef100_UPI000013EAED	2	3	7.70%	583	65071	6.6	CD166 antigen precursor (Activated leukocyte-cell adhesion molecule) (ALCAM).
UniRef100_Q13740-2	2	3	7.90%	570	63666	7.1	Isoform 2 of Q13740
UniRef100_P08637	2	5	7.50%	254	29089	8.1	Low affinity immunoglobulin gamma Fc region receptor III-A precursor
UniRef100_Q6PIJ0	2	5	7.50%	254	29057	8.1	FCGR3A protein
UniRef100_Q65ZM6	2	5	8.20%	233	26702	8.1	CD16
UniRef100_Q5EBR4	2	5	7.50%	254	29041	8.1	FCGR3A protein
UniRef100_Q53FL6	2	5	7.30%	259	29542	8	FCGR3A protein variant
UniRef100_Q53FJ0	2	5	7.20%	263	29924	8	FCGR3A protein variant
UniRef100_P12035	6	17	7.30%	629	64504	6.5	Keratin, type II cytoskeletal 3
UniRef100_UPI000013EEC8	6	17	7.30%	628	64417	6.5	keratin 3
UniRef100_P25786	2	2	7.20%	263	29556	6.6	Proteasome subunit alpha type 1
UniRef100_Q53YE8	2	2	7.20%	263	29598	6.6	Proteasome (Prosome, macropain) subunit, alpha type, 1
UniRef100_P25786-2	2	2	7.10%	269	30239	7	Isoform Long of P25786
UniRef100_P13473	3	17	7.10%	410	44961	5.6	Lysosome-associated membrane glycoprotein 2 precursor
UniRef100_Q9UD93	3	17	7.10%	410	45043	5.9	Lysosomal membrane glycoprotein LAMP-2 homolog
UniRef100_Q6Q3G8	3	17	7.10%	411	45170	5.9	Lysosomal-associated membrane protein 2C
UniRef100_P13473-2	3	17	7.10%	410	44956	5.7	Isoform LAMP

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P00491	2	2	6.90%	289	32118	6.9	Purine nucleoside phosphorylase
UniRef100_UPI0000112E78	2	2	6.90%	289	32148	6.9	purine nucleoside phosphorylase
UniRef100_Q3SYH6	2	5	6.90%	277	30705	7.3	Collectin sub-family member 10
UniRef100_Q9Y6Z7	2	5	6.90%	277	30733	7.7	Collectin 34
UniRef100_Q6UW19	2	5	6.90%	277	30645	7.3	COLEC10
UniRef100_P14625	4	5	6.70%	803	92469	4.8	Endoplasmin precursor
UniRef100_Q5CAQ5	4	5	6.70%	802	92340	4.9	Tumor rejection antigen (Gp96) 1
UniRef100_Q9H4A9	2	2	6.60%	486	53365	6.5	Dipeptidase 2 precursor
UniRef100_UPI00004569AB	2	2	8.00%	400	43973	6.1	Dipeptidase 2 precursor (EC 3.4.13.19).
UniRef100_UPI000013D7DC	2	2	6.60%	486	53306	6.4	Dipeptidase 2 precursor (EC 3.4.13.19).
UniRef100_Q9H4A9-2	2	2	8.00%	399	43887	6.2	Isoform 2 of Q9H4A9
UniRef100_P40925	2	3	6.60%	334	36426	7.3	Malate dehydrogenase, cytoplasmic
UniRef100_Q07954	24	38	6.50%	4544	504579	5.4	Low-density lipoprotein receptor-related protein 1 precursor
UniRef100_UPI00001B044F	24	38	6.50%	4544	504610	5.4	low density lipoprotein-related protein 1
UniRef100_Q7Z7M8	2	2	6.50%	397	43396	8.3	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 8
UniRef100_O15204	2	2	6.40%	470	52775	7.3	ADAM DEC1 precursor
UniRef100_Q9UKU6	5	5	6.20%	1024	116999	7	Thyrotropin-releasing hormone-degrading ectoenzyme
UniRef100_Q9H8L6	9	24	6.20%	949	104417	5.8	Multimerin-2 precursor
UniRef100_UPI000013F046	9	24	6.20%	949	104409	5.9	Multimerin-2 precursor (EMILIN-3) (Elastin microfibril interface located protein 3) (Elastin microfibril interfacer 3) (EndoGlyx-1 p125/p140 subunit).
UniRef100_Q9UKP6	2	3	6.20%	389	42130	10.7	Urotensin II receptor
UniRef100_Q9Y6R7	22	32	6.10%	5405	572072	5.3	IgGFc-binding protein precursor
UniRef100_UPI0000120C9E	22	32	6.10%	5405	572101	5.3	Fc fragment of IgG binding protein
UniRef100_Q16706	4	5	6.10%	1144	131084	7.6	Alpha-mannosidase 2
UniRef100_UPI000013D193	4	5	6.10%	1144	131140	7.6	mannosidase, alpha, class 2A, member 1
UniRef100_P04066	2	4	6.10%	461	53176	6.7	Tissue alpha-L-fucosidase precursor
UniRef100_UPI0000D61E8A	2	4	6.30%	443	50911	6.9	Tissue alpha-L-fucosidase precursor (EC 3.2.1.51) (Alpha-L-fucosidase I) (Alpha-L-fucoside fucohydrolase).
UniRef100_P03951	3	6	5.90%	625	70109	8.1	Coagulation factor XI precursor (EC 3.4.21.27) (Plasma thromboplastin antecedent) (PTA) (FXI) [Contains: Coagulation factor XIa heavy chain; Coagulation factor XIa light chain]
UniRef100_UPI00004572B5	3	6	6.50%	573	64053	8.3	Coagulation factor XI precursor (EC 3.4.21.27) (Plasma thromboplastin antecedent) (PTA) (FXI) [Contains: Coagulation factor XIa heavy chain; Coagulation factor XIa light chain].
UniRef100_P03951-2	3	6	6.50%	571	63840	8.3	Isoform 2 of P03951
UniRef100_P01876	2	2	5.90%	353	37655	6.5	Ig alpha-1 chain C region
UniRef100_UPI0000F30352	2	2	5.90%	353	37697	6.5	Immunoglobulin heavy chain C gene segment
UniRef100_Q9BRV0	2	2	4.20%	500	54154	6.7	IGHA1 protein
UniRef100_Q96KX8	2	2	4.20%	496	53392	7.8	IGHA1 protein
UniRef100_Q96K68	2	2	4.30%	494	53088	6.9	CDNA FLJ14473 fis, clone MAMMA1001080, highly similar to Homo sapiens SNC73 protein (SNC73) mRNA
UniRef100_Q96DK0	2	2	4.20%	496	53533	6.7	CDNA FLJ25298 fis, clone STM07683, highly similar to Protein Tro alpha1 H,myeloma
UniRef100_Q8NCL6	2	2	4.30%	493	53224	6.5	CDNA FLJ90170 fis, clone MAMMA1000370, highly similar to Ig alpha-1 chain C region
UniRef100_Q8N5K4	2	2	4.20%	499	53376	6.7	IGHA1 protein
UniRef100_Q6ZW64	2	2	4.30%	494	53321	6.5	CDNA FLJ41552 fis, clone COLON2004478, highly similar to Protein Tro alpha1 H,myeloma
UniRef100_Q6N092	2	2	4.00%	519	56424	6.9	Hypothetical protein DKFZp686K18196
UniRef100_Q6N090	2	2	4.20%	506	54389	6.6	Hypothetical protein DKFZp686G21220
UniRef100_Q6MZW0	2	2	4.20%	506	54460	6.8	Hypothetical protein DKFZp686J11235
UniRef100_Q6GMX2	2	2	4.30%	493	52865	7.1	IGHA1 protein

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q569J1	2	2	4.30%	493	53158	7.2	IGHA1 protein
UniRef100_Q13201	8	25	5.80%	1228	138110	7.9	Multimerin-1 precursor
UniRef100_P05787	4	17	5.80%	483	53704	5.6	Keratin, type II cytoskeletal 8
UniRef100_P05362	2	4	5.60%	532	57825	8	Intercellular adhesion molecule 1 precursor
UniRef100_UPI000012D132	2	4	5.60%	532	57826	7.7	intercellular adhesion molecule 1 precursor
UniRef100_Q5NKV8	2	4	5.60%	532	57882	7.7	Intercellular adhesion molecule 1
UniRef100_Q5NKV7	2	4	5.70%	528	57502	7.7	Intercellular adhesion molecule 1
UniRef100_Q15463	2	4	10.90%	276	30221	8.4	Cell surface glycoprotein
UniRef100_Q9Y5Y7	2	7	5.60%	322	35213	8.3	Lymphatic vessel endothelial hyaluronic acid receptor 1 precursor
UniRef100_P05556	3	3	5.50%	798	88465	5.4	Integrin beta-1 precursor
UniRef100_UPI0000160C2A	3	3	5.30%	825	91620	5.4	integrin beta 1 isoform 1C-1 precursor
UniRef100_UPI0000160759	3	3	5.60%	789	87446	5.5	integrin beta 1 isoform 1B precursor
UniRef100_UPI000013E7B1	3	3	5.50%	801	88884	5.5	integrin beta 1 isoform 1D precursor
UniRef100_UPI000013DBE0	3	3	5.40%	819	91035	5.4	integrin beta 1 isoform 1C-2 precursor
UniRef100_Q8WUM6	3	3	5.50%	798	88415	5.4	Integrin, beta 1
UniRef100_Q7Z3V1	3	3	5.30%	823	91131	5.5	Integrin beta
UniRef100_P05556-5	3	3	5.50%	801	88934	5.5	Isoform Beta
UniRef100_P05556-4	3	3	5.40%	819	91085	5.5	Isoform Beta
UniRef100_P05556-3	3	3	5.30%	825	91670	5.5	Isoform Beta
UniRef100_P05556-2	3	3	5.60%	789	87496	5.5	Isoform Beta
UniRef100_P10619	2	4	5.40%	480	54466	6.6	Lysosomal protective protein precursor (EC 3.4.16.5) (Cathepsin A) (Carboxypeptidase C) (Protective protein for beta-galactosidase) [Contains: Lysosomal protective protein 32 kDa chain; Lysosomal protective protein 20 kDa chain]
UniRef100_Q59EV6	2	4	5.20%	497	56120	6.6	Carrier family 6 , member 8 variant
UniRef100_Q96HR3	2	20	5.10%	178	20277	8.3	Thyroid hormone receptor-associated protein 6
UniRef100_P23470	4	6	4.80%	1445	162028	6.5	Receptor-type tyrosine-protein phosphatase gamma precursor
UniRef100_UPI00001AEBFB	4	6	4.80%	1445	162003	6.4	Receptor-type tyrosine-protein phosphatase gamma precursor (EC 3.1.3.48) (Protein-tyrosine phosphatase gamma) (R-PTP-gamma).
UniRef100_UPI0000132994	4	6	4.80%	1445	162058	6.5	protein tyrosine phosphatase, receptor type, G precursor
UniRef100_P23470-2	4	6	4.90%	1416	158795	6.2	Isoform 2 of P23470
UniRef100_P07602	2	7	4.80%	524	58113	5.2	Proactivator polypeptide precursor [Contains: Saposin A (Protein A); Saposin B-Val; Saposin B (Sphingolipid activator protein 1) (SAP-1) (Cerebroside sulfate activator) (CSAct) (Dispersin) (Sulfatide/GM1 activator); Saposin C (Co-beta-glucosidase) (A1 activator) (Glucosylceramidase activator) (Sphingolipid activator protein 2) (SAP-2); Saposin D (Protein C) (Component C)]
UniRef100_Q5JQ37	2	7	4.50%	559	61693	5.2	Prosaposin
UniRef100_Q59EN5	2	7	4.70%	530	58727	5.1	Prosaposin variant
UniRef100_Q53FJ5	2	7	4.80%	524	58141	5.2	Prosaposin (Variant Gaucher disease and variant metachromatic leukodystrophy) variant
UniRef100_P07602-2	2	7	4.80%	526	58356	5.1	Isoform Sap
UniRef100_Q8N6C8	2	6	4.80%	439	47472	8.1	Leukocyte immunoglobulin-like receptor subfamily A member 3 precursor
UniRef100_UPI0000070FC0	2	6	4.80%	439	47490	8.1	leukocyte immunoglobulin-like receptor, subfamily A (without TM domain), member 3
UniRef100_Q5TF06	4	5	4.50%	1346	149457	6.7	OTTHUMP00000016557
UniRef100_UPI000013D61D	4	5	4.60%	1326	147129	6.5	Probable G-protein coupled receptor 116 precursor.
UniRef100_P12109	4	5	4.50%	1028	108529	5.4	Collagen alpha-1(VI) chain precursor
UniRef100_Q15063	2	2	4.40%	836	93314	7.5	Periostin precursor
UniRef100_UPI00000747E8	2	2	4.40%	836	93332	7.7	periostin, osteoblast specific factor
UniRef100_Q5VSY8	2	2	4.70%	779	87021	7.8	Periostin, osteoblast specific factor

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q5VSY7	2	2	4.60%	809	90424	7.4	Periostin, osteoblast specific factor
UniRef100_Q5VSY6	2	2	4.60%	808	90143	8	Periostin, osteoblast specific factor
UniRef100_Q29XZ0	2	2	4.90%	751	83868	8.3	Periodontal ligament-specific periostin
UniRef100_Q15063-3	2	2	4.70%	782	87383	7.7	Isoform 3 of Q15063
UniRef100_Q14515	2	3	4.40%	664	75216	4.8	SPARC-like protein 1 precursor
UniRef100_UPI000013DCE3	2	3	4.40%	664	75208	4.8	SPARC-like protein 1 precursor (High endothelial venule protein) (Hevin) (MAST 9).
UniRef100_UPI0000048D6A	2	3	4.40%	664	75248	4.8	SPARC-like 1
UniRef100_Q8N4S1	2	3	4.40%	664	75230	4.8	SPARC-like 1
UniRef100_Q59EG0	8	18	4.30%	2331	246410	7.2	Basement membrane-specific heparan sulfate proteoglycan core protein variant
UniRef100_P22105	14	19	4.20%	4289	464461	5.3	Tenascin-X precursor
UniRef100_UPI0000D626B5	14	19	4.20%	4309	466129	5.3	Cyclic AMP-dependent transcription factor ATF-6 beta (Activating transcription factor 6 beta) (ATF6-beta) (cAMP-responsive element- binding protein-like 1) (cAMP response element-binding protein-related protein) (Creb-rp) (Protein G13).
UniRef100_UPI0000530314	14	19	4.20%	4289	464330	5.3	tenascin XB isoform 1
UniRef100_Q9NPK9	14	19	4.20%	4288	464241	5.3	DJ34F7.1.1 (Tenascin XB (Isoform 1))
UniRef100_Q5ST74	14	19	4.30%	4222	456149	5.2	Tenascin XB
UniRef100_Q5SQD3	14	19	4.30%	4222	456107	5.2	Tenascin XB
UniRef100_Q5JNX3	14	19	5.50%	3295	358549	5.1	Tenascin XB
UniRef100_Q14118	2	5	4.10%	895	97581	8.6	Dystroglycan precursor (Dystrophin-associated glycoprotein 1) [Contains: Alpha-dystroglycan (Alpha-DG); Beta-dystroglycan (Beta- DG)]
UniRef100_UPI000013EDAE	2	5	4.10%	895	97441	8.6	Dystroglycan precursor (Dystrophin-associated glycoprotein 1) [Contains: Alpha-dystroglycan (Alpha-DG); Beta-dystroglycan (Beta- DG)].
UniRef100_Q969J9	2	5	4.10%	895	97541	8.6	Dystroglycan 1
UniRef100_Q9BTY2	2	2	4.10%	467	54061	6.2	Plasma alpha-L-fucosidase precursor
UniRef100_UPI0000073C10	2	2	4.10%	467	54067	6.2	fucosidase, alpha-L- 2, plasma
UniRef100_P98160	12	23	3.80%	4391	468830	6.5	Basement membrane-specific heparan sulfate proteoglycan core protein precursor
UniRef100_UPI0000D626C6	12	23	3.80%	4346	464081	6.5	Basement membrane-specific heparan sulfate proteoglycan core protein precursor (HSPG) (Perlecan) (PLC).
UniRef100_Q5VU27	12	23	3.80%	4391	468835	6.5	Heparan sulfate proteoglycan 2
UniRef100_Q15465	2	2	3.70%	462	49607	8	Sonic hedgehog protein precursor (SHH) (HHG-1) [Contains: Sonic hedgehog protein N-product; Sonic hedgehog protein C-product]
UniRef100_P22897	3	4	3.60%	1456	166011	6.5	Macrophage mannose receptor 1 precursor
UniRef100_Q5VSK2	3	4	3.60%	1456	166045	6.5	Mannose receptor C type 1-like protein 1
UniRef100_Q0Z8D6	3	4	3.60%	1456	165977	6.5	Mannose receptor
UniRef100_P07942	3	4	3.50%	1786	198065	5	Laminin subunit beta-1 precursor
UniRef100_Q8TAS6	3	4	5.70%	1083	118913	4.9	LAMB1 protein
UniRef100_Q14D91	3	4	3.50%	1786	198037	4.9	Laminin, beta 1
UniRef100_P35590	2	2	3.30%	1138	125090	7	Tyrosine-protein kinase receptor Tie-1 precursor
UniRef100_P16070	2	9	3.00%	742	81554	5.3	CD44 antigen precursor
UniRef100_UPI000037848D	2	9	4.50%	493	53411	5.4	CD44 antigen isoform 3 precursor
UniRef100_UPI000037848C	2	9	3.10%	699	76612	5.3	CD44 antigen isoform 2 precursor
UniRef100_UPI000013D3FE	2	9	3.00%	742	81538	5.3	CD44 antigen isoform 1 precursor
UniRef100_Q9H5A7	2	9	3.30%	676	73929	5.3	CD44 molecule
UniRef100_Q9H5A6	2	9	4.70%	470	50728	5.4	CD44 molecule
UniRef100_Q9H5A5	2	9	3.10%	719	78854	5.3	CD44 molecule
UniRef100_Q9H5A4	2	9	6.50%	338	36733	5.4	CD44 molecule
UniRef100_Q9H5A3	2	9	8.10%	271	29391	5.2	CD44 molecule

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P16070-9	2	9	3.30%	675	74212	5.2	Isoform 9 of P16070
UniRef100_P16070-8	2	9	3.30%	674	74404	5.2	Isoform 8 of P16070
UniRef100_P16070-7	2	9	3.10%	713	78461	5.4	Isoform 7 of P16070
UniRef100_P16070-6	2	9	3.10%	699	76692	5.3	Isoform 6 of P16070
UniRef100_P16070-5	2	9	3.00%	734	80806	5.3	Isoform 5 of P16070
UniRef100_P16070-4	2	9	3.10%	699	76628	5.3	Isoform 4 of P16070
UniRef100_P16070-3	2	9	3.10%	711	77999	5.4	Isoform 3 of P16070
UniRef100_P16070-17	2	9	3.20%	691	75945	5.3	Isoform 17 of P16070
UniRef100_P16070-16	2	9	3.30%	668	73138	5.4	Isoform 16 of P16070
UniRef100_P16070-15	2	9	7.50%	294	32075	5.2	Isoform 15 of P16070
UniRef100_P16070-14	2	9	5.60%	396	43157	5.3	Isoform 14 of P16070
UniRef100_P16070-13	2	9	5.20%	425	46249	5.2	Isoform 13 of P16070
UniRef100_P16070-11	2	9	5.10%	429	46565	5.7	Isoform 11 of P16070
UniRef100_P16070-10	2	9	4.50%	493	53399	5.4	Isoform 10 of P16070
UniRef100_P12111	6	11	2.90%	3176	343551	6.8	Collagen alpha-3(VI) chain precursor
UniRef100_UPI000046D378	6	11	3.10%	3010	325293	6.5	alpha 3 type VI collagen isoform 2 precursor
UniRef100_UPI0000456F3C	6	11	3.10%	2971	321353	7.3	alpha 3 type VI collagen isoform 5 precursor
UniRef100_UPI0000456F3A	6	11	3.10%	2977	322000	6.9	alpha 3 type VI collagen isoform 3 precursor
UniRef100_P12111-2	6	11	3.10%	2971	321351	7.5	Isoform 2 of P12111
UniRef100_Q7Z7G0	2	2	2.80%	1075	118642	9.4	Target of Nesh-SH3 precursor
UniRef100_UPI0000D61B42	2	2	4.60%	655	72282	8.6	Target of Nesh-SH3 precursor (Tarsh) (Nesh-binding protein) (NeshBP) (ABI gene family member 3-binding protein).
UniRef100_UPI0000D61B41	2	2	3.80%	784	86861	10	Target of Nesh-SH3 precursor (Tarsh) (Nesh-binding protein) (NeshBP) (ABI gene family member 3-binding protein).
UniRef100_UPI000036718A	2	2	2.80%	1074	118486	9.4	Target of Nesh-SH3 precursor (Tarsh) (Nesh-binding protein) (NeshBP) (ABI gene family member 3-binding protein).
UniRef100_Q7Z7G0-4	2	2	3.80%	784	86789	10	Isoform 4 of Q7Z7G0
UniRef100_Q7Z7G0-3	2	2	4.60%	655	72267	8.6	Isoform 3 of Q7Z7G0
UniRef100_P27487	2	2	2.70%	766	88279	6	Dipeptidyl peptidase 4 (EC 3.4.14.5) (Dipeptidyl peptidase IV) (DPP IV) (T-cell activation antigen CD26) (TP103) (Adenosine deaminase complexing protein 2) (ADABP) [Contains: Dipeptidyl peptidase 4 membrane form (Dipeptidyl peptidase IV membrane form); Dipeptidyl peptidase 4 soluble form (Dipeptidyl peptidase IV soluble form)]
UniRef100_Q4LDE5	5	5	2.40%	3574	390549	5.5	Sushi, von Willebrand factor type A, EGF and pentraxin domain- containing protein 1
UniRef100_UPI0000D618EA	5	5	2.40%	3571	390199	5.5	polydom
UniRef100_UPI0000D618E9	5	5	2.40%	3574	390563	5.5	polydom
UniRef100_UPI00006C0F16	5	5	2.40%	3574	390507	5.5	polydom
UniRef100_Q5VTE4	5	5	2.40%	3548	387517	5.5	Sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1
UniRef100_P20023	2	2	2.40%	1033	112974	7.5	Complement receptor type 2 precursor
UniRef100_UPI00004562F0	2	2	2.50%	1006	110294	7.8	Complement receptor type 2 precursor (Cr2) (Complement C3d receptor) (Epstein-Barr virus receptor) (EBV receptor) (CD21 antigen).
UniRef100_Q5VW87	2	2	2.40%	1033	112916	7.5	Complement component (3d/Epstein Barr virus) receptor 2
UniRef100_Q5VW86	2	2	2.30%	1092	119160	7.5	Complement component (3d/Epstein Barr virus) receptor 2
UniRef100_Q5VW85	2	2	2.60%	971	106381	7.5	Complement component (3d/Epstein Barr virus) receptor 2
UniRef100_Q5BKT9	2	2	2.40%	1033	113001	7.5	Complement component (3d/Epstein Barr virus) receptor 2
UniRef100_Q53EL2	2	2	2.30%	1092	119218	7.5	Complement component (3d/Epstein Barr virus) receptor 2 isoform 1 variant (Complement component (3d/Epstein Barr virus) receptor 2)
UniRef100_P20023-4	2	2	2.30%	1084	118347	7.5	Isoform D of P20023

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P20023-3	2	2	2.30%	1092	119228	7.5	Isoform C of P20023
UniRef100_P20023-2	2	2	2.50%	1007	110466	7.7	Isoform B of P20023
UniRef100_Q76LX8	3	3	2.30%	1427	153604	7.2	ADAMTS-13 precursor
UniRef100_Q76LX8-3	3	3	2.50%	1340	144517	7.1	Isoform 3 of Q76LX8
UniRef100_Q76LX8-2	3	3	2.40%	1371	147804	7.2	Isoform 2 of Q76LX8
UniRef100_Q6UY14	2	3	2.30%	1074	116545	8.3	ADAMTS-like protein 4 precursor
UniRef100_Q6UY14-2	2	3	2.90%	877	95132	8.3	Isoform 2 of Q6UY14
UniRef100_Q92859	2	3	2.20%	1461	160016	6.5	Neogenin precursor
UniRef100_UPI0000366A6D	2	3	2.30%	1408	154303	6.4	Neogenin precursor.
UniRef100_UPI000012FF30	2	3	2.20%	1461	159959	6.5	neogenin homolog 1
UniRef100_Q92859-2	2	3	2.30%	1408	154304	6.4	Isoform 2 of Q92859
UniRef100_P39060	3	5	2.10%	1754	178159	6	Collagen alpha-1(XVIII) chain precursor [Contains: Endostatin]
UniRef100_UPI0000DB273B	3	5	2.40%	1516	153767	5.7	alpha 1 type XVIII collagen isoform 1 precursor
UniRef100_UPI0000D6255D	3	5	2.10%	1755	178377	6.1	Collagen alpha-1(XVIII) chain precursor [Contains: Endostatin].
UniRef100_UPI0000D6255C	3	5	2.50%	1476	150048	5.7	Collagen alpha-1(XVIII) chain precursor [Contains: Endostatin].
UniRef100_UPI0000D6255B	3	5	2.80%	1339	135917	6.5	Collagen alpha-1(XVIII) chain precursor [Contains: Endostatin].
UniRef100_UPI00004F6EDB	3	5	2.80%	1336	135510	6.5	alpha 1 type XVIII collagen isoform 2 precursor
UniRef100_Q8NG19	3	5	14.20%	261	26745	9.3	Multi-functional protein MFP
UniRef100_P39060-2	3	5	2.80%	1339	135761	6.5	Isoform 3 of P39060
UniRef100_P39060-1	3	5	2.40%	1519	154018	5.7	Isoform 2 of P39060
UniRef100_P12821	2	3	2.10%	1306	149714	6.4	Angiotensin-converting enzyme, somatic isoform precursor (EC 3.4.15.1) (Dipeptidyl carboxypeptidase I) (Kininase II) (CD143 antigen) [Contains: Angiotensin-converting enzyme, somatic isoform, soluble form]
UniRef100_P35555	3	6	2.00%	2871	312312	4.9	Fibrillin-1 precursor
UniRef100_UPI000045684D	3	6	2.00%	2871	312236	4.9	Fibrillin-1 precursor.
UniRef100_UPI0000163B0B	3	6	2.00%	2871	312237	4.9	fibrillin 1 precursor
UniRef100_P39059	2	2	1.90%	1388	141720	5	Collagen alpha-1(XV) chain precursor [Contains: Endostatin (Endostatin-XV) (Restin) (Related to endostatin)]
UniRef100_UPI0000D618D9	2	2	1.90%	1388	141703	5	Collagen alpha-1(XV) chain precursor [Contains: Endostatin (Endostatin-XV) (Restin) (Related to endostatin)].
UniRef100_P08519	6	11	1.80%	4548	501323	5.9	Apolipoprotein(a) precursor (EC 3.4.21.-) (Apo(a)) (Lp(a))
UniRef100_Q5VTD7	6	11	4.00%	2040	226544	6.1	Lipoprotein, Lp
UniRef100_Q1HP67	6	11	4.00%	2040	226514	6.1	Lipoprotein, Lp
UniRef100_P21333	4	9	1.70%	2647	280737	6.1	Filamin-A
UniRef100_UPI0000D61DF8	4	9	1.80%	2607	276576	6	Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding protein) (Actin-binding protein 280) (ABP-280) (Nonmuscle filamin).
UniRef100_UPI0000D61DF7	4	9	1.70%	2639	280044	6	Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding protein) (Actin-binding protein 280) (ABP-280) (Nonmuscle filamin).
UniRef100_UPI00004578B4	4	9	1.70%	2647	280765	6	Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding protein) (Actin-binding protein 280) (ABP-280) (Nonmuscle filamin).
UniRef100_Q8NF52	4	9	1.70%	2651	281428	6.2	FLJ00343 protein
UniRef100_Q60FE6	4	9	1.80%	2612	277503	6	Filamin A
UniRef100_Q60FE5	4	9	1.80%	2620	278224	6.1	Filamin A
UniRef100_Q5HY54	4	9	1.80%	2607	276548	6	Filamin A, alpha
UniRef100_Q5HY53	4	9	1.70%	2639	280016	6	Filamin A, alpha
UniRef100_P02452	2	4	1.50%	1464	138912	5.8	Collagen alpha-1(I) chain precursor
UniRef100_UPI000013C88B	2	4	1.50%	1464	138942	5.8	Collagen alpha-1(I) chain precursor.

Supplemental Table 2A: Protein Groups Identified in the Human Serum Proteome Analysis

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P15924	2	2	1.40%	2871	331774	6.8	Desmoplakin
UniRef100_Q4LE79	2	2	1.70%	2319	265192	7.3	DSP variant protein
UniRef100_P15924-2	2	2	1.70%	2271	260045	7	Isoform DPII of P15924
UniRef100_A4D0P9	3	6	1.20%	3460	388389	5.9	Reelin
UniRef100_UPI000020F855	3	6	1.20%	3427	384094	5.7	Reelin precursor (EC 3.4.21.-).
UniRef100_Q5ISM4	3	6	1.30%	3246	363731	5.6	Reelin
UniRef100_P78509-2	3	6	1.20%	3458	388217	5.9	Isoform 2 of P78509
UniRef100_P78509	3	6	1.20%	3460	388403	5.9	Reelin precursor
UniRef100_A4D0Q0	3	6	1.20%	3458	388203	5.9	Reelin
UniRef100_O75369	2	3	1.20%	2602	278193	5.7	Filamin-B
UniRef100_UPI000045712A	2	3	1.50%	2150	230812	5.5	Filamin-B (FLN-B) (Beta-filamin) (Actin-binding-like protein) (Thyroid autoantigen) (Truncated actin-binding protein) (Truncated ABP) (ABP- 280 homolog) (ABP-278) (Filamin 3) (Filamin homolog 1) (Fh1).
UniRef100_UPI0000457129	2	3	1.20%	2578	275692	5.8	Filamin-B (FLN-B) (Beta-filamin) (Actin-binding-like protein) (Thyroid autoantigen) (Truncated actin-binding protein) (Truncated ABP) (ABP- 280 homolog) (ABP-278) (Filamin 3) (Filamin homolog 1) (Fh1).
UniRef100_UPI0000457128	2	3	1.20%	2602	278188	5.7	Filamin-B (FLN-B) (Beta-filamin) (Actin-binding-like protein) (Thyroid autoantigen) (Truncated actin-binding protein) (Truncated ABP) (ABP- 280 homolog) (ABP-278) (Filamin 3) (Filamin homolog 1) (Fh1).
UniRef100_UPI000036716E	2	3	1.20%	2561	273906	5.7	Filamin-B (FLN-B) (Beta-filamin) (Actin-binding-like protein) (Thyroid autoantigen) (Truncated actin-binding protein) (Truncated ABP) (ABP- 280 homolog) (ABP-278) (Filamin 3) (Filamin homolog 1) (Fh1).
UniRef100_UPI00001AEC01	2	3	1.20%	2602	278162	5.7	filamin B, beta (actin binding protein 278)
UniRef100_Q60FE7	2	3	1.20%	2591	276936	5.7	Filamin B
UniRef100_O75369-6	2	3	1.30%	2537	271442	5.7	Isoform 6 of O75369
UniRef100_O75369-3	2	3	1.20%	2561	273938	5.7	Isoform 3 of O75369
UniRef100_O75369-2	2	3	1.20%	2578	275697	5.8	Isoform 2 of O75369
UniRef100_Q96RW7	2	2	0.50%	5635	613396	6.5	Hemicentin-1 precursor
UniRef100_UPI00004578EF	2	2	0.50%	5633	613165	6.5	Hemicentin-1 precursor (Fibulin-6) (FIBL-6).

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

The data was searched with 100 ppm precursor tolerance and partial tryptic boundary, as indicated in "Methods"
The search results were filtered using the "default" filter: 10 ppm, full tryptic boundary, and ΔCn >=0.05
Only proteins with two or more peptides are listed. The global non-redundant peptide FDR for this dataset is 0.01%. Protein FDR is 0.08%
Protein Groups are separated by horizontal lines

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	4	11	100.00%	34	3884	6	Hemoglobin delta-beta fusion protein
UniRef100_P	3	5	100.00%	24	2771	4	Heat shock protein HSP 90-beta
UniRef100_Q	22	110	94.70%	76	8391	7	Hemoglobin alpha 2
UniRef100_P	20	286	88.40%	147	15998	7	Hemoglobin subunit beta
UniRef100_Q	2	6	88.00%	25	2927	8	Hemoglobin beta chain, HB beta
UniRef100_P	18	144	85.70%	147	16055	8	Hemoglobin subunit delta
UniRef100_Q	14	137	85.70%	105	11459	7	Hemoglobin Lepore-Baltimore
UniRef100_Q	15	202	85.70%	105	11446	7	Hemoglobin beta
UniRef100_P	49	266	84.00%	400	44092	5	Keratin, type I cytoskeletal 19
UniRef100_P	27	193	83.90%	199	22391	8	Transgelin-2
UniRef100_U	27	193	75.90%	220	24454	8	Transgelin-2 (SM22-alpha homolog).
UniRef100_P	27	360	83.80%	142	15258	9	Hemoglobin subunit alpha
UniRef100_Q	27	360	83.80%	142	15281	9	Alpha 2 globin variant
UniRef100_Q	18	271	83.00%	147	16051	8	Mutant beta-globin
UniRef100_Q	24	90	81.90%	199	22110	8	Peroxiredoxin-1
UniRef100_P	7	16	81.70%	115	11665	5	60S acidic ribosomal protein P2
UniRef100_O	6	12	81.30%	91	9614	5	Hepatitis B virus X-interacting protein
UniRef100_U	6	12	42.80%	173	18158	6	hepatitis B virus x-interacting protein
UniRef100_Q	16	206	81.20%	128	13964	7	Hemoglobin beta subunit variant
UniRef100_Q	14	224	81.00%	105	11501	7	Mutant hemoglobin beta chain
UniRef100_P	23	70	80.90%	152	17149	6	Nucleoside diphosphate kinase A
UniRef100_P	15	329	80.70%	135	14716	6	Galectin-1
UniRef100_P	11	48	80.60%	93	10834	7	Protein S100-A8
UniRef100_P	13	54	80.30%	127	14478	5	Nuclear transport factor 2
UniRef100_P	10	19	80.20%	121	13569	5	Replication protein A 14 kDa subunit
UniRef100_Q	13	131	80.20%	101	10928	7	HBB protein
UniRef100_P	29	87	79.90%	364	39420	8	Fructose-bisphosphate aldolase A
UniRef100_P	11	26	79.80%	163	18658	5	S-phase kinase-associated protein 1A
UniRef100_P	27	95	79.50%	249	26669	7	Triosephosphate isomerase
UniRef100_Q	28	48	79.20%	390	43062	5	Interleukin enhancer-binding factor 2
UniRef100_U	28	48	79.40%	389	42931	5	Interleukin enhancer-binding factor 2 (Nuclear factor of activated T- cells 45 kDa).
UniRef100_O	10	19	78.90%	114	12774	5	SH3 domain-binding glutamic acid-rich-like protein
UniRef100_Q	12	251	78.90%	71	7799	7	Beta-actin
UniRef100_P	110	1221	78.30%	609	69367	6	Serum albumin precursor
UniRef100_Q	18	302	78.20%	142	15272	9	Hemoglobin alpha 1-2 hybrid
UniRef100_P	49	333	77.20%	430	48058	6	Keratin, type I cytoskeletal 18

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	29	44	77.10%	472	52391	6	Selenium binding protein 1
UniRef100_U	29	44	76.20%	478	53062	7	Selenium-binding protein 1.
UniRef100_P	49	945	77.10%	375	41737	6	Actin, cytoplasmic 1
UniRef100_Q	49	945	78.50%	368	41005	6	Actin, beta
UniRef100_Q	49	945	77.10%	375	41765	6	Beta actin variant
UniRef100_P	49	945	77.10%	375	41793	6	Actin, cytoplasmic 2
UniRef100_P	19	80	77.10%	205	22783	6	Heat-shock protein beta-1
UniRef100_U	24	125	76.80%	164	18707	5	Keratin, type I cytoskeletal 19 (Cytokeratin-19) (CK-19) (Keratin-19) (K19).
UniRef100_Q	14	42	76.80%	151	16961	5	Myosin, light chain 6, alkali, smooth muscle and non-muscle
UniRef100_Q	22	55	76.60%	201	22611	9	Transgelin
UniRef100_Q	9	57	76.40%	123	13941	6	Thioredoxin-like protein 5
UniRef100_P	5	19	76.20%	80	9128	#	U6 snRNA-associated Sm-like protein LSm6
UniRef100_P	55	780	75.90%	453	51512	6	Fibrinogen gamma chain precursor
UniRef100_Q	55	780	78.70%	437	49497	6	Fibrinogen, gamma polypeptide
UniRef100_U	6	232	75.00%	76	8621	7	Ubiquitin
UniRef100_P	13	30	74.90%	187	21057	8	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (Prostatic-binding protein) (HCNPpp) (Neuropolypeptide h3) (Raf kinase inhibitor protein) (RKIP) [Contains: Hippocampal cholinergic neurostimulating peptide (HCNP)]
UniRef100_P	28	78	74.80%	254	28804	7	Phosphoglycerate mutase 1
UniRef100_U	28	78	74.80%	254	28850	7	PREDICTED: similar to Phosphoglycerate mutase 1 (Phosphoglycerate mutase isozyme B) (PGAM-B) (BPG-dependent PGAM 1) isoform 1
UniRef100_Q	28	78	74.80%	254	28832	7	Phosphoglycerate mutase 1 (Brain) variant
UniRef100_Q	9	24	74.70%	95	10835	7	U6 snRNA-associated Sm-like protein LSm2
UniRef100_P	17	50	74.60%	114	13242	6	Protein S100-A9
UniRef100_P	25	99	74.30%	245	27745	5	14-3-3 protein zeta/delta
UniRef100_Q	34	40	74.10%	475	52878	6	Cytosolic nonspecific dipeptidase
UniRef100_U	34	40	74.10%	475	52897	6	Cytosolic nonspecific dipeptidase (Glutamate carboxypeptidase-like protein 1) (CNDP dipeptidase 2).
UniRef100_P	57	322	74.00%	531	57937	8	Pyruvate kinase isozymes M1/M2
UniRef100_P	23	61	73.70%	247	28303	5	14-3-3 protein gamma
UniRef100_P	23	62	73.60%	246	28082	5	14-3-3 protein beta/alpha
UniRef100_P	23	62	74.20%	244	27850	5	Isoform Short of P31946
UniRef100_P	18	48	73.50%	215	23897	6	Ras-related protein Rab-14
UniRef100_P	16	70	72.50%	207	23490	7	Ras-related protein Rab-7a
UniRef100_Q	16	31	72.40%	185	21228	8	Calcyclin binding protein
UniRef100_Q	16	31	58.80%	228	26210	8	Calcyclin-binding protein
UniRef100_P	10	134	72.40%	105	11740	7	Protein S100-A11
UniRef100_P	46	435	72.30%	444	49671	5	Tubulin beta chain
UniRef100_P	44	400	72.10%	445	49831	5	Tubulin beta-2C chain
UniRef100_Q	44	400	72.10%	445	49840	5	Tubulin, beta 2C
UniRef100_Q	21	55	72.00%	189	19891	7	Protein DJ-1

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	13	30	71.90%	153	16470	6	BTF3L4 protein
UniRef100_U	13	30	72.40%	152	16409	6	Transcription factor BTF3 homolog 4 (Basic transcription factor 3-like 4).
UniRef100_Q	13	30	69.60%	158	17271	6	Transcription factor BTF3 homolog 4
UniRef100_P	15	64	71.90%	135	15850	5	Retinol-binding protein I, cellular
UniRef100_O	6	15	71.90%	96	10403	5	U6 snRNA-associated Sm-like protein LSm8
UniRef100_P	15	38	71.80%	216	23483	8	Ras-related protein Rab-5C
UniRef100_Q	21	109	71.50%	375	41075	5	Hypothetical protein DKFZp434G0719
UniRef100_Q	16	26	71.50%	253	28772	6	Chloride intracellular channel protein 4
UniRef100_Q	13	87	70.50%	105	11418	8	Peptidylprolyl isomerase A
UniRef100_P	23	79	70.40%	152	17298	8	Nucleoside diphosphate kinase B
UniRef100_P	19	43	70.30%	317	35077	8	Guanine nucleotide-binding protein subunit beta 2-like 1
UniRef100_Q	19	43	64.30%	347	37889	8	Lung cancer oncogene 7
UniRef100_Q	28	58	70.20%	289	32660	6	Inorganic pyrophosphatase
UniRef100_P	12	26	69.90%	146	17164	6	Protein mago nashi homolog
UniRef100_Q	12	26	68.90%	148	17276	6	Protein mago nashi homolog 2
UniRef100_P	27	119	69.80%	255	29174	5	14-3-3 protein epsilon
UniRef100_P	16	32	69.70%	218	24579	7	Hypoxanthine-guanine phosphoribosyltransferase
UniRef100_Q	16	32	69.70%	218	24588	7	HPRT1 protein
UniRef100_P	53	819	69.40%	432	49880	6	Glial fibrillary acidic protein, astrocyte
UniRef100_P	141	466	69.20%	1663	2E+05	6	Complement C3 precursor [Contains: Complement C3 beta chain; Complement C3 alpha chain; C3a anaphylatoxin; Complement C3b alpha' chain; Complement C3c alpha' chain fragment 1; Complement C3dg fragment; Complement C3g fragment; Complement C3d fragment; Complement C3f fragment; Complement C3c alpha' chain fragment 2]
UniRef100_P	23	159	68.70%	166	18502	8	Cofilin-1
UniRef100_Q	23	74	68.60%	239	27349	6	Cell migration-inducing protein 22
UniRef100_Q	23	74	68.60%	239	27362	6	Proteasome activator complex subunit 2
UniRef100_Q	23	74	68.60%	239	27402	6	Full-length cDNA clone CS0DJ015YJ12 of T cells (Jurkat cell line) of Homo sapiens
UniRef100_O	18	41	68.50%	241	26923	5	Chloride intracellular channel protein 1
UniRef100_Q	18	41	68.50%	241	27015	5	Chloride intracellular channel 1 variant
UniRef100_P	8	17	68.40%	158	17977	7	Isoform 2 of P24666
UniRef100_P	10	24	68.30%	126	13802	7	Histidine triad nucleotide-binding protein 1
UniRef100_P	26	35	68.20%	289	32118	7	Purine nucleoside phosphorylase
UniRef100_Q	21	24	68.00%	272	30629	6	Capping protein (Actin filament) muscle Z-line, beta
UniRef100_Q	21	24	61.50%	301	33781	6	Capping protein (Actin filament) muscle Z-line, beta
UniRef100_P	15	52	67.90%	212	23546	7	Ras-related protein Rab-2A
UniRef100_P	23	45	67.70%	325	36573	7	Alcohol dehydrogenase [NADP+]
UniRef100_P	16	31	67.50%	194	21635	9	Adenylate kinase isoenzyme 1
UniRef100_Q	16	31	62.40%	210	23411	9	Adenylate kinase 1
UniRef100_Q	16	31	67.50%	194	21619	9	Adenylate kinase 1 variant
UniRef100_P	54	267	67.40%	531	58062	8	Isoform M1 of P14618
UniRef100_P	12	28	67.40%	89	10366	7	Dynein light chain 1, cytoplasmic

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	17	35	67.40%	89	10350	7	Dynein light chain 2, cytoplasmic
UniRef100_Q	22	30	67.30%	324	36748	6	Protein FAM49B
UniRef100_Q	204	683	67.10%	2452	3E+05	5	Isoform 3 of Q13813
UniRef100_P	17	44	67.10%	286	32949	6	F-actin capping protein subunit alpha-2
UniRef100_Q	17	44	67.10%	286	32967	6	Capping protein (Actin filament) muscle Z-line, alpha 2 variant
UniRef100_P	10	21	67.10%	152	17138	7	Ubiquitin-conjugating enzyme E2 N
UniRef100_O	100	287	67.00%	911	1E+05	5	Alpha-actinin-4
UniRef100_Q	206	693	66.80%	2472	3E+05	5	Spectrin alpha chain, brain
UniRef100_Q	205	689	66.70%	2477	3E+05	5	Isoform 2 of Q13813
UniRef100_P	20	52	66.70%	327	37187	6	Serine/threonine-protein phosphatase PP1-beta catalytic subunit
UniRef100_P	22	95	66.50%	224	25035	6	Peroxiredoxin-6
UniRef100_P	72	161	66.40%	806	89322	5	Transitional endoplasmic reticulum ATPase (TER ATPase) (15S Mg(2+)- ATPase p97 subunit)
UniRef100_P	25	33	66.40%	360	41390	7	Mitogen-activated protein kinase 1
UniRef100_U	25	33	62.90%	380	43553	7	Mitogen-activated protein kinase 1
UniRef100_P	40	150	66.20%	417	44615	8	Phosphoglycerate kinase 1
UniRef100_P	20	245	66.20%	210	23356	6	Glutathione S-transferase P
UniRef100_P	96	265	66.10%	892	1E+05	5	Alpha-actinin-1
UniRef100_P	48	679	66.10%	466	53652	5	Vimentin
UniRef100_Q	5	12	65.90%	44	4894	5	Glyceraldehyde 3-phosphate dehydrogenase
UniRef100_P	37	56	65.80%	445	50663	7	Rab GDP dissociation inhibitor beta
UniRef100_P	8	21	65.80%	158	18042	7	Low molecular weight phosphotyrosine protein phosphatase
UniRef100_Q	8	21	63.00%	165	18698	8	Acid phosphatase 1 isoform c variant
UniRef100_P	4	18	65.80%	76	8496	9	Small nuclear ribonucleoprotein G
UniRef100_Q	4	18	78.10%	64	7101	7	SNRPG protein
UniRef100_P	10	49	65.70%	105	11737	5	Thioredoxin
UniRef100_P	5	16	65.70%	67	7645	8	DNA-directed RNA polymerase II 7.6 kDa polypeptide
UniRef100_Q	204	533	65.20%	2364	3E+05	6	Spectrin beta chain, brain 1
UniRef100_Q	155	458	65.20%	1675	2E+05	6	Clathrin heavy chain 1
UniRef100_Q	155	458	66.60%	1639	2E+05	6	Isoform 2 of Q00610
UniRef100_Q	9	15	65.20%	184	20749	8	Glucosamine 6-phosphate N-acetyltransferase
UniRef100_Q	16	31	65.20%	135	15164	7	Fatty acid-binding protein, epidermal
UniRef100_P	11	49	65.20%	92	10804	9	Small nuclear ribonucleoprotein E
UniRef100_Q	14	37	65.10%	218	24488	6	Ras-related protein Rab-11B
UniRef100_P	19	72	64.80%	193	20567	9	Cysteine and glycine-rich protein 1
UniRef100_P	29	311	64.60%	353	37430	9	Heterogeneous nuclear ribonucleoproteins A2/B1
UniRef100_U	29	311	64.80%	352	37298	9	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2 / hnRNP B1).
UniRef100_P	20	52	64.60%	240	26788	5	Hepatoma-derived growth factor
UniRef100_O	11	31	64.60%	127	13331	5	Gamma-synuclein
UniRef100_Q	30	352	64.40%	449	49823	5	Tubulin alpha 6 variant
UniRef100_U	30	352	64.50%	448	49764	5	Tubulin alpha-6 chain (Alpha-tubulin 6).
UniRef100_Q	30	352	64.40%	449	49895	5	Tubulin alpha-6 chain

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P	15	86	64.40%	205	22678	6	Ras-related protein Rab-1A
UniRef100_P	34	409	64.10%	451	50152	5	Tubulin alpha-ubiquitous chain
UniRef100_Q	34	349	64.10%	451	50136	5	Tubulin alpha-3 chain
UniRef100_P	203	1153	64.00%	2647	3E+05	6	Filamin-A
UniRef100_Q	203	1153	64.20%	2639	3E+05	6	Filamin A, alpha
UniRef100_P	75	889	64.00%	491	55928	8	Fibrinogen beta chain precursor [Contains: Fibrinopeptide B]
UniRef100_Q	75	889	64.00%	491	55916	8	Fibrinogen beta chain
UniRef100_O	15	25	63.90%	227	26227	9	Cleavage and polyadenylation specificity factor 5
UniRef100_P	10	37	63.90%	147	15887	6	Transthyretin precursor
UniRef100_Q	358	1361	63.70%	4525	5E+05	6	Plectin 3
UniRef100_U	358	1361	63.70%	4525	5E+05	6	Plectin-1 (PLTN) (PCN) (Hemidesmosomal protein 1) (HD1).
UniRef100_Q	47	288	63.50%	572	65135	7	Lamin A/C
UniRef100_Q	33	50	63.40%	459	51805	5	FK506-binding protein 4
UniRef100_Q	8	18	63.40%	142	15945	6	Coactosin-like protein
UniRef100_Q	356	1358	63.30%	4547	5E+05	6	Isoform 4 of Q15149
UniRef100_U	356	1358	63.30%	4547	5E+05	6	Plectin-1 (PLTN) (PCN) (Hemidesmosomal protein 1) (HD1).
UniRef100_U	356	1358	63.30%	4547	5E+05	6	plectin 1 isoform 11
UniRef100_Q	356	1352	63.20%	4570	5E+05	6	Isoform 3 of Q15149
UniRef100_Q	356	1358	63.10%	4574	5E+05	6	Isoform 2 of Q15149
UniRef100_U	356	1358	63.10%	4574	5E+05	6	Plectin-1 (PLTN) (PCN) (Hemidesmosomal protein 1) (HD1).
UniRef100_Q	356	1358	63.10%	4574	5E+05	6	Plectin 1
UniRef100_P	36	406	63.10%	434	47169	7	Alpha-enolase
UniRef100_Q	36	406	63.10%	434	47141	7	Enolase 1 variant
UniRef100_Q	36	406	63.10%	434	47197	7	Enolase 1 variant
UniRef100_Q	23	60	63.10%	249	28723	6	Proteasome activator complex subunit 1
UniRef100_P	13	33	63.10%	225	24764	5	Elongation factor 1-beta
UniRef100_Q	8	21	63.10%	103	11801	7	Protein S100-A16
UniRef100_P	50	243	63.00%	646	70898	6	Heat shock cognate 71 kDa protein
UniRef100_U	8	19	63.00%	127	13735	6	Transthyretin
UniRef100_U	8	19	63.00%	127	13719	6	Transthyretin
UniRef100_P	29	46	62.80%	592	64616	7	Bifunctional purine biosynthesis protein PURH [Includes: Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) (5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase) (AICAR transformylase); IMP cyclohydrolase (EC 3.5.4.10) (Inosinicase) (IMP synthetase) (ATIC)]
UniRef100_P	11	24	62.80%	145	17040	#	40S ribosomal protein S15
UniRef100_Q	11	24	67.40%	135	15812	#	RIG homolog
UniRef100_Q	11	62	62.70%	201	22171	6	Ras-related protein Rab-1B
UniRef100_P	17	53	62.60%	198	21892	6	Peroxiredoxin-2
UniRef100_P	7	12	62.60%	147	16829	5	Bis(5'-nucleosyl)-tetraphosphatase [asymmetrical]
UniRef100_P	93	205	62.40%	1134	1E+05	6	Vinculin
UniRef100_P	93	205	66.40%	1066	1E+05	6	Isoform 1 of P18206

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P	25	62	62.40%	535	57488	6	T-complex protein 1 subunit beta
UniRef100_U	44	151	62.30%	639	65433	8	keratin 2
UniRef100_P	27	101	62.30%	334	36639	6	L-lactate dehydrogenase B chain
UniRef100_P	56	177	62.20%	732	82705	6	ATP-dependent DNA helicase 2 subunit 2
UniRef100_Q	39	334	62.20%	445	49953	5	Tubulin beta-2B chain
UniRef100_Q	39	335	62.20%	445	49907	5	Tubulin beta-2A chain
UniRef100_P	9	20	62.20%	201	22988	5	Rho GDP-dissociation inhibitor 2
UniRef100_P	30	73	62.10%	406	46154	6	Eukaryotic initiation factor 4A-I
UniRef100_Q	357	1359	61.90%	4684	5E+05	6	Plectin-1
UniRef100_U	357	1359	61.90%	4684	5E+05	6	Plectin-1 (PLTN) (PCN) (Hemidesmosomal protein 1) (HD1).
UniRef100_Q	357	1359	61.90%	4684	5E+05	6	Plectin 6
UniRef100_P	7	20	61.90%	118	12895	6	Myotrophin
UniRef100_P	11	14	61.70%	282	31463	7	S-formylglutathione hydrolase
UniRef100_P	17	48	61.50%	286	32923	6	F-actin capping protein subunit alpha-1
UniRef100_P	46	141	61.40%	788	85238	4	Nuclear autoantigenic sperm protein
UniRef100_Q	16	24	61.40%	298	33233	6	Isoform 2 of Q9HC38
UniRef100_Q	16	24	36.30%	504	55012	9	Uncharacterized protein C17orf25
UniRef100_P	37	320	61.30%	444	49586	5	Tubulin beta-4 chain
UniRef100_Q	32	180	61.30%	432	48106	5	Keratin, type I cytoskeletal 17
UniRef100_Q	32	180	62.20%	426	47603	5	CDNA FLJ38023 fis, clone CTONG2012901, highly similar to KERATIN, TYPE I CYTOSKELETAL 17
UniRef100_P	19	88	61.00%	154	16832	5	Eukaryotic translation initiation factor 5A-1
UniRef100_P	19	88	51.10%	184	20170	7	Isoform 2 of P63241
UniRef100_P	6	27	61.00%	100	11175	7	Apolipoprotein A-II precursor (Apo-AII) (ApoA-II) [Contains: Apolipoprotein A-II(1-76)]
UniRef100_Q	12	44	60.90%	174	19889	6	RNA-binding protein 8A
UniRef100_P	54	171	60.70%	858	95338	7	Elongation factor 2
UniRef100_Q	7	15	60.70%	140	15088	6	Profilin 2
UniRef100_P	106	360	60.50%	1657	2E+05	7	Ras GTPase-activating-like protein IQGAP1
UniRef100_P	22	83	60.50%	281	31122	5	Elongation factor 1-delta
UniRef100_Q	22	83	26.30%	647	71422	6	EEF1D protein
UniRef100_P	7	65	60.50%	147	16140	7	Hemoglobin subunit gamma-1
UniRef100_P	64	344	60.40%	724	83264	5	Heat shock protein HSP 90-beta
UniRef100_U	64	344	59.40%	736	84758	5	Heat shock protein HSP 90-beta (HSP 84) (HSP 90).
UniRef100_Q	28	116	60.30%	375	41273	7	Full-length cDNA clone CS0DD006YL02 of Neuroblastoma of Homo sapiens
UniRef100_P	7	20	60.20%	113	12732	8	Eukaryotic translation initiation factor 1
UniRef100_Q	176	504	60.00%	2541	3E+05	6	Talin-1
UniRef100_P	15	23	60.00%	260	29246	7	Carbonic anhydrase 2
UniRef100_P	16	49	60.00%	185	21418	5	Chromobox protein homolog 1
UniRef100_P	12	33	60.00%	165	18506	8	Destrin
UniRef100_P	13	260	60.00%	140	15054	8	Profilin-1
UniRef100_Q	9	17	60.00%	125	13507	5	Mitogen-activated protein-binding protein-interacting protein

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P	4	11	60.00%	85	9118	9	Ubiquitin-fold modifier 1 precursor
UniRef100_P	18	31	59.60%	277	30375	8	Carbonyl reductase [NADPH] 1 (EC 1.1.1.184) (NADPH-dependent carbonyl reductase 1) (Prostaglandin-E(2) 9-reductase)
UniRef100_P	65	259	59.50%	1058	1E+05	6	Ubiquitin-activating enzyme E1
UniRef100_U	33	99	59.50%	684	73911	6	Dihydropyrimidinase-related protein 3 (DRP-3) (Unc-33-like phosphoprotein) (ULIP protein) (Collapsin response mediator protein 4) (CRMP-4).
UniRef100_P	16	37	59.50%	168	19667	8	Actin-related protein 2/3 complex subunit 4
UniRef100_U	16	37	59.90%	167	19488	8	Tubulin--tyrosine ligase-like protein 3 (HOTTL).
UniRef100_P	27	301	59.40%	293	32338	5	Isoform C1 of P07910
UniRef100_P	12	78	59.40%	180	20530	7	ADP-ribosylation factor 5
UniRef100_P	15	89	59.40%	180	20511	7	ADP-ribosylation factor 4
UniRef100_P	48	293	59.30%	664	74140	7	Lamin-A/C
UniRef100_Q	48	293	59.30%	664	74082	7	Lamin A/C transcript variant 1
UniRef100_P	16	36	59.30%	108	11951	8	FK506-binding protein 1A
UniRef100_Q	16	36	62.10%	103	11424	9	Peptidyl-prolyl cis-trans isomerase
UniRef100_Q	21	44	59.20%	407	46402	6	Eukaryotic initiation factor 4A-II
UniRef100_Q	21	44	59.10%	408	46489	6	Isoform 2 of Q14240
UniRef100_P	19	37	59.20%	223	24824	6	Ubiquitin carboxyl-terminal hydrolase isozyme L1
UniRef100_P	34	397	59.10%	335	36053	9	Glyceraldehyde-3-phosphate dehydrogenase
UniRef100_P	14	26	59.00%	261	29484	8	Proteasome subunit alpha type 4
UniRef100_P	16	24	58.90%	263	29556	7	Proteasome subunit alpha type 1
UniRef100_Q	16	24	58.90%	263	29598	7	Proteasome (Prosome, macropain) subunit, alpha type, 1
UniRef100_P	16	24	57.60%	269	30239	7	Isoform Long of P25786
UniRef100_O	12	26	58.90%	258	27547	6	6-phosphogluconolactonase
UniRef100_U	42	135	58.70%	623	62064	5	keratin 9
UniRef100_P	18	21	58.60%	261	28769	5	Proliferating cell nuclear antigen
UniRef100_Q	18	21	58.60%	261	28706	5	Proliferating cell nuclear antigen
UniRef100_P	60	164	58.50%	698	77050	7	Serotransferrin precursor
UniRef100_Q	60	164	58.50%	698	77080	7	Transferrin variant
UniRef100_U	28	87	58.50%	475	51673	8	adenylyl cyclase-associated protein
UniRef100_Q	16	52	58.50%	246	28219	5	14-3-3 protein eta
UniRef100_U	43	415	58.40%	644	66039	8	keratin 1
UniRef100_P	26	40	58.40%	447	50583	5	Rab GDP dissociation inhibitor alpha
UniRef100_P	9	27	58.30%	115	12784	#	60S ribosomal protein L30
UniRef100_P	10	131	58.30%	115	12476	8	Macrophage migration inhibitory factor
UniRef100_Q	7	11	58.20%	91	9937	5	U6 snRNA-associated Sm-like protein LSm5
UniRef100_P	22	41	58.10%	339	38604	8	Annexin A2
UniRef100_U	22	41	55.20%	357	40411	8	annexin A2 isoform 1
UniRef100_Q	22	41	58.10%	339	38576	8	Annexin A2
UniRef100_Q	12	79	58.10%	234	24793	6	IGL@ protein
UniRef100_Q	9	17	58.00%	112	12473	5	Transcription elongation factor B polypeptide 1

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	159	468	57.80%	2591	3E+05	6	Filamin B
UniRef100_U	159	468	57.50%	2602	3E+05	6	filamin B, beta (actin binding protein 278)
UniRef100_P	19	39	57.80%	315	36112	5	Eukaryotic translation initiation factor 2 subunit 1
UniRef100_P	10	25	57.80%	154	17862	9	Ubiquitin-conjugating enzyme E2 L3
UniRef100_Q	6	7	57.80%	64	7706	#	H/ACA ribonucleoprotein complex subunit 3
UniRef100_P	20	82	57.70%	267	30778	6	Apolipoprotein A-I precursor (Apo-AI) (ApoA-I) [Contains: Apolipoprotein A-I(1-242)]
UniRef100_Q	12	21	57.60%	184	20778	5	Lactoylglutathione lyase
UniRef100_O	10	15	57.60%	151	16320	6	Actin-related protein 2/3 complex subunit 5
UniRef100_Q	10	17	57.50%	181	20555	9	Malignant T cell amplified sequence 1
UniRef100_Q	68	102	57.40%	1224	1E+05	8	Coatomer protein complex, subunit alpha
UniRef100_Q	68	102	57.00%	1233	1E+05	8	COPA protein
UniRef100_P	87	269	57.30%	1474	2E+05	6	Alpha-2-macroglobulin precursor
UniRef100_U	87	269	57.30%	1474	2E+05	6	alpha-2-macroglobulin precursor
UniRef100_Q	6	16	57.30%	103	11575	6	Actin-like protein
UniRef100_P	24	38	57.20%	320	35937	5	Annexin A5
UniRef100_P	15	76	57.20%	243	26688	#	40S ribosomal protein S3
UniRef100_P	44	167	57.10%	609	69843	7	ATP-dependent DNA helicase 2 subunit 1
UniRef100_P	20	46	57.10%	196	22222	6	UMP-CMP kinase
UniRef100_P	7	13	57.10%	77	8533	9	Cysteine-rich protein 1
UniRef100_Q	3	12	56.90%	72	8006	9	Guanine nucleotide-binding protein G(I)/G(S)/G(O) gamma-12 subunit precursor
UniRef100_O	16	21	56.80%	308	33392	6	3'(2'),5'-bisphosphate nucleotidase 1
UniRef100_O	27	56	56.40%	606	66194	7	WD repeat protein 1
UniRef100_Q	27	56	54.80%	624	68171	7	WD repeat-containing protein 1 isoform 1 variant
UniRef100_P	13	18	56.30%	309	35594	6	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform
UniRef100_O	11	12	56.10%	285	29644	6	NG,NG-dimethylarginine dimethylaminohydrolase 2
UniRef100_P	19	36	56.10%	246	27399	7	Proteasome subunit alpha type 6
UniRef100_U	12	297	56.10%	214	23481	5	HUMANIZED ANTIBODY HFE7A, LIGHT CHAIN
UniRef100_P	7	10	56.10%	148	16537	9	Lysozyme C precursor
UniRef100_Q	34	103	56.00%	698	75509	8	Isoform 4 of Q12906
UniRef100_Q	34	103	55.40%	706	76502	8	Isoform 6 of Q12906
UniRef100_P	31	98	56.00%	464	52602	7	Antithrombin-III precursor
UniRef100_O	21	41	56.00%	414	46659	7	Isocitrate dehydrogenase [NADP] cytoplasmic (EC 1.1.1.42) (Cytosolic NADP-isocitrate dehydrogenase) (Oxalosuccinate decarboxylase) (IDH) (NADP(+)-specific ICDH)
UniRef100_P	31	158	56.00%	332	36689	8	L-lactate dehydrogenase A chain
UniRef100_P	14	47	56.00%	248	27774	5	14-3-3 protein sigma
UniRef100_U	34	419	55.90%	469	51386	6	keratin 7
UniRef100_P	14	34	55.90%	324	35924	#	Nuclease sensitive element-binding protein 1
UniRef100_P	11	34	55.90%	118	13527	#	Small nuclear ribonucleoprotein Sm D2
UniRef100_Q	25	55	55.80%	572	62294	6	Dihydropyrimidinase-related protein 2
UniRef100_Q	25	55	50.80%	628	68184	6	Dihydropyrimidinase-like 2 variant
UniRef100_U	12	295	55.80%	215	23281	6	IGM-KAPPA COLD AGGLUTININ (LIGHT CHAIN)

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P	13	88	55.80%	138	15693	5	Cellular retinoic acid-binding protein 2
UniRef100_Q	6	21	55.80%	86	10135	6	Splicing factor 3B subunit 5
UniRef100_P	17	36	55.70%	461	49974	5	Ribonuclease inhibitor
UniRef100_P	45	78	55.60%	968	1E+05	6	Alanyl-tRNA synthetase, cytoplasmic
UniRef100_U	45	78	55.60%	968	1E+05	6	Alanyl-tRNA synthetase, cytoplasmic (EC 6.1.1.7) (Alanine--tRNA ligase) (AlaRS) (Renal carcinoma antigen NY-REN-42).
UniRef100_P	36	123	55.50%	641	70038	6	Heat shock 70 kDa protein 1
UniRef100_U	36	123	55.50%	641	70025	6	heat shock 70kDa protein 1B
UniRef100_Q	36	123	55.50%	641	70052	6	Heat shock 70kDa protein 1A
UniRef100_P	10	41	55.50%	146	16445	#	40S ribosomal protein S16
UniRef100_U	13	88	55.50%	137	15601	5	Cellular retinoic acid-binding protein 2
UniRef100_P	13	33	55.40%	193	21768	6	Transforming protein RhoA precursor
UniRef100_P	10	31	55.40%	184	20825	6	Ras-related protein Rap-1b precursor
UniRef100_P	18	40	55.20%	268	28316	5	Calpain small subunit 1
UniRef100_P	14	43	55.20%	183	21226	6	Ferritin heavy chain
UniRef100_U	14	43	41.40%	244	27725	7	Ferritin heavy chain (EC 1.16.3.1) (Ferritin H subunit) (Proliferation-inducing gene 15 protein).
UniRef100_P	18	24	55.10%	374	39724	8	Alcohol dehydrogenase class 3 (EC 1.1.1.1) (Alcohol dehydrogenase class III) (Alcohol dehydrogenase class chi chain) (S- (hydroxymethyl)glutathione dehydrogenase)
UniRef100_U	18	24	55.20%	373	39617	8	Alcohol dehydrogenase class 3 chi chain (EC 1.1.1.1) (Alcohol dehydrogenase class III chi chain) (S-(hydroxymethyl)glutathione dehydrogenase) (EC 1.1.1.284) (Glutathione-dependent formaldehyde dehydrogenase) (FDH).
UniRef100_P	13	71	55.10%	214	22026	9	Peroxiredoxin-5, mitochondrial precursor
UniRef100_U	13	71	55.10%	214	22086	9	Peroxiredoxin-5, mitochondrial precursor (EC 1.11.1.15) (Prx-V) (Peroxisomal antioxidant enzyme) (PLP) (Thioredoxin reductase) (Thioredoxin peroxidase PMP20) (Antioxidant enzyme B166) (AOEB166) (TPx type VI) (Liver tissue 2D-page spot 71B) (Alu corepresso
UniRef100_Q	9	271	55.10%	156	17905	#	Ribosomal protein S27a
UniRef100_P	8	20	55.10%	98	11140	8	Cystatin-B
UniRef100_O	21	27	55.00%	300	34333	7	Actin-related protein 2/3 complex subunit 2
UniRef100_Q	84	236	54.90%	1270	1E+05	7	ATP-dependent RNA helicase A
UniRef100_U	84	236	53.00%	1315	1E+05	7	ATP-dependent RNA helicase A (EC 3.6.1.-) (Nuclear DNA helicase II) (NDH II) (DEAH box protein 9).
UniRef100_P	28	104	54.90%	437	50119	7	Elongation factor 1-gamma
UniRef100_U	28	104	55.00%	436	50016	7	Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma).
UniRef100_U	28	104	55.20%	435	49917	7	Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma).
UniRef100_P	49	73	54.80%	953	1E+05	6	Coatomer subunit beta
UniRef100_P	26	34	54.80%	491	55521	7	Nicotinamide phosphoribosyltransferase
UniRef100_P	10	21	54.80%	135	15550	#	40S ribosomal protein S17
UniRef100_O	19	62	54.70%	137	15529	9	Putative nucleoside diphosphate kinase
UniRef100_Q	25	78	54.60%	474	51830	8	CAP, adenylate cyclase-associated protein 1
UniRef100_P	9	51	54.60%	119	13282	#	Small nuclear ribonucleoprotein Sm D1
UniRef100_P	50	551	54.50%	483	53704	6	Keratin, type II cytoskeletal 8

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	13	30	54.50%	268	29999	5	Microtubule-associated protein RP/EB family member 1
UniRef100_P	8	34	54.50%	165	17819	9	60S ribosomal protein L12
UniRef100_P	48	77	54.40%	971	1E+05	6	Exportin-2
UniRef100_P	48	77	55.90%	945	1E+05	6	Isoform 3 of P55060
UniRef100_P	33	410	54.40%	469	51418	6	Keratin, type II cytoskeletal 7
UniRef100_Q	10	10	54.40%	228	24679	7	Protein-L-isoaspartate (D-aspartate) O-methyltransferase
UniRef100_Q	10	10	54.60%	227	24636	7	Protein-L-isoaspartate (D-aspartate) O-methyltransferase
UniRef100_O	16	26	54.20%	308	34482	5	Coatomer subunit epsilon
UniRef100_U	13	280	54.20%	212	23248	8	IGG1-KAPPA 3D6 FAB (LIGHT CHAIN)
UniRef100_P	10	31	54.20%	192	21863	#	60S ribosomal protein L9
UniRef100_Q	7	12	54.20%	153	17201	8	H/ACA ribonucleoprotein complex subunit 2
UniRef100_P	9	13	54.10%	207	23171	8	Metalloproteinase inhibitor 1 precursor
UniRef100_Q	4	25	54.10%	109	11646	8	Myosin-reactive immunoglobulin light chain variable region
UniRef100_P	33	75	53.90%	662	75534	6	Interferon-induced GTP-binding protein Mx1
UniRef100_P	36	133	53.90%	586	66408	5	Lamin-B1
UniRef100_P	24	98	53.90%	531	57221	9	Polypyrimidine tract-binding protein 1
UniRef100_U	24	98	51.30%	557	59693	9	Polypyrimidine tract-binding protein 1 (PTB) (Heterogeneous nuclear ribonucleoprotein I) (hnRNP I) (57 kDa RNA-binding protein PPTB-1).
UniRef100_Q	24	98	51.30%	557	59633	9	Polypyrimidine tract binding protein 1
UniRef100_P	24	98	52.00%	550	59037	9	Isoform 2 of P26599
UniRef100_Q	77	124	53.80%	1230	1E+05	6	Cullin-associated NEDD8-dissociated protein 1
UniRef100_Q	4	6	53.80%	119	13370	6	Vacuolar ATP synthase subunit F
UniRef100_Q	54	114	53.60%	840	94331	5	Heat shock 70kDa protein 4
UniRef100_P	12	92	53.60%	181	20601	7	ADP-ribosylation factor 3
UniRef100_P	12	92	53.60%	181	20697	7	ADP-ribosylation factor 1
UniRef100_P	21	71	53.50%	245	27764	5	14-3-3 protein theta
UniRef100_Q	42	87	53.40%	874	97718	6	Coatomer subunit gamma
UniRef100_Q	6	59	53.40%	103	11555	8	Actin-like protein
UniRef100_P	18	46	53.30%	330	37512	6	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit
UniRef100_Q	18	46	51.60%	341	38631	7	Protein phosphatase type 1 catalytic subunit
UniRef100_P	15	123	53.30%	165	18012	8	Peptidyl-prolyl cis-trans isomerase A
UniRef100_P	11	31	53.30%	165	17887	8	Interferon-induced 17 kDa protein precursor [Contains: Ubiquitin cross-reactive protein (hUCRP) (Interferon-induced 15 kDa protein)]
UniRef100_P	28	56	53.20%	483	53140	7	6-phosphogluconate dehydrogenase, decarboxylating
UniRef100_O	14	21	53.20%	248	27887	9	Proteasome subunit alpha type 7
UniRef100_Q	14	21	55.50%	238	26714	9	Hypothetical protein
UniRef100_P	43	88	53.10%	714	81890	6	Calpain-1 catalytic subunit
UniRef100_Q	43	88	53.10%	714	81831	6	CAPN1 protein
UniRef100_Q	12	14	53.00%	283	31236	7	S-methyl-5-thioadenosine phosphorylase
UniRef100_Q	135	259	52.90%	2548	3E+05	7	FASN variant protein

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_U	135	259	52.90%	2548	3E+05	7	Fatty acid synthase (EC 2.3.1.85) [Includes: [Acyl-carrier-protein] S- acetyltransferase (EC 2.3.1.38); [Acyl-carrier-protein] S- malonyltransferase (EC 2.3.1.39); 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41); 3-oxoacyl-[acyl-carrier-protein] r
UniRef100_A	37	142	52.90%	751	84307	5	RRBP1 protein
UniRef100_P	7	34	52.90%	104	12000	7	Pterin-4-alpha-carbinolamine dehydratase
UniRef100_Q	16	27	52.80%	271	31284	5	Ubiquitin thioesterase OTUB1
UniRef100_U	13	279	52.80%	214	23409	7	PROTEIN (ANTIBODY (LIGHT CHAIN))
UniRef100_P	12	22	52.80%	142	16786	6	Thioredoxin-like protein 4A
UniRef100_Q	5	9	52.80%	144	16297	5	Placental protein 25
UniRef100_P	10	14	52.70%	245	26599	5	Eukaryotic translation initiation factor 6 (eIF-6) (B4 integrin interactor) (CAB) (p27(BBP)) (B(2)GCN homolog)
UniRef100_Q	10	14	53.10%	243	26349	5	P27BBP protein
UniRef100_Q	7	9	52.70%	150	16588	8	Dual specificity protein phosphatase 23
UniRef100_U	134	770	52.60%	2355	3E+05	6	fibronectin 1 isoform 3 preproprotein
UniRef100_P	31	120	52.60%	418	46737	6	Alpha-1-antitrypsin precursor
UniRef100_Q	22	33	52.50%	474	52951	6	Vitamin D-binding protein variant
UniRef100_P	25	41	52.50%	379	42742	6	Leukocyte elastase inhibitor
UniRef100_U	132	759	52.30%	2296	3E+05	6	fibronectin 1 isoform 5 preproprotein
UniRef100_P	25	44	52.30%	545	60534	7	T-complex protein 1 subunit gamma
UniRef100_U	25	44	52.40%	544	60463	7	chaperonin containing TCP1, subunit 3 isoform b
UniRef100_Q	25	44	54.60%	522	57972	7	Chaperonin containing TCP1, subunit 3
UniRef100_Q	16	109	52.20%	356	37498	7	Poly(rC)-binding protein 1
UniRef100_U	16	109	52.20%	356	37526	7	poly(rC) binding protein 1
UniRef100_P	14	90	52.20%	295	32854	5	40S ribosomal protein SA
UniRef100_Q	10	17	52.20%	182	20446	7	VPS29 protein
UniRef100_Q	10	17	52.20%	182	20506	7	Vacuolar protein sorting-associated protein 29
UniRef100_U	133	761	52.10%	2386	3E+05	6	Fibronectin precursor (FN) (Cold-insoluble globulin) (CIG).
UniRef100_P	3	15	52.10%	94	10201	7	Neutrophil defensin 1 precursor (HNP-1) (HP-1) (HP1) (Defensin, alpha 1) [Contains: HP 1-56; Neutrophil defensin 2 (HNP-2) (HP-2) (HP2)]
UniRef100_P	3	15	52.10%	94	10245	6	Neutrophil defensin 3 precursor (HNP-3) (HP-3) (HP3) (Defensin, alpha 3) [Contains: HP 3-56; Neutrophil defensin 2 (HNP-2) (HP-2) (HP2)]
UniRef100_P	133	733	52.00%	2386	3E+05	6	Fibronectin precursor
UniRef100_P	27	54	52.00%	710	78182	8	Lactotransferrin precursor (EC 3.4.21.-) (Lactoferrin) (Talalactoferrin alfa) [Contains: Kaliocin-1; Lactoferroxin A; Lactoferroxin B; Lactoferroxin C]
UniRef100_A	10	60	52.00%	102	11377	#	HIST2H4B protein
UniRef100_P	10	60	51.50%	103	11367	#	Histone H4
UniRef100_O	58	95	51.90%	1071	1E+05	6	Exportin-1
UniRef100_U	58	95	52.00%	1070	1E+05	6	Exportin-1 (Exp1) (Chromosome region maintenance 1 protein homolog).
UniRef100_P	22	66	51.90%	462	51676	7	Hemopexin precursor
UniRef100_U	12	294	51.90%	214	23270	8	Fab 4E10
UniRef100_U	12	294	51.60%	215	23472	7	F105 LIGHT CHAIN

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	13	72	51.90%	183	20811	5	Chromobox protein homolog 3
UniRef100_P	41	131	51.80%	906	1E+05	6	Catenin alpha-1
UniRef100_P	27	36	51.80%	627	70289	5	Plastin-2
UniRef100_Q	27	36	51.80%	627	70289	5	Lymphocyte cytosolic protein 1
UniRef100_P	16	19	51.60%	413	46248	7	Aspartate aminotransferase, cytoplasmic
UniRef100_Q	10	15	51.60%	277	31540	9	Ras suppressor protein 1
UniRef100_P	17	34	51.60%	217	24831	#	60S ribosomal protein L10a
UniRef100_U	17	34	51.90%	216	24700	#	60S ribosomal protein L10a (CSA-19).
UniRef100_P	64	106	51.50%	1231	1E+05	7	Complement factor H precursor
UniRef100_P	63	720	51.50%	866	94973	6	Fibrinogen alpha chain precursor [Contains: Fibrinopeptide A]
UniRef100_Q	131	417	51.40%	2101	2E+05	6	Isoform 2 of Q14980
UniRef100_P	20	40	51.40%	418	47371	6	Actin-like protein 3
UniRef100_P	13	41	51.40%	317	34274	6	60S acidic ribosomal protein P0
UniRef100_Q	13	41	51.40%	317	34302	6	Ribosomal protein P0 variant
UniRef100_U	12	276	51.40%	220	24185	7	IGG Light chain
UniRef100_P	14	30	51.30%	318	35554	8	DNA-(apurinic or apyrimidinic site) lyase
UniRef100_P	15	31	51.30%	234	25899	7	Proteasome subunit alpha type 2
UniRef100_Q	15	31	51.30%	234	25841	8	Proteasome alpha 2 subunit variant
UniRef100_Q	132	419	51.20%	2115	2E+05	6	Nuclear mitotic apparatus protein 1
UniRef100_Q	9	13	51.20%	160	18048	5	Uncharacterized protein C1orf123
UniRef100_P	34	73	51.10%	577	67820	6	Moesin
UniRef100_P	31	62	51.10%	558	63147	8	Glucose-6-phosphate isomerase
UniRef100_P	17	44	51.10%	323	36984	7	Serine/threonine-protein phosphatase PP1-gamma catalytic subunit
UniRef100_Q	17	44	56.10%	294	33774	5	Serine/threonine phosphatase 1 gamma
UniRef100_P	17	44	49.00%	337	38518	6	Isoform Gamma
UniRef100_P	6	8	51.00%	202	22277	8	Complement component C8 gamma chain precursor
UniRef100_Q	6	8	51.00%	202	22219	9	Complement component 8, gamma polypeptide
UniRef100_Q	6	8	51.00%	202	22196	9	Complement component 8, gamma polypeptide
UniRef100_Q	30	239	50.90%	450	50433	5	Tubulin beta-3 chain
UniRef100_P	7	10	50.90%	171	19794	5	Myosin regulatory light chain 2, nonsarcomeric
UniRef100_Q	7	10	50.60%	172	19779	5	Myosin regulatory light chain 2-B, smooth muscle isoform
UniRef100_O	112	237	50.80%	2136	2E+05	6	U5 small nuclear ribonucleoprotein 200 kDa helicase
UniRef100_Q	15	16	50.80%	297	33602	7	CDA11
UniRef100_P	7	26	50.80%	128	14787	9	60S ribosomal protein L22
UniRef100_Q	7	26	50.80%	128	14818	9	Heparin-binding protein HBp15
UniRef100_P	6	10	50.70%	150	17143	5	DNA-directed RNA polymerases I, II, and III 17.1 kDa polypeptide
UniRef100_P	12	30	50.60%	87	10044	7	Acyl-CoA-binding protein
UniRef100_Q	12	30	50.00%	88	10145	7	Diazepam binding inhibitor, splice form 1c
UniRef100_Q	12	30	42.30%	104	11793	6	Diazepam-binding protein
UniRef100_Q	27	52	50.50%	709	77981	8	Lactoferrin
UniRef100_P	10	13	50.30%	302	33825	6	Spermidine synthase

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_O	6	6	50.30%	191	21868	5	Programmed cell death protein 6
UniRef100_Q	6	6	50.30%	191	21896	5	Programmed cell death 6 variant
UniRef100_Q	6	6	50.80%	189	21664	5	Programmed cell death 6
UniRef100_Q	5	8	50.30%	163	17663	5	Protein FAM96B
UniRef100_P	6	11	50.30%	151	16570	8	Epididymal secretory protein E1 precursor
UniRef100_Q	6	11	50.30%	151	16584	8	Niemann-Pick disease, type C2 variant
UniRef100_P	64	161	50.10%	1065	1E+05	6	Ceruloplasmin precursor
UniRef100_P	46	192	50.10%	593	59519	5	Keratin, type I cytoskeletal 10
UniRef100_U	46	192	50.90%	584	58827	5	Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10).
UniRef100_U	46	192	50.90%	584	58827	5	keratin 10
UniRef100_Q	55	104	50.00%	876	97170	5	Importin beta-1 subunit
UniRef100_P	38	133	50.00%	732	83267	6	Coagulation factor XIII A chain precursor
UniRef100_U	38	133	50.00%	732	83268	6	coagulation factor XIII A1 subunit precursor
UniRef100_Q	38	133	48.30%	757	85956	6	Coagulation factor XIII A chain variant
UniRef100_P	28	78	50.00%	408	46837	7	Lupus La protein
UniRef100_Q	11	15	50.00%	280	31896	8	Four and a half LIM domains 1 variant
UniRef100_Q	11	15	50.00%	280	31895	8	FHL1 protein
UniRef100_P	12	13	50.00%	208	22897	9	Proteasome subunit beta type 5 precursor
UniRef100_Q	12	13	39.10%	266	28810	7	Hypothetical protein DKFZp686I0180
UniRef100_Q	9	16	50.00%	210	22346	6	Abhydrolase domain-containing protein 14B
UniRef100_O	2	3	50.00%	76	8544	4	Heat shock factor-binding protein 1
UniRef100_U	2	3	45.80%	83	9349	4	Heat shock factor-binding protein 1 (Nasopharyngeal carcinoma- associated antigen 13) (NPC-A-13).
UniRef100_O	12	52	49.80%	329	36072	7	PDZ and LIM domain protein 1
UniRef100_Q	16	22	49.80%	329	35870	8	NADP-dependent leukotriene B4 12-hydroxydehydrogenase
UniRef100_U	16	22	49.80%	329	35886	8	NADP-dependent leukotriene B4 12-hydroxydehydrogenase
UniRef100_U	131	757	49.70%	2477	3E+05	6	fibronectin 1 isoform 1 preproprotein
UniRef100_P	24	42	49.70%	519	56166	8	Cytosol aminopeptidase
UniRef100_P	11	42	49.70%	191	22225	6	Chromobox protein homolog 5
UniRef100_P	7	9	49.70%	195	21995	5	BH3-interacting domain death agonist (BID) (p22 BID) [Contains: BH3- interacting domain death agonist p15 (p15 BID); BH3-interacting domain death agonist p13 (p13 BID); BH3-interacting domain death agonist p11 (p11 BID)]
UniRef100_P	23	51	49.60%	548	59621	6	T-complex protein 1 subunit theta
UniRef100_Q	5	20	49.60%	129	13988	#	Histone H2A type 2-C
UniRef100_Q	5	20	49.20%	130	14095	#	Histone H2A type 2-A
UniRef100_Q	37	55	49.40%	893	99327	6	Major vault protein
UniRef100_P	34	71	49.40%	623	67878	8	Transketolase
UniRef100_Q	34	71	49.40%	623	67906	8	Transketolase variant
UniRef100_P	17	18	49.40%	417	48142	4	Calreticulin precursor
UniRef100_Q	17	18	50.70%	406	46919	4	Calreticulin variant
UniRef100_P	14	31	49.40%	241	26411	5	Proteasome subunit alpha type 5

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P	16	21	49.30%	383	42625	9	Chitinase-3-like protein 1 precursor
UniRef100_UI	16	21	49.30%	383	42613	9	chitinase 3-like 1
UniRef100_P	10	15	49.30%	217	25206	6	Growth factor receptor-bound protein 2
UniRef100_P	17	26	49.20%	323	36375	6	Annexin A3
UniRef100_UI	17	26	49.20%	323	36417	6	Annexin A3 (Annexin III) (Lipocortin III) (Placental anticoagulant protein III) (PAP-III) (35-alpha calcimedin) (Inositol 1,2-cyclic phosphate 2-phosphohydrolase).
UniRef100_P	9	25	49.20%	193	22006	7	Rho-related GTP-binding protein RhoC precursor
UniRef100_Q	9	25	50.30%	189	21580	7	Ras homolog gene family, member C
UniRef100_P	6	22	49.20%	130	14091	#	Histone H2A type 1
UniRef100_UI	6	22	41.30%	155	16610	#	H2A histone family, member J isoform 2
UniRef100_Q	6	22	49.60%	129	14019	#	H2A histone family, member J
UniRef100_Q	6	22	50.00%	128	13936	#	Histone H2A type 1-J
UniRef100_Q	6	22	50.00%	128	13906	#	Histone H2A type 1-H
UniRef100_P	6	22	49.20%	130	14107	#	Histone H2A type 1-D
UniRef100_Q	23	71	49.10%	428	48991	6	Spliceosome RNA helicase BAT1
UniRef100_Q	23	71	49.10%	428	49019	6	HLA-B associated transcript 1 variant
UniRef100_UI	12	226	49.10%	212	23072	7	Fab 48d light chain
UniRef100_UI	12	280	49.10%	212	22991	6	IMMUNOGLOBULIN
UniRef100_UI	12	280	48.60%	214	23352	8	KAPPA LIGHT CHAIN OF IG
UniRef100_UI	12	280	48.60%	214	23409	7	IGG1-KAPPA 4D5 FAB (LIGHT CHAIN)
UniRef100_UI	12	280	48.60%	214	23571	8	CAMPATH-1H ANTIBODY
UniRef100_Q	283	601	49.00%	4646	5E+05	6	Dynein heavy chain, cytosolic
UniRef100_Q	13	18	49.00%	261	29916	7	Pyridoxine 5'-phosphate oxidase variant
UniRef100_Q	13	18	49.00%	261	29988	7	Pyridoxine-5'-phosphate oxidase
UniRef100_P	9	18	49.00%	157	17170	9	Putative RNA-binding protein 3
UniRef100_UI	47	56	48.90%	1102	1E+05	6	Ubiquitin carboxyl-terminal hydrolase 7 (EC 3.1.2.15) (Ubiquitin thioesterase 7) (Ubiquitin-specific-processing protease 7) (Deubiquitinating enzyme 7) (Herpesvirus-associated ubiquitin-specific protease).
UniRef100_Q	47	56	48.90%	1102	1E+05	6	Ubiquitin carboxyl-terminal hydrolase 7
UniRef100_P	31	40	48.90%	611	69285	6	Leukotriene A-4 hydrolase (EC 3.3.2.6) (LTA-4 hydrolase) (Leukotriene A(4) hydrolase)
UniRef100_P	28	75	48.80%	406	45205	7	Haptoglobin precursor [Contains: Haptoglobin alpha chain; Haptoglobin beta chain]
UniRef100_P	28	320	48.70%	448	49924	5	Tubulin alpha-1 chain
UniRef100_P	16	33	48.70%	345	38298	8	Beta-2-glycoprotein 1 precursor (Beta-2-glycoprotein I) (Apolipoprotein H) (Apo-H) (B2GPI) (Beta(2)GPI)
UniRef100_UI	16	33	48.70%	345	38312	8	apolipoprotein H precursor
UniRef100_Q	86	201	48.60%	1615	2E+05	7	Apolipoprotein B variant
UniRef100_P	39	104	48.60%	782	85697	6	Gelsolin precursor
UniRef100_UI	12	228	48.60%	214	23459	8	Fab 412d heavy chain
UniRef100_O	5	7	48.60%	142	16311	5	DNA-directed RNA polymerase II 16 kDa polypeptide
UniRef100_P	20	117	48.50%	326	35885	8	Ig gamma-2 chain C region

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P6	7	10	48.50%	200	22407	5	Ubiquitin-conjugating enzyme E2-25 kDa (EC 6.3.2.19) (Ubiquitin- protein ligase) (Ubiquitin carrier protein) (E2(25K))
UniRef100_P3	9	19	48.50%	206	22119	8	Flavin reductase
UniRef100_UI	9	19	47.40%	211	22594	8	Flavin reductase (EC 1.5.1.30) (FR) (NADPH-dependent diaphorase) (NADPH-flavin reductase) (FLR) (Biliverdin reductase B) (EC 1.3.1.24) (BVR-B) (Biliverdin-IX beta-reductase) (Green heme-binding protein) (GHBP).
UniRef100_Q	28	33	48.40%	737	82589	5	Dipeptidyl-peptidase 3
UniRef100_Q	12	21	48.40%	219	24328	5	ADP-sugar pyrophosphatase
UniRef100_UI	12	21	45.70%	232	25895	5	ADP-sugar pyrophosphatase (EC 3.6.1.13) (EC 3.6.1.-) (Nucleoside diphosphate-linked moiety X motif 5) (Nudix motif 5) (YSA1H).
UniRef100_Q	8	10	48.40%	192	21184	5	Apoptosis regulator BAX, membrane isoform alpha
UniRef100_Q	8	10	52.00%	179	19718	5	Bax-sigma
UniRef100_Q	8	10	53.80%	173	19312	6	Bax isoform psi
UniRef100_Q	8	10	42.70%	218	24220	8	Apoptosis regulator BAX, cytoplasmic isoform beta
UniRef100_O	6	12	48.30%	89	10059	6	Barrier-to-autointegration factor
UniRef100_P3	39	50	48.20%	906	1E+05	5	Coatomer subunit beta'
UniRef100_Q	5	9	48.20%	110	12405	8	PHD finger-like domain-containing protein 5A
UniRef100_UI	252	566	48.10%	4563	5E+05	7	apolipoprotein B precursor
UniRef100_P(	9	23	48.10%	154	15936	6	Superoxide dismutase [Cu-Zn]
UniRef100_UI	9	23	47.40%	156	16122	6	Superoxide dismutase [Cu-Zn] (EC 1.15.1.1).
UniRef100_Q	46	102	48.00%	964	1E+05	8	EBNA-2 co-activator variant
UniRef100_Q	46	102	50.90%	910	1E+05	7	Staphylococcal nuclease domain-containing protein 1
UniRef100_P3	20	45	47.90%	411	46871	7	Eukaryotic initiation factor 4A-III
UniRef100_Q	10	15	47.90%	280	31355	5	Thioredoxin-like 1 variant
UniRef100_P6	7	8	47.70%	193	22245	5	Neurocalcin-delta
UniRef100_P4	9	22	47.70%	132	14515	7	40S ribosomal protein S12
UniRef100_P1	4	12	47.70%	86	10192	7	Cytochrome c oxidase subunit VIb isoform 1
UniRef100_P6	10	75	47.70%	86	9725	5	Small nuclear ribonucleoprotein F
UniRef100_P3	103	151	47.60%	1960	2E+05	6	Myosin-9
UniRef100_UI	11	275	47.60%	212	23145	8	Fab 47e light chain
UniRef100_P1	6	11	47.60%	143	15145	#	Histone H2A.x
UniRef100_P6	8	36	47.60%	126	13916	#	Small nuclear ribonucleoprotein Sm D3
UniRef100_Q	7	18	47.50%	204	21640	6	Uncharacterized protein C9orf142
UniRef100_P3	6	23	47.50%	118	12712	7	D-dopachrome decarboxylase
UniRef100_P1	5	8	47.50%	99	11140	#	Acylphosphatase-2
UniRef100_P6	10	40	47.40%	194	22127	#	40S ribosomal protein S7
UniRef100_P3	21	34	47.30%	562	61449	7	Phosphoglucomutase-1
UniRef100_UI	21	34	47.20%	564	61633	7	Phosphoglucomutase-1 (EC 5.4.2.2) (Glucose phosphomutase 1) (PGM 1).
UniRef100_Q	21	34	47.30%	562	61370	7	Phosphoglucomutase 1
UniRef100_UI	18	78	47.30%	347	38111	8	Immunoglobulin heavy chain C gene segment
UniRef100_P(	8	22	47.30%	201	21899	7	Glutathione peroxidase 1

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_U	8	22	46.80%	203	21938	7	glutathione peroxidase 1 isoform 1
UniRef100_Q	8	24	47.20%	125	14585	9	Pre-mRNA branch site protein p14
UniRef100_P	31	105	47.10%	558	60187	7	Heterogeneous nuclear ribonucleoprotein L
UniRef100_U	31	105	44.70%	589	64133	8	heterogeneous nuclear ribonucleoprotein L isoform a
UniRef100_Q	31	105	47.10%	558	60233	7	HNRPL protein
UniRef100_O	8	22	47.10%	206	22238	5	Tumor protein D54
UniRef100_U	8	22	44.30%	219	23739	6	Tumor protein D54 (hD54) (Tumor protein D52-like 2).
UniRef100_Q	8	22	44.10%	220	23787	6	Tumor protein D52-like 2
UniRef100_Q	8	22	42.40%	229	24854	6	Tumor protein D52-like 2
UniRef100_Q	9	17	47.10%	189	20967	5	Calcyphosin
UniRef100_O	6	13	47.10%	174	19108	5	c-Myc-responsive protein Rcl
UniRef100_Q	5	8	47.10%	170	18681	5	CDNA: FLJ21190 fis, clone CAS12333
UniRef100_Q	4	5	47.10%	138	15196	7	Chromosome 6 open reading frame 86
UniRef100_A	4	8	47.10%	121	12897	7	Rheumatoid factor G9 light chain
UniRef100_P	6	10	47.10%	70	8218	#	60S ribosomal protein L38
UniRef100_Q	15	16	47.00%	298	32237	7	Isochorismatase domain-containing protein 1
UniRef100_Q	10	218	47.00%	234	25390	7	IGKC protein
UniRef100_P	8	24	46.90%	213	23871	6	Ras-related protein Rab-4A
UniRef100_Q	8	24	45.90%	218	24390	6	RAB4A, member RAS oncogene family
UniRef100_Q	8	24	45.90%	218	24332	7	RAB4A, member RAS oncogene family variant
UniRef100_P	15	56	46.90%	175	20020	6	Ferritin light chain
UniRef100_Q	15	56	46.90%	175	19986	6	Ferritin, light polypeptide
UniRef100_Q	15	56	46.90%	175	20062	6	Ferritin, light polypeptide
UniRef100_Q	15	56	46.90%	175	19992	6	Ferritin
UniRef100_A	5	9	46.90%	96	10393	9	A30
UniRef100_U	5	9	42.50%	106	11518	8	IGM MEZ IMMUNOGLOBULIN
UniRef100_A	5	9	46.90%	96	10420	9	A30 protein
UniRef100_Q	20	43	46.80%	541	57996	5	Siah binding protein 1
UniRef100_U	20	43	46.80%	541	58115	5	fuse-binding protein-interacting repressor isoform b
UniRef100_Q	20	43	46.70%	542	58172	5	FBP-interacting repressor
UniRef100_Q	12	45	46.80%	248	27745	#	Splicing factor, arginine/serine-rich 1
UniRef100_O	6	12	46.80%	188	21008	5	Uncharacterized protein C7orf24
UniRef100_Q	11	21	46.70%	195	21627	6	Apoptosis-associated speck-like protein containing a CARD
UniRef100_P	8	142	46.60%	146	16009	8	Hemoglobin subunit beta
UniRef100_Q	3	6	46.60%	103	11953	6	MYCBP protein
UniRef100_Q	3	6	46.60%	103	11967	6	C-Myc-binding protein
UniRef100_Q	53	281	46.50%	854	98113	5	Heat shock protein HSP 90-alpha 2
UniRef100_O	16	73	46.50%	372	39617	#	Core histone macro-H2A.1
UniRef100_Q	27	162	46.50%	361	38669	9	CTCL tumor antigen HD-CL-08
UniRef100_P	7	18	46.50%	198	22588	9	Neutrophil gelatinase-associated lipocalin precursor

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_U	7	18	46.00%	200	22902	9	Neutrophil gelatinase-associated lipocalin precursor (NGAL) (p25) (25 kDa alpha-2-microglobulin-related subunit of MMP-9) (Lipocalin-2) (Oncogene 24p3).
UniRef100_Q	7	18	46.50%	198	22562	9	LCN2 protein
UniRef100_Q	7	18	46.00%	200	22788	9	Lipocalin 2
UniRef100_Q	4	9	46.50%	142	15069	#	PIN4 protein
UniRef100_U	4	9	42.30%	156	16608	#	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)
UniRef100_Q	4	9	50.40%	131	13810	#	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4
UniRef100_Q	4	9	46.80%	141	14892	#	PIN4 protein
UniRef100_P	20	41	46.40%	412	46530	8	Argininosuccinate synthase
UniRef100_U	20	41	46.20%	413	46617	8	Argininosuccinate synthase
UniRef100_P	4	24	46.40%	69	7841	#	40S ribosomal protein S28
UniRef100_U	4	24	46.40%	69	7823	#	ribosomal protein S28 (RPS28), mRNA
UniRef100_Q	14	28	46.30%	393	41920	6	Synaptic vesicle membrane protein VAT-1 homolog
UniRef100_Q	12	25	46.30%	244	27969	6	CLE
UniRef100_Q	12	25	46.30%	244	28068	7	Protein C14orf166
UniRef100_Q	11	12	46.20%	279	32193	8	Four and a half LIM domains protein 2
UniRef100_U	11	12	34.70%	372	42073	8	Four and a half LIM domains protein 2 (FHL-2) (Skeletal muscle LIM- protein 3) (SLIM 3) (LIM domain protein DRAL).
UniRef100_Q	11	12	33.20%	389	44177	8	FHL2 isoform 5
UniRef100_Q	11	12	46.20%	279	32196	7	Four and a half LIM-domain protein 2
UniRef100_P	7	32	46.20%	130	14839	#	40S ribosomal protein S15a
UniRef100_P	44	93	46.10%	1014	1E+05	9	Poly [ADP-ribose] polymerase 1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+) ADP-ribosyltransferase 1)
UniRef100_Q	7	8	46.00%	198	21819	6	COMM domain-containing protein 9
UniRef100_P	4	9	46.00%	113	12452	5	Dynein light chain Tctex-type 1
UniRef100_P	35	85	45.90%	764	85533	7	Complement factor B precursor (EC 3.4.21.47) (C3/C5 convertase) (Properdin factor B) (Glycine-rich beta glycoprotein) (GBG) (PBF2) [Contains: Complement factor B Ba fragment; Complement factor B Bb fragment]
UniRef100_P	8	109	45.90%	146	16007	8	Hemoglobin subunit beta
UniRef100_P	12	25	45.80%	249	28585	4	Acidic leucine-rich nuclear phosphoprotein 32 family member A
UniRef100_U	12	25	46.20%	247	28325	4	Acidic leucine-rich nuclear phosphoprotein 32 family member A (Potent heat-stable protein phosphatase 2A inhibitor I1PP2A) (Acidic nuclear phosphoprotein pp32) (Leucine-rich acidic nuclear protein) (Lanp) (Putative HLA-DR-associated protein I) (PHAPI) (Ma
UniRef100_Q	12	25	45.80%	249	28557	4	Acidic (Leucine-rich) nuclear phosphoprotein 32 family, member A variant
UniRef100_Q	10	57	45.80%	166	18737	8	Cofilin-2
UniRef100_P	11	59	45.70%	208	24205	#	40S ribosomal protein S8
UniRef100_Q	3	8	45.70%	81	9056	6	Uncharacterized protein C6orf115
UniRef100_U	3	8	20.10%	184	20402	7	PREDICTED: similar to Protein C6orf115
UniRef100_P	16	27	45.60%	241	26489	8	Proteasome subunit beta type 1 precursor
UniRef100_Q	16	27	45.60%	241	26491	8	Proteasome beta 1 subunit variant
UniRef100_Q	12	25	45.60%	228	26183	6	Translin

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P	6	28	45.60%	180	19608	6	Adenine phosphoribosyltransferase
UniRef100_P	5	67	45.60%	147	16043	8	Hemoglobin subunit gamma-1
UniRef100_P	7	29	45.60%	90	10180	6	Protein S100-A6
UniRef100_Q	13	15	45.50%	376	42917	6	Proteasome 26S non-ATPase subunit 13 isoform 1 variant
UniRef100_U	13	15	45.50%	376	42946	6	26S proteasome non-ATPase regulatory subunit 13 (26S proteasome regulatory subunit S11) (26S proteasome regulatory subunit p40.5).
UniRef100_Q	13	15	45.40%	377	42671	6	HSPC027
UniRef100_Q	13	15	45.50%	376	42918	6	26S proteasome non-ATPase regulatory subunit 13
UniRef100_P	9	24	45.50%	178	19592	8	Cellular nucleic acid-binding protein
UniRef100_Q	9	24	47.40%	171	18871	8	Cellular nucleic acid binding protein beta variant 1
UniRef100_Q	5	11	45.50%	99	11250	5	Dpy-30-like protein
UniRef100_Q	41	61	45.40%	908	1E+05	5	26S proteasome non-ATPase regulatory subunit 2
UniRef100_Q	41	61	45.10%	913	1E+05	5	Proteasome 26S non-ATPase subunit 2 variant
UniRef100_Q	41	61	45.40%	908	1E+05	5	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 2
UniRef100_P	8	19	45.40%	229	25569	6	Platelet-activating factor acetylhydrolase IB subunit beta
UniRef100_P	35	49	45.30%	835	93308	5	Isoform Short of P45974
UniRef100_U	35	49	45.30%	835	93394	5	Ubiquitin isopeptidase T
UniRef100_P	32	153	45.30%	590	62378	8	Keratin, type II cytoskeletal 5
UniRef100_P	24	87	45.20%	423	47651	6	Alpha-1-antichymotrypsin precursor (ACT) [Contains: Alpha-1- antichymotrypsin His-Pro-less]
UniRef100_Q	11	276	45.20%	219	24030	8	Immunoblobulin light chain
UniRef100_Q	11	276	41.40%	239	26235	8	Hypothetical protein
UniRef100_Q	11	276	41.20%	240	26234	7	IGKV1-5 protein
UniRef100_P	9	26	45.20%	177	19463	8	Cellular nucleic acid-binding protein
UniRef100_Q	9	26	47.10%	170	18742	8	Cellular nucleic acid-binding protein
UniRef100_Q	19	30	45.10%	505	55210	7	UPF0027 protein C22orf28
UniRef100_P	12	24	45.10%	264	29204	6	Proteasome subunit beta type 4 precursor
UniRef100_Q	34	46	44.90%	858	96865	5	Heat-shock protein 105 kDa
UniRef100_O	7	10	44.80%	174	19811	9	Eukaryotic translation elongation factor 1 epsilon-1
UniRef100_P	7	20	44.80%	143	15585	#	Midkine precursor
UniRef100_P	21	48	44.70%	501	57136	7	Aspartyl-tRNA synthetase, cytoplasmic
UniRef100_O	11	32	44.70%	215	24741	9	Vesicle-trafficking protein SEC22b
UniRef100_Q	4	26	44.70%	114	11568	4	RPLP1 protein
UniRef100_P	46	114	44.60%	1170	1E+05	5	Thrombospondin-1 precursor
UniRef100_Q	46	114	42.60%	1225	1E+05	5	Thrombospondin 1 variant
UniRef100_Q	29	34	44.60%	790	91839	6	Nuclear cap-binding protein subunit 1
UniRef100_P	35	355	44.60%	462	50141	9	Elongation factor 1-alpha 1
UniRef100_Q	35	355	44.60%	462	50185	9	Eukaryotic translation elongation factor 1 alpha 1
UniRef100_Q	35	355	44.60%	462	50123	9	Eukaryotic translation elongation factor 1 alpha 1
UniRef100_Q	35	355	44.60%	462	50185	9	Eukaryotic translation elongation factor 1 alpha-like 3
UniRef100_Q	35	355	44.60%	462	50125	9	Eukaryotic translation elongation factor 1 alpha 1 variant
UniRef100_Q	35	355	44.60%	462	50142	9	Eukaryotic translation elongation factor 1 alpha 1 variant

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	35	355	44.60%	462	50111	9	Eukaryotic translation elongation factor 1 alpha 1 variant
UniRef100_Q	35	355	44.60%	462	50113	9	Eukaryotic translation elongation factor 1 alpha 1 variant
UniRef100_Q	8	8	44.60%	276	30580	7	Nitrilase family member 2
UniRef100_Q	8	8	44.60%	276	30608	7	Nit protein 2
UniRef100_Q	13	46	44.60%	175	20039	6	Ferritin, light polypeptide
UniRef100_Q	12	42	44.60%	130	15040	5	Astrocytic phosphoprotein PEA-15
UniRef100_Q	12	42	44.60%	130	15068	5	PEA15 protein
UniRef100_Q	12	24	44.50%	290	33112	7	Translin-associated protein X
UniRef100_O	8	10	44.50%	272	31444	6	TIP41-like protein
UniRef100_U	34	78	44.40%	914	1E+05	7	Transmembrane protein 110.
UniRef100_P	31	51	44.40%	770	88068	6	Signal transducer and activator of transcription 3
UniRef100_Q	29	234	44.40%	478	52667	8	IGHM protein
UniRef100_P	19	28	44.40%	394	44761	7	Actin-like protein 2
UniRef100_Q	7	12	44.40%	169	19015	8	Nucleoside diphosphate kinase 3
UniRef100_U	65	172	44.30%	1609	2E+05	5	laminin, gamma 1 precursor
UniRef100_P	12	57	44.30%	327	35941	7	Ig gamma-4 chain C region
UniRef100_U	12	57	44.30%	327	35983	7	Immunoglobulin heavy chain C gene segment
UniRef100_P	10	20	44.30%	296	33428	6	Biliverdin reductase A precursor
UniRef100_P	14	38	44.30%	201	23512	5	Alpha-1-acid glycoprotein 1 precursor
UniRef100_Q	14	38	44.30%	201	23540	5	Orosomucoid 1
UniRef100_P	8	14	44.30%	201	22836	7	Proteasome subunit beta type 2
UniRef100_P	8	9	44.30%	185	20478	8	Dual specificity protein phosphatase 3
UniRef100_P	4	10	44.30%	115	13015	#	40S ribosomal protein S26
UniRef100_Q	4	10	44.30%	115	13001	#	OTTHUMP00000018641
UniRef100_Q	14	19	44.20%	513	57544	7	Smu-1 suppressor of mec-8 and unc-52 protein homolog
UniRef100_Q	20	35	44.20%	385	42838	5	Hypothetical protein DKFZp686E12175
UniRef100_U	20	35	44.00%	386	42982	5	Branched-chain-amino-acid aminotransferase, cytosolic (EC 2.6.1.42) (BCAT(c)) (ECA39 protein).
UniRef100_U	20	35	44.00%	386	42966	5	branched chain aminotransferase 1, cytosolic
UniRef100_Q	14	18	44.20%	346	38450	5	SUMO-activating enzyme subunit 1
UniRef100_Q	13	51	44.20%	321	35893	7	GDP-L-fucose synthetase (EC 1.1.1.271) (Protein FX) (Red cell NADP(H)- binding protein)
UniRef100_P	6	8	44.20%	172	19827	5	Myosin regulatory light chain 2, smooth muscle isoform
UniRef100_Q	6	8	44.20%	172	19893	5	Regulatory myosin light chain long version
UniRef100_Q	6	8	44.20%	172	19849	5	MYL9 protein
UniRef100_Q	4	9	44.20%	104	11662	5	Protein S100-A14
UniRef100_P	19	204	44.10%	440	48562	6	Isoform 3 of P61978
UniRef100_Q	19	204	45.30%	428	47557	6	Heterogeneous nuclear ribonucleoprotein K
UniRef100_P	27	403	44.10%	372	38846	9	Heterogeneous nuclear ribonucleoprotein A1
UniRef100_U	27	403	51.20%	320	34223	9	Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand RNA-binding protein) (hnRNP core protein A1).
UniRef100_U	27	403	44.10%	372	38747	9	heterogeneous nuclear ribonucleoprotein A1 isoform b

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	27	403	61.40%	267	29386	9	HNRPA1 protein
UniRef100_P	27	403	51.20%	320	34196	9	Heterogeneous nuclear ribonucleoprotein A1
UniRef100_Q	7	12	44.10%	245	26724	8	3-hydroxybutyrate dehydrogenase type 2
UniRef100_P	9	47	44.10%	152	17719	#	40S ribosomal protein S18
UniRef100_O	7	9	44.10%	152	17637	8	Ubiquitin/ISG15-conjugating enzyme E2 L6
UniRef100_Q	14	23	44.00%	393	44446	5	Hypothetical protein
UniRef100_P	20	57	44.00%	248	28522	5	Tropomyosin alpha-4 chain
UniRef100_Q	9	53	44.00%	234	25148	7	IGL@ protein
UniRef100_Q	10	74	44.00%	234	24910	7	Hypothetical protein
UniRef100_A	34	54	43.90%	814	92482	5	Eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa
UniRef100_P	34	54	40.90%	873	99039	5	Isoform 2 of P55884
UniRef100_P	34	54	43.90%	814	92492	5	Eukaryotic translation initiation factor 3 subunit 9
UniRef100_A	34	54	46.10%	775	88681	5	Eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa
UniRef100_P	25	45	43.90%	693	76715	7	GMP synthase [glutamine-hydrolyzing]
UniRef100_P	13	17	43.90%	271	31540	7	Phosphatidylinositol transfer protein beta isoform
UniRef100_UI	7	57	43.90%	155	16959	5	Heat shock protein HSP 90-beta (HSP 84) (HSP 90).
UniRef100_Q	107	336	43.80%	2725	3E+05	6	Filamin-C
UniRef100_UI	107	336	44.10%	2705	3E+05	6	Filamin-C (Gamma-filamin) (Filamin-2) (Protein FLNc) (Actin-binding- like protein) (ABP-L) (ABP-280-like protein).
UniRef100_UI	107	336	43.80%	2725	3E+05	6	gamma filamin
UniRef100_Q	107	336	44.30%	2692	3E+05	6	Isoform 2 of Q14315
UniRef100_P	33	52	43.80%	843	96696	7	Glycogen phosphorylase, brain form
UniRef100_P	13	27	43.70%	437	49031	6	Eukaryotic peptide chain release factor subunit 1
UniRef100_Q	16	96	43.70%	373	39525	7	Poly(RC)-binding protein 2 isoform b variant
IPITrypsinPIG	19	974	43.70%	231	24409	7	TRYP_PIG
gi|12345|prg	19	974	45.30%	223	23476	8	Promega sequencing grade modified trypsin
UniRef100_P	9	10	43.60%	289	32668	7	Glucosamine-6-phosphate isomerase
UniRef100_Q	6	10	43.50%	154	17328	6	Prefoldin subunit 5
UniRef100_Q	6	12	43.50%	124	13623	7	Mitogen-activated protein kinase kinase 1-interacting protein 1
UniRef100_P	220	641	43.40%	4128	5E+05	7	DNA-dependent protein kinase catalytic subunit
UniRef100_UI	220	641	43.40%	4127	5E+05	7	DNA-dependent protein kinase catalytic subunit (EC 2.7.11.1) (DNA-PK catalytic subunit) (DNA-PKcs) (DNPK1) (p460).
UniRef100_P	22	116	43.40%	472	51622	5	Keratin, type I cytoskeletal 14
UniRef100_UI	22	116	43.40%	472	51561	5	Keratin, type I cytoskeletal 14 (Cytokeratin-14) (CK-14) (Keratin-14) (K14).
UniRef100_P	12	23	43.40%	334	36426	7	Malate dehydrogenase, cytoplasmic
UniRef100_P	7	14	43.40%	182	20456	7	ADP-ribosylation factor-like protein 3
UniRef100_Q	7	14	43.40%	182	20474	7	ARL3 protein
UniRef100_Q	110	215	43.30%	2335	3E+05	9	Pre-mRNA-processing-splicing factor 8
UniRef100_Q	43	78	43.30%	972	1E+05	5	116 kDa U5 small nuclear ribonucleoprotein component
UniRef100_UI	43	78	43.30%	972	1E+05	5	U5 snRNP-specific protein, 116 kD
UniRef100_Q	43	78	43.30%	972	1E+05	5	U5-116KD protein

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	19	26	43.30%	504	55181	7	Pre-mRNA-processing factor 19
UniRef100_O	13	22	43.30%	434	47047	5	Mannose-6-phosphate receptor-binding protein 1
UniRef100_P	13	58	43.30%	263	29598	#	40S ribosomal protein S4, X isoform
UniRef100_Q	13	58	46.90%	243	27260	#	RPS4X protein
UniRef100_P	12	28	43.30%	201	23603	5	Alpha-1-acid glycoprotein 2 precursor
UniRef100_Q	12	28	43.30%	201	23615	5	ORM2 protein
UniRef100_Q	11	35	43.20%	361	41487	7	Septin-2
UniRef100_Q	44	73	43.10%	1217	1E+05	7	Structural maintenance of chromosomes protein 3
UniRef100_Q	15	16	43.10%	504	56196	6	26S proteasome non-ATPase regulatory subunit 5
UniRef100_P	12	39	43.10%	255	28416	9	U2 small nuclear ribonucleoprotein A'
UniRef100_Q	58	91	42.90%	1140	1E+05	5	DNA damage-binding protein 1
UniRef100_O	13	29	42.90%	312	35102	6	Pyridoxal kinase
UniRef100_P	13	17	42.90%	198	21676	6	Sorcin
UniRef100_U	13	17	46.40%	183	20345	5	sorcin isoform b
UniRef100_Q	2	2	42.90%	98	10643	5	V1-22 protein
UniRef100_U	2	2	35.90%	117	12681	5	Immunoglobulin Lambda light chain V gene segment
UniRef100_P	24	43	42.80%	589	65309	5	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
UniRef100_U	24	43	43.30%	582	64677	5	Protein phosphatase 2
UniRef100_Q	28	231	42.80%	472	51725	8	Hypothetical protein DKFZp686P15220
UniRef100_Q	233	391	42.60%	5430	6E+05	5	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5
UniRef100_P	10	10	42.60%	303	33730	7	Cell division protein kinase 4
UniRef100_P	7	9	42.60%	230	26183	5	Ubiquitin carboxyl-terminal hydrolase isozyme L3
UniRef100_Q	9	25	42.60%	209	23420	8	Hypothetical protein DKFZp313C1541
UniRef100_Q	9	25	41.20%	216	24214	8	Ras-related protein Rab-2B
UniRef100_Q	6	8	42.60%	209	23226	5	COP9 signalosome complex subunit 8
UniRef100_P	10	16	42.60%	197	22658	7	Prefoldin subunit 3
UniRef100_Q	5	8	42.60%	122	13104	8	Uncharacterized protein C7orf48
UniRef100_Q	26	219	42.50%	475	52043	8	Hypothetical protein DKFZp686G11190
UniRef100_Q	26	219	42.10%	480	52613	8	Hypothetical protein DKFZp686O01196
UniRef100_Q	6	12	42.50%	186	21539	8	ADP-ribosylation factor-like protein 8B
UniRef100_P	4	5	42.50%	134	15330	5	Cytochrome b5
UniRef100_Q	4	5	43.20%	132	14572	6	Cytochrome b-5 isoform 1 variant
UniRef100_P	4	5	58.20%	98	11268	5	Isoform 2 of P00167
UniRef100_Q	10	73	42.40%	236	25024	8	Hypothetical protein
UniRef100_Q	4	10	42.40%	125	14199	5	TRM112-like protein
UniRef100_Q	30	99	42.30%	835	88550	6	Transcription intermediary factor 1-beta
UniRef100_Q	30	99	46.90%	753	79474	6	Isoform 2 of Q13263
UniRef100_P	13	18	42.30%	376	42614	7	Alpha-centractin
UniRef100_O	6	8	42.30%	175	19979	9	Anterior gradient protein 2 homolog precursor
UniRef100_Q	6	8	42.30%	175	19963	9	Anterior gradient 2 homolog

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_U	76	210	42.20%	2110	2E+05	5	Tenascin precursor (TN) (Tenascin-C) (TN-C) (Hexabrachion) (Cytotactin) (Neuronectin) (GMEM) (JI) (Myotendinous antigen) (Glioma- associated-extracellular matrix antigen) (GP 150-225).
UniRef100_Q	5	5	42.20%	199	22745	7	COMM domain-containing protein 2
UniRef100_Q	5	8	42.20%	154	16648	7	Prefoldin subunit 2
UniRef100_Q	8	11	42.10%	261	28933	5	Enolase-phosphatase E1
UniRef100_Q	10	75	42.10%	233	24867	5	IGLV3-25 protein
UniRef100_Q	5	5	42.10%	183	21090	5	COMM domain-containing protein 8
UniRef100_A	9	37	42.10%	126	13916	#	H2B histone family, member S
UniRef100_Q	9	37	42.10%	126	13952	#	Histone H2B type 1-L
UniRef100_Q	9	37	42.10%	126	13989	#	Histone H2B type 1-M
UniRef100_Q	9	37	42.10%	126	13922	#	Histone H2B type 1-N
UniRef100_Q	9	37	42.10%	126	13892	#	Histone H2B type 1-H
UniRef100_Q	9	37	42.10%	126	13920	#	Histone H2B type 2-F
UniRef100_P	9	37	42.40%	125	13819	#	Histone H2B type 1-C/E/F/G/I
UniRef100_P	9	37	42.10%	126	13936	#	Histone H2B type 1-D
UniRef100_P	9	37	42.10%	126	13944	#	Histone H2B type F-S
UniRef100_O	9	37	42.10%	126	13890	#	Histone H2B type 1-K
UniRef100_P	10	37	42.10%	126	13904	#	Histone H2B type 1-J
UniRef100_Q	10	37	42.10%	126	13908	#	Histone H2B type 3-B
UniRef100_Q	10	37	42.10%	126	13920	#	Histone H2B type 2-E
UniRef100_P	10	37	42.10%	126	13950	#	Histone H2B type 1-B
UniRef100_P	10	37	42.10%	126	13906	#	Histone H2B type 1-O
UniRef100_P	26	71	42.00%	719	81308	7	DNA replication licensing factor MCM7
UniRef100_Q	25	45	42.00%	600	67689	5	Lamin-B2
UniRef100_Q	32	126	42.00%	597	65039	7	IGHM protein
UniRef100_Q	15	27	42.00%	348	38499	6	Hypothetical protein CAPG
UniRef100_Q	5	10	42.00%	181	21210	8	Regulator of G-protein signalling 10
UniRef100_Q	6	18	42.00%	88	9380	9	SH3 domain binding glutamic acid-rich protein like 3
UniRef100_U	6	18	16.40%	225	23699	9	SH3 domain-binding glutamic acid-rich-like protein 3 (SH3 domain- binding protein 1) (SH3BP-1).
UniRef100_Q	6	18	39.80%	93	10438	5	SH3 domain-binding glutamic acid-rich-like protein 3
UniRef100_Q	6	18	16.40%	226	23838	9	Hypothetical protein
UniRef100_P	18	29	41.90%	418	46342	6	Pigment epithelium-derived factor precursor
UniRef100_Q	8	23	41.90%	160	18697	5	Prostaglandin E synthase 3
UniRef100_Q	5	11	41.90%	172	17900	7	Uncharacterized potential DNA-binding protein C17orf49
UniRef100_A	4	33	41.90%	105	11246	8	C7 protein
UniRef100_P	4	9	41.90%	86	10112	8	Signal recognition particle 9 kDa protein
UniRef100_P	17	36	41.80%	505	56782	6	Protein disulfide-isomerase A3 precursor
UniRef100_P	14	16	41.80%	483	54417	9	Probable ATP-dependent RNA helicase DDX6
UniRef100_U	14	16	42.80%	472	53216	9	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P	19	30	41.80%	471	53165	6	Tryptophanyl-tRNA synthetase, cytoplasmic
UniRef100_U	19	30	45.80%	430	48852	7	tryptophanyl-tRNA synthetase isoform b
UniRef100_P	11	21	41.80%	208	22742	9	Peptidyl-prolyl cis-trans isomerase B precursor
UniRef100_U	11	21	40.30%	216	23743	9	peptidylprolyl isomerase B precursor
UniRef100_Q	11	21	40.30%	216	23728	9	Peptidyl-prolyl cis-trans isomerase
UniRef100_P	9	21	41.80%	208	22493	9	Cysteine-rich protein 2
UniRef100_Q	9	21	41.80%	208	22494	9	Cysteine-rich protein 2 variant
UniRef100_Q	7	10	41.80%	189	21097	6	Heme-binding protein 1
UniRef100_P	9	150	41.80%	146	15808	8	Hemoglobin subunit delta
UniRef100_Q	32	123	41.70%	597	65305	8	IGHM protein
UniRef100_Q	32	123	41.70%	597	65275	8	IGHM protein
UniRef100_Q	32	123	41.70%	597	65301	8	IGHM protein
UniRef100_Q	13	19	41.70%	343	39602	6	Protein arginine methyltransferase 1
UniRef100_U	13	19	39.80%	359	41255	6	Protein arginine N-methyltransferase 1 (EC 2.1.1.-) (Interferon receptor 1-bound protein 4).
UniRef100_Q	13	19	40.60%	352	40417	6	PRMT1 protein
UniRef100_Q	13	19	41.20%	347	39929	6	HRMT1L2 protein
UniRef100_Q	9	14	41.70%	271	30540	6	Peroxiredoxin-4
UniRef100_O	8	13	41.70%	108	12855	5	Tubulin-specific chaperone A
UniRef100_O	29	52	41.60%	939	1E+05	7	AP-2 complex subunit alpha-2
UniRef100_Q	29	52	41.60%	940	1E+05	7	Adaptor-related protein complex 2, alpha 2 subunit variant
UniRef100_P	9	11	41.60%	149	16838	4	Calmodulin
UniRef100_P	4	6	41.60%	125	14523	5	DNA-directed RNA polymerase II subunit I
UniRef100_Q	14	17	41.50%	429	49398	7	Septin-11
UniRef100_Q	12	276	41.50%	236	25936	8	IGKC protein
UniRef100_Q	35	40	41.40%	953	1E+05	5	26S proteasome non-ATPase regulatory subunit 1
UniRef100_P	15	23	41.40%	418	46441	9	Serpin H1 precursor
UniRef100_O	11	15	41.40%	285	31122	6	NG,NG-dimethylarginine dimethylaminohydrolase 1
UniRef100_Q	11	275	41.40%	239	26246	8	IGKV2-24 protein
UniRef100_P	7	35	41.40%	145	16060	#	40S ribosomal protein S19
UniRef100_Q	7	35	38.20%	157	17282	#	Ribosomal protein S19
UniRef100_P	12	19	41.30%	404	45518	5	cAMP-dependent protein kinase type II-alpha regulatory subunit
UniRef100_Q	12	19	43.70%	382	43067	5	PRKAR2A protein
UniRef100_Q	9	52	41.20%	233	24855	7	IGL@ protein
UniRef100_Q	6	10	41.20%	153	16941	7	Actin-related protein 2/3 complex subunit 5-like protein
UniRef100_Q	14	34	41.10%	326	36092	9	ELAV-like protein 1
UniRef100_Q	6	21	41.10%	73	8547	8	Ubiquitin-like protein 5
UniRef100_Q	79	213	41.00%	2201	2E+05	5	Tenascin C
UniRef100_Q	15	22	41.00%	463	51157	6	RuvB-like 2
UniRef100_Q	7	10	41.00%	173	19815	9	Protein tyrosine phosphatase type IVA protein 1 (EC 3.1.3.48) (Protein-tyrosine phosphatase 4a1) (Protein-tyrosine phosphatase of regenerating liver 1) (PRL-1) (PTP(CAAXI))
UniRef100_P	20	42	40.90%	628	67405	6	Lutheran blood group glycoprotein precursor

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	10	27	40.90%	308	32055	6	Asparaginase-like protein 1
UniRef100_A	10	74	40.90%	235	24747	6	Hypothetical protein
UniRef100_P	5	10	40.90%	137	14494	9	Ribonuclease UK114
UniRef100_Q	24	38	40.80%	683	74681	8	Transforming growth factor-beta-induced protein ig-h3 precursor
UniRef100_U	24	38	40.90%	682	74591	7	Transforming growth factor-beta-induced protein ig-h3 precursor (Beta ig-h3) (Kerato-epithelin) (RGD-containing collagen-associated protein) (RGD-CAP).
UniRef100_P	23	75	40.80%	654	72333	5	78 kDa glucose-regulated protein precursor (GRP 78) (Heat shock 70 kDa protein 5) (Immunoglobulin heavy chain-binding protein) (BiP) (Endoplasmic reticulum lumenal Ca(2+)-binding protein grp78)
UniRef100_O	37	65	40.70%	1097	1E+05	5	Importin beta-3
UniRef100_U	37	65	40.00%	1115	1E+05	5	RAN binding protein 5
UniRef100_Q	15	25	40.70%	396	44744	8	Putative GTP-binding protein 9
UniRef100_O	12	18	40.70%	327	38170	7	Vacuolar protein sorting-associated protein 26A
UniRef100_U	9	223	40.70%	214	23341	7	ANTIBODY 2F5 (LIGHT CHAIN)
UniRef100_Q	4	12	40.70%	86	10117	7	BolA-like protein 2
UniRef100_P	8	9	40.60%	244	25789	7	Dihydropteridine reductase
UniRef100_U	8	9	40.60%	244	25804	7	quinoid dihydropteridine reductase
UniRef100_P	11	30	40.50%	346	38714	7	Annexin A1
UniRef100_P	17	47	40.50%	284	32723	5	Isoform 2 of P67936
UniRef100_A	5	8	40.50%	116	12528	8	Rheumatoid factor C6 light chain
UniRef100_Q	38	73	40.40%	949	1E+05	5	AP-1 complex subunit beta-1
UniRef100_U	38	73	40.70%	942	1E+05	5	adaptor-related protein complex 1 beta 1 subunit isoform b
UniRef100_U	38	73	40.40%	949	1E+05	5	adaptor-related protein complex 1 beta 1 subunit isoform a
UniRef100_Q	38	73	40.80%	939	1E+05	5	AP1B1 protein
UniRef100_Q	38	73	40.70%	942	1E+05	5	Isoform B of Q10567
UniRef100_Q	20	34	40.40%	522	56085	9	Protein RCC2
UniRef100_Q	6	12	40.40%	240	27872	9	Splicing factor U2AF 35 kDa subunit
UniRef100_Q	10	73	40.40%	235	24888	7	IGL@ protein
UniRef100_U	10	73	44.20%	215	22666	8	Fab 447-52D, light chain
UniRef100_Q	9	53	40.40%	235	24858	8	IGL@ protein
UniRef100_U	9	53	44.00%	216	22799	7	IMMUNOGLOBULIN LAMBDA DIMER MCG (LIGHT CHAIN)
UniRef100_A	10	74	40.40%	235	24655	8	Lambda-chain precursor
UniRef100_Q	6	12	40.40%	161	17745	5	UPF0404 protein C11orf59
UniRef100_P	5	7	40.40%	156	16533	6	Cyclin-dependent kinase inhibitor 2A, isoforms 1/2/3
UniRef100_P	29	113	40.30%	730	77516	9	Heterogeneous nuclear ribonucleoprotein M
UniRef100_P	29	113	42.50%	691	73621	9	Isoform 2 of P52272
UniRef100_Q	10	75	40.30%	236	25021	8	IGL@ protein
UniRef100_P	13	25	40.20%	348	38518	6	Macrophage-capping protein
UniRef100_Q	8	18	40.20%	244	27326	5	Tubulin folding cofactor B
UniRef100_P	9	35	40.20%	204	22876	#	40S ribosomal protein S5
UniRef100_P	4	10	40.20%	102	10932	9	10 kDa heat shock protein, mitochondrial

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	4	10	42.30%	97	10295	9	Chaperonin 10-related protein
UniRef100_P	9	26	40.20%	92	10713	5	Protein S100-B
UniRef100_P	10	11	40.10%	367	40787	6	Uroporphyrinogen decarboxylase
UniRef100_Q	10	11	40.10%	367	40803	6	Uroporphyrinogen decarboxylase
UniRef100_P	10	18	40.10%	172	19595	5	Translationally-controlled tumor protein
UniRef100_O	8	13	40.10%	177	19208	8	Peptidyl-prolyl cis-trans isomerase H
UniRef100_P	24	47	40.00%	543	62639	7	Stress-induced-phosphoprotein 1
UniRef100_O	8	10	40.00%	225	26131	6	Breast carcinoma amplified sequence 2
UniRef100_Q	50	95	39.90%	1233	1E+05	8	Structural maintenance of chromosomes protein 1A
UniRef100_P	32	104	39.90%	586	69413	6	Ezrin
UniRef100_U	32	104	39.70%	589	69688	6	Ezrin (p81) (Cytovillin) (Villin-2).
UniRef100_Q	32	104	39.90%	586	69242	6	Villin 2
UniRef100_Q	7	10	39.80%	103	11602	5	U6 snRNA-associated Sm-like protein LSm7
UniRef100_U	7	10	40.20%	102	11528	5	U6 snRNA-associated Sm-like protein LSm7.
UniRef100_P	5	27	39.80%	83	9111	9	40S ribosomal protein S21
UniRef100_Q	5	27	40.70%	81	8850	9	RPS21 protein
UniRef100_Q	58	126	39.70%	1217	1E+05	5	Splicing factor 3B subunit 3
UniRef100_Q	25	81	39.70%	923	1E+05	5	Protein KIAA1967
UniRef100_U	25	81	39.60%	925	1E+05	5	p30 DBC protein
UniRef100_Q	34	84	39.70%	821	92889	5	DNA replication licensing factor MCM6
UniRef100_P	19	40	39.70%	556	60344	6	T-complex protein 1 subunit alpha
UniRef100_Q	19	32	39.70%	501	58849	5	Splicing factor 3A subunit 3
UniRef100_Q	10	26	39.70%	290	33489	4	Protein SET
UniRef100_Q	53	81	39.60%	1357	2E+05	6	Kinectin
UniRef100_Q	8	8	39.50%	337	38609	6	Scavenger mRNA-decapping enzyme DcpS
UniRef100_Q	17	45	39.40%	493	52865	7	IGHA1 protein
UniRef100_Q	16	28	39.40%	406	45151	9	Hypothetical protein
UniRef100_Q	16	28	40.60%	394	43787	7	Proliferation-associated protein 2G4
UniRef100_Q	16	28	42.90%	373	41681	8	PA2G4 protein
UniRef100_P	11	14	39.40%	391	45144	8	Casein kinase II subunit alpha
UniRef100_U	11	14	39.00%	395	45682	8	Casein kinase II subunit alpha (EC 2.7.11.1) (CK II).
UniRef100_Q	11	14	38.80%	397	45909	8	CSNK2A1 protein
UniRef100_Q	11	14	39.40%	312	34353	8	Multisynthetase complex auxiliary component p43 [Contains: Endothelial monocyte-activating polypeptide 2 (EMAP-II) (Small inducible cytokine subfamily E member 1)]
UniRef100_Q	11	28	39.40%	277	32103	4	Isoform 2 of Q01105
UniRef100_U	11	28	39.40%	277	32134	4	SET translocation (myeloid leukemia-associated)
UniRef100_P	9	50	39.40%	216	24423	8	GTP-binding nuclear protein Ran
UniRef100_P	4	4	39.40%	188	21425	8	Isoform 2B of P01116
UniRef100_P	7	29	39.40%	175	20159	7	Alpha crystallin B chain (Alpha(B)-crystallin)
UniRef100_P	7	15	39.40%	142	17018	6	AP-2 complex subunit sigma-1
UniRef100_O	32	46	39.30%	962	1E+05	5	General vesicular transport factor p115

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_UI	32	46	39.30%	962	1E+05	5	vesicle docking protein p115
UniRef100_Q	29	234	39.30%	544	60102	8	IGHG1 protein
UniRef100_Q	10	223	39.30%	239	26024	6	IGKV1-5 protein
UniRef100_P	6	19	39.30%	84	9461	#	40S ribosomal protein S27
UniRef100_Q	164	459	39.20%	4391	5E+05	7	Heparan sulfate proteoglycan 2
UniRef100_UI	164	459	39.60%	4346	5E+05	7	Basement membrane-specific heparan sulfate proteoglycan core protein precursor (HSPG) (Perlecan) (PLC).
UniRef100_P	11	21	39.20%	380	42593	9	Flap endonuclease 1
UniRef100_P	19	30	39.20%	337	37540	7	Transaldolase
UniRef100_Q	10	12	39.20%	227	26319	6	Isopentenyl-diphosphate Delta-isomerase 1
UniRef100_UI	10	12	38.20%	233	26862	6	Isopentenyl-diphosphate delta isomerase
UniRef100_Q	10	12	36.20%	246	28515	7	IDI1 protein
UniRef100_P	4	4	39.20%	189	21229	5	GTPase NRas precursor
UniRef100_P	4	4	39.20%	189	21298	5	GTPase HRas precursor
UniRef100_Q	26	57	39.10%	747	85105	5	Heterogeneous nuclear ribonucleoprotein U-like protein 2
UniRef100_Q	20	31	39.10%	650	72596	6	Aminopeptidase B
UniRef100_P	164	460	39.00%	4391	5E+05	7	Basement membrane-specific heparan sulfate proteoglycan core protein precursor
UniRef100_Q	52	81	39.00%	1312	2E+05	7	DNA repair protein RAD50
UniRef100_Q	52	81	38.80%	1318	2E+05	7	Isoform 2 of Q92878
UniRef100_Q	17	22	39.00%	508	56940	8	UTP--glucose-1-phosphate uridylyltransferase 2
UniRef100_O	47	115	38.90%	1304	1E+05	7	Splicing factor 3B subunit 1
UniRef100_UI	47	115	38.90%	1304	1E+05	7	splicing factor 3b, subunit 1 isoform 1
UniRef100_P	21	29	38.90%	627	70436	6	Plastin-3
UniRef100_UI	21	29	38.70%	630	70811	6	plastin 3
UniRef100_P	13	13	38.90%	522	56257	9	Glutathione reductase, mitochondrial precursor
UniRef100_UI	11	15	38.90%	435	48392	5	nucleoredoxin
UniRef100_Q	11	31	38.90%	329	36414	6	Calponin-3
UniRef100_Q	8	10	38.90%	288	31675	8	Apolipoprotein A-I-binding protein
UniRef100_Q	8	10	38.90%	288	31689	8	ApoA-I binding protein precursor
UniRef100_P	7	22	38.90%	175	20082	9	ADP-ribosylation factor 6
UniRef100_Q	7	22	38.90%	175	20211	9	ADP-ribosylation factor 6
UniRef100_P	19	65	38.80%	531	58024	7	T-complex protein 1 subunit zeta
UniRef100_Q	19	65	38.90%	529	57762	7	Chaperonin containing TCP1, subunit 6A isoform a variant
UniRef100_Q	13	22	38.80%	374	42503	6	PCI domain containing 1
UniRef100_Q	19	24	38.70%	538	57564	6	Nicotinate phosphoribosyltransferase-like protein
UniRef100_Q	5	20	38.70%	124	12993	5	WAP four-disulfide core domain protein 2 precursor
UniRef100_P	36	67	38.60%	1101	1E+05	7	ATP-citrate synthase (EC 2.3.3.8) (ATP-citrate (pro-S-)-lyase)
UniRef100_UI	36	67	39.00%	1091	1E+05	7	ATP citrate lyase isoform 2
UniRef100_P	17	40	38.60%	541	59671	6	T-complex protein 1 subunit epsilon
UniRef100_Q	8	49	38.60%	233	24899	7	IGLV3-21 protein
UniRef100_Q	9	12	38.50%	218	25060	5	Eukaryotic translation initiation factor 3 subunit 12

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P4	10	27	38.50%	205	22949	7	Proteasome subunit beta type 3
UniRef100_Q9	7	9	38.50%	195	21273	7	Nucleoside diphosphate-linked moiety X motif 16
UniRef100_A0	47	95	38.40%	1512	2E+05	7	EPRS protein
UniRef100_Q	54	60	38.40%	1411	2E+05	6	Early endosome antigen 1
UniRef100_UI	54	60	38.40%	1411	2E+05	6	Early endosome antigen 1 (Endosome-associated protein p162) (Zinc finger FYVE domain-containing protein 2).
UniRef100_P5	37	50	38.40%	919	1E+05	6	Puromycin-sensitive aminopeptidase
UniRef100_UI	37	50	40.30%	875	98503	5	aminopeptidase puromycin sensitive
UniRef100_Q9	31	39	38.40%	796	91707	6	Vacuolar protein sorting-associated protein 35
UniRef100_P3	23	50	38.40%	583	68564	6	Radixin
UniRef100_O	9	11	38.40%	352	39930	7	Eukaryotic translation initiation factor 3 subunit 3
UniRef100_Q5	9	11	38.70%	349	39610	6	Hypothetical protein
UniRef100_Q5	9	11	38.40%	352	39914	7	Eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa variant
UniRef100_Q6	11	17	38.40%	349	39548	7	Twinfilin-2
UniRef100_Q9	9	18	38.40%	328	35668	7	Glyoxylate reductase/hydroxypyruvate reductase
UniRef100_P0	15	25	38.30%	412	44552	7	Cathepsin D precursor (EC 3.4.23.5) [Contains: Cathepsin D light chain; Cathepsin D heavy chain]
UniRef100_Q5	9	11	38.30%	332	35536	7	Putative quinone oxidoreductase
UniRef100_Q	7	16	38.30%	193	20954	9	Cysteine and glycine-rich protein 2
UniRef100_Q9	41	75	38.20%	1047	1E+05	6	FACT complex subunit SPT16
UniRef100_P6	10	40	38.20%	204	24146	#	60S ribosomal protein L15
UniRef100_Q5	10	40	38.20%	204	24174	#	Ribosomal protein L15 pseudogene 3
UniRef100_Q8	8	38	38.20%	191	21259	7	Cell division control protein 42 homolog precursor
UniRef100_UI	8	38	38.00%	192	21346	7	Human Cell Division Cycle 42 (CDC42)
UniRef100_O	8	13	38.20%	178	20547	9	Actin-related protein 2/3 complex subunit 3
UniRef100_P4	7	30	38.20%	144	16460	5	Eukaryotic translation initiation factor 1A, X-chromosomal
UniRef100_UI	5	18	38.20%	123	13072	7	PREDICTED: similar to D-dopachrome decarboxylase (D-dopachrome tautomerase) (Phenylpyruvate tautomerase II)
UniRef100_O0	6	20	38.20%	68	7402	7	Copper transport protein ATOX1
UniRef100_UI	6	20	38.20%	68	7449	7	Copper transport protein ATOX1 (Metal transport protein ATX1).
UniRef100_Q6	6	20	38.20%	68	7388	7	ATOX1 protein
UniRef100_P4	8	29	38.10%	194	22591	#	40S ribosomal protein S9
UniRef100_P9	4	11	38.10%	105	11749	#	Cytochrome c
UniRef100_Q7	4	11	38.10%	84	9477	#	40S ribosomal protein S27-like protein
UniRef100_UI	4	11	32.00%	100	11346	9	40S ribosomal protein S27-like protein.
UniRef100_P0	12	38	38.00%	355	40451	6	Guanine nucleotide-binding protein G(i), alpha-2 subunit
UniRef100_P1	31	60	37.90%	803	92469	5	Endoplasmin precursor
UniRef100_Q5	31	60	37.90%	802	92340	5	Tumor rejection antigen (Gp96) 1
UniRef100_Q9	17	45	37.90%	496	53392	8	IGHA1 protein
UniRef100_P0	11	24	37.90%	317	36154	6	Apolipoprotein E precursor
UniRef100_P3	8	17	37.90%	261	28048	8	Sepiapterin reductase

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	8	17	37.90%	261	28101	8	Sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) variant
UniRef100_Q	6	10	37.90%	182	20652	5	MIR-interacting saposin-like protein precursor
UniRef100_Q	21	38	37.80%	543	59341	8	Chaperonin containing TCP1, subunit 7 (Eta) variant
UniRef100_Q	21	38	37.80%	543	59367	8	T-complex protein 1 subunit eta
UniRef100_Q	21	38	37.80%	543	59329	8	CCT7 protein
UniRef100_P	5	16	37.80%	201	23010	6	Plasma retinol-binding protein precursor (PRBP) (RBP) [Contains: Plasma retinol-binding protein(1-182); Plasma retinol-binding protein(1-181); Plasma retinol-binding protein(1-179); Plasma retinol-binding protein(1-176)]
UniRef100_Q	5	16	38.20%	199	22944	6	Retinol binding protein 4, plasma
UniRef100_P	5	7	37.80%	172	19294	6	DNA-directed RNA polymerase II 19 kDa polypeptide
UniRef100_Q	4	10	37.80%	143	14804	9	L antigen family member 3
UniRef100_A	53	123	37.70%	1744	2E+05	7	Complement component C4B (Childo blood group) (Complement component C4B (Childo blood group) 2)
UniRef100_Q	8	15	37.70%	305	33581	6	WD repeat protein 61
UniRef100_Q	51	185	37.60%	1410	2E+05	9	Ribosome-binding protein 1
UniRef100_P	42	66	37.60%	1266	1E+05	6	Isoleucyl-tRNA synthetase, cytoplasmic
UniRef100_Q	42	66	37.20%	1279	1E+05	6	Isoleucyl-tRNA synthetase, cytoplasmic variant
UniRef100_O	20	81	37.60%	623	69603	9	Heterogeneous nuclear ribonucleoprotein Q
UniRef100_Q	20	81	41.60%	562	62656	8	OTTHUMP00000016816
UniRef100_Q	20	81	51.70%	453	50651	7	Hypothetical protein
UniRef100_Q	13	14	37.60%	425	47820	5	Histone-binding protein RBBP7
UniRef100_Q	13	14	34.10%	469	52314	5	Retinoblastoma binding protein 7
UniRef100_Q	13	14	38.10%	420	47273	5	Retinoblastoma binding protein 7
UniRef100_O	12	23	37.60%	372	40950	8	Actin-related protein 2/3 complex subunit 1B
UniRef100_U	12	23	37.80%	370	40821	9	PREDICTED: similar to Actin-related protein 2/3 complex subunit 1B (ARP2/3 complex 41 kDa subunit) (p41-ARC)
UniRef100_Q	11	27	37.60%	250	28673	4	Acidic (Leucine-rich) nuclear phosphoprotein 32 family, member B variant
UniRef100_Q	11	27	37.50%	251	28788	4	Acidic leucine-rich nuclear phosphoprotein 32 family member B
UniRef100_Q	9	12	37.50%	360	40369	6	TXNDC5 protein
UniRef100_Q	9	12	31.20%	432	47629	6	Thioredoxin domain-containing protein 5 precursor
UniRef100_P	4	11	37.50%	104	11553	9	Platelet factor 4 variant precursor (PF4var1) (PF4alt) (CXCL4L1) [Contains: Platelet factor 4 variant(4-74); Platelet factor 4 variant(5-74); Platelet factor 4 variant(6-74)]
UniRef100_Q	11	15	37.40%	425	47656	5	Histone-binding protein RBBP4
UniRef100_Q	12	15	37.40%	270	31806	7	Phosphatidylinositol transfer protein alpha isoform
UniRef100_U	12	15	37.30%	271	31934	7	Phosphatidylinositol transfer protein alpha isoform (PtdIns transfer protein alpha) (PtdInsTP) (PI-TP-alpha).
UniRef100_Q	12	15	32.00%	316	35900	8	PITPNA protein
UniRef100_P	8	12	37.30%	244	27507	6	Glutathione S-transferase theta-2
UniRef100_Q	8	12	39.60%	230	25948	8	Em:AP000351.3 protein
UniRef100_Q	8	12	37.30%	244	27532	7	GSTT2 protein
UniRef100_P	5	8	37.30%	142	16713	5	Glia maturation factor beta

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_UI	5	8	34.40%	154	18218	6	Glia maturation factor beta (GMF-beta).
UniRef100_Q	5	8	34.40%	154	18110	5	GMFB protein
UniRef100_P	9	11	37.20%	298	33930	9	Cell division protein kinase 2
UniRef100_O	6	10	37.20%	242	27310	9	Hypothetical protein 44M2.1
UniRef100_UI	6	10	20.50%	439	48549	9	THUMP domain-containing protein 1.
UniRef100_Q	6	10	25.50%	353	39315	8	THUMP domain-containing protein 1
UniRef100_Q	6	10	20.50%	439	48491	9	Hypothetical protein DKFZp686C1054
UniRef100_P	8	10	37.20%	215	24942	6	Casein kinase II subunit beta
UniRef100_Q	8	10	34.20%	234	26926	6	Casein kinase 2, beta polypeptide
UniRef100_Q	8	10	35.10%	228	26673	6	Casein kinase 2, beta polypeptide
UniRef100_Q	8	10	43.00%	186	21609	5	Casein kinase 2, beta polypeptide
UniRef100_P	6	8	37.20%	183	20900	8	NEDD8-conjugating enzyme Ubc12
UniRef100_UI	6	8	37.80%	180	20639	8	NEDD8-conjugating enzyme Ubc12
UniRef100_O	4	8	37.20%	129	14583	9	Prefoldin subunit 6
UniRef100_P	7	21	37.00%	127	14395	#	Activated RNA polymerase II transcriptional coactivator p15
UniRef100_UI	7	21	37.00%	127	14365	#	activated RNA polymerase II transcription cofactor 4
UniRef100_Q	7	21	35.10%	134	15135	9	Activated RNA polymerase II transcription cofactor 4 variant
UniRef100_Q	23	66	36.90%	710	72897	8	KHSRP protein
UniRef100_UI	23	66	36.50%	717	73805	8	Far upstream element-binding protein 2 (FUSE-binding protein 2) (KH type-splicing regulatory protein) (KSRP) (p75).
UniRef100_Q	17	22	36.90%	493	54530	7	Fascin
UniRef100_UI	17	22	36.90%	493	54640	8	Fascin (Singed-like protein) (55 kDa actin-bundling protein) (p55).
UniRef100_Q	17	22	36.40%	500	55136	7	FSCN1 protein
UniRef100_P	13	24	36.90%	425	47079	7	Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole- succinocarboxamide synthase (EC 6.3.2.6) (SAICAR synthetase); Phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21) (AIR carboxylase) (AIRC)]
UniRef100_UI	13	24	34.80%	451	49679	8	Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole- succinocarboxamide synthase (EC 6.3.2.6) (SAICAR synthetase); Phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21) (AIR carboxylase) (AIRC)].
UniRef100_P	25	315	36.90%	377	42009	5	Actin, aortic smooth muscle
UniRef100_P	25	315	36.90%	377	42019	5	Actin, alpha cardiac muscle 1
UniRef100_P	5	9	36.90%	179	20257	8	ARMET protein precursor
UniRef100_UI	5	9	35.70%	185	21144	9	arginine-rich, mutated in early stage tumors
UniRef100_P	5	9	36.90%	149	17302	6	Stathmin
UniRef100_Q	5	9	36.90%	149	17337	6	Stathmin 1/oncoprotein 18
UniRef100_P	19	91	36.80%	473	51268	5	Keratin, type I cytoskeletal 16
UniRef100_O	4	5	36.80%	136	14874	9	SNARE-associated protein Snapin
UniRef100_UI	22	64	36.70%	711	73161	7	KH-type splicing regulatory protein (FUSE binding protein 2)
UniRef100_Q	8	9	36.70%	335	36427	6	Probable O-sialoglycoprotein endopeptidase
UniRef100_P	8	19	36.70%	215	23707	8	Ras-related protein Rab-5B
UniRef100_Q	28	60	36.60%	868	96023	7	Programmed cell death 6-interacting protein

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	31	122	36.60%	620	68125	7	IGHM protein
UniRef100_Q	15	51	36.60%	232	27176	5	Hypothetical protein DKFZp686J1372
UniRef100_U	15	51	34.30%	248	28916	5	Tropomyosin alpha-3 chain (Tropomyosin-3) (Tropomyosin gamma) (hTM5).
UniRef100_U	15	51	34.30%	248	29079	5	Tropomyosin alpha-3 chain (Tropomyosin-3) (Tropomyosin gamma) (hTM5).
UniRef100_Q	15	51	34.30%	248	29033	5	Tropomyosin 3
UniRef100_Q	15	51	34.30%	248	28870	5	Tropomyosin 3
UniRef100_Q	15	51	36.60%	232	27175	5	Tropomyosin 3
UniRef100_P	7	14	36.60%	101	11728	6	Protein S100-A4
UniRef100_Q	65	140	36.50%	1786	2E+05	5	Laminin, beta 1
UniRef100_Q	18	49	36.50%	529	59578	9	Nucleolar protein NOP5
UniRef100_P	10	14	36.50%	510	54637	9	Fumarate hydratase, mitochondrial precursor
UniRef100_P	10	14	39.80%	467	50213	7	Isoform Cytoplasmic of P07954
UniRef100_O	10	17	36.50%	359	39589	7	Aflatoxin B1 aldehyde reductase member 2
UniRef100_Q	8	12	36.50%	293	32789	8	Exosome complex exonuclease RRP4
UniRef100_P	33	57	36.40%	937	1E+05	5	AP-2 complex subunit beta-1
UniRef100_U	33	57	35.80%	953	1E+05	5	AP-2 complex subunit beta-1 (Adapter-related protein complex 2 beta-1 subunit) (Beta-adaptin) (Plasma membrane adaptor HA2/AP2 adaptin beta subunit) (Clathrin assembly protein complex 2 beta large chain) (AP105B).
UniRef100_U	33	57	36.30%	939	1E+05	5	AP-2 complex subunit beta-1 (Adapter-related protein complex 2 beta-1 subunit) (Beta-adaptin) (Plasma membrane adaptor HA2/AP2 adaptin beta subunit) (Clathrin assembly protein complex 2 beta large chain) (AP105B).
UniRef100_Q	33	57	35.90%	951	1E+05	5	Ap2b1 protein
UniRef100_P	7	26	36.40%	165	18898	#	40S ribosomal protein S10
UniRef100_P	8	25	36.40%	151	16273	#	40S ribosomal protein S14
UniRef100_Q	3	4	36.40%	140	15805	9	Similar to CG14903-PA
UniRef100_Q	2	4	36.40%	121	13857	5	Short coiled-coil protein
UniRef100_Q	2	4	35.20%	125	14032	6	Short coiled-coil protein
UniRef100_Q	2	4	53.70%	82	9355	5	Short coiled-coil protein SCOCO
UniRef100_Q	2	4	36.10%	122	13895	5	CDNA FLJ14891 fis, clone PLACE1004256, weakly similar to Mus musculus short coiled coil protein SCOCO (Scoc) mRNA
UniRef100_Q	2	4	38.30%	115	12905	5	Similar to short coiled-coil protein
UniRef100_U	32	97	36.30%	911	1E+05	7	inter-alpha (globulin) inhibitor H1
UniRef100_P	6	13	36.30%	157	17779	#	60S ribosomal protein L24
UniRef100_P	65	141	36.20%	1786	2E+05	5	Laminin subunit beta-1 precursor
UniRef100_Q	17	21	36.20%	456	50228	6	RuvB-like 1
UniRef100_Q	11	11	36.20%	406	46269	6	COP9 signalosome complex subunit 4
UniRef100_P	12	19	36.20%	276	30354	8	Proteasome subunit beta type 8 precursor
UniRef100_Q	12	19	36.80%	272	29696	6	PSMB8 protein
UniRef100_Q	12	19	36.20%	276	30354	7	Proteasome subunit beta type
UniRef100_Q	12	19	39.70%	252	27850	8	Proteasome (Prosome, macropain) subunit, beta type, 8
UniRef100_Q	12	19	36.80%	272	29770	6	Proteasome subunit beta type

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	11	14	36.10%	313	35079	8	WD repeat protein 82
UniRef100_P	8	23	36.10%	158	18431	#	40S ribosomal protein S11
UniRef100_P	3	4	36.10%	147	16687	8	Ubiquitin-conjugating enzyme E2 D3 (EC 6.3.2.19) (Ubiquitin-protein ligase D3) (Ubiquitin carrier protein D3) (Ubiquitin-conjugating enzyme E2-17 kDa 3) (E2(17)KB 3)
UniRef100_U	3	4	35.30%	150	16910	7	Ubiquitin-conjugating enzyme E2 D3 (EC 6.3.2.19) (Ubiquitin-protein ligase D3) (Ubiquitin carrier protein D3) (Ubiquitin-conjugating enzyme E2-17 kDa 3) (E2(17)KB 3).
UniRef100_U	3	4	35.30%	150	16943	7	Ubiquitin-conjugating enzyme E2 D3 (EC 6.3.2.19) (Ubiquitin-protein ligase D3) (Ubiquitin carrier protein D3) (Ubiquitin-conjugating enzyme E2-17 kDa 3) (E2(17)KB 3).
UniRef100_U	3	4	35.60%	149	16893	8	ubiquitin-conjugating enzyme E2D 3 isoform 3
UniRef100_Q	3	4	44.90%	118	13635	8	Ubiquitin-conjugating enzyme
UniRef100_Q	3	4	35.80%	148	16785	7	CDNA FLJ38503 fis, clone HCHON2000056, highly similar to UBIQUITIN- CONJUGATING ENZYME E2-17 kDa 3
UniRef100_P	3	4	36.10%	147	16735	8	Ubiquitin-conjugating enzyme E2 D2 (EC 6.3.2.19) (Ubiquitin-protein ligase D2) (Ubiquitin carrier protein D2) (Ubiquitin-conjugating enzyme E2-17 kDa 2) (E2(17)KB 2)
UniRef100_Q	4	4	36.10%	108	11834	9	Myosin-reactive immunoglobulin light chain variable region
UniRef100_P	15	18	36.00%	509	57411	6	Histidyl-tRNA synthetase, cytoplasmic
UniRef100_P	12	23	36.00%	472	51110	8	Eukaryotic translation initiation factor 2 subunit 3
UniRef100_P	9	12	36.00%	392	42911	6	Selenide, water dikinase 1
UniRef100_P	13	19	36.00%	264	29574	6	Nicotinamide N-methyltransferase
UniRef100_P	8	11	36.00%	261	28870	7	Carbonic anhydrase 1
UniRef100_P	7	14	36.00%	136	15798	#	60S ribosomal protein L27
UniRef100_Q	12	28	35.90%	326	36900	6	Uncharacterized protein C20orf77
UniRef100_Q	6	6	35.90%	251	27383	6	Uncharacterized protein C11orf68
UniRef100_U	6	6	35.90%	251	27355	6	Uncharacterized protein C11orf68 (Basophilic leukemia expressed protein Bles03) (Protein p5326).
UniRef100_A	7	17	35.90%	198	20925	6	CutA divalent cation tolerance homolog
UniRef100_O	7	17	39.70%	179	19116	6	Protein CutA precursor
UniRef100_A	14	28	35.80%	433	50263	9	Hypothetical protein DKFZp686F17268
UniRef100_U	14	28	35.40%	438	50809	9	Septin-7 (CDC10 protein homolog).
UniRef100_Q	14	28	37.20%	417	48659	9	Septin 7
UniRef100_Q	14	28	37.10%	418	48774	9	Predicted protein product of Nbla02942
UniRef100_Q	14	28	35.60%	436	50581	9	Isoform 2 of Q16181
UniRef100_Q	14	28	35.50%	437	50680	9	Septin-7
UniRef100_P	7	8	35.80%	366	41268	5	Spermine synthase
UniRef100_Q	13	17	35.80%	372	40058	#	Core histone macro-H2A.2
UniRef100_Q	10	65	35.80%	285	30588	8	Isoform 3 of Q99729
UniRef100_Q	28	29	35.70%	1169	1E+05	6	Ankyrin repeat and FYVE domain-containing protein 1
UniRef100_U	28	29	35.70%	1168	1E+05	6	Ankyrin repeat and FYVE domain-containing protein 1 (Ankyrin repeats hooked to a zinc finger motif).
UniRef100_P	8	11	35.70%	297	34095	8	Cell division control protein 2 homolog

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_U	8	11	35.70%	297	34081	8	Cell division control protein 2 homolog (EC 2.7.11.22) (EC 2.7.11.23) (p34 protein kinase) (Cyclin-dependent kinase 1) (CDK1).
UniRef100_O	5	7	35.70%	230	24670	7	Acyl-protein thioesterase 1
UniRef100_O	5	7	38.30%	214	22875	7	Isoform 2 of O75608
UniRef100_Q	4	4	35.70%	199	21764	7	COMM domain-containing protein 4
UniRef100_P	23	46	35.60%	810	90569	7	Plasminogen precursor (EC 3.4.21.7) [Contains: Plasmin heavy chain A; Activation peptide; Angiostatin; Plasmin heavy chain A, short form; Plasmin light chain B]
UniRef100_P	26	38	35.60%	775	87799	7	Glutaminyl-tRNA synthetase
UniRef100_Q	26	38	35.60%	775	87711	7	Glutaminyl-tRNA synthetase variant
UniRef100_Q	23	49	35.60%	644	67560	8	Far upstream element-binding protein 1
UniRef100_U	23	49	35.00%	655	68904	8	Far upstream element-binding protein 1 (FUSE-binding protein 1) (FBP) (DNA helicase V) (HDH V).
UniRef100_U	23	49	35.20%	651	68491	7	Far upstream element-binding protein 1 (FUSE-binding protein 1) (FBP) (DNA helicase V) (HDH V).
UniRef100_Q	23	49	35.10%	653	68605	7	Isoform 2 of Q96AE4
UniRef100_P	12	35	35.60%	264	29945	#	40S ribosomal protein S3a
UniRef100_Q	12	35	35.60%	264	29975	#	Ribosomal protein S3A
UniRef100_Q	22	24	35.40%	765	86161	7	Protein transport protein Sec23A
UniRef100_Q	19	48	35.40%	745	81745	6	Plakoglobin
UniRef100_Q	19	48	33.70%	784	85651	7	JUP protein
UniRef100_Q	19	48	35.40%	745	81717	6	Gamma-catenin
UniRef100_P	13	15	35.40%	511	55366	7	Alpha-aminoadipic semialdehyde dehydrogenase
UniRef100_P	11	20	35.40%	495	54273	6	Alpha-1B-glycoprotein precursor
UniRef100_Q	10	17	35.40%	325	35701	6	BTB/POZ domain-containing protein KCTD12
UniRef100_P	8	12	35.40%	144	17000	9	Protein BUD31 homolog
UniRef100_P	3	7	35.40%	99	11261	9	Acylphosphatase-1
UniRef100_U	3	7	47.90%	73	8322	#	Acylphosphatase-1 (EC 3.6.1.7) (Acylphosphate phosphohydrolase 1) (Acylphosphatase, organ-common type isozyme) (Acylphosphatase, erythrocyte isozyme).
UniRef100_P	13	32	35.30%	348	39008	7	Haptoglobin-related protein precursor
UniRef100_P	13	32	31.90%	385	43056	7	Isoform 2 of P00739
UniRef100_P	11	23	35.30%	204	23207	5	Rho GDP-dissociation inhibitor 1
UniRef100_P	4	8	35.30%	119	13715	7	Beta-2-microglobulin precursor [Contains: Beta-2-microglobulin variant pI 5.3]
UniRef100_Q	4	8	35.30%	119	13697	7	B2M protein
UniRef100_Q	10	10	35.20%	344	37376	6	N-acetylglucosamine kinase
UniRef100_P	4	12	35.20%	128	14174	9	NHP2-like protein 1
UniRef100_U	4	12	34.60%	130	14318	9	U4/U6.U5 tri-snRNP 15.5 kDa protein
UniRef100_Q	4	10	35.20%	125	13833	6	14 kDa phosphohistidine phosphatase
UniRef100_U	4	10	30.60%	144	16144	6	14 kDa phosphohistidine phosphatase
UniRef100_P	33	57	35.10%	904	1E+05	6	DNA replication licensing factor MCM2
UniRef100_P	8	29	35.10%	225	25486	#	U2 small nuclear ribonucleoprotein B''
UniRef100_Q	7	11	35.10%	194	21446	6	Inosine triphosphate pyrophosphatase

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	5	5	35.10%	188	20783	#	Trafficking protein particle complex subunit 5
UniRef100_Q	31	53	35.00%	1139	1E+05	5	DCTN1 protein
UniRef100_Q	10	15	35.00%	274	28649	8	Pyrroline-5-carboxylate reductase-like
UniRef100_O	61	165	34.90%	2045	2E+05	6	Agrin precursor
UniRef100_P	13	53	34.90%	338	38429	7	Lumican precursor
UniRef100_Q	14	20	34.80%	466	53263	9	Adaptor-related protein complex 1, mu 1 subunit variant
UniRef100_Q	14	20	38.30%	423	48587	7	AP-1 complex subunit mu-1
UniRef100_U	27	39	34.70%	955	1E+05	8	adaptor-related protein complex 2, alpha 1 subunit isoform 2
UniRef100_U	27	39	33.90%	977	1E+05	7	adaptor-related protein complex 2, alpha 1 subunit isoform 1
UniRef100_Q	24	116	34.70%	723	79844	8	Heterogeneous nuclear ribonucleoprotein U
UniRef100_O	15	44	34.70%	427	49130	6	ATP-dependent RNA helicase DDX39
UniRef100_P	6	9	34.70%	297	33178	7	3-mercaptopyruvate sulfurtransferase
UniRef100_P	10	40	34.70%	248	29226	#	60S ribosomal protein L7
UniRef100_U	10	40	32.00%	269	31621	#	RPL7 protein.
UniRef100_Q	10	40	27.00%	318	37022	#	RPL7 protein
UniRef100_U	6	11	34.70%	202	22537	6	Tetranectin precursor (TN) (C-type lectin domain family 3 member B) (Plasminogen kringle 4-binding protein).
UniRef100_P	4	11	34.70%	101	10845	9	Platelet factor 4 precursor
UniRef100_Q	4	11	64.80%	54	6033	#	PF 4-derived endothelial cell growth inhibitor PEAK II
UniRef100_P	21	47	34.60%	703	77261	5	Fibulin-1 precursor
UniRef100_U	21	47	34.60%	703	77242	5	fibulin 1 isoform D
UniRef100_U	21	47	34.60%	703	77214	5	Fibulin-1 precursor.
UniRef100_Q	6	8	34.60%	162	18885	8	Sorting nexin 12
UniRef100_U	6	8	32.60%	172	19819	8	Sorting nexin-12.
UniRef100_Q	6	8	32.60%	172	19730	8	Sorting nexin-12
UniRef100_Q	5	12	34.60%	81	9072	8	NEDD8 precursor
UniRef100_U	5	12	34.60%	81	8905	7	NEDD8
UniRef100_Q	16	38	34.50%	519	56424	7	Hypothetical protein DKFZp686K18196
UniRef100_Q	16	38	36.10%	496	53533	7	CDNA FLJ25298 fis, clone STM07683, highly similar to Protein Tro alpha1 H,myeloma
UniRef100_Q	16	38	35.90%	499	53376	7	IGHA1 protein
UniRef100_Q	16	38	36.20%	494	53321	7	CDNA FLJ41552 fis, clone COLON2004478, highly similar to Protein Tro alpha1 H,myeloma
UniRef100_Q	9	62	34.50%	232	24795	6	IGL@ protein
UniRef100_U	6	8	34.40%	291	31821	5	Exosome complex exonuclease RRP42 (EC 3.1.13.-) (Ribosomal RNA- processing protein 42) (Exosome component 7) (p8).
UniRef100_U	5	5	34.40%	186	21337	7	Peroxiredoxin-4 (EC 1.11.1.15) (Prx-IV) (Thioredoxin peroxidase AO372) (Thioredoxin-dependent peroxide reductase A0372) (Antioxidant enzyme AOE372) (AOE37-2).
UniRef100_O	3	4	34.40%	122	14210	7	Prefoldin subunit 1
UniRef100_Q	22	32	34.30%	740	82432	7	ATP-dependent RNA helicase DDX1
UniRef100_P	3	16	34.30%	143	15808	#	40S ribosomal protein S23
UniRef100_U	3	16	32.00%	153	16681	#	PREDICTED: similar to ribosomal protein S23
UniRef100_U	3	16	34.30%	143	15790	#	40S ribosomal protein S23.

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P	12	30	34.20%	284	32990	5	Isoform 2 of P07951
UniRef100_Q	5	9	34.20%	161	18155	7	Peptidyl-prolyl cis-trans isomerase-like 3
UniRef100_A	7	11	34.10%	211	23467	9	Ras-related C3 botulinum toxin substrate 1
UniRef100_P	7	11	37.50%	192	21450	9	Ras-related C3 botulinum toxin substrate 1 precursor
UniRef100_A	7	11	48.60%	148	16797	9	Ras-related C3 botulinum toxin substrate 1
UniRef100_Q	19	57	34.00%	636	71214	8	HNRPR protein
UniRef100_Q	7	9	34.00%	315	35117	7	Ester hydrolase C11orf54
UniRef100_P	11	166	33.90%	434	47269	5	Gamma-enolase
UniRef100_Q	10	11	33.90%	404	42136	7	Acetyl-CoA acetyltransferase, cytosolic variant
UniRef100_Q	10	11	34.50%	397	41351	7	Acetyl-CoA acetyltransferase, cytosolic
UniRef100_Q	10	12	33.90%	327	36163	6	COP9 signalosome complex subunit 6
UniRef100_P	14	15	33.80%	474	52385	6	Glutathione synthetase
UniRef100_Q	9	15	33.80%	325	36502	6	Eukaryotic translation initiation factor 3 subunit 2
UniRef100_Q	9	15	33.80%	325	36500	6	Eukaryotic translation initiation factor 3, subunit 2 beta, 36kDa variant
UniRef100_Q	5	6	33.80%	240	26443	7	IAH1 protein
UniRef100_Q	5	6	35.10%	231	25635	7	IAH1 protein
UniRef100_Q	5	6	32.70%	248	27599	5	Isoamyl acetate-hydrolyzing esterase 1 homolog
UniRef100_Q	6	13	33.80%	148	16253	7	Dynein, light chain, roadblock-type 1
UniRef100_Q	6	13	52.10%	96	10922	7	Dynein light chain roadblock-type 1
UniRef100_P	6	18	33.70%	104	12259	6	Enhancer of rudimentary homolog
UniRef100_Q	5	15	33.70%	98	11471	6	Protein S100-A13
UniRef100_P	17	30	33.60%	660	75379	7	Arginyl-tRNA synthetase, cytoplasmic
UniRef100_O	20	64	33.60%	633	70943	8	Heterogeneous nuclear ribonucleoprotein R
UniRef100_Q	10	10	33.60%	423	47873	7	COP9 signalosome complex subunit 3
UniRef100_Q	3	6	33.60%	131	14711	5	Chromatin accessibility complex protein 1
UniRef100_Q	18	36	33.50%	597	68048	6	Lysyl-tRNA synthetase
UniRef100_U	18	36	32.00%	625	71497	7	Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) (LysRS).
UniRef100_Q	18	36	32.00%	625	71384	7	Lysyl-tRNA synthetase
UniRef100_P	7	8	33.50%	257	30005	7	26S proteasome non-ATPase regulatory subunit 8
UniRef100_Q	7	8	33.50%	257	29922	7	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 8
UniRef100_Q	6	7	33.50%	227	24434	7	Candidate tumor suppressor in ovarian cancer 2
UniRef100_Q	6	7	33.50%	227	24418	7	Candidate tumor suppressor OVCA2
UniRef100_Q	8	8	33.40%	314	35620	6	Hypothetical protein FLJ11151
UniRef100_U	8	8	33.40%	314	35548	6	CDNA FLJ11151 fis, clone PLACE1006883.
UniRef100_Q	8	8	33.40%	314	35624	6	CDNA FLJ12648 fis, clone NT2RM4002018
UniRef100_P	7	16	33.40%	314	34920	8	Tumor-associated calcium signal transducer 1 precursor
UniRef100_U	7	16	33.40%	314	34902	8	tumor-associated calcium signal transducer 1 precursor
UniRef100_Q	7	16	33.40%	314	34960	8	TACSTD1 protein
UniRef100_Q	7	16	33.40%	314	34932	8	TACSTD1 protein
UniRef100_P	10	25	33.40%	293	31324	#	40S ribosomal protein S2
UniRef100_U	10	25	33.40%	293	31438	#	similar to ribosomal protein S2 (LOC646294), mRNA

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	10	25	33.40%	293	31385	#	Ribosomal protein S2
UniRef100_P	14	21	33.30%	493	54739	7	Phospholipid transfer protein precursor
UniRef100_P	12	22	33.30%	381	42982	5	cAMP-dependent protein kinase type I-alpha regulatory subunit
UniRef100_Q	12	22	33.30%	381	42948	5	Hypothetical protein DKFZp779L0468
UniRef100_Q	6	10	33.30%	231	25734	7	Platelet-activating factor acetylhydrolase IB subunit gamma
UniRef100_P	6	37	33.30%	207	23668	9	Ras-related protein Rab-8A
UniRef100_Q	4	8	33.30%	198	22367	7	GTP-binding protein SAR1a
UniRef100_O	4	5	33.30%	153	17561	9	Histone deacetylase complex subunit SAP18
UniRef100_Q	31	56	33.20%	1156	1E+05	6	Scavenger receptor cysteine-rich type 1 protein M130 precursor (CD163 antigen) (Hemoglobin scavenger receptor) [Contains: Soluble CD163 (sCD163)]
UniRef100_Q	31	56	33.30%	1154	1E+05	6	Isoform 4 of Q86VB7
UniRef100_Q	31	56	34.30%	1121	1E+05	6	Isoform 3 of Q86VB7
UniRef100_Q	31	56	33.10%	1161	1E+05	6	Isoform 2 of Q86VB7
UniRef100_P	20	33	33.20%	750	87335	6	Signal transducer and activator of transcription 1-alpha/beta
UniRef100_P	11	12	33.20%	494	53802	6	4-trimethylaminobutyraldehyde dehydrogenase
UniRef100_Q	6	10	33.20%	193	22774	#	Uncharacterized protein C16orf80
UniRef100_P	16	36	33.10%	432	47716	6	Adenosylhomocysteinase
UniRef100_Q	9	13	33.10%	359	40308	7	Sialic acid synthase
UniRef100_Q	12	30	33.10%	284	32815	5	Tropomyosin 2
UniRef100_P	11	18	33.10%	254	29506	6	Proteasome activator complex subunit 3
UniRef100_P	11	18	31.50%	267	30887	6	Isoform 2 of P61289
UniRef100_O	4	7	33.10%	178	19344	5	Nucleoplasmin-3
UniRef100_Q	5	31	33.10%	172	18648	#	Cold-inducible RNA-binding protein
UniRef100_P	74	210	33.00%	2349	3E+05	5	Nucleoprotein TPR
UniRef100_Q	74	210	32.80%	2363	3E+05	5	Translocated promoter region
UniRef100_Q	13	21	33.00%	640	71224	5	SUMO-activating enzyme subunit 2
UniRef100_P	13	35	33.00%	454	50670	9	Lamina-associated polypeptide 2, isoforms beta/gamma (Thymopoietin, isoforms beta/gamma) (TP beta/gamma) (Thymopoietin-related peptide isoforms beta/gamma) (TPRP isoforms beta/gamma) [Contains: Thymopoietin (TP) (Splenin); Thymopentin (TP5)]
UniRef100_P	6	13	33.00%	321	33784	#	rRNA 2'-O-methyltransferase fibrillarin
UniRef100_Q	6	13	40.80%	260	28449	9	FBL protein
UniRef100_P	10	19	33.00%	303	33777	7	Crk-like protein
UniRef100_Q	9	13	33.00%	282	29130	8	Insulin-like growth factor-binding protein 7 precursor
UniRef100_P	8	10	33.00%	273	28936	8	Proteasome subunit beta type 10 precursor
UniRef100_Q	5	6	33.00%	197	21820	8	Lin-7 homolog C variant
UniRef100_Q	5	6	33.00%	197	21834	8	Lin-7 homolog C
UniRef100_Q	2	7	33.00%	100	11309	9	Vesicle-associated membrane protein 3
UniRef100_Q	2	7	33.00%	100	11310	7	Vesicle-associated membrane protein 3
UniRef100_Q	25	126	32.90%	806	88980	6	Isoform Short of Q00839
UniRef100_Q	7	13	32.90%	225	24348	8	Ras-related protein Rab-21
UniRef100_O	16	40	32.80%	579	63720	9	Insulin-like growth factor 2 mRNA-binding protein 3

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_U	16	40	32.80%	579	63705	9	insulin-like growth factor 2 mRNA binding protein 3
UniRef100_P	4	5	32.80%	137	15594	5	Immunoglobulin J chain
UniRef100_P	23	46	32.70%	1010	1E+05	7	Trifunctional purine biosynthetic protein adenosine-3 [Includes: Phosphoribosylamine--glycine ligase (EC 6.3.4.13) (GARS) (Glycinamide ribonucleotide synthetase) (Phosphoribosylglycinamide synthetase); Phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1) (AIRS) (Phosphoribosyl-aminoimidazole synthetase) (AIR synthase); Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2) (GART) (GAR transformylase) (5'-phosphoribosylglycinamide transformylase)]
UniRef100_Q	23	46	31.50%	1046	1E+05	7	Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase isoform 1 variant
UniRef100_Q	23	46	32.70%	1010	1E+05	7	Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase
UniRef100_O	14	18	32.70%	548	62943	6	Asparaginyl-tRNA synthetase, cytoplasmic
UniRef100_Q	14	18	32.70%	548	62911	6	Asparaginyl-tRNA synthetase variant
UniRef100_P	10	19	32.70%	352	38999	6	AMBP protein precursor [Contains: Alpha-1-microglobulin (Protein HC) (Complex-forming glycoprotein heterogeneous in charge) (Alpha-1 microglycoprotein); Inter-alpha-trypsin inhibitor light chain (ITI-LC) (Bikunin) (HI-30)]
UniRef100_A	2	4	32.70%	113	12388	9	Cold agglutinin FS-1 L-chain
UniRef100_U	2	4	30.30%	122	13446	8	ANTI EGFR ANTIBODY FV REGION
UniRef100_P	2	4	32.70%	113	12316	6	Ig kappa chain V-II region TEW
UniRef100_P	24	42	32.60%	847	97149	7	Glycogen phosphorylase, liver form
UniRef100_Q	9	17	32.60%	368	42209	7	Twinfilin-1
UniRef100_U	9	17	32.60%	368	42362	8	Twinfilin-1 (Protein A6) (Protein tyrosine kinase 9).
UniRef100_Q	9	17	32.30%	372	42389	7	TWF1 protein
UniRef100_Q	9	17	34.30%	350	40283	7	Isoform 1 of Q12792
UniRef100_P	11	16	32.60%	316	35853	7	Aldose reductase
UniRef100_Q	20	255	32.50%	449	50094	5	Tubulin alpha-8 chain
UniRef100_Q	10	32	32.40%	404	45250	6	PSMC3 protein
UniRef100_Q	8	15	32.40%	358	40668	6	Serine/threonine-protein phosphatase 2A regulatory subunit B'
UniRef100_Q	8	15	35.90%	323	36775	6	Isoform 1 of Q15257
UniRef100_P	10	25	32.40%	284	32876	5	Isoform 3 of P09493
UniRef100_P	7	12	32.40%	241	27566	7	Glutathione transferase omega-1
UniRef100_Q	4	6	32.40%	170	19550	6	HD domain containing 2
UniRef100_Q	4	6	32.40%	170	19491	5	CGI-130 protein
UniRef100_Q	4	6	25.20%	218	24850	6	HD domain-containing protein 2
UniRef100_Q	4	6	27.00%	204	23419	6	HD domain containing 2
UniRef100_Q	10	20	32.30%	575	58977	8	Dihydroxyacetone kinase
UniRef100_U	10	20	32.30%	575	58947	8	dihydroxyacetone kinase 2
UniRef100_P	9	20	32.30%	158	18007	9	SUMO-conjugating enzyme UBC9

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_U	9	20	27.70%	184	20458	9	SUMO-conjugating enzyme UBC9 (EC 6.3.2.-) (SUMO-protein ligase) (Ubiquitin-conjugating enzyme E2 I) (Ubiquitin-protein ligase I) (Ubiquitin carrier protein I) (Ubiquitin carrier protein 9) (p18).
UniRef100_Q	9	20	27.70%	184	20444	9	Ubiquitin-conjugating enzyme E2I
UniRef100_Q	20	26	32.20%	807	90974	6	Spondin-1 precursor
UniRef100_U	20	26	32.30%	806	90903	6	Spondin-1 precursor (F-spondin) (Vascular smooth muscle cell growth- promoting factor).
UniRef100_P	7	8	32.20%	367	39325	6	Alpha-2-HS-glycoprotein precursor (Fetuin-A) (Alpha-2-Z-globulin) (Ba- alpha-2-glycoprotein) [Contains: Alpha-2-HS-glycoprotein chain A; Alpha-2-HS-glycoprotein chain B]
UniRef100_U	7	8	32.20%	367	39341	6	Alpha-2-HS-glycoprotein precursor (Fetuin-A) (Alpha-2-Z-globulin) (Ba- alpha-2-glycoprotein) [Contains: Alpha-2-HS-glycoprotein chain A; Alpha-2-HS-glycoprotein chain B].
UniRef100_Q	11	24	32.20%	307	34930	#	Leucine-rich repeat-containing protein 59
UniRef100_P	7	21	32.10%	140	14865	#	60S ribosomal protein L23
UniRef100_U	7	21	32.10%	140	14811	#	60S ribosomal protein L23 (Ribosomal protein L17).
UniRef100_Q	7	21	33.60%	134	14150	#	Similar to ribosomal protein L23
UniRef100_Q	28	88	32.00%	793	88886	5	Splicing factor 3 subunit 1
UniRef100_P	13	19	32.00%	353	40532	5	Farnesyl pyrophosphate synthetase (FPP synthetase) (FPS) (Farnesyl diphosphate synthetase) [Includes: Dimethylallyltranstransferase (EC 2.5.1.1); Geranyltranstransferase (EC 2.5.1.10)]
UniRef100_P	2	2	32.00%	100	10729	6	Ig kappa chain V-III region NG9 precursor
UniRef100_Q	2	4	32.00%	75	8745	6	Probable protein BRICK1
UniRef100_U	2	4	22.20%	108	12158	7	UPI00004570B9 UniRef100 entry
UniRef100_Q	2	4	22.60%	106	12046	7	Isoform 2 of Q8WUW1
UniRef100_Q	25	123	31.90%	824	90514	6	Heterogeneous nuclear ribonucleoprotein U
UniRef100_Q	7	10	31.80%	311	34005	7	Phosphopantothenate--cysteine ligase
UniRef100_Q	7	10	31.80%	176	20748	6	Vacuolar protein sorting-associated protein 25
UniRef100_P	13	34	31.70%	511	57210	6	Coatomer subunit delta
UniRef100_U	13	34	29.30%	552	61626	6	Coatomer subunit delta (Delta-coat protein) (Delta-COP) (Archain).
UniRef100_Q	13	34	29.30%	552	61598	6	Hypothetical protein DKFZp686M09245
UniRef100_P	7	7	31.70%	350	41213	9	Casein kinase II subunit alpha'
UniRef100_Q	11	11	31.60%	370	40423	8	Phosphoserine aminotransferase
UniRef100_P	10	25	31.60%	297	34363	#	60S ribosomal protein L5
UniRef100_P	6	9	31.60%	177	20198	5	Coatomer subunit zeta-1
UniRef100_Q	6	9	31.60%	177	20267	5	Coatomer protein complex, subunit zeta 1 variant
UniRef100_P	5	11	31.60%	114	12640	8	Ig kappa chain V-IV region Len
UniRef100_U	5	11	31.60%	114	12625	8	IMMUNOGLOBULIN LIGHT CHAIN VARIABLE DOMAIN
UniRef100_O	30	49	31.50%	1038	1E+05	5	Importin-7
UniRef100_Q	8	10	31.50%	298	33811	6	Golgi phosphoprotein 3
UniRef100_P	6	9	31.50%	222	24722	8	Superoxide dismutase [Mn], mitochondrial precursor
UniRef100_U	6	9	31.50%	222	24750	8	manganese superoxide dismutase isoform A precursor
UniRef100_P	3	7	31.50%	108	11939	5	Ig kappa chain V-I region AU
UniRef100_P	20	55	31.40%	808	90981	6	DNA replication licensing factor MCM3

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	20	55	31.40%	808	90981	6	Minichromosome maintenance protein 3 variant
UniRef100_P	13	116	31.40%	449	49229	6	Heterogeneous nuclear ribonucleoprotein H
UniRef100_U	13	116	29.90%	472	51230	7	Heterogeneous nuclear ribonucleoprotein H (hnRNP H).
UniRef100_Q	13	116	31.40%	449	49130	6	HNRPH1 protein
UniRef100_P	7	8	31.40%	338	36814	7	Fructose-1,6-bisphosphatase 1
UniRef100_P	4	7	31.40%	210	24551	6	DNA-directed RNA polymerase II 23 kDa polypeptide
UniRef100_U	4	7	31.40%	210	24611	6	DNA directed RNA polymerase II polypeptide E
UniRef100_Q	3	7	31.40%	118	13133	5	Transcription elongation factor B polypeptide 2
UniRef100_U	3	7	23.00%	161	17911	6	elongin B isoform b
UniRef100_Q	37	55	31.30%	1299	1E+05	5	Diaphanous 1 variant
UniRef100_Q	37	55	31.90%	1272	1E+05	6	Diaphanous 1
UniRef100_O	13	38	31.30%	533	56651	7	D-3-phosphoglycerate dehydrogenase
UniRef100_P	7	8	31.30%	307	35080	5	Serine/threonine-protein phosphatase 4 catalytic subunit
UniRef100_Q	8	17	31.30%	166	18237	8	Peptidyl-prolyl cis-trans isomerase-like 1
UniRef100_Q	5	7	31.30%	147	16860	5	DNA polymerase epsilon subunit 3
UniRef100_U	5	7	31.30%	147	16872	5	DNA polymerase epsilon subunit 3
UniRef100_Q	5	11	31.30%	147	15892	8	Calcium-regulated heat stable protein 1
UniRef100_P	19	42	31.20%	781	85497	6	Catenin beta-1
UniRef100_U	19	42	31.50%	774	84766	6	PREDICTED: similar to catenin (cadherin-associated protein), beta 1, 88kDa
UniRef100_U	19	42	34.80%	702	77207	7	PREDICTED: similar to Beta-catenin
UniRef100_U	19	42	35.20%	694	75927	7	PREDICTED: similar to catenin (cadherin-associated protein), beta 1, 88kDa
UniRef100_P	20	28	31.20%	734	82286	8	DNA replication licensing factor MCM5
UniRef100_Q	20	28	31.20%	734	82237	8	Minichromosome maintenance deficient protein 5 variant
UniRef100_P	15	22	31.20%	592	67903	6	Interferon-induced guanylate-binding protein 1
UniRef100_P	14	30	31.20%	539	57924	8	T-complex protein 1 subunit delta
UniRef100_P	12	27	31.20%	250	26188	9	Galectin-3
UniRef100_Q	12	27	31.20%	250	26152	9	LGALS3 protein
UniRef100_Q	12	27	31.20%	250	26161	9	LGALS3 protein
UniRef100_Q	12	27	30.20%	258	27118	8	LGALS3 protein variant
UniRef100_P	3	6	31.20%	125	14311	8	Biogenesis of lysosome-related organelles complex-1 subunit 1
UniRef100_P	13	20	31.10%	515	59257	7	Glucose-6-phosphate 1-dehydrogenase
UniRef100_U	13	20	29.40%	545	62468	8	glucose-6-phosphate dehydrogenase isoform a
UniRef100_Q	13	20	33.70%	475	54824	7	Glucose-6-phosphate dehydrogenase
UniRef100_Q	13	20	33.70%	475	54825	7	Glucose-6-phosphate 1-dehydrogenase
UniRef100_Q	13	20	33.70%	475	54857	7	Glucose-6-phosphate 1-dehydrogenase
UniRef100_P	13	20	28.50%	561	63827	7	Isoform Long of P11413
UniRef100_P	7	12	31.10%	322	35541	6	Protein SEC13 homolog
UniRef100_A	8	15	31.10%	273	31682	6	MHC class I antigen
UniRef100_A	8	15	31.10%	273	31799	6	MHC class I antigen
UniRef100_A	8	15	31.10%	273	31636	6	MHC class I antigen
UniRef100_P	8	23	31.10%	228	26680	5	Isoform 2 of P09493

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	5	5	31.10%	212	24702	8	Programmed cell death protein 10
UniRef100_P	6	43	31.10%	164	19330	#	Splicing factor, arginine/serine-rich 3
UniRef100_U	6	43	34.00%	150	16821	6	Fusion protein consists of immunoglobin G-Bin
UniRef100_U	6	43	34.00%	150	16835	6	Fusion protein consists of immunoglobin G-Bin
UniRef100_A	2	2	31.10%	106	12218	7	FTO protein
UniRef100_U	2	2	6.50%	505	58282	5	fatso
UniRef100_Q	2	2	6.50%	507	58456	5	KIAA1752 protein
UniRef100_Q	2	2	26.00%	127	14936	9	Hypothetical protein
UniRef100_Q	31	60	31.00%	1156	1E+05	6	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin c2 isoform b variant
UniRef100_Q	31	60	31.70%	1130	1E+05	6	Isoform 2 of Q8TAQ2
UniRef100_Q	31	60	29.50%	1214	1E+05	6	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily C member 2
UniRef100_Q	31	60	30.80%	1164	1E+05	6	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin c2 isoform b variant
UniRef100_P	8	20	31.00%	345	37419	7	GMP reductase 1
UniRef100_U	8	20	31.00%	345	37385	7	guanosine monophosphate reductase
UniRef100_Q	4	16	31.00%	248	27385	7	Eukaryotic translation initiation factor 4H
UniRef100_Q	4	16	33.80%	228	25200	8	Isoform Short of Q15056
UniRef100_P	6	9	31.00%	197	22128	8	Phospholipid hydroperoxide glutathione peroxidase, mitochondrial precursor
UniRef100_U	6	9	26.10%	234	26948	#	glutathione peroxidase 4 isoform C precursor
UniRef100_U	6	9	31.00%	197	22025	8	glutathione peroxidase 4 isoform A precursor
UniRef100_P	6	9	35.90%	170	19478	8	Isoform Cytoplasmic of P36969
UniRef100_Q	3	6	31.00%	100	11438	7	Vesicle-associated membrane protein 8
UniRef100_O	12	17	30.90%	456	52904	8	26S proteasome non-ATPase regulatory subunit 12
UniRef100_Q	5	41	30.90%	188	21634	#	60S ribosomal protein L18
UniRef100_Q	5	41	35.40%	164	18732	#	Ribosomal protein L18
UniRef100_Q	2	6	30.90%	97	10405	5	V2-17 protein
UniRef100_Q	33	56	30.80%	1278	1E+05	6	Dynactin-1
UniRef100_O	35	36	30.80%	1150	1E+05	5	Nardilysin precursor
UniRef100_U	35	36	30.80%	1151	1E+05	5	Nardilysin precursor (EC 3.4.24.61) (N-arginine dibasic convertase) (NRD convertase) (NRD-C).
UniRef100_U	35	36	30.80%	1150	1E+05	5	Nardilysin precursor (EC 3.4.24.61) (N-arginine dibasic convertase) (NRD convertase) (NRD-C).
UniRef100_U	35	36	29.00%	1219	1E+05	5	nardilysin (N-arginine dibasic convertase)
UniRef100_Q	35	36	29.00%	1219	1E+05	5	Nardilysin
UniRef100_O	35	36	29.10%	1218	1E+05	5	Isoform 2 of O43847
UniRef100_O	25	39	30.80%	795	90933	8	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15
UniRef100_P	17	19	30.80%	723	83435	7	Threonyl-tRNA synthetase, cytoplasmic
UniRef100_Q	17	19	32.70%	682	78606	7	TARS protein
UniRef100_Q	17	19	30.80%	723	83445	7	Threonyl-tRNA synthetase variant

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P	12	88	30.80%	415	45672	6	Heterogeneous nuclear ribonucleoprotein F
UniRef100_O	8	13	30.80%	328	37155	7	Mitotic checkpoint protein BUB3
UniRef100_Q	3	7	30.80%	107	11520	9	Anti-streptococcal/anti-myosin immunoglobulin kappa light chain variable region
UniRef100_Q	3	7	30.60%	108	11738	8	Myosin-reactive immunoglobulin light chain variable region
UniRef100_P	22	106	30.70%	564	60200	8	Keratin, type II cytoskeletal 6C
UniRef100_P	22	106	30.70%	564	60045	8	Keratin, type II cytoskeletal 6A
UniRef100_U	9	11	30.70%	440	50928	6	Septin-8.
UniRef100_U	9	11	29.30%	460	53163	7	Septin-8.
UniRef100_Q	38	44	30.60%	1253	1E+05	7	Cytoplasmic FMR1-interacting protein 1
UniRef100_Q	12	14	30.60%	435	49655	#	AP-2 complex subunit mu-1
UniRef100_U	12	14	30.70%	433	49390	#	AP-2 complex subunit mu-1 (Adaptin mu-1) (AP-2 mu-2 chain) (Clathrin coat assembly protein AP50) (Clathrin coat-associated protein AP50) (Plasma membrane adaptor AP-2 50 kDa protein) (HA2 50 kDa subunit) (Clathrin assembly protein complex 2 medium chain).
UniRef100_U	12	14	30.60%	435	49656	#	AP-2 complex subunit mu-1 (Adaptin mu-1) (AP-2 mu-2 chain) (Clathrin coat assembly protein AP50) (Clathrin coat-associated protein AP50) (Plasma membrane adaptor AP-2 50 kDa protein) (HA2 50 kDa subunit) (Clathrin assembly protein complex 2 medium chain).
UniRef100_O	11	19	30.60%	422	47464	7	26S proteasome non-ATPase regulatory subunit 11
UniRef100_Q	11	19	30.50%	423	47535	7	Proteasome 26S non-ATPase subunit 11 variant
UniRef100_P	7	15	30.60%	340	37331	6	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 2
UniRef100_Q	10	16	30.50%	439	50436	6	Rho GTPase-activating protein 1
UniRef100_A	7	13	30.40%	273	31679	6	MHC class I antigen
UniRef100_Q	7	9	30.40%	260	29910	6	DnaJ homolog subfamily C member 9
UniRef100_Q	17	20	30.30%	564	66696	6	Eukaryotic translation initiation factor 3 subunit 6 interacting protein variant
UniRef100_Q	17	20	30.30%	564	66727	6	Eukaryotic translation initiation factor 3 subunit 6-interacting protein
UniRef100_Q	17	20	28.20%	607	70902	7	DJ1014D13.1 protein
UniRef100_Q	17	20	30.30%	564	66739	6	MSTP005
UniRef100_Q	17	20	30.30%	564	66753	6	Eukaryotic translation initiation factor 3 subunit 6 interacting protein variant
UniRef100_P	13	22	30.30%	485	53154	6	Angiotensinogen precursor (Serpin A8) [Contains: Angiotensin-1 (Angiotensin I) (Ang I); Angiotensin-2 (Angiotensin II) (Ang II); Angiotensin-3 (Angiotensin III) (Ang III) (Des-Asp[1]-angiotensin II)]
UniRef100_Q	13	22	30.30%	485	53114	6	Angiotensinogen (Serine (Or cysteine) proteinase inhibitor, clade A (Alpha-1 antiproteinase, antitrypsin), member 8)
UniRef100_Q	13	22	29.90%	491	53778	6	Angiotensinogen variant
UniRef100_P	6	8	30.30%	218	25745	6	Glutathione S-transferase Mu 2
UniRef100_U	6	8	34.20%	193	22876	5	Glutathione S-transferase Mu 4 (EC 2.5.1.18) (GSTM4-4) (GST class-mu 4) (GTS-Mu2).
UniRef100_U	6	8	27.80%	237	27676	6	Glutathione S-transferase Mu 4 (EC 2.5.1.18) (GSTM4-4) (GST class-mu 4) (GTS-Mu2).
UniRef100_U	6	8	30.00%	220	26098	6	Glutathione S-transferase Mu 4 (EC 2.5.1.18) (GSTM4-4) (GST class-mu 4) (GTS-Mu2).
UniRef100_Q	6	8	30.30%	218	25685	6	Glutathione S-transferase M2
UniRef100_P	8	9	30.20%	338	35531	9	Malate dehydrogenase, mitochondrial precursor
UniRef100_U	8	9	30.20%	338	35503	9	mitochondrial malate dehydrogenase precursor
UniRef100_Q	8	9	30.20%	338	35559	9	MDH2 protein

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	6	10	30.20%	192	21995	6	Phosphomevalonate kinase
UniRef100_P	3	4	30.20%	106	11776	8	Glutaredoxin-1
UniRef100_P	9	29	30.10%	389	44173	8	26S protease regulatory subunit S10B
UniRef100_Q	5	16	30.10%	206	22977	5	Ras-related protein Rab-18
UniRef100_P	4	4	30.10%	136	15075	8	Galectin-7
UniRef100_P	50	88	30.00%	1897	2E+05	6	Receptor-type tyrosine-protein phosphatase F precursor
UniRef100_U	50	88	30.00%	1897	2E+05	6	Receptor-type tyrosine-protein phosphatase F precursor (EC 3.1.3.48) (LAR protein) (Leukocyte antigen related).
UniRef100_Q	50	88	30.00%	1898	2E+05	6	Protein tyrosine phosphatase, receptor type, F
UniRef100_Q	50	88	29.70%	1918	2E+05	6	LAR
UniRef100_Q	50	88	29.90%	1907	2E+05	6	Protein tyrosine phosphatase, receptor type, F
UniRef100_P	9	21	30.00%	253	28766	9	Phosphoglycerate mutase 2
UniRef100_O	7	19	30.00%	243	27228	7	Vesicle-associated membrane protein-associated protein B/C
UniRef100_P	28	57	29.90%	1172	1E+05	5	Thrombospondin-2 precursor
UniRef100_Q	28	57	29.90%	1172	1E+05	5	Thrombospondin 2
UniRef100_Q	8	13	29.90%	401	44231	5	Dynactin subunit 2
UniRef100_U	8	13	29.60%	406	44722	5	Dynactin subunit 2 (Dynactin complex 50 kDa subunit) (50 kDa dynein- associated polypeptide) (p50 dynamitin) (DCTN-50).
UniRef100_U	8	13	29.60%	406	44820	5	dynactin 2
UniRef100_P	8	19	29.90%	304	33872	6	Proto-oncogene C-crk
UniRef100_Q	8	19	29.90%	304	33831	6	V-crk sarcoma virus CT10 oncogene homolog
UniRef100_Q	84	192	29.80%	3063	3E+05	6	Collagen type XII alpha 1
UniRef100_U	84	192	29.80%	3063	3E+05	6	Collagen alpha-1(XII) chain precursor.
UniRef100_Q	20	40	29.80%	709	81075	7	FACT complex subunit SSRP1
UniRef100_P	14	15	29.80%	617	68304	6	Vacuolar ATP synthase catalytic subunit A
UniRef100_P	11	15	29.80%	456	50097	7	Adenylosuccinate synthetase isozyme 2
UniRef100_Q	12	13	29.80%	389	45531	6	26S proteasome non-ATPase regulatory subunit 6
UniRef100_Q	11	12	29.80%	356	40229	7	Vesicular integral-membrane protein VIP36 precursor
UniRef100_P	10	23	29.80%	339	37822	6	Cathepsin B precursor (EC 3.4.22.1) (Cathepsin B1) (APP secretase) (APPS) [Contains: Cathepsin B light chain; Cathepsin B heavy chain]
UniRef100_A	5	29	29.80%	238	25145	8	Anti-(ED-B) scFV
UniRef100_A	5	29	29.80%	238	25156	8	Anti-TeTox scFv
UniRef100_A	5	29	29.80%	238	25003	8	Anti-IFN-G scFv
UniRef100_A	5	29	29.80%	238	24970	8	Anti-FactorVIII scFv
UniRef100_A	5	29	29.80%	238	25223	8	Anti-HCS scFv
UniRef100_A	5	29	29.80%	238	25164	8	Anti-TN-C scFv
UniRef100_A	5	29	29.80%	238	25161	8	Anti-(ED-B) scFV
UniRef100_A	5	29	29.80%	238	25193	8	Anti-(ED-B) scFV
UniRef100_A	5	29	29.80%	238	25205	8	Anti-(ED-B) scFV
UniRef100_Q	11	46	29.70%	414	44740	6	TAR DNA-binding protein 43
UniRef100_U	11	46	41.30%	298	33730	7	TAR DNA-binding protein 43 (TDP-43).

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	11	46	41.70%	295	33462	7	TAR DNA binding protein
UniRef100_Q	7	15	29.70%	145	16363	8	Ubiquitin-conjugating enzyme E2 variant 2
UniRef100_U	7	15	29.90%	144	16384	8	Ubiquitin-conjugating enzyme E2 variant 2 (MMS2) (Enterocyte differentiation-associated factor EDAF-1) (Enterocyte differentiation- promoting factor) (EDPF-1) (Vitamin D3-inducible protein) (DDVit 1).
UniRef100_P	4	10	29.70%	128	13894	9	Platelet basic protein precursor (PBP) (Small inducible cytokine B7) (CXCL7) (Leukocyte-derived growth factor) (LDGF) (Macrophage-derived growth factor) (MDGF) [Contains: Connective tissue-activating peptide III (CTAP-III) (Low-affinity platelet factor IV) (LA-PF4); TC-2; Connective tissue-activating peptide III(1-81) (CTAP-III(1-81)); Beta- thromboglobulin (Beta-TG); Neutrophil-activating peptide 2(74) (NAP- 2(74)); Neutrophil-activating peptide 2(73) (NAP-2(73)); Neutrophil-activating peptide 2 (NAP-2); TC-1; Neutrophil-activating peptide 2(1- 66) (NAP-2(1-66)); Neutrophil-activating peptide 2(1-63) (NAP-2(1- 63))]
UniRef100_P	4	5	29.70%	101	11557	6	Small ubiquitin-related modifier 1 precursor
UniRef100_P	35	65	29.60%	1264	1E+05	8	Valyl-tRNA synthetase
UniRef100_U	35	65	29.60%	1264	1E+05	8	Valyl-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA ligase) (ValRS) (Protein G7a).
UniRef100_P	19	135	29.60%	707	76150	9	Splicing factor, proline- and glutamine-rich
UniRef100_O	10	21	29.60%	514	57674	9	H/ACA ribonucleoprotein complex subunit 4
UniRef100_Q	12	93	29.60%	355	38434	8	Heterogeneous nuclear ribonucleoprotein D0
UniRef100_Q	12	93	34.30%	306	32835	8	Isoform 3 of Q14103
UniRef100_U	6	7	29.60%	321	34006	6	hypothetical protein LOC283871
UniRef100_Q	13	35	29.60%	307	32550	9	RNA binding protein (Autoantigenic, hnRNP-associated with lethal yellow) long isoform variant (RNA binding protein, autoantigenic) (HnRNP-associated with lethal yellow homolog (Mouse))
UniRef100_Q	13	35	31.40%	290	30364	#	Isoform 1 of Q9UKM9
UniRef100_Q	13	35	29.70%	306	32463	9	RNA-binding protein Raly
UniRef100_Q	13	35	38.40%	237	24665	#	RNA binding protein, autoantigenic (HnRNP-associated with lethal yellow homolog (Mouse))
UniRef100_O	5	7	29.60%	162	18762	9	Sorting nexin-3
UniRef100_O	16	40	29.50%	594	66050	9	Nucleolar protein Nop56
UniRef100_Q	14	35	29.50%	586	65402	9	Septin-9
UniRef100_U	14	35	30.80%	562	62865	8	Septin-9 (MLL septin-like fusion protein) (MLL septin-like fusion protein MSF-A) (Ovarian/Breast septin) (Ov/Br septin) (Septin D1).
UniRef100_Q	14	35	29.90%	579	64682	8	Isoform 5 of Q9UHD8
UniRef100_Q	14	35	30.50%	568	63666	8	Isoform 2 of Q9UHD8
UniRef100_P	7	12	29.50%	397	44868	7	DnaJ homolog subfamily A member 1
UniRef100_Q	7	12	35.30%	331	37045	9	DnaJA2
UniRef100_P	9	35	29.50%	346	36926	7	Heterogeneous nuclear ribonucleoprotein H3
UniRef100_Q	9	35	29.50%	346	36926	7	Heterogeneous nuclear ribonucleoprotein H3 isoform a variant
UniRef100_P	9	35	30.80%	331	35239	7	Isoform 2 of P31942
UniRef100_Q	5	8	29.50%	237	27508	6	DCN1-like protein 5
UniRef100_P	14	17	29.40%	739	83140	7	Glycyl-tRNA synthetase
UniRef100_U	14	17	29.40%	739	83166	7	glycyl-tRNA synthetase
UniRef100_U	14	17	31.70%	685	77531	6	Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS).

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	11	19	29.40%	489	54235	6	Coronin-1B
UniRef100_P	12	17	29.40%	445	52221	6	Eukaryotic translation initiation factor 3 subunit 6
UniRef100_Q	12	17	29.40%	445	52206	6	EIF3S6 protein
UniRef100_Q	12	13	29.40%	419	48162	7	Basic leucine zipper and W2 domain-containing protein 2
UniRef100_P	9	10	29.40%	395	43661	7	S-adenosylmethionine synthetase isoform type-2
UniRef100_UI	9	10	29.30%	396	43748	7	S-adenosylmethionine synthetase isoform type-
UniRef100_O	4	7	29.40%	231	24737	7	Acyl-protein thioesterase 2
UniRef100_Q	179	316	29.30%	5938	7E+05	5	Microtubule-actin crosslinking factor 1
UniRef100_Q	179	316	29.30%	5938	7E+05	5	Microtubule-actin cross-linking factor 1, isoform 4
UniRef100_O	33	35	29.30%	1485	2E+05	6	Intron-binding protein aquarius
UniRef100_UI	33	35	28.60%	1521	2E+05	7	Intron-binding protein aquarius (Intron-binding protein of 160 kDa) (IBP160).
UniRef100_P	17	28	29.30%	597	67033	7	C4b-binding protein alpha chain precursor
UniRef100_Q	11	28	29.20%	500	54154	7	IGHA1 protein
UniRef100_P	7	7	29.20%	295	33233	5	Alpha-soluble NSF attachment protein
UniRef100_P	7	14	29.20%	226	25505	8	Glutathione peroxidase 3 precursor
UniRef100_UI	7	14	29.20%	226	25402	8	plasma glutathione peroxidase 3 precursor
UniRef100_P	13	22	29.10%	646	71608	6	Cell surface glycoprotein MUC18 precursor
UniRef100_Q	12	24	29.10%	344	39587	#	Splicing factor, arginine/serine-rich 6
UniRef100_Q	12	24	35.80%	279	31865	#	Arginine/serine-rich splicing factor 6 variant
UniRef100_Q	12	24	29.90%	335	38419	#	Isoform SRP55
UniRef100_O	9	14	29.10%	357	37564	5	Eukaryotic translation initiation factor 3 subunit 5
UniRef100_P	24	183	29.00%	710	76615	5	Nucleolin
UniRef100_UI	24	183	30.00%	687	74427	5	Nucleolin (Protein C23).
UniRef100_Q	24	183	34.20%	603	65962	5	CDNA FLJ45706 fis, clone FEBRA2028457, highly similar to Nucleolin
UniRef100_P	24	183	30.00%	687	74397	5	Isoform 2 of P19338
UniRef100_Q	8	9	29.00%	410	46324	7	WD repeat and FYVE domain-containing protein 1
UniRef100_UI	8	9	32.40%	367	41317	7	WD repeat and FYVE domain-containing protein 1 (WD40- and FYVE domain- containing protein 1) (Phosphoinositide-binding protein 1) (FENS-1) (Zinc finger FYVE domain-containing protein 17).
UniRef100_Q	29	54	28.90%	1041	1E+05	5	Importin-9
UniRef100_Q	15	25	28.90%	634	74667	9	Hypothetical protein
UniRef100_Q	15	25	22.50%	812	96864	9	EIF3S10 protein
UniRef100_Q	15	25	28.80%	636	74908	9	EIF3S10 protein
UniRef100_Q	15	25	28.60%	640	75395	9	EIF3S10 protein
UniRef100_Q	15	25	13.20%	1382	2E+05	7	Eukaryotic translation initiation factor 3, subunit 10 theta, 150/170kDa
UniRef100_Q	15	25	13.20%	1382	2E+05	7	Eukaryotic translation initiation factor 3 subunit 10
UniRef100_Q	11	22	28.90%	440	48121	5	Protein disulfide-isomerase A6 precursor
UniRef100_Q	11	22	25.80%	492	53901	5	Isoform 2 of Q15084
UniRef100_Q	8	17	28.90%	266	30434	4	Acidic (Leucine-rich) nuclear phosphoprotein 32 family, member E variant
UniRef100_Q	8	17	28.70%	268	30692	4	Acidic leucine-rich nuclear phosphoprotein 32 family member E
UniRef100_Q	5	5	28.90%	190	21495	5	Protein LZIC

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	15	27	28.80%	642	72380	6	Sec1 family domain-containing protein 1
UniRef100_O	7	7	28.80%	399	45283	8	LanC-like protein 1
UniRef100_Q	7	7	28.80%	399	45267	8	LANCL1 protein
UniRef100_P	8	15	28.80%	368	41654	8	Biglycan precursor
UniRef100_Q	8	15	28.80%	368	41655	7	Biglycan preproprotein variant
UniRef100_Q	8	15	28.80%	368	41605	8	Biglycan preproprotein variant
UniRef100_P	6	35	28.80%	208	23593	6	Ras-related protein Rab-6A
UniRef100_Q	6	35	28.80%	208	23550	5	RAB6A protein
UniRef100_P	6	35	28.80%	208	23549	6	Isoform 2 of P20340
UniRef100_Q	5	8	28.80%	205	22875	5	Heme-binding protein 2
UniRef100_Q	3	5	28.80%	125	14211	#	COMM domain containing 6
UniRef100_U	3	5	28.80%	125	14257	#	COMM domain-containing protein 6.
UniRef100_Q	3	5	42.40%	85	9638	6	COMM domain-containing protein 6
UniRef100_O	3	4	28.80%	118	13758	9	Vacuolar ATP synthase subunit G 1
UniRef100_P	8	10	28.70%	376	42293	6	Beta-centractin
UniRef100_Q	8	10	32.80%	329	37097	7	Beta-centractin
UniRef100_O	3	4	28.70%	150	17420	6	Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit delta
UniRef100_P	3	9	28.70%	136	15328	#	Histone H3.3
UniRef100_Q	25	34	28.60%	1003	1E+05	9	Putative helicase MOV-10
UniRef100_P	18	63	28.60%	636	70671	#	Polyadenylate-binding protein 1 (Poly(A)-binding protein 1)
UniRef100_U	18	63	33.20%	548	61318	9	Polyadenylate-binding protein 1 (Poly(A)-binding protein 1) (PABP 1).
UniRef100_P	18	63	33.30%	547	61181	9	Isoform 2 of P11940
UniRef100_P	16	144	28.60%	294	32575	5	Nucleophosmin
UniRef100_P	16	144	31.70%	265	29465	5	Isoform 2 of P06748
UniRef100_Q	9	49	28.60%	220	23787	#	RPL14 protein
UniRef100_P	5	19	28.60%	133	15423	#	40S ribosomal protein S24
UniRef100_Q	5	19	28.80%	132	15326	#	Hypothetical protein DKFZp686N1586
UniRef100_Q	5	19	29.20%	130	15069	#	Ribosomal protein S24
UniRef100_Q	3	7	28.60%	105	12254	#	60S ribosomal protein L36
UniRef100_O	62	99	28.50%	2390	3E+05	6	Spectrin beta chain, brain 2
UniRef100_U	62	99	28.50%	2390	3E+05	6	Spectrin beta chain, brain 2 (Spectrin, non-erythroid beta chain 2) (Beta-III spectrin).
UniRef100_O	62	99	28.80%	2365	3E+05	6	Isoform 2 of O15020
UniRef100_Q	19	27	28.50%	629	70353	6	Plastin-1
UniRef100_Q	19	27	28.50%	629	70323	6	PLS1 protein
UniRef100_Q	11	18	28.50%	558	61068	6	Myo-inositol 1-phosphate synthase A1
UniRef100_Q	11	18	28.50%	558	61084	6	CDNA FLJ10463 fis, clone NT2RP1001543, moderately similar to MYO- INOSITOL-1-PHOSPHATE SYNTHASE
UniRef100_Q	11	18	37.00%	430	47146	5	Hypothetical protein DKFZp434A0612
UniRef100_Q	20	72	28.50%	550	60883	8	EEF1D protein
UniRef100_Q	13	17	28.40%	592	67931	6	Guanylate binding protein 1, interferon-inducible, 67kDa
UniRef100_Q	9	11	28.40%	483	55756	6	Septin-8

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_UI	9	11	31.90%	430	49916	6	Septin-8.
UniRef100_UI	9	11	31.00%	442	51178	6	Septin-8.
UniRef100_Q	9	11	31.90%	429	49814	6	Isoform 2 of Q92599
UniRef100_Q	2	3	28.40%	116	13196	5	Similar to RIKEN cDNA A430101B06 gene
UniRef100_Q	28	31	28.30%	1204	1E+05	6	Exportin-5
UniRef100_UI	28	31	28.30%	1204	1E+05	6	Exportin-5 (Exp5) (Ran-binding protein 21).
UniRef100_P	2	2	28.30%	92	10275	#	60S ribosomal protein L37a
UniRef100_Q	18	60	28.20%	737	81068	8	DEAD box polypeptide 17 isoform p82 variant
UniRef100_UI	18	60	31.90%	652	72576	9	Probable ATP-dependent RNA helicase DDX17 (EC 3.6.1.-) (DEAD box protein 17) (RNA-dependent helicase p72) (DEAD box protein p72).
UniRef100_UI	18	60	28.50%	729	80255	8	Probable ATP-dependent RNA helicase DDX17 (EC 3.6.1.-) (DEAD box protein 17) (RNA-dependent helicase p72) (DEAD box protein p72).
UniRef100_UI	18	60	28.50%	729	80273	8	DEAD box polypeptide 17 isoform p82
UniRef100_Q	18	60	31.90%	652	72557	9	Isoform 3 of Q92841
UniRef100_Q	18	60	31.90%	652	72542	9	Isoform 2 of Q92841
UniRef100_Q	18	60	32.00%	650	72372	9	Probable ATP-dependent RNA helicase DDX17
UniRef100_Q	15	45	28.20%	394	42819	6	Transformation-related protein 14
UniRef100_UI	15	45	28.20%	394	42834	6	Protein NDRG1 (N-myc downstream-regulated gene 1 protein) (Differentiation-related gene 1 protein) (DRG-1) (Reducing agents and tunicamycin-responsive protein) (RTP) (Nickel-specific induction protein Cap43) (Rit42).
UniRef100_Q	15	45	28.20%	394	42835	6	Protein NDRG1
UniRef100_Q	15	45	34.40%	323	35226	6	CDNA FLJ38330 fis, clone FCBBF3025280, highly similar to NDRG1 PROTEIN
UniRef100_P	8	11	28.20%	319	35883	6	Annexin A4
UniRef100_Q	8	11	30.10%	299	33552	6	ANXA4 protein
UniRef100_Q	6	8	28.20%	227	25795	6	Hypothetical protein PPA2
UniRef100_Q	6	8	21.00%	305	34658	9	Isoform 3 of Q9H2U2
UniRef100_Q	6	8	18.30%	349	39638	7	Isoform 2 of Q9H2U2
UniRef100_Q	6	8	19.20%	334	37920	7	Inorganic pyrophosphatase 2, mitochondrial precursor
UniRef100_P	4	18	28.20%	213	23587	6	Ras-related protein Rab-4B
UniRef100_Q	4	18	52.20%	115	12982	5	Ras-related GTP-binding protein
UniRef100_P	4	18	24.20%	248	27506	6	Isoform 2 of P61018
UniRef100_P	4	9	28.20%	206	22168	9	Transcription factor BTF3
UniRef100_Q	4	9	28.40%	204	22031	#	Transcription factor BTF3
UniRef100_P	9	9	28.10%	501	54862	7	Retinal dehydrogenase 1
UniRef100_Q	8	13	28.10%	370	40572	5	P47 protein isoform a variant
UniRef100_Q	8	13	28.10%	370	40573	5	NSFL1 cofactor p47
UniRef100_Q	8	13	28.00%	372	40816	5	NSFL1 (P97) cofactor
UniRef100_Q	7	7	28.10%	342	37766	7	Aldose 1-epimerase
UniRef100_A	2	5	28.10%	96	10352	5	V2-7 protein
UniRef100_P	72	156	28.00%	2871	3E+05	7	Desmoplakin
UniRef100_P	13	15	28.00%	649	73456	8	ATP-dependent DNA helicase Q1

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_U	13	15	28.00%	649	73457	8	RecQ protein-like isoform 1
UniRef100_O	5	5	28.00%	275	30344	8	Proline synthetase co-transcribed bacterial homolog protein
UniRef100_Q	4	4	28.00%	211	23769	7	Polyamine-modulated factor 1
UniRef100_Q	4	4	28.80%	205	23339	6	Polyamine-modulated factor 1
UniRef100_O	4	10	28.00%	125	14285	6	Programmed cell death protein 5
UniRef100_P	22	73	27.90%	946	1E+05	7	Inter-alpha-trypsin inhibitor heavy chain H2 precursor
UniRef100_Q	22	73	27.90%	946	1E+05	7	Inter-alpha (Globulin) inhibitor H2
UniRef100_Q	22	73	28.20%	935	1E+05	7	Inter-alpha (Globulin) inhibitor H2
UniRef100_Q	12	41	27.90%	466	52138	6	Ras-GTPase-activating protein SH3-domain-binding protein variant
UniRef100_Q	11	18	27.90%	423	48109	8	Adaptor-related protein complex 1, mu 2 subunit variant
UniRef100_Q	11	18	27.90%	423	48109	8	AP-1 complex subunit mu-2
UniRef100_O	5	5	27.90%	305	35144	6	Serine/threonine-protein phosphatase 6
UniRef100_Q	5	5	28.10%	303	34814	6	Serine/threonine protein phosphatase catalytic subunit
UniRef100_Q	6	6	27.90%	305	33712	7	Translation initiation factor eIF-2B subunit alpha
UniRef100_Q	5	28	27.90%	208	23462	6	Ras-related protein Rab-6B
UniRef100_P	6	9	27.90%	201	23310	5	Ran-specific GTPase-activating protein
UniRef100_Q	4	4	27.90%	190	21307	6	MURR1 variant
UniRef100_Q	4	4	27.90%	190	21178	6	COMM domain-containing protein 1
UniRef100_P	17	36	27.80%	683	74462	5	Isoform C of P23142
UniRef100_U	17	36	27.80%	683	74434	5	Fibulin-1 precursor.
UniRef100_A	11	28	27.80%	662	73333	7	Adducin 1
UniRef100_P	11	28	24.00%	768	84303	6	Isoform 3 of P35611
UniRef100_P	11	28	25.00%	737	80955	6	Alpha-adducin
UniRef100_Q	3	4	27.80%	209	23484	8	D-tyrosyl-tRNA deacylase 1 homolog
UniRef100_Q	3	4	27.80%	209	23424	8	Probable D-tyrosyl-tRNA(Tyr) deacylase 1
UniRef100_P	37	38	27.70%	1532	2E+05	7	Glycogen debranching enzyme (Glycogen debrancher) [Includes: 4-alpha- glucanotransferase (EC 2.4.1.25) (Oligo-1,4-1,4-glucantransferase); Amylo-alpha-1,6-glucosidase (EC 3.2.1.33) (Amylo-1,6-glucosidase) (Dextrin 6-alpha-D-glucosidase)]
UniRef100_U	37	38	27.60%	1534	2E+05	7	Glycogen debranching enzyme (Glycogen debrancher) [Includes: 4-alpha- glucanotransferase (EC 2.4.1.25) (Oligo-1,4-1,4-glucantransferase); Amylo-alpha-1,6-glucosidase (EC 3.2.1.33) (Amylo-1,6-glucosidase) (Dextrin 6-alpha-D-glucosidase)].
UniRef100_Q	37	38	27.70%	1533	2E+05	7	Amylo-1,6-glucosidase, 4-alpha-glucanotransferase isoform 1 variant
UniRef100_Q	22	42	27.70%	1081	1E+05	5	Importin-4
UniRef100_Q	22	42	27.60%	1083	1E+05	5	Isoform 2 of Q8TEX9
UniRef100_P	12	51	27.70%	375	42674	9	Protein DEK
UniRef100_Q	7	18	27.70%	224	25177	9	FK506-binding protein 3
UniRef100_Q	7	18	27.70%	224	25204	9	FK506-binding protein 3 variant
UniRef100_P	2	3	27.70%	83	9396	#	Cytochrome c oxidase polypeptide VIIa-liver/heart, mitochondrial precursor
UniRef100_U	2	3	20.00%	115	12844	9	Cytochrome c oxidase polypeptide VIIa-liver/heart, mitochondrial precursor (EC 1.9.3.1) (Cytochrome c oxidase subunit VIIa-L) (VIIaL).
UniRef100_Q	2	3	27.70%	83	9426	#	Cytochrome c oxidase subunit VIIa polypeptide 2

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P	12	14	27.60%	529	57862	5	Importin alpha-2 subunit
UniRef100_Q	12	14	27.60%	529	57965	5	Karyopherin alpha 2
UniRef100_Q	5	5	27.60%	214	23787	6	Osteoclast-stimulating factor 1
UniRef100_A	36	58	27.50%	1632	2E+05	8	DNMT1 protein
UniRef100_P	36	58	27.70%	1616	2E+05	8	DNA (cytosine-5)-methyltransferase 1
UniRef100_Q	16	88	27.50%	465	51325	7	Hypothetical protein
UniRef100_P	9	11	27.50%	364	39456	7	Fructose-bisphosphate aldolase C
UniRef100_Q	4	4	27.50%	211	23338	9	Protein syndesmos
UniRef100_P	5	35	27.50%	200	22541	8	Ras-related protein Rab-10
UniRef100_U	5	35	27.50%	200	22469	9	ras-related GTP-binding protein RAB10
UniRef100_Q	4	9	27.50%	167	19127	8	Protein tyrosine phosphatase type IVA protein 2 (EC 3.1.3.48) (Protein-tyrosine phosphatase 4a2) (Protein-tyrosine phosphatase of regenerating liver 2) (PRL-2) (PTP(CAAXII))
UniRef100_P	17	49	27.40%	780	85018	8	6-phosphofructokinase, liver type
UniRef100_Q	14	33	27.40%	478	51857	7	Hypothetical protein
UniRef100_P	13	39	27.40%	215	24894	6	High mobility group protein B1
UniRef100_U	13	39	30.70%	192	22066	#	High mobility group protein HMG1 (High mobility group 1 protein)
UniRef100_Q	13	39	36.40%	162	18808	#	High-mobility group box 1
UniRef100_Q	13	39	37.30%	158	18311	#	High-mobility group box 1
UniRef100_Q	13	39	33.50%	176	20164	#	High-mobility group box 1 variant
UniRef100_Q	13	39	27.40%	215	24993	6	HMG-1
UniRef100_P	21	45	27.30%	863	96558	7	DNA replication licensing factor MCM4
UniRef100_Q	18	27	27.30%	699	78806	7	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1
UniRef100_U	18	27	28.00%	681	76747	7	glucosamine-fructose-6-phosphate aminotransferase
UniRef100_Q	18	27	28.00%	681	76759	7	Isoform 2 of Q06210
UniRef100_O	6	15	27.30%	333	36049	6	PDZ domain-containing protein GIPC1
UniRef100_U	6	15	38.60%	236	26072	6	regulator of G-protein signalling 19 interacting protein 1 isoform 2
UniRef100_Q	7	7	27.30%	245	28043	7	Carboxymethylenebutenolidase homolog
UniRef100_Q	7	7	27.30%	245	28048	7	Carboxymethylenebutenolidase homolog
UniRef100_Q	3	3	27.30%	176	19444	5	TATA-binding protein-associated phosphoprotein
UniRef100_Q	3	3	27.30%	176	19472	5	Down-regulator of transcription 1 variant
UniRef100_P	13	72	27.20%	449	49264	6	Heterogeneous nuclear ribonucleoprotein H'
UniRef100_P	5	9	27.20%	158	18733	6	AP-1 complex subunit sigma-1A
UniRef100_P	3	13	27.20%	125	13938	8	Interferon-induced transmembrane protein 1
UniRef100_U	3	13	27.20%	125	13912	8	interferon induced transmembrane protein 1 (9-27)
UniRef100_P	7	34	27.10%	266	29996	#	60S ribosomal protein L7a
UniRef100_U	7	34	26.70%	270	30548	#	similar to 60S ribosomal protein L7a (Surfeit locus protein 3) (LOC645846), mRNA
UniRef100_U	7	34	27.10%	266	30042	#	PREDICTED: similar to 60S ribosomal protein L7a isoform 3
UniRef100_Q	14	61	27.00%	626	72201	7	SAM domain and HD domain-containing protein 1
UniRef100_P	9	11	27.00%	482	49955	6	Thymidine phosphorylase precursor
UniRef100_Q	18	43	26.90%	784	85596	8	6-phosphofructokinase type C
UniRef100_Q	8	17	26.90%	379	43615	#	Cell growth-regulating nucleolar protein

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_U	8	17	26.90%	379	43634	#	hypothetical protein FLJ20425
UniRef100_Q	5	6	26.90%	357	38297	8	Sorbitol dehydrogenase
UniRef100_U	5	6	26.90%	357	38312	8	sorbitol dehydrogenase
UniRef100_Q	7	7	26.90%	323	37231	9	Mortality factor 4 like 1
UniRef100_Q	7	7	24.00%	362	41474	9	Mortality factor 4-like protein 1
UniRef100_P	4	5	26.90%	201	22838	6	Ras-related protein Rab-9
UniRef100_Q	3	3	26.90%	145	16832	9	Trafficking protein particle complex subunit 1
UniRef100_O	18	37	26.80%	822	91391	7	AP-1 complex subunit gamma-1
UniRef100_U	18	37	26.70%	825	91723	7	adaptor-related protein complex 1, gamma 1 subunit isoform a
UniRef100_U	18	37	26.80%	822	91351	7	adaptor-related protein complex 1, gamma 1 subunit isoform b
UniRef100_Q	18	37	26.70%	825	91757	7	Adaptor-related protein complex 1, gamma 1 subunit
UniRef100_Q	16	19	26.80%	745	86983	7	Cullin-2
UniRef100_A	7	12	26.80%	298	34402	6	MHC class I antigen
UniRef100_P	7	8	26.80%	246	27992	8	B-cell receptor-associated protein 31
UniRef100_Q	7	8	26.80%	246	27931	8	B-cell receptor-associated protein 31 variant
UniRef100_U	4	20	26.80%	220	23809	9	ANTIBODY A5B7 (HEAVY CHAIN)
UniRef100_Q	3	3	26.80%	194	22083	#	MGC11257 protein
UniRef100_O	8	14	26.70%	419	49513	6	Histone acetyltransferase type B catalytic subunit
UniRef100_Q	8	17	26.70%	360	41564	5	Protein phosphatase 1 regulatory subunit 7
UniRef100_Q	5	5	26.70%	322	34911	6	Transcriptional activator protein Pur-alpha
UniRef100_Q	5	5	26.70%	322	34911	7	Purine-rich element binding protein A
UniRef100_Q	5	5	26.70%	322	34939	7	Purine-rich element binding protein A
UniRef100_Q	5	5	30.20%	285	32015	7	PURA protein
UniRef100_Q	5	5	28.70%	300	34166	9	PURA protein
UniRef100_P	14	17	26.60%	587	63542	5	Ran GTPase-activating protein 1
UniRef100_O	8	20	26.60%	546	59272	4	Protein phosphatase 2C isoform gamma
UniRef100_P	7	15	26.60%	496	56806	8	Glycylpeptide N-tetradecanoyltransferase 1
UniRef100_U	7	15	26.50%	498	56978	8	Glycylpeptide N-tetradecanoyltransferase 1 (EC 2.3.1.97) (Peptide N- myristoyltransferase 1) (Myristoyl-CoA:protein N-myristoyltransferase 1) (NMT 1) (Type I N-myristoyltransferase).
UniRef100_Q	7	15	26.70%	494	56604	8	NMT1 protein
UniRef100_P	7	15	31.70%	416	48141	8	Isoform Short of P30419
UniRef100_O	11	115	26.60%	293	32142	5	Heterogeneous nuclear ribonucleoprotein C-like 1
UniRef100_Q	8	9	26.50%	499	54707	7	Thioredoxin reductase 1, cytoplasmic precursor
UniRef100_U	8	9	22.60%	585	64401	8	CDNA FLJ46672 fis, clone TRACH3009008, highly similar to Thioredoxin reductase (EC 1.6.4.5).
UniRef100_U	8	9	20.30%	651	71153	8	CDNA FLJ46672 fis, clone TRACH3009008, highly similar to Thioredoxin reductase (EC 1.6.4.5).
UniRef100_U	8	9	26.50%	499	54604	7	thioredoxin reductase 1
UniRef100_Q	8	9	26.60%	497	54615	7	Thioredoxin reductase GRIM-12
UniRef100_Q	8	9	24.00%	549	60212	7	KM-102-derived reductase-like factor
UniRef100_Q	8	9	26.60%	497	54575	7	TXNRD1 protein

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	7	13	26.50%	441	51172	6	UPF0364 protein C6orf211
UniRef100_P	7	16	26.50%	359	39747	9	Decorin precursor
UniRef100_U	3	3	26.50%	113	13171	5	family with sequence similarity 127, member A
UniRef100_Q	2	3	26.50%	83	9046	4	Novel protein
UniRef100_Q	22	30	26.40%	1070	1E+05	7	Tyrosine-protein kinase-like 7 precursor
UniRef100_U	22	30	27.90%	1015	1E+05	7	Tyrosine-protein kinase-like 7 precursor (Colon carcinoma kinase 4) (CCK-4).
UniRef100_Q	22	30	27.90%	1014	1E+05	7	Transmembrane receptor PTK7-4
UniRef100_P	9	10	26.40%	484	54889	7	Adenylosuccinate lyase
UniRef100_Q	9	10	26.40%	484	54871	7	Adenylosuccinate lyase
UniRef100_P	10	24	26.40%	375	40076	6	Monocyte differentiation antigen CD14 precursor (Myeloid cell-specific leucine-rich glycoprotein) [Contains: Monocyte differentiation antigen CD14, urinary form; Monocyte differentiation antigen CD14, membrane- bound form]
UniRef100_Q	38	74	26.30%	1845	2E+05	7	Proteasome-associated protein ECM29 homolog
UniRef100_U	38	74	24.10%	2017	2E+05	9	PREDICTED: similar to Proteasome-associated protein ECM29 homolog (Ecm29)
UniRef100_U	38	74	26.50%	1833	2E+05	7	Proteasome-associated protein ECM29 homolog (Ecm29).
UniRef100_U	38	74	26.40%	1839	2E+05	7	Proteasome-associated protein ECM29 homolog (Ecm29).
UniRef100_A	4	5	26.30%	152	17174	5	Ubiquitin-conjugating enzyme E2H
UniRef100_Q	4	5	26.30%	152	17184	5	Ubiquitin-conjugating enzyme
UniRef100_P	4	5	21.90%	183	20655	5	Ubiquitin-conjugating enzyme E2 H
UniRef100_O	3	3	26.30%	133	15179	5	U6 snRNA-associated Sm-like protein LSm1
UniRef100_Q	10	17	26.20%	504	56770	6	Apoptosis inhibitor 5
UniRef100_U	10	17	25.30%	521	58472	7	Apoptosis inhibitor 5 (API-5) (Fibroblast growth factor 2-interacting factor) (FIF) (Protein XAGL) (Antiapoptosis clone 11 protein) (AAC- 11).
UniRef100_Q	10	17	26.40%	500	56099	6	Isoform 4 of Q9BZZ5
UniRef100_Q	10	17	25.90%	510	57561	6	Apoptosis inhibitor 5
UniRef100_Q	18	128	26.20%	446	49857	5	Tubulin beta-6 chain
UniRef100_P	10	44	26.20%	427	47697	#	60S ribosomal protein L4
UniRef100_U	10	44	26.30%	426	47566	#	60S ribosomal protein L4 (L1).
UniRef100_Q	10	44	25.40%	441	48996	#	Ribosomal protein L4 variant
UniRef100_P	4	4	26.20%	275	31441	5	DNA-directed RNA polymerase II 33 kDa polypeptide
UniRef100_P	15	40	26.10%	614	69148	9	Probable ATP-dependent RNA helicase DDX5
UniRef100_Q	15	22	26.00%	776	89678	8	Cullin-1
UniRef100_P	15	19	26.00%	645	72933	5	Protein disulfide-isomerase A4 precursor
UniRef100_Q	19	154	26.00%	447	50090	5	Tubulin beta-6 chain
UniRef100_O	5	11	26.00%	246	28082	7	Phosphomannomutase 2
UniRef100_P	5	6	25.90%	363	39609	5	UV excision repair protein RAD23 homolog A
UniRef100_Q	5	6	24.80%	379	41256	5	UV excision repair protein RAD23 homolog A variant
UniRef100_O	7	9	25.90%	347	38088	6	CD5 antigen-like precursor
UniRef100_P	7	9	25.90%	255	28433	5	Proteasome subunit alpha type 3
UniRef100_Q	7	9	25.90%	255	28415	5	Proteasome subunit alpha type
UniRef100_P	7	9	26.60%	248	27647	5	Isoform 2 of P25788

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P	5	6	25.90%	193	22313	5	Hippocalcin-like protein 1
UniRef100_Q	2	2	25.90%	81	8702	6	Rearranged Vl3l segment
UniRef100_Q	16	35	25.80%	656	71492	7	Isoform 3 of Q13421
UniRef100_Q	16	35	27.20%	621	67941	6	Isoform 4 of Q13421
UniRef100_Q	16	35	27.20%	622	68070	6	Isoform 2 of Q13421
UniRef100_P	10	16	25.80%	528	59144	7	Tyrosyl-tRNA synthetase, cytoplasmic
UniRef100_Q	10	54	25.80%	476	52421	8	Hypothetical protein DKFZp686M24218
UniRef100_P	12	51	25.80%	391	42332	#	Heterogeneous nuclear ribonucleoprotein G
UniRef100_P	5	8	25.80%	295	33872	6	Zinc-alpha-2-glycoprotein precursor
UniRef100_Q	5	8	25.50%	298	34259	6	Alpha-2-glycoprotein 1, zinc-binding
UniRef100_Q	5	8	25.50%	298	34245	6	Alpha-2-glycoprotein 1, zinc-binding
UniRef100_P	5	7	25.80%	252	26706	#	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial precursor
UniRef100_U	5	7	26.00%	250	26552	#	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial precursor (EC 3.6.1.23) (dUTPase) (dUTP pyrophosphatase).
UniRef100_Q	5	7	25.80%	252	26563	9	DUTP pyrophosphatase
UniRef100_Q	5	7	39.60%	164	17748	7	DUT protein
UniRef100_Q	3	3	25.80%	209	23850	7	Glycolipid transfer protein
UniRef100_O	2	4	25.80%	124	13693	8	Ribonuclease P protein subunit p14
UniRef100_U	62	296	25.70%	2971	3E+05	7	alpha 3 type VI collagen isoform 5 precursor
UniRef100_Q	13	79	25.70%	471	54232	9	Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (p54(nrb))
UniRef100_P	4	4	25.70%	292	33295	5	Histamine N-methyltransferase
UniRef100_P	6	28	25.70%	249	28681	#	40S ribosomal protein S6
UniRef100_Q	6	28	25.70%	249	28709	#	Ribosomal protein S6
UniRef100_Q	8	25	25.70%	245	28509	5	Tropomyosin 1 alpha variant 6
UniRef100_Q	3	12	25.70%	101	11529	9	Enhancer of yellow 2 homolog
UniRef100_U	3	12	25.70%	101	11526	9	enhancer of yellow 2 homolog
UniRef100_Q	2	5	25.70%	101	11380	5	Ubiquitin-related modifier 1 homolog
UniRef100_O	8	15	25.60%	429	47461	6	Actin-like protein 6A
UniRef100_Q	8	15	25.60%	429	47381	6	BAF53A protein
UniRef100_Q	8	15	25.60%	429	47481	6	Actin-like 6A isoform 1 variant
UniRef100_Q	7	17	25.60%	309	33621	8	Calponin 2 isoform a variant
UniRef100_Q	7	17	25.60%	309	33697	7	Calponin-2
UniRef100_Q	7	17	25.60%	309	33709	7	CNN2 protein
UniRef100_P	5	6	25.60%	254	28607	5	HLA class II histocompatibility antigen, DR alpha chain precursor
UniRef100_U	5	6	36.30%	179	20821	5	HLA class II histocompatibility antigen, DR a
UniRef100_U	5	6	35.50%	183	21264	5	HLA class II histocompatibility antigen, DR a
UniRef100_U	5	6	25.60%	254	28621	5	major histocompatibility complex, class II, DR alpha precursor
UniRef100_Q	8	44	25.60%	238	27367	#	Splicing factor, arginine/serine-rich 7
UniRef100_U	8	44	44.50%	137	15763	#	Splicing factor, arginine/serine-rich 7 (Splicing factor 9G8).
UniRef100_Q	8	44	46.20%	132	15257	#	Isoform 3 of Q16629

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	8	44	45.20%	135	15573	#	Isoform 2 of Q16629
UniRef100_Q	5	12	25.60%	215	23384	5	Nascent polypeptide-associated complex subunit alpha
UniRef100_P	39	117	25.50%	1798	2E+05	7	Laminin subunit beta-2 precursor
UniRef100_U	39	117	25.50%	1798	2E+05	7	laminin, beta 2 precursor
UniRef100_A	8	15	25.50%	431	48294	5	Src homology 3 domain-containing protein HIP-55
UniRef100_Q	8	15	25.60%	430	48207	5	Drebrin-like protein
UniRef100_P	3	6	25.50%	110	12538	#	60S ribosomal protein L35a
UniRef100_Q	73	132	25.40%	3280	4E+05	7	RING finger protein 213
UniRef100_O	31	32	25.40%	1388	2E+05	6	Rho-associated protein kinase 2
UniRef100_U	31	32	25.40%	1388	2E+05	6	Rho-associated, coiled-coil containing protein kinase 2
UniRef100_P	12	19	25.40%	583	65720	8	Complement factor I precursor (EC 3.4.21.45) (C3B/C4B inactivator) [Contains: Complement factor I heavy chain; Complement factor I light chain]
UniRef100_U	12	19	25.40%	583	65750	8	Complement factor I precursor (EC 3.4.21.45) (C3B/C4B inactivator) [Contains: Complement factor I heavy chain; Complement factor I light chain].
UniRef100_P	6	7	25.40%	351	40590	9	cAMP-dependent protein kinase, alpha-catalytic subunit
UniRef100_P	11	118	25.40%	378	39595	9	Heterogeneous nuclear ribonucleoprotein A3
UniRef100_P	11	118	27.00%	356	37029	8	Isoform 2 of P51991
UniRef100_Q	4	4	25.40%	169	19398	9	N-acetyltransferase 13
UniRef100_Q	7	8	25.30%	297	30816	6	Nicotinate-nucleotide pyrophosphorylase [carboxylating]
UniRef100_U	7	8	25.30%	297	30846	6	Nicotinate-nucleotide pyrophosphorylase [carboxylating] (EC 2.4.2.19) (Quinolinate phosphoribosyltransferase [decarboxylating]) (QAPRTase) (QPRTase).
UniRef100_Q	4	6	25.30%	221	25425	6	Vacuolar protein sorting-associated protein 28 homolog
UniRef100_P	5	12	25.30%	198	21642	5	Syndecan-4 precursor
UniRef100_Q	5	12	25.30%	198	21608	5	Syndecan 4 variant
UniRef100_P	27	71	25.20%	1184	1E+05	5	Fibulin-2 precursor
UniRef100_Q	27	71	24.20%	1231	1E+05	5	Fibulin 2
UniRef100_Q	9	12	25.20%	485	53439	8	Hypothetical protein DNPEP
UniRef100_Q	9	12	25.70%	475	52428	7	Aspartyl aminopeptidase
UniRef100_P	8	15	25.20%	409	43171	5	UV excision repair protein RAD23 homolog B
UniRef100_P	5	6	25.20%	266	30160	7	HLA class II histocompatibility antigen, DRB1-11 beta chain precursor
UniRef100_Q	3	3	25.20%	202	22966	7	COMM domain-containing protein 10
UniRef100_Q	15	35	25.10%	746	84138	6	Chromosome 9 open reading frame 88
UniRef100_Q	15	35	25.50%	733	82683	6	Niban-like protein
UniRef100_Q	4	5	25.10%	259	28536	6	Haloacid dehalogenase-like hydrolase domain-containing protein 2
UniRef100_U	4	5	24.40%	266	29349	6	haloacid dehalogenase-like hydrolase domain containing 2
UniRef100_Q	4	8	25.10%	175	19661	7	TP53RK-binding protein
UniRef100_Q	4	8	20.60%	214	23854	7	Isoform 3 of Q9Y3C4
UniRef100_Q	20	21	25.00%	1087	1E+05	6	Exportin-7
UniRef100_U	20	21	25.00%	1087	1E+05	6	Exportin-7 (Exp7) (Ran-binding protein 16).
UniRef100_U	20	21	25.00%	1087	1E+05	6	exportin 7
UniRef100_Q	9	14	25.00%	424	48618	6	BZW1 protein variant

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	9	14	25.30%	419	48043	6	Basic leucine zipper and W2 domain-containing protein 1
UniRef100_P	2	3	25.00%	108	11393	7	Ig lambda chain V-III region SH
UniRef100_Q	19	24	24.90%	820	95647	#	Probable ATP-dependent RNA helicase DDX23
UniRef100_U	19	24	24.90%	820	95583	#	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23
UniRef100_P	9	26	24.90%	406	45626	8	26S protease regulatory subunit 8
UniRef100_U	9	26	25.10%	402	45292	8	26S protease regulatory subunit 8 (Proteasome 26S subunit ATPase 5) (Proteasome subunit p45) (p45/SUG) (Thyroid hormone receptor- interacting protein 1) (TRIP1).
UniRef100_P	10	14	24.90%	381	42644	6	Creatine kinase B-type
UniRef100_Q	10	14	24.90%	381	42675	6	CKB protein
UniRef100_Q	7	10	24.90%	334	37579	7	COP9 signalosome complex subunit 5
UniRef100_P	5	17	24.90%	217	25097	6	Eukaryotic translation initiation factor 4E
UniRef100_Q	5	17	24.90%	217	25067	6	Eukaryotic translation initiation factor 4E
UniRef100_P	8	8	24.80%	483	53083	8	Serine hydroxymethyltransferase, cytosolic
UniRef100_Q	8	8	24.80%	483	53117	8	Serine hydroxymethyltransferase 1
UniRef100_Q	8	8	24.80%	483	53155	8	Serine hydroxymethyltransferase 1 (Soluble) isoform 1 variant
UniRef100_P	8	8	27.00%	444	49028	8	Isoform 2 of P34896
UniRef100_P	5	8	24.80%	330	35398	8	PDZ and LIM domain protein 4
UniRef100_P	6	21	24.80%	282	31280	#	U1 small nuclear ribonucleoprotein A
UniRef100_P	3	5	24.80%	137	15566	5	Cellular retinoic acid-binding protein 1
UniRef100_Q	2	2	24.80%	129	14665	5	Huntingtin-interacting protein HYPK
UniRef100_Q	2	2	18.30%	175	19332	5	Huntingtin-interacting protein HYPK
UniRef100_Q	15	24	24.70%	612	68283	7	Phosphoglucomutase-2
UniRef100_O	10	13	24.70%	534	60978	8	26S proteasome non-ATPase regulatory subunit 3
UniRef100_Q	10	13	24.70%	534	60946	8	PSMD3 protein
UniRef100_O	12	14	24.70%	542	59852	6	Phosphoacetylglucosamine mutase
UniRef100_O	12	14	26.60%	504	55489	6	Isoform 2 of O95394
UniRef100_Q	12	18	24.70%	474	53281	7	Coronin, actin binding protein, 1C variant
UniRef100_Q	12	18	24.70%	474	53249	7	Coronin-1C
UniRef100_P	6	13	24.70%	340	37377	6	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1
UniRef100_U	6	13	25.70%	327	36045	6	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1).
UniRef100_P	9	31	24.70%	288	33666	#	Arginine/serine-rich-splicing factor 10
UniRef100_U	9	31	24.60%	289	33699	#	Arginine/serine-rich-splicing factor 10 (Transformer-2-beta) (HTRA2- beta) (Transformer 2 protein homolog).
UniRef100_Q	9	31	25.70%	276	32321	#	Hypothetical protein DKFZp686F18120
UniRef100_Q	9	31	25.50%	278	32274	#	Splicing factor, arginine/serine-rich 10 (Transformer 2 homolog, Drosophila) variant
UniRef100_P	9	31	37.80%	188	21935	#	Isoform 3 of P62995
UniRef100_U	5	21	24.70%	231	24741	8	Fab 447-52D, heavy chain
UniRef100_O	3	3	24.70%	186	21000	6	Retinoblastoma-binding protein 9
UniRef100_P	42	68	24.60%	2225	2E+05	7	CAD protein [Includes: Glutamine-dependent carbamoyl-phosphate synthase (EC 6.3.5.5); Aspartate carbamoyltransferase (EC 2.1.3.2); Dihydroorotase (EC 3.5.2.3)]
UniRef100_Q	42	68	25.40%	2151	2E+05	7	Hypothetical protein CAD

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_A	21	23	24.50%	1183	1E+05	6	Neuronal cell adhesion molecule
UniRef100_U	21	23	23.40%	1238	1E+05	6	Neuronal cell adhesion molecule precursor (Nr-CAM) (NgCAM-related cell adhesion molecule) (Ng-CAM-related) (hBravo).
UniRef100_U	21	23	24.50%	1182	1E+05	6	Neuronal cell adhesion molecule precursor (Nr-CAM) (NgCAM-related cell adhesion molecule) (Ng-CAM-related) (hBravo).
UniRef100_U	21	23	24.50%	1185	1E+05	6	Neuronal cell adhesion molecule precursor (Nr-CAM) (NgCAM-related cell adhesion molecule) (Ng-CAM-related) (hBravo).
UniRef100_U	21	23	22.20%	1306	1E+05	6	Neuronal cell adhesion molecule precursor (Nr-CAM) (NgCAM-related cell adhesion molecule) (Ng-CAM-related) (hBravo).
UniRef100_U	21	23	22.10%	1310	1E+05	6	Neuronal cell adhesion molecule precursor (Nr-CAM) (NgCAM-related cell adhesion molecule) (Ng-CAM-related) (hBravo).
UniRef100_U	21	23	22.20%	1304	1E+05	6	neuronal cell adhesion molecule isoform A precursor
UniRef100_Q	21	23	22.20%	1308	1E+05	6	Isoform 5 of Q92823
UniRef100_Q	21	23	24.50%	1183	1E+05	6	Isoform 4 of Q92823
UniRef100_Q	21	23	24.60%	1180	1E+05	6	Isoform 3 of Q92823
UniRef100_Q	21	23	23.50%	1236	1E+05	6	Isoform 2 of Q92823
UniRef100_Q	21	23	22.20%	1304	1E+05	6	Neuronal cell adhesion molecule precursor
UniRef100_Q	21	23	24.60%	1180	1E+05	6	NRCAM protein
UniRef100_Q	21	23	24.30%	1192	1E+05	6	NRCAM protein
UniRef100_Q	9	11	24.50%	457	51212	6	FK506-binding protein 5
UniRef100_U	9	11	24.50%	457	51154	6	FK506-binding protein 5 (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (51 kDa FK506-binding protein) (FKBP- 51) (54 kDa progesterone receptor-associated immunophilin) (FKBP54) (P54) (FF1 antigen) (HSP90-binding immunophilin) (Andr
UniRef100_Q	9	11	24.50%	457	51198	6	FK506 binding protein 5 variant
UniRef100_Q	9	11	24.50%	457	51178	6	FK506 binding protein 5
UniRef100_Q	9	11	24.50%	367	40542	9	Developmentally-regulated GTP-binding protein 1
UniRef100_Q	8	10	24.50%	331	38243	5	Nuclear migration protein nudC
UniRef100_O	5	5	24.50%	310	34577	7	26S proteasome non-ATPase regulatory subunit 14
UniRef100_Q	5	5	29.30%	259	28772	7	10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610303K13 product:26S proteasome-associated pad1 homolog, full insert sequence
UniRef100_P	5	7	24.50%	277	30189	5	Inositol monophosphatase (EC 3.1.3.25) (IMPase) (IMP) (Inositol-1(or 4)-monophosphatase)
UniRef100_P	4	6	24.50%	261	29149	5	Gamma-interferon-inducible lysosomal thiol reductase precursor
UniRef100_U	4	6	24.70%	259	28903	5	Gamma-interferon-inducible lysosomal thiol reductase precursor (Gamma- interferon-inducible protein IP-30).
UniRef100_Q	4	6	25.60%	250	27964	5	Interferon, gamma-inducible protein 30
UniRef100_Q	4	6	25.60%	250	27936	5	Interferon, gamma-inducible protein 30
UniRef100_P	5	10	24.50%	151	17222	#	40S ribosomal protein S13
UniRef100_P	2	2	24.50%	98	11006	6	Cystatin-A
UniRef100_Q	18	22	24.40%	895	1E+05	8	Cullin-4B
UniRef100_U	18	22	24.20%	900	1E+05	8	Cullin-4B (CUL-4B).
UniRef100_U	18	22	23.80%	917	1E+05	8	Cullin-4B (CUL-4B).

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	18	22	23.90%	913	1E+05	7	Cullin 4B
UniRef100_Q	14	16	24.40%	767	86479	7	Protein transport protein Sec23B
UniRef100_Q	4	22	24.40%	176	20762	#	60S ribosomal protein L18a
UniRef100_Q	3	6	24.40%	131	14142	#	Myosin-reactive immunoglobulin heavy chain variable region
UniRef100_Q	2	4	24.40%	82	8969	8	Immediate early response 3-interacting protein 1
UniRef100_U	19	112	24.30%	564	60067	8	keratin 6B
UniRef100_Q	6	6	24.30%	387	42650	6	CDNA FLJ14257 fis, clone PLACE1000547, highly similar to Homo sapiens GDP-mannose pyrophosphorylase B (GMPPB) mRNA
UniRef100_U	6	6	26.10%	360	39834	7	GDP-mannose pyrophosphorylase B isoform 2
UniRef100_U	6	6	24.30%	387	42622	6	GDP-mannose pyrophosphorylase B isoform 2
UniRef100_Q	6	6	26.10%	360	39862	7	GDP-mannose pyrophosphorylase B
UniRef100_Q	4	7	24.30%	214	23730	5	Haloacid dehalogenase-like hydrolase domain-containing protein 1A
UniRef100_Q	3	3	24.30%	107	12312	7	SH3 domain binding glutamic acid-rich protein like 2
UniRef100_Q	3	3	24.30%	107	12326	7	SH3 domain-binding glutamic acid-rich-like protein 2
UniRef100_Q	3	3	24.30%	107	12314	7	SH3 domain binding glutamic acid-rich protein like 2
UniRef100_Q	8	18	24.20%	392	46514	#	Putative RNA-binding protein Luc7-like 2
UniRef100_U	8	18	23.70%	401	47506	#	Putative RNA-binding protein Luc7-like 2.
UniRef100_P	6	18	24.20%	211	24261	#	60S ribosomal protein L13
UniRef100_Q	6	18	24.20%	211	24265	#	Ribosomal protein L13
UniRef100_Q	11	30	24.10%	528	60593	5	Golgi resident protein GCP60
UniRef100_U	8	58	24.10%	345	39576	5	UPI0000D622D2 UniRef100 entry
UniRef100_P	7	8	24.10%	324	37025	7	26S proteasome non-ATPase regulatory subunit 7
UniRef100_Q	2	4	24.10%	116	12294	5	Amyloid lambda 6 light chain variable region SAR
UniRef100_Q	2	4	24.10%	108	11419	7	Resistin precursor
UniRef100_P	3	6	24.10%	83	9332	9	Apolipoprotein C-I precursor
UniRef100_Q	44	97	24.00%	2322	3E+05	6	Chondroitin sulfate proteoglycan 4 precursor
UniRef100_U	44	97	24.00%	2322	3E+05	6	chondroitin sulfate proteoglycan 4
UniRef100_P	16	67	24.00%	847	94623	6	Matrin-3
UniRef100_P	8	26	24.00%	433	48634	6	26S protease regulatory subunit 7
UniRef100_Q	8	26	24.00%	433	48618	6	Hypothetical protein Nbla10058
UniRef100_A	3	6	24.00%	179	20296	5	Nudix (Nucleoside diphosphate linked moiety X)-type motif 1
UniRef100_Q	3	6	27.60%	156	17984	5	Nudix (Nucleoside diphosphate linked moiety X)-type motif 1
UniRef100_Q	3	6	27.60%	156	17951	5	Nudix (Nucleoside diphosphate linked moiety X)-type motif 1
UniRef100_P	3	6	21.80%	197	22552	5	7,8-dihydro-8-oxoguanine triphosphatase
UniRef100_P	4	18	24.00%	125	13742	#	40S ribosomal protein S25
UniRef100_U	4	18	24.20%	124	13614	#	PREDICTED: similar to 40S ribosomal protein S25
UniRef100_U	4	18	24.20%	124	13588	#	UPI000013DB63 UniRef100 entry
UniRef100_U	4	18	24.20%	124	13615	#	PREDICTED: similar to 40S ribosomal protein S25
UniRef100_P	24	26	23.90%	1174	1E+05	7	DNA-directed RNA polymerase II 140 kDa polypeptide
UniRef100_Q	6	13	23.90%	393	45571	7	Paraspeckle protein 1 beta isoform
UniRef100_Q	6	13	18.00%	523	58744	7	Paraspeckle component 1

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	4	6	23.90%	264	29622	6	COP9 signalosome complex subunit 7b
UniRef100_P	8	16	23.90%	209	24034	8	High mobility group protein B2
UniRef100_Q	8	16	24.00%	208	23905	8	High-mobility group box 2
UniRef100_Q	39	54	23.80%	1810	2E+05	5	Protein KIAA1429
UniRef100_U	39	54	23.80%	1812	2E+05	5	hypothetical protein LOC25962 isoform 1
UniRef100_Q	39	54	24.00%	1795	2E+05	5	KIAA1429 protein
UniRef100_O	13	27	23.80%	794	89595	7	Uncharacterized protein KIAA0776
UniRef100_P	13	19	23.80%	559	63173	6	Complement component C9 precursor [Contains: Complement component C9a; Complement component C9b]
UniRef100_P	10	18	23.80%	508	57116	5	Protein disulfide-isomerase precursor
UniRef100_Q	5	12	23.80%	227	23790	6	Upstream regulatory element binding protein 1
UniRef100_P	7	13	23.70%	325	37251	8	LIM and senescent cell antigen-like-containing domain protein 1
UniRef100_U	7	13	19.40%	396	45508	8	LIM and senescent cell antigen-like-containing domain protein 3 (Particularly interesting new Cys-His protein 3) (PINCH-3).
UniRef100_U	7	13	19.90%	387	44390	8	LIM and senescent cell antigen-like-containing domain protein 1 (Particularly interesting new Cys-His protein 1) (PINCH-1) (Renal carcinoma antigen NY-REN-48).
UniRef100_P	4	5	23.70%	270	29247	6	Replication protein A 32 kDa subunit
UniRef100_P	4	5	17.90%	358	38810	9	Isoform 3 of P15927
UniRef100_P	4	5	23.00%	278	30156	7	Isoform 2 of P15927
UniRef100_Q	3	3	23.70%	236	26318	6	Guanidinoacetate N-methyltransferase
UniRef100_Q	3	7	23.70%	152	16938	9	Mitochondrial fission 1 protein
UniRef100_U	3	7	23.70%	152	16980	9	tetratricopeptide repeat domain 11
UniRef100_Q	39	87	23.60%	1816	2E+05	6	LAMA4 protein
UniRef100_O	16	16	23.60%	962	1E+05	5	Exportin-T (tRNA exportin) (Exportin(tRNA))
UniRef100_U	16	16	23.60%	963	1E+05	6	Exportin-T (tRNA exportin) (Exportin(tRNA)).
UniRef100_P	6	13	23.60%	440	49185	6	26S protease regulatory subunit 4
UniRef100_Q	6	13	23.60%	440	49127	6	Proteasome (Prosome, macropain) 26S subunit, ATPase, 1
UniRef100_Q	6	13	23.60%	440	49213	6	Proteasome 26S ATPase subunit 1 variant
UniRef100_Q	5	6	23.60%	365	40833	8	LIM and cysteine-rich domains protein 1
UniRef100_Q	7	18	23.60%	314	35611	5	Uncharacterized protein C20orf116 precursor
UniRef100_U	7	18	23.60%	314	35595	5	Uncharacterized protein C20orf116 precursor.
UniRef100_Q	7	13	23.50%	221	25797	8	Ubiquitin-conjugating enzyme E2 variant 1
UniRef100_U	7	13	14.10%	370	42210	7	ubiquitin-conjugating enzyme E2 Kua-UEV isoform 1
UniRef100_Q	7	13	35.40%	147	16495	8	Ubiquitin-conjugating enzyme E2 variant 1
UniRef100_Q	7	13	30.60%	170	19307	9	Isoform 7 of Q13404
UniRef100_Q	7	13	30.60%	170	19228	8	Isoform 2 of Q13404
UniRef100_Q	27	34	23.40%	1479	2E+05	6	Macrophage mannose receptor 2 precursor
UniRef100_U	27	34	23.40%	1479	2E+05	6	mannose receptor, C type 2
UniRef100_U	16	117	23.40%	376	42003	6	hypothetical protein LOC345651
UniRef100_Q	6	8	23.40%	269	31129	7	Golgi phosphoprotein 3-like
UniRef100_Q	6	8	22.10%	285	32767	6	Golgi phosphoprotein 3-like

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P	4	16	23.40%	184	21397	#	60S ribosomal protein L17
UniRef100_U	4	16	23.20%	185	21441	#	60S ribosomal protein L17 (L23).
UniRef100_Q	4	16	23.40%	184	21416	#	Ribosomal protein L17
UniRef100_Q	20	54	23.30%	785	88256	9	Gamma-interferon-inducible protein Ifi-16
UniRef100_Q	20	54	25.10%	729	82096	9	Isoform 2 of Q16666
UniRef100_P	4	5	23.30%	288	32819	8	Heme oxygenase 1
UniRef100_U	4	5	23.30%	287	32652	9	Heme oxygenase 1 (EC 1.14.99.3) (HO-1).
UniRef100_O	7	23	23.30%	262	31301	#	FUS-interacting serine-arginine-rich protein 1
UniRef100_U	7	23	25.00%	244	29195	#	PREDICTED: similar to FUS-interacting serine-arginine-rich protein 1 (TLS-associated protein with Ser-Arg repeats) (TLS-associated protein with SR repeats) (TASR) (TLS-associated serine-arginine protein) (TLS-associated SR protein) (Neural-specific SR protein... isoform 3
UniRef100_U	7	23	57.50%	106	12581	9	PREDICTED: similar to FUS interacting protein (serine-arginine rich) 1
UniRef100_Q	7	23	33.30%	183	22222	#	FUS interacting protein (Serine/arginine-rich) 1
UniRef100_Q	7	23	33.50%	182	22135	#	FUS interacting protein (Serine/arginine-rich) 1
UniRef100_Q	7	23	35.30%	173	21000	#	FUS interacting protein (Serine/arginine-rich) 1
UniRef100_Q	7	23	35.50%	172	20913	#	FUS interacting protein (Serine/arginine-rich) 1
UniRef100_Q	7	23	23.40%	261	31213	#	FUS interacting protein (Serine/arginine-rich) 1
UniRef100_Q	7	23	23.30%	262	31282	#	FUS interacting protein (Serine-arginine rich) 1 isoform 2 variant
UniRef100_P	4	7	23.30%	270	30651	6	Complement factor H-related protein 2 precursor
UniRef100_P	4	7	25.90%	243	27897	7	Isoform Short of P36980
UniRef100_Q	5	12	23.30%	249	27893	9	Vesicle-associated membrane protein-associated protein A
UniRef100_U	5	12	19.70%	294	32614	9	vesicle-associated membrane protein-associated protein A isoform 1
UniRef100_Q	3	7	23.30%	150	17068	7	Ionized calcium-binding adapter molecule 2
UniRef100_U	3	7	19.80%	177	20058	8	Ionized calcium-binding adapter molecule 2.
UniRef100_U	3	7	24.60%	142	16191	9	Ionized calcium-binding adapter molecule 2.
UniRef100_Q	3	7	24.60%	142	16183	9	Isoform 3 of Q9BQI0
UniRef100_Q	3	7	19.90%	176	20015	8	Isoform 2 of Q9BQI0
UniRef100_Q	2	3	23.30%	133	15237	6	DNA-directed RNA polymerase I subunit D
UniRef100_P	2	3	23.30%	116	13062	6	Dynein light chain Tctex-type 3
UniRef100_U	2	3	17.80%	152	16979	6	Dynein light chain Tctex-type 3 (T-complex-associated testis-expressed 1-like) (Protein 91/23).
UniRef100_Q	86	190	23.20%	4374	5E+05	5	E3 ubiquitin-protein ligase HUWE1
UniRef100_Q	86	190	23.30%	4365	5E+05	5	Isoform 3 of Q7Z6Z7
UniRef100_Q	86	190	23.30%	4358	5E+05	5	Isoform 2 of Q7Z6Z7
UniRef100_P	10	10	23.20%	616	68138	7	Replication protein A 70 kDa DNA-binding subunit
UniRef100_Q	7	25	23.20%	393	43135	8	PAI-1 mRNA-binding protein
UniRef100_Q	7	25	23.50%	387	42441	8	Hypothetical protein DKFZp686P17171
UniRef100_Q	7	25	23.50%	387	42427	8	PAI-1 mRNA-binding protein
UniRef100_O	3	11	23.20%	198	22092	5	Density-regulated protein
UniRef100_U	3	11	23.10%	199	22285	6	Density-regulated protein (DRP) (Protein DRP1) (Smooth muscle cell- associated protein 3) (SMAP-3).
UniRef100_P	2	9	23.20%	95	10871	6	Small ubiquitin-related modifier 2 precursor

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_UI	2	9	29.70%	74	8368	5	Small ubiquitin-related modifier 2 precursor (SUMO-2) (Ubiquitin-like protein SMT3B) (SMT3 homolog 2) (Sentrin-2) (HSMT3) (SUMO-3).
UniRef100_UI	2	9	31.00%	71	8111	5	SMT3 suppressor of mif two 3 homolog 2 isoform b precursor
UniRef100_UI	2	9	23.20%	95	10839	6	PREDICTED: similar to SMT3 suppressor of mif two 3 homolog 2
UniRef100_Q	27	29	23.10%	1531	2E+05	6	UDP-glucose:glycoprotein glucosyltransferase 1 precursor
UniRef100_UI	27	29	22.70%	1557	2E+05	6	UDP-glucose:glycoprotein glucosyltransferase 1 precursor (EC 2.4.1.-) (UDP-glucose ceramide glucosyltransferase-like 1) (UDP-- Glc:glycoprotein glucosyltransferase) (HUGT1).
UniRef100_UI	27	29	22.70%	1555	2E+05	6	UDP-glucose ceramide glucosyltransferase-like 1 isoform 1
UniRef100_Q	6	10	23.10%	390	43476	6	Polymerase I and transcript release factor
UniRef100_P	5	8	23.10%	350	39384	6	Glycogenin-1
UniRef100_UI	5	8	31.40%	258	28857	5	Glycogenin-1 (EC 2.4.1.186).
UniRef100_Q	5	8	24.50%	331	37246	5	GYG1 protein
UniRef100_Q	5	8	24.30%	333	37479	5	GYG protein
UniRef100_P	5	8	31.20%	260	29057	5	Isoform GN
UniRef100_P	6	6	23.10%	286	31514	6	Interferon-induced 35 kDa protein
UniRef100_UI	6	6	22.90%	288	31777	6	Interferon-induced 35 kDa protein (IFP 35).
UniRef100_P	6	6	22.90%	288	31745	6	Isoform 2 of P80217
UniRef100_P	3	4	23.10%	147	16858	7	Bis(5'-adenosyl)-triphosphatase
UniRef100_Q	2	14	23.10%	121	13436	8	Immunglobulin heavy chain variable region
UniRef100_P	40	100	23.00%	2468	3E+05	5	Microtubule-associated protein 1B (MAP 1B) [Contains: MAP1 light chain LC1]
UniRef100_UI	40	100	23.00%	2468	3E+05	5	Microtubule-associated protein 1B (MAP 1B) [Contains: MAP1 light chain LC1].
UniRef100_Q	16	30	23.00%	890	1E+05	5	Transportin-1
UniRef100_UI	16	30	22.80%	898	1E+05	5	transportin 1 isoform 1
UniRef100_Q	5	16	23.00%	282	32689	#	Transformer-2 protein homolog
UniRef100_Q	6	16	23.00%	261	29717	7	LIM and SH3 domain protein 1
UniRef100_UI	6	16	18.60%	322	35773	9	LIM and SH3 domain protein 1 (LASP-1) (MLN 50).
UniRef100_Q	6	16	18.60%	323	36014	9	Isoform 2 of Q14847
UniRef100_Q	8	12	23.00%	239	27560	8	mRNA turnover protein 4 homolog
UniRef100_P	5	10	23.00%	135	15860	#	60S ribosomal protein L32
UniRef100_UI	5	10	23.00%	135	15751	#	PREDICTED: similar to 60S ribosomal protein L32
UniRef100_Q	6	8	22.90%	423	47708	6	WD repeat protein 12
UniRef100_UI	6	8	22.90%	423	47544	6	WD repeat domain 12 protein
UniRef100_P	4	10	22.90%	210	23671	6	Nuclear protein Hcc-1
UniRef100_Q	4	10	32.00%	150	16830	#	CIP29 protein
UniRef100_P	3	4	22.90%	109	12457	7	Transcription initiation factor IIA gamma chain
UniRef100_Q	21	29	22.80%	1496	2E+05	7	Peroxidasin homolog
UniRef100_Q	17	22	22.80%	1192	1E+05	6	Tubulin-specific chaperone D
UniRef100_UI	17	22	22.80%	1192	1E+05	6	beta-tubulin cofactor D
UniRef100_Q	17	22	21.80%	1248	1E+05	6	Isoform 4 of Q9BTW9
UniRef100_Q	15	35	22.80%	877	98116	6	SF3B2 protein
UniRef100_Q	15	35	22.40%	894	1E+05	6	SF3B2 protein

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P	14	36	22.80%	500	55154	7	Plasma protease C1 inhibitor precursor
UniRef100_U	14	36	34.20%	333	37303	8	Plasma protease C1 inhibitor precursor (C1 Inh) (C1Inh) (C1 esterase inhibitor) (C1-inhibiting factor).
UniRef100_Q	14	36	34.20%	333	37288	8	Serine/cysteine proteinase inhibitor clade G member 1 splice variant 2
UniRef100_P	9	35	22.80%	491	54566	6	Alpha-2-antiplasmin precursor
UniRef100_Q	9	35	22.80%	491	54594	6	SERPINF2 protein
UniRef100_Q	6	10	22.80%	372	42244	6	Alpha-parvin
UniRef100_Q	2	6	22.80%	145	16298	9	Mitochondrial import receptor subunit TOM20 homolog
UniRef100_P	4	13	22.80%	136	14570	#	Signal recognition particle 14 kDa protein
UniRef100_Q	4	13	22.80%	136	14514	#	Signal recognition particle 14kD
UniRef100_P	10	43	22.70%	475	53501	9	Splicing factor U2AF 65 kDa subunit (U2 auxiliary factor 65 kDa subunit) (U2 snRNP auxiliary factor large subunit) (hU2AF(65))
UniRef100_U	10	43	22.60%	477	53728	9	Splicing factor U2AF 65 kDa subunit (U2 auxiliary factor 65 kDa subunit) (U2 snRNP auxiliary factor large subunit) (hU2AF(65)).
UniRef100_Q	10	43	22.90%	471	53121	9	U2 small nuclear RNA auxiliary factor 2
UniRef100_Q	6	7	22.70%	445	46804	8	von Willebrand factor A domain-containing protein 1
UniRef100_Q	4	4	22.70%	203	23363	9	ARL-6-interacting protein 1
UniRef100_Q	4	11	22.70%	198	22410	6	SAR1a gene homolog 2 variant
UniRef100_Q	4	11	22.70%	198	22410	6	GTP-binding protein SAR1b
UniRef100_O	3	5	22.70%	132	14889	6	Fatty acid-binding protein, brain
UniRef100_Q	3	5	18.10%	166	18829	6	Hypothetical protein DKFZp547J2313
UniRef100_Q	3	5	29.10%	103	11698	8	Hypothetical protein
UniRef100_A	16	28	22.50%	839	99723	6	RBM25 protein
UniRef100_U	16	28	22.40%	843	1E+05	6	RNA binding motif protein 25
UniRef100_P	16	28	24.10%	784	94122	6	Probable RNA-binding protein 25
UniRef100_O	10	21	22.50%	613	66901	9	Apoptosis-inducing factor 1, mitochondrial precursor
UniRef100_O	10	21	22.70%	609	66295	9	Isoform 3 of O95831
UniRef100_P	9	16	22.50%	494	56069	5	Ubiquitin carboxyl-terminal hydrolase 14
UniRef100_U	9	16	24.20%	459	52386	6	ubiquitin specific protease 14 isoform b
UniRef100_Q	8	28	22.50%	271	30069	6	COMT protein
UniRef100_Q	8	28	33.50%	182	20045	6	COMT protein
UniRef100_O	20	26	22.40%	1208	1E+05	6	Neural cell adhesion molecule L1-like protein precursor
UniRef100_U	20	26	22.10%	1224	1E+05	6	cell adhesion molecule with homology to L1CAM precursor
UniRef100_O	20	26	22.10%	1224	1E+05	6	Isoform 2 of O00533
UniRef100_Q	15	22	22.40%	768	88930	9	Cullin-3
UniRef100_Q	15	22	23.10%	744	86234	8	Isoform 2 of Q13618
UniRef100_Q	6	12	22.40%	330	37662	8	Complement factor H-related protein 1 precursor
UniRef100_Q	6	12	22.40%	330	37651	7	Complement factor H-related 1
UniRef100_Q	6	12	27.30%	271	30858	8	Complement factor H-related 1
UniRef100_O	7	13	22.30%	494	55024	7	UDP-glucose 6-dehydrogenase
UniRef100_Q	3	3	22.30%	224	24670	7	COMM domain-containing protein 5

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P4	3	14	22.30%	148	16561	#	60S ribosomal protein L27a
UniRef100_UI	3	14	22.30%	148	16622	#	PREDICTED: similar to 60S ribosomal protein L27a
UniRef100_Q	3	14	31.10%	106	12015	#	Ribosomal protein L27a
UniRef100_Q	3	14	22.30%	148	16478	#	Ribosomal protein L27a
UniRef100_Q	2	2	22.30%	103	11761	8	Pterin-4-alpha-carbinolamine dehydratase 2
UniRef100_UI	2	2	17.70%	130	14365	9	pterin-4 alpha-carbinolamine dehydratase 2
UniRef100_P	4	19	22.20%	257	28025	#	60S ribosomal protein L8
UniRef100_Q	3	3	22.20%	225	26032	6	Preimplantation protein 3
UniRef100_Q	3	3	25.90%	193	22318	6	Isoform 2 of Q9Y3A3
UniRef100_O	4	8	22.20%	180	20274	5	Trafficking protein particle complex subunit 3
UniRef100_P	3	4	22.20%	117	13667	8	Gamma-aminobutyric acid receptor-associated protein-like 2 (GABA(A) receptor-associated protein-like 2)
UniRef100_Q	2	2	22.20%	108	11594	7	Anti-streptococcal/anti-myosin immunoglobulin lambda light chain variable region
UniRef100_P	12	20	22.10%	705	80174	6	Complement C1r subcomponent precursor (EC 3.4.21.41) (Complement component 1, r subcomponent) [Contains: Complement C1r subcomponent heavy chain; Complement C1r subcomponent light chain]
UniRef100_UI	12	20	22.10%	705	80200	6	complement component 1, r subcomponent
UniRef100_Q	12	20	22.10%	705	80300	6	Complement component 1, r subcomponent variant
UniRef100_Q	12	20	22.10%	705	80241	6	Complement component 1, r subcomponent variant
UniRef100_P	8	9	22.10%	493	54548	6	Xaa-Pro dipeptidase
UniRef100_Q	5	11	22.10%	411	46476	8	Uncharacterized protein C1orf58
UniRef100_Q	8	10	22.00%	350	38380	5	Unr-interacting protein
UniRef100_Q	8	10	22.00%	350	38438	5	Serine-threonine kinase receptor-associated protein
UniRef100_Q	8	10	22.00%	350	38452	5	Hypothetical protein DKFZp564N1778
UniRef100_A	5	9	22.00%	273	31694	7	MHC class I antigen
UniRef100_A	5	8	22.00%	273	31642	6	MHC class I antigen
UniRef100_A	5	8	22.00%	273	31437	6	MHC class I antigen
UniRef100_A	5	8	22.00%	273	31467	6	MHC class I antigen
UniRef100_A	5	8	16.40%	365	40842	6	MHC class I antigen
UniRef100_A	5	8	22.70%	264	30518	5	MHC class I antigen
UniRef100_A	5	8	20.20%	297	33777	6	MHC class I antigen
UniRef100_O	7	13	22.00%	277	30850	6	Carbonyl reductase [NADPH] 3
UniRef100_Q	8	9	21.90%	475	53489	5	Ataxin-10
UniRef100_A	14	22	21.80%	923	1E+05	6	Transportin 3
UniRef100_Q	14	22	22.10%	909	1E+05	6	Isoform 4 of Q9Y5L0
UniRef100_Q	10	12	21.80%	717	82922	8	Cleavage stimulation factor 77 kDa subunit
UniRef100_P	5	10	21.80%	372	40090	#	DNA-binding protein A
UniRef100_UI	5	10	21.80%	372	40060	#	cold shock domain protein A
UniRef100_Q	5	10	26.70%	303	31947	#	CSDA protein
UniRef100_P	5	10	23.70%	342	37021	#	Isoform 3 of P16989
UniRef100_P	11	34	21.80%	284	32819	5	Tropomyosin alpha-3 chain

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_U	11	34	21.80%	285	32996	5	Tropomyosin alpha-3 chain (Tropomyosin-3) (Tropomyosin gamma) (hTM5).
UniRef100_U	11	34	21.80%	285	32950	5	tropomyosin 3 isoform 1
UniRef100_P	5	8	21.80%	225	26560	6	Glutathione S-transferase Mu 3
UniRef100_Q	5	8	21.20%	231	27202	6	Glutathione S-transferase M3 variant
UniRef100_P	2	2	21.80%	170	19509	5	Ubiquitin-conjugating enzyme E2 G1
UniRef100_Q	11	31	21.70%	585	65331	5	Galectin-3-binding protein precursor
UniRef100_Q	9	14	21.60%	541	60542	6	DKFZP564J0863 protein
UniRef100_Q	9	14	21.60%	541	60559	6	Hypothetical protein DKFZp564J0863
UniRef100_P	8	26	21.60%	449	52495	6	Clusterin precursor (Complement-associated protein SP-40,40) (Complement cytolysis inhibitor) (CLI) (NA1/NA2) (Apolipoprotein J) (Apo-J) (Testosterone-repressed prostate message 2) (TRPM-2) [Contains: Clusterin beta chain (ApoJalpha) (Complement cytolysis inhibitor a chain); Clusterin alpha chain (ApoJbeta) (Complement cytolysis inhibitor b chain)]
UniRef100_Q	7	13	21.60%	375	42823	5	Nucleosome assembly protein 1-like 4
UniRef100_U	7	13	21.50%	377	43011	5	Nucleosome assembly protein 1-like 4 (Nucleosome assembly protein 2) (NAP2).
UniRef100_Q	4	6	21.60%	231	26389	6	Phosphoribosyl transferase domain-containing protein 1
UniRef100_Q	4	6	22.20%	225	25673	6	HHGP
UniRef100_Q	4	9	21.60%	176	18985	9	Protein CGI-38
UniRef100_Q	2	2	21.60%	125	14116	8	Uncharacterized protein C1orf31
UniRef100_U	2	2	17.40%	155	18007	#	Novel protein.
UniRef100_Q	2	2	34.20%	79	9428	8	Isoform 3 of Q5JTJ3
UniRef100_Q	2	2	17.30%	156	18094	#	Isoform 2 of Q5JTJ3
UniRef100_P	3	11	21.60%	111	12203	4	Prothymosin alpha [Contains: Thymosin alpha-1]
UniRef100_Q	3	11	21.80%	110	12016	4	Prothymosin, alpha
UniRef100_Q	3	11	21.80%	110	12044	4	Prothymosin alpha protein
UniRef100_Q	3	11	21.80%	110	12055	4	OTTHUMP00000018545
UniRef100_Q	3	11	21.80%	110	12047	4	Prothymosin alpha
UniRef100_Q	3	11	22.00%	109	11959	4	Prothymosin alpha
UniRef100_Q	3	11	21.80%	110	12085	4	Prothymosin alpha
UniRef100_P	3	11	21.80%	110	12074	4	Isoform 2 of P06454
UniRef100_P	5	5	21.50%	386	43215	7	Methionine aminopeptidase 1
UniRef100_P	2	3	21.50%	121	13842	7	Protein yippee-like 5
UniRef100_P	16	18	21.40%	917	1E+05	7	Hexokinase-1
UniRef100_U	16	18	21.70%	905	1E+05	7	Hexokinase-1 (EC 2.7.1.1) (Hexokinase type I) (HK I) (Brain form hexokinase).
UniRef100_P	16	18	21.70%	905	1E+05	7	Isoform 4 of P19367
UniRef100_O	8	12	21.40%	637	72684	6	Protein arginine N-methyltransferase 5
UniRef100_U	8	12	21.90%	620	71320	7	protein arginine methyltransferase 5 isoform b
UniRef100_Q	13	27	21.40%	630	70990	8	Tripartite motif-containing protein 25
UniRef100_Q	13	27	21.00%	644	72250	8	Tripartite motif-containing 25 variant
UniRef100_Q	4	7	21.40%	201	23383	7	5'(3')-deoxyribonucleotidase, cytosolic type
UniRef100_Q	4	7	36.80%	117	13299	7	Isoform 2 of Q8TCD5
UniRef100_O	2	3	21.40%	196	21731	9	Peptidoglycan recognition protein precursor

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	15	19	21.30%	944	1E+05	6	Neutral alpha-glucosidase AB precursor
UniRef100_Q	15	19	20.80%	966	1E+05	6	Isoform 2 of Q14697
UniRef100_Q	13	36	21.30%	644	70783	9	Polyadenylate-binding protein 4 (Poly(A)-binding protein 4) (PABP 4) (Inducible poly(A)-binding protein)
UniRef100_Q	13	36	20.80%	660	72361	9	PABPC4 protein
UniRef100_Q	13	36	20.80%	660	72391	9	Poly(A) binding protein, cytoplasmic 4
UniRef100_Q	13	36	22.30%	615	67971	#	Poly(A) binding protein, cytoplasmic 4
UniRef100_P	7	8	21.30%	376	42404	6	Serpin B9
UniRef100_Q	63	119	21.20%	3695	4E+05	7	Laminin alpha5 chain precursor
UniRef100_Q	8	17	21.20%	481	51476	#	SF3A2 protein
UniRef100_Q	8	17	22.00%	464	49256	#	Splicing factor 3A subunit 2
UniRef100_Q	5	9	21.20%	363	38947	5	Poly(ADP-ribose) glycohydrolase ARH3
UniRef100_U	5	9	22.20%	347	37805	5	ADP-ribosylhydrolase 3
UniRef100_P	6	36	21.20%	240	24610	#	Small nuclear ribonucleoprotein-associated proteins B and B'
UniRef100_U	6	36	21.60%	236	26362	9	Small nuclear ribonucleoprotein-associated protein N (snRNP-N) (Sm protein N) (Sm-N) (SmN) (Sm-D) (Tissue-specific-splicing protein).
UniRef100_U	6	36	21.10%	242	27236	9	Small nuclear ribonucleoprotein-associated proteins B and B' (snRNP-B) (Sm protein B/B') (Sm-B/Sm-B') (SmB/SmB').
UniRef100_U	6	36	17.80%	287	29862	#	Small nuclear ribonucleoprotein-associated proteins B and B' (snRNP-B) (Sm protein B/B') (Sm-B/Sm-B') (SmB/SmB').
UniRef100_Q	6	36	21.00%	243	27267	9	Small nuclear ribonucleoprotein B'
UniRef100_Q	6	36	21.80%	234	24088	#	SNRPB protein
UniRef100_Q	6	36	22.10%	231	23656	#	Small nuclear ribonucleoprotein polypeptides B and B1
UniRef100_Q	6	36	22.10%	231	23657	#	Small nuclear ribonucleoprotein polypeptide B
UniRef100_Q	6	36	17.90%	285	29671	#	SNRPB protein
UniRef100_P	6	36	21.20%	240	24614	#	Small nuclear ribonucleoprotein-associated protein N
UniRef100_P	6	36	17.60%	289	30032	#	Isoform SM
UniRef100_Q	2	4	21.20%	208	23279	6	Protein FADD
UniRef100_P	4	6	21.20%	156	17695	#	60S ribosomal protein L23a
UniRef100_P	30	43	21.10%	1970	2E+05	7	DNA-directed RNA polymerase II largest subunit
UniRef100_P	12	23	21.10%	622	70037	6	Prothrombin precursor (EC 3.4.21.5) (Coagulation factor II) [Contains: Activation peptide fragment 1; Activation peptide fragment 2; Thrombin light chain; Thrombin heavy chain]
UniRef100_U	12	23	21.10%	622	69961	6	Prothrombin precursor (EC 3.4.21.5) (Coagulation factor II) [Contains: Activation peptide fragment 1; Activation peptide fragment 2; Thrombin light chain; Thrombin heavy chain].
UniRef100_Q	12	23	21.10%	622	70009	6	Coagulation factor II
UniRef100_Q	12	23	21.10%	622	70136	6	Coagulation factor II variant
UniRef100_Q	12	23	21.10%	622	70064	6	Coagulation factor II variant
UniRef100_Q	12	23	21.10%	622	69965	6	Prothrombin
UniRef100_P	5	5	21.10%	454	49831	5	Ca(2+)/calmodulin-dependent protein kinase phosphatase
UniRef100_Q	5	5	21.20%	453	49702	5	Protein phosphatase 1F
UniRef100_Q	7	9	21.10%	421	47996	8	Testin

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P	9	19	21.10%	369	41332	5	Hsc70-interacting protein
UniRef100_P	6	7	21.10%	298	33922	6	Mimecan precursor
UniRef100_U	6	7	19.90%	316	36096	7	osteoglycin preproprotein isoform 1
UniRef100_Q	6	7	21.10%	298	33922	6	Osteoglycin OG
UniRef100_Q	5	17	21.10%	289	32917	7	P15RS protein
UniRef100_Q	5	17	19.60%	312	35720	8	Cyclin-dependent kinase inhibitor-related protein
UniRef100_Q	3	3	21.10%	152	17025	8	Uncharacterized protein C6orf130
UniRef100_U	3	3	20.40%	157	17607	8	Uncharacterized protein C6orf130.
UniRef100_Q	28	36	21.00%	1550	2E+05	6	Protein ALO17
UniRef100_Q	28	36	20.30%	1599	2E+05	6	Isoform 3 of Q9HCF4
UniRef100_A	7	13	21.00%	348	39150	7	MHC class I antigen
UniRef100_A	7	13	24.50%	298	34245	6	MHC Class I antigen
UniRef100_Q	4	5	21.00%	329	35207	8	Quinone oxidoreductase
UniRef100_U	4	5	23.40%	295	31528	9	Quinone oxidoreductase (EC 1.6.5.5) (NADPH:quinone reductase) (Zeta- crystallin).
UniRef100_A	4	13	21.00%	219	23245	5	Proteasome (Prosome, macropain) subunit beta type 9
UniRef100_P	4	13	22.00%	209	22328	5	Isoform LMP2.S of P28065
UniRef100_P	4	13	21.00%	219	23264	5	Proteasome subunit beta type 9 precursor
UniRef100_A	4	13	23.50%	196	20942	5	Proteasome (Prosome, macropain) subunit beta type 9
UniRef100_P	3	5	21.00%	157	18615	6	AP-1 complex subunit sigma-2
UniRef100_O	7	8	20.90%	556	62412	7	Glypican-4 precursor
UniRef100_Q	4	9	20.90%	320	35349	8	Multisynthetase complex auxiliary component p38
UniRef100_P	6	11	20.90%	301	34235	8	NADH-cytochrome b5 reductase (EC 1.6.2.2) (B5R) (Diaphorase-1) (Cytochrome b5 reductase 3) [Contains: NADH-cytochrome b5 reductase membrane-bound form; NADH-cytochrome b5 reductase soluble form]
UniRef100_Q	4	5	20.90%	239	27614	5	Phosducin-like protein 3
UniRef100_Q	4	13	20.90%	139	15350	#	U6 snRNA-associated Sm-like protein LSm4
UniRef100_P	11	25	20.80%	573	61055	6	60 kDa heat shock protein, mitochondrial precursor
UniRef100_U	11	25	20.70%	575	61213	6	60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 kDa chaperonin) (CPN60) (Heat shock protein 60) (HSP-60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein) (HuCHA60).
UniRef100_Q	9	10	20.80%	514	55595	6	F-box-like/WD repeat protein TBL1XR1
UniRef100_P	4	6	20.80%	212	24422	9	ER lumen protein retaining receptor 2
UniRef100_P	9	9	20.70%	599	69069	6	Afamin precursor
UniRef100_Q	7	11	20.70%	488	55364	6	Histone deacetylase 2
UniRef100_P	3	3	20.70%	363	40764	6	Adenosine deaminase
UniRef100_P	17	86	20.60%	641	70375	6	Heat shock 70 kDa protein 1L
UniRef100_Q	17	86	20.60%	641	70404	6	Heat shock 70kDa protein 1-like variant
UniRef100_Q	4	5	20.60%	446	49346	5	CDNA FLJ90195 fis, clone MAMMA1001310
UniRef100_Q	4	5	20.60%	446	49419	5	Glutamate-rich WD repeat-containing protein 1
UniRef100_Q	4	5	20.70%	445	49260	5	KIAA1942 protein
UniRef100_Q	6	16	20.60%	364	40314	7	RNA-binding protein 4

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_U	6	16	20.50%	365	40841	8	RNA binding motif protein 4 (RBM4), mRNA
UniRef100_Q	5	5	20.60%	330	37191	6	Protein FAM98B
UniRef100_U	5	5	15.70%	433	45547	9	family with sequence similarity 98, member B isoform 1
UniRef100_P	5	10	20.60%	301	33970	8	Transcription elongation factor A protein 1
UniRef100_O	4	4	20.60%	223	24654	7	26S proteasome non-ATPase regulatory subunit 9
UniRef100_U	4	4	20.60%	223	24682	7	proteasome 26S non-ATPase subunit 9
UniRef100_U	52	95	20.50%	2813	3E+05	6	von Willebrand factor precursor (vWF) [Contains: von Willebrand antigen 2 (von Willebrand antigen II)].
UniRef100_U	52	95	20.50%	2813	3E+05	6	von Willebrand factor preproprotein
UniRef100_Q	8	35	20.50%	390	42142	#	RNA-binding motif protein X-linked-like 1
UniRef100_Q	3	3	20.50%	293	33933	6	F-box only protein 6
UniRef100_Q	3	3	20.50%	302	32904	5	Deoxyhypusine hydroxylase
UniRef100_P	2	6	20.50%	132	14326	9	Antileukoproteinase precursor
UniRef100_P	16	34	20.40%	998	1E+05	6	General transcription factor II-I
UniRef100_U	16	34	21.30%	957	1E+05	8	general transcription factor II, i isoform 4
UniRef100_Q	16	34	20.90%	976	1E+05	8	General transcription factor II, i
UniRef100_P	16	34	20.90%	977	1E+05	7	Isoform 4 of P78347
UniRef100_P	16	34	20.90%	978	1E+05	7	Isoform 3 of P78347
UniRef100_P	16	34	21.30%	957	1E+05	8	Isoform 2 of P78347
UniRef100_Q	10	18	20.40%	638	71457	5	Cytoplasmic dynein 1 intermediate chain 2
UniRef100_U	10	18	20.30%	641	71709	5	Cytoplasmic dynein 1 intermediate chain 2 (Dynein intermediate chain 2, cytosolic) (DH IC-2) (Cytoplasmic dynein intermediate chain 2).
UniRef100_Q	10	18	21.20%	612	68354	5	Cytoplasmic dynein intermediate chain 2C
UniRef100_Q	10	18	21.20%	612	68426	5	DYNC1I2 protein
UniRef100_Q	10	18	21.20%	612	68412	5	DYNC1I2 protein
UniRef100_Q	10	18	21.30%	611	68298	5	Isoform 2F of Q13409
UniRef100_Q	10	18	20.40%	637	71328	5	Isoform 2E of Q13409
UniRef100_Q	10	18	20.60%	632	70645	5	Isoform 2B of Q13409
UniRef100_P	9	11	20.40%	499	57071	7	Heparin cofactor 2 precursor
UniRef100_Q	9	11	20.40%	499	56957	7	Serpin peptidase inhibitor, clade D (Heparin cofactor), member 1
UniRef100_O	2	2	20.40%	216	24182	9	Maleylacetoacetate isomerase
UniRef100_Q	2	2	20.40%	216	24083	8	GSTZ1 protein
UniRef100_Q	4	6	20.40%	167	19458	7	Ufm1-conjugating enzyme 1
UniRef100_U	4	6	20.40%	167	19467	8	Ufm1-conjugating enzyme 1
UniRef100_Q	19	34	20.30%	1268	1E+05	7	Vigilin
UniRef100_Q	19	34	20.30%	1268	1E+05	7	Hypothetical protein HDLBP
UniRef100_Q	4	5	20.30%	291	33049	7	PCTP-like protein
UniRef100_Q	4	4	20.30%	296	31698	7	Pyridoxal phosphate phosphatase
UniRef100_U	4	4	19.60%	306	32907	7	Pyridoxal phosphate phosphatase
UniRef100_U	4	4	20.10%	298	31826	7	PYRIDOXAL PHOSPHATE PHOSPHATASE
UniRef100_P	3	8	20.30%	128	13553	#	Histone H2A.Z

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_U	3	8	17.30%	150	15488	#	Histone H2AV (H2A.F/Z).
UniRef100_Q	3	8	20.30%	128	13509	#	Histone H2AV
UniRef100_P	2	2	20.30%	79	9660	9	Cyclin-dependent kinases regulatory subunit 1
UniRef100_U	2	2	20.30%	79	9660	9	PREDICTED: similar to Cyclin-dependent kinases regulatory subunit 1 (CKS-1) (Sid 1334)
UniRef100_U	2	2	20.30%	79	9687	8	PREDICTED: similar to Cyclin-dependent kinases regulatory subunit 1 (CKS-1) (Sid 1334)
UniRef100_Q	2	2	23.90%	67	8027	6	CDC28 protein kinase regulatory subunit 1B
UniRef100_Q	7	9	20.20%	327	35896	8	Nitrilase homolog 1
UniRef100_Q	7	9	21.20%	312	34323	7	Isoform 5 of Q86X76
UniRef100_P	3	5	20.20%	332	31555	4	Myristoylated alanine-rich C-kinase substrate
UniRef100_Q	2	3	20.20%	228	26749	5	Protein C20orf11
UniRef100_P	4	5	20.20%	223	25387	7	Serum amyloid P-component precursor (SAP) (9.5S alpha-1-glycoprotein) [Contains: Serum amyloid P-component(1-203)]
UniRef100_U	3	35	20.20%	223	23701	9	IGG1-KAPPA 4D5 FAB (HEAVY CHAIN)
UniRef100_U	3	35	20.30%	222	23655	9	chimera of Fab2C4: "humanized" murine monoclo
UniRef100_U	3	35	20.20%	223	23723	9	IGG1-KAPPA 4D5 FAB (HEAVY CHAIN)
UniRef100_O	18	30	20.10%	1030	1E+05	5	Huntingtin-interacting protein 1
UniRef100_Q	18	30	20.00%	1037	1E+05	5	Huntingtin interacting protein 1
UniRef100_Q	14	24	20.10%	866	1E+05	7	NMDA receptor-regulated protein 1
UniRef100_Q	7	8	20.10%	463	51852	6	NEDD8-activating enzyme E1 catalytic subunit
UniRef100_Q	4	5	20.10%	384	42191	6	ACY1L2 protein
UniRef100_Q	4	5	17.70%	436	47776	6	Aminoacylase 1-like protein 2
UniRef100_Q	7	14	20.10%	189	21493	8	Receptor expression-enhancing protein 5
UniRef100_Q	2	3	20.10%	134	15314	5	Prefoldin subunit 4
UniRef100_O	8	11	20.00%	521	57887	5	Importin alpha-4 subunit
UniRef100_Q	6	15	20.00%	415	45687	9	Apolipoprotein L2 variant
UniRef100_U	6	15	24.60%	337	37122	7	Apolipoprotein-L2 (Apolipoprotein L-II) (ApoL-II).
UniRef100_Q	6	15	24.60%	337	37092	7	Apolipoprotein-L2
UniRef100_Q	4	6	20.00%	360	41293	6	Mitogen-activated protein kinase 14
UniRef100_Q	4	6	20.00%	360	41493	6	Mitogen-activated protein kinase 14
UniRef100_O	4	5	20.00%	245	28362	9	Eukaryotic translation initiation factor 4E type 2
UniRef100_U	4	5	19.20%	255	29289	8	Eukaryotic translation initiation factor 4E type 2 (eIF4E type 2) (eIF-4E type 2) (mRNA cap-binding protein type 3) (Eukaryotic translation initiation factor 4E-like 3) (Eukaryotic translation initiation factor 4E homologous protein) (mRNA cap-binding pro
UniRef100_Q	4	5	20.20%	243	27829	8	Eukaryotic translation initiation factor 4E member 2 variant
UniRef100_O	4	6	20.00%	200	22980	8	High mobility group protein B3
UniRef100_U	4	6	19.20%	208	23744	9	PREDICTED: similar to high-mobility group box 3
UniRef100_Q	3	3	20.00%	195	22151	6	COMM domain-containing protein 3
UniRef100_Q	3	5	20.00%	115	12530	6	Putative thiosulfate sulfurtransferase KAT
UniRef100_U	3	5	19.20%	120	13059	6	Junctional adhesion molecule A precursor (JAM-A) (Junctional adhesion molecule 1) (JAM-1) (Platelet adhesion molecule 1) (PAM-1) (Platelet F11 receptor) (CD321 antigen).
UniRef100_Q	3	5	18.90%	122	13189	7	Isoform 4 of Q8NFU3

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	3	5	21.10%	109	11750	6	Isoform 3 of Q8NFU3
UniRef100_Q	3	5	31.10%	74	8274	5	Isoform 2 of Q8NFU3
UniRef100_Q	12	16	19.90%	780	90955	8	Cullin-5
UniRef100_P	11	13	19.90%	748	85473	7	Cysteinyl-tRNA synthetase, cytoplasmic
UniRef100_U	11	13	20.20%	738	84472	6	cysteinyl-tRNA synthetase isoform d
UniRef100_Q	11	13	17.90%	831	94638	7	Hypothetical protein DKFZp686F1612
UniRef100_P	11	13	20.50%	726	82846	7	Isoform 2 of P49589
UniRef100_P	9	11	19.90%	732	81225	6	Acylamino-acid-releasing enzyme
UniRef100_Q	9	13	19.90%	583	63473	8	Leucine-rich repeat-containing protein 47
UniRef100_P	13	22	19.90%	538	60671	8	60 kDa SS-A/Ro ribonucleoprotein
UniRef100_Q	3	3	19.90%	297	33325	5	SAPK substrate protein 1
UniRef100_O	4	8	19.90%	261	29816	6	Syntaxin-7
UniRef100_U	4	8	19.90%	261	29846	6	syntaxin 7
UniRef100_O	4	8	21.80%	239	27400	5	Isoform 2 of O15400
UniRef100_P	3	9	19.90%	181	20418	6	ADP-ribosylation factor-like protein 1
UniRef100_O	12	37	19.80%	662	73244	7	ATP-dependent RNA helicase DDX3X
UniRef100_Q	7	10	19.80%	334	38164	9	Hypothetical protein
UniRef100_U	7	10	13.90%	474	53291	7	coiled-coil domain containing 6
UniRef100_Q	7	10	13.90%	474	53295	7	Coiled-coil domain containing 6
UniRef100_Q	7	10	11.30%	585	65917	7	Coiled-coil domain-containing protein 6
UniRef100_Q	2	16	19.80%	121	13536	9	RAB4B protein
UniRef100_P	2	3	19.80%	91	10739	4	Ubiquinol-cytochrome c reductase complex 11 kDa protein, mitochondrial precursor
UniRef100_Q	2	3	21.20%	85	9953	6	UQCRH protein
UniRef100_A	14	29	19.70%	913	1E+05	6	Cell migration-inducing protein 17
UniRef100_U	14	29	19.70%	914	1E+05	6	PREDICTED: similar to eukaryotic translation initiation factor 3, subunit 8, 110kDa isoform 1
UniRef100_Q	14	29	19.70%	913	1E+05	6	Eukaryotic translation initiation factor 3 subunit 8
UniRef100_P	10	33	19.70%	524	58113	5	Proactivator polypeptide precursor [Contains: Saposin A (Protein A); Saposin B-Val; Saposin B (Sphingolipid activator protein 1) (SAP-1) (Cerebroside sulfate activator) (CSAct) (Dispersin) (Sulfatide/GM1 activator); Saposin C (Co-beta-glucosidase) (A1 activator) (Glucosylceramidase activator) (Sphingolipid activator protein 2) (SAP-2); Saposin D (Protein C) (Component C)]
UniRef100_Q	10	33	18.40%	559	61693	5	Prosaposin
UniRef100_Q	10	33	19.40%	530	58727	5	Prosaposin variant
UniRef100_Q	10	33	19.70%	524	58141	5	Prosaposin (Variant Gaucher disease and variant metachromatic leukodystrophy) variant
UniRef100_P	10	33	19.60%	526	58356	5	Isoform Sap
UniRef100_U	9	59	19.70%	422	46229	5	UPI0000D622CC UniRef100 entry
UniRef100_Q	4	4	19.70%	300	34294	7	Chromosome 2 open reading frame 4 short form
UniRef100_Q	4	4	19.90%	297	33733	7	Protein memo
UniRef100_O	2	2	19.70%	198	22418	7	Synaptobrevin homolog YKT6
UniRef100_Q	2	2	20.40%	191	21607	7	SNARE protein Ykt6
UniRef100_Q	4	5	19.70%	173	18795	7	Uncharacterized protein C19orf10 precursor

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_O	8	8	19.60%	536	60030	5	Importin alpha-7 subunit
UniRef100_U	8	8	19.50%	539	60342	5	Importin alpha-7 subunit (Karyopherin alpha-6).
UniRef100_Q	6	8	19.60%	332	37490	8	Cysteine and histidine-rich domain-containing protein 1
UniRef100_Q	6	8	19.60%	332	37437	8	CHORD containing protein-1
gi|21689593|	2	3	19.60%	138	14722	5	rubber elongation factor [Hevea brasiliensis]
UniRef100_P	2	2	19.60%	102	11845	5	U6 snRNA-associated Sm-like protein LSm3
UniRef100_P	8	9	19.50%	591	67047	8	Complement component C8 beta chain precursor
UniRef100_U	8	9	19.50%	591	66948	8	complement component 8, beta polypeptide preproprotein
UniRef100_Q	8	9	29.60%	389	45036	9	Hypothetical protein
UniRef100_P	10	21	19.50%	591	66690	7	CTP synthase 1
UniRef100_U	10	21	19.50%	591	66705	6	CTP synthase
UniRef100_Q	8	17	19.50%	395	44650	8	Acid ceramidase precursor (EC 3.5.1.23) (Acylsphingosine deacylase) (N-acylsphingosine amidohydrolase) (AC) (Putative 32 kDa heart protein) (PHP32) [Contains: Acid ceramidase subunit alpha; Acid ceramidase subunit beta]
UniRef100_U	8	17	18.70%	411	46494	8	N-acylsphingosine amidohydrolase (acid ceramidase) 1 isoform b
UniRef100_Q	8	17	19.50%	395	44692	8	N-acylsphingosine amidohydrolase (Acid ceramidase) 1 preproprotein isoform a variant
UniRef100_Q	8	25	19.50%	221	25476	#	Splicing factor, arginine/serine-rich 2
UniRef100_Q	8	25	19.50%	221	25502	#	Splicing factor, arginine/serine-rich 2 variant
UniRef100_Q	2	2	19.50%	154	17218	9	Golgi-associated plant pathogenesis-related protein 1
UniRef100_P	2	5	19.50%	113	12497	7	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1
UniRef100_P	6	26	19.40%	403	46109	#	60S ribosomal protein L3
UniRef100_U	6	26	22.10%	353	40027	#	60S ribosomal protein L3 (HIV-1 TAR RNA-binding protein B) (TARBP-B).
UniRef100_U	6	26	22.00%	354	40152	#	ribosomal protein L3 isoform b
UniRef100_U	6	26	19.40%	402	45978	#	60S ribosomal protein L3 (HIV-1 TAR RNA-binding protein B) (TARBP-B).
UniRef100_Q	6	26	22.70%	343	39383	#	Ribosomal protein L3
UniRef100_A	5	7	19.40%	387	42737	6	CADM1 protein
UniRef100_U	5	7	17.00%	442	48509	5	immunoglobulin superfamily, member 4D
UniRef100_Q	5	7	17.00%	442	48537	5	Nectin-like protein 2
UniRef100_Q	5	7	16.90%	443	48648	5	Immunoglobulin superfamily member 4
UniRef100_A	5	7	18.10%	415	45780	5	CADM1 protein
UniRef100_Q	4	7	19.40%	314	35020	6	Cyclophilin-33B
UniRef100_Q	4	7	20.30%	301	33431	6	Peptidyl-prolyl cis-trans isomerase E
UniRef100_Q	4	7	19.40%	314	34991	6	Peptidyl-prolyl cis-trans isomerase
UniRef100_Q	4	7	20.60%	296	33085	6	Peptidyl-prolyl cis-trans isomerase
UniRef100_Q	5	6	19.40%	309	34412	7	Ketosamine-3-kinase
UniRef100_P	3	3	19.40%	217	24010	5	Grancalcin
UniRef100_P	4	10	19.40%	196	22123	5	Rho-related GTP-binding protein RhoB precursor
UniRef100_Q	18	31	19.30%	1375	2E+05	5	Nidogen-2 precursor
UniRef100_P	9	28	19.30%	514	55805	7	Inosine-5'-monophosphate dehydrogenase 2
UniRef100_A	6	10	19.30%	368	41206	7	Major histocompatibility complex, class I, C
UniRef100_A	6	10	17.90%	397	44216	7	Major histocompatibility complex, class I, C

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_A	6	10	19.10%	372	41363	6	Major histocompatibility complex, class I, C
UniRef100_Q	3	3	19.30%	187	20869	8	CDNA FLJ46021 fis, clone SPLEN2021231
UniRef100_P	4	20	19.30%	119	13373	#	40S ribosomal protein S20
UniRef100_Q	16	22	19.20%	1066	1E+05	5	Ubiquitin conjugation factor E4 A
UniRef100_Q	16	22	19.10%	1073	1E+05	5	Isoform 2 of Q14139
UniRef100_P	8	10	19.20%	677	76690	6	NADPH--cytochrome P450 reductase
UniRef100_Q	8	10	19.10%	680	77018	6	Hypothetical protein DKFZp686G04235
UniRef100_Q	5	11	19.10%	371	43728	#	Putative RNA-binding protein Luc7-like 1
UniRef100_Q	5	11	21.80%	325	38405	#	Isoform 2 of Q9NQ29
UniRef100_P	6	6	19.10%	303	34632	5	SPARC precursor
UniRef100_Q	5	7	19.10%	277	29937	8	Proteasome subunit beta type
UniRef100_Q	5	7	19.10%	277	29965	8	Proteasome subunit beta type 7 precursor
UniRef100_Q	5	7	19.10%	277	30018	8	Proteasome (Prosome, macropain) subunit, beta type, 7
UniRef100_O	18	25	19.00%	1338	1E+05	6	Phosphoribosylformylglycinamidine synthase
UniRef100_U	18	25	19.00%	1338	1E+05	6	phosphoribosylformylglycinamidine synthase
UniRef100_Q	13	55	19.00%	793	93250	6	Caldesmon
UniRef100_U	13	55	19.00%	793	93231	6	caldesmon 1 isoform 1
UniRef100_Q	13	55	28.40%	532	61213	7	Isoform 5 of Q05682
UniRef100_Q	13	55	28.10%	538	62663	6	Isoform 4 of Q05682
UniRef100_Q	13	55	27.10%	558	64256	7	Isoform 3 of Q05682
UniRef100_Q	13	55	26.80%	564	65707	7	Isoform 2 of Q05682
UniRef100_Q	6	6	19.00%	431	48358	7	Cleavage stimulation factor 50 kDa subunit
UniRef100_O	2	4	19.00%	226	24428	6	26S proteasome non-ATPase regulatory subunit 10
UniRef100_Q	2	4	19.00%	226	24458	6	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 10
UniRef100_Q	2	4	22.30%	193	20808	7	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 10
UniRef100_P	3	5	19.00%	189	21276	5	Apolipoprotein D precursor
UniRef100_P	9	11	18.90%	700	80009	5	Calpain-2 catalytic subunit precursor
UniRef100_U	9	11	18.90%	700	79995	5	Calpain-2 catalytic subunit precursor (EC 3.4.22.53) (Calpain-2 large subunit) (Calcium-activated neutral proteinase 2) (CANP 2) (Calpain M- type) (M-calpain) (Millimolar-calpain) (Calpain large polypeptide L2).
UniRef100_U	9	11	18.90%	700	79996	5	Calpain-2 catalytic subunit precursor (EC 3.4.22.53) (Calpain-2 large subunit) (Calcium-activated neutral proteinase 2) (CANP 2) (Calpain M- type) (M-calpain) (Millimolar-calpain) (Calpain large polypeptide L2).
UniRef100_U	9	11	18.90%	700	80007	5	calpain 2, large subunit
UniRef100_Q	9	11	18.10%	729	83109	5	Calpain 2, large [catalytic] subunit variant
UniRef100_P	7	10	18.90%	528	59425	4	Glucosidase 2 subunit beta precursor
UniRef100_U	7	10	19.00%	525	59178	4	protein kinase C substrate 80K-H isoform 2
UniRef100_Q	5	6	18.90%	482	54121	6	Ras GTPase-activating protein-binding protein 2
UniRef100_Q	5	6	20.30%	449	50817	5	Isoform B of Q9UN86
UniRef100_Q	4	6	18.90%	259	30124	5	DCN1-like protein 1

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_U	4	6	19.00%	258	29993	5	DCN1-like protein 1 (Defective in cullin neddylation protein 1-like protein 1) (DCUN1 domain-containing protein 1) (Squamous cell carcinoma-related oncogene).
UniRef100_P	16	22	18.80%	889	98399	7	Iron-responsive element-binding protein 1
UniRef100_P	7	8	18.80%	591	67183	6	Interferon-induced guanylate-binding protein 2
UniRef100_U	7	8	18.80%	591	67209	6	guanylate binding protein 2, interferon-inducible
UniRef100_Q	7	8	18.80%	591	67153	6	GBP2 protein
UniRef100_Q	7	8	18.80%	591	67234	6	Guanylate binding protein 2, interferon-inducible
UniRef100_Q	7	10	18.80%	586	65678	7	CTP synthase 2
UniRef100_U	7	10	18.80%	586	65626	7	CTP synthase 2 (EC 6.3.4.2) (UTP--ammonia ligase 2) (CTP synthetase 2).
UniRef100_Q	6	6	18.80%	399	46030	9	PCI domain-containing protein 2
UniRef100_U	6	6	18.80%	398	45907	9	PCI domain-containing protein 2 (CSN12-like protein).
UniRef100_U	6	6	19.80%	379	44176	9	PCI domain-containing protein 2 (CSN12-like protein).
UniRef100_Q	6	6	16.60%	453	52100	9	Isoform 4 of Q5JVF3
UniRef100_Q	6	6	18.90%	397	45773	9	Isoform 2 of Q5JVF3
UniRef100_U	6	16	18.80%	260	29603	5	PREDICTED: similar to 14-3-3 protein epsilon (14-3-3E) (Mitochondrial import stimulation factor L subunit) (MSF L)
UniRef100_P	3	5	18.80%	240	27335	8	Glutathione S-transferase theta-1
UniRef100_U	3	5	18.80%	240	27263	8	glutathione S-transferase theta 1
UniRef100_Q	3	5	18.80%	240	27349	8	Glutathione S-transferase theta 1
UniRef100_P	2	3	18.80%	112	11896	9	Ig lambda chain V-I region HA
UniRef100_P	6	8	18.70%	461	51026	7	Coronin-1A
UniRef100_Q	4	5	18.70%	262	29601	7	Spindlin-1
UniRef100_U	4	5	20.20%	242	27488	6	Spindlin-1
UniRef100_U	4	5	19.90%	246	28053	6	Spindlin-1 (Ovarian cancer-related protein).
UniRef100_A	4	19	18.70%	219	21879	#	Liver histone H1e
UniRef100_Q	4	19	18.70%	219	21893	#	Histone cluster 1, H1e
UniRef100_P	4	19	19.20%	213	21365	#	Histone H1.2
UniRef100_P	4	19	18.60%	221	22350	#	Histone H1.3
UniRef100_P	4	19	18.70%	219	21865	#	Histone H1.4
UniRef100_Q	9	12	18.60%	625	68259	6	Clathrin interactor 1
UniRef100_Q	6	9	18.60%	414	46382	5	Secernin-1
UniRef100_P	4	4	18.60%	361	39330	7	Porphobilinogen deaminase
UniRef100_P	5	7	18.60%	318	34769	7	Ribose-phosphate pyrophosphokinase II
UniRef100_Q	5	7	18.40%	321	35054	6	Phosphoribosyl pyrophosphate synthetase 2
UniRef100_Q	4	8	18.60%	306	32749	5	Polyadenylate-binding protein 2 (Poly(A)-binding protein 2) (Poly(A)- binding protein II) (PABII) (Polyadenylate-binding nuclear protein 1) (Nuclear poly(A)-binding protein 1)
UniRef100_Q	4	8	19.30%	296	31497	5	Isoform 2 of Q86U42
UniRef100_P	4	6	18.60%	236	25809	5	CD81 antigen
UniRef100_U	4	6	16.10%	274	29806	7	CD81 antigen (26 kDa cell surface protein TAPA-1) (Target of the antiproliferative antibody 1) (Tetraspanin-28) (Tspan-28).
UniRef100_Q	4	8	18.60%	221	25542	9	Splicing factor, arginine/serine-rich 9

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_O	2	4	18.60%	140	16445	7	Trafficking protein particle complex subunit 2
UniRef100_U	2	4	18.10%	144	17020	7	Trafficking protein particle complex subunit 2 (Sedlin) (MBP-1- interacting protein 2A) (MIP-2A).
UniRef100_U	2	4	17.70%	147	17217	7	Trafficking protein particle complex subunit 2 (Sedlin) (MBP-1- interacting protein 2A) (MIP-2A).
UniRef100_O	2	4	17.70%	147	17260	7	Isoform 2 of O14582
UniRef100_Q	2	3	18.60%	113	12683	6	RING-box protein 2
UniRef100_P	11	95	18.50%	639	70021	6	Heat shock-related 70 kDa protein 2
UniRef100_O	10	22	18.50%	530	60103	9	PC4 and SFRS1-interacting protein
UniRef100_A	6	17	18.50%	449	47958	7	Procollagen C-endopeptidase enhancer
UniRef100_Q	6	17	18.50%	449	47973	7	Procollagen C-endopeptidase enhancer 1 precursor
UniRef100_Q	6	9	18.50%	341	39774	8	MO25-like protein
UniRef100_Q	6	9	18.50%	341	39869	7	Calcium-binding protein 39
UniRef100_Q	2	2	18.50%	270	29165	6	Phospholysine phosphohistidine inorganic pyrophosphate phosphatase
UniRef100_U	2	2	18.50%	270	29221	6	phospholysine phosphohistidine inorganic pyrophosphate phosphatase
UniRef100_Q	2	2	18.50%	270	29193	6	Phospholysine phosphohistidine inorganic pyrophosphate phosphatase
UniRef100_P	2	2	18.50%	173	18999	6	Translocon-associated protein subunit delta precursor
UniRef100_U	17	24	18.40%	1247	1E+05	5	nidogen 1 precursor
UniRef100_Q	6	31	18.40%	424	44386	9	Splicing factor 3B subunit 4
UniRef100_Q	6	31	18.40%	424	44387	8	Splicing factor 3b, subunit 4 variant
UniRef100_Q	4	6	18.40%	245	26383	7	Exosome complex exonuclease RRP41
UniRef100_Q	3	4	18.40%	163	18243	9	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1
UniRef100_Q	9	10	18.30%	482	55847	7	Interferon-induced protein with tetratricopeptide repeats 5
UniRef100_P	6	14	18.30%	410	46638	7	Platelet-activating factor acetylhydrolase IB subunit alpha
UniRef100_Q	4	10	18.30%	312	35124	8	Hypothetical protein DKFZp779H1622
UniRef100_Q	3	4	18.30%	273	31773	7	MHC class I antigen
UniRef100_Q	6	18	18.30%	257	26888	#	THO complex subunit 4
UniRef100_U	3	25	18.30%	229	24421	8	IGG1-KAPPA 3D6 FAB (HEAVY CHAIN)
UniRef100_Q	3	4	18.30%	197	21726	7	Guanylate kinase
UniRef100_Q	3	4	16.60%	217	23711	8	Guanylate kinase 1
UniRef100_Q	3	4	14.20%	253	27578	6	Guanylate kinase 1
UniRef100_Q	3	4	18.10%	199	21999	6	Guanylate kinase 1
UniRef100_Q	3	4	14.90%	242	26279	9	Guanylate kinase 1
UniRef100_O	2	3	18.30%	186	21119	6	Dynactin subunit 3
UniRef100_O	2	3	21.50%	158	18001	6	Isoform 3 of O75935
UniRef100_A	10	19	18.20%	917	1E+05	6	Scaffold attachment factor B
UniRef100_Q	10	19	18.30%	915	1E+05	6	Scaffold attachment factor B
UniRef100_Q	6	8	18.20%	554	63522	5	Chronic myelogenous leukemia tumor antigen 66 short form
UniRef100_U	6	8	17.30%	583	66756	5	NudC domain containing 1
UniRef100_Q	6	8	17.30%	583	66790	5	NudC domain containing 1
UniRef100_Q	6	8	17.30%	583	66776	5	NudC domain-containing protein 1
UniRef100_Q	5	13	18.20%	340	37567	6	Guanine nucleotide-binding protein subunit beta 4
UniRef100_A	2	5	18.20%	121	13103	#	NANUC-1 heavy chain

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_A	2	5	16.50%	133	14604	#	NANUC-2 heavy chain
UniRef100_O	13	15	18.10%	925	1E+05	6	Probable ATP-dependent RNA helicase DDX58
UniRef100_Q	8	17	18.10%	531	60577	#	Parafibromin
UniRef100_UI	8	17	18.10%	531	60577	#	Parafibromin (Cell division cycle protein 73 homolog) (Hyperparathyroidism 2 protein).
UniRef100_P	5	14	18.10%	421	47579	9	2',3'-cyclic-nucleotide 3'-phosphodiesterase
UniRef100_P	5	14	19.00%	401	45099	9	Isoform CNPI of P09543
UniRef100_P	23	39	18.00%	1676	2E+05	7	Complement C5 precursor [Contains: Complement C5 beta chain; Complement C5 alpha chain; C5a anaphylatoxin; Complement C5 alpha' chain]
UniRef100_Q	23	39	18.00%	1676	2E+05	7	Complement component 5
UniRef100_Q	23	39	18.00%	1676	2E+05	7	Complement component 5
UniRef100_Q	16	103	18.00%	499	55152	5	Keratin-8-like protein 1
UniRef100_A	7	16	18.00%	440	49490	#	Hypothetical protein
UniRef100_Q	7	16	17.00%	464	52165	#	RSL1D1 protein
UniRef100_O	7	16	16.10%	490	54973	#	Ribosomal L1 domain-containing protein 1
UniRef100_A	7	16	25.60%	308	35115	#	Hypothetical protein
UniRef100_Q	2	5	18.00%	122	13407	#	Selenoprotein H
UniRef100_UI	2	5	18.00%	122	13303	#	selenoprotein H
UniRef100_Q	8	11	17.90%	585	65701	7	FARSB protein
UniRef100_UI	8	11	17.80%	589	66116	7	phenylalanyl-tRNA synthetase, beta subunit
UniRef100_Q	8	11	17.80%	589	66130	7	Phenylalanyl-tRNA synthetase beta chain
UniRef100_O	5	6	17.90%	521	57811	5	Importin alpha-3 subunit
UniRef100_Q	5	6	17.90%	521	57901	5	Karyopherin alpha 3
UniRef100_Q	4	8	17.90%	407	43383	9	DAZ-associated protein 1
UniRef100_Q	4	8	19.30%	378	40530	8	Isoform 2 of Q96EP5
UniRef100_Q	6	8	17.90%	386	42315	6	Protein phosphatase methylesterase 1
UniRef100_UI	6	8	17.70%	389	42669	6	Protein phosphatase methylesterase 1 (EC 3.1.1.-) (PME-1).
UniRef100_Q	3	29	17.90%	201	23025	8	Ras-related protein Rab-35
UniRef100_UI	3	29	17.90%	201	23053	8	Ras-related protein Rab-35 (Rab-1C) (GTP-binding protein RAY).
UniRef100_P	2	3	17.90%	117	13293	6	DNA-directed RNA polymerase II subunit J
UniRef100_UI	2	3	11.80%	178	18673	6	DNA-directed RNA polymerase II subunit J (EC 2.7.7.6) (DNA-directed RNA polymerase II 13.3 kDa polypeptide) (RPB11).
UniRef100_Q	2	3	16.50%	127	14131	6	RPB11a protein
UniRef100_Q	2	3	18.30%	115	13074	6	RPB11b1alpha protein
UniRef100_Q	2	3	13.10%	160	17172	7	MGC13098 protein
UniRef100_Q	2	3	11.70%	179	18885	6	MGC13098 protein
UniRef100_Q	2	3	11.70%	180	19038	7	MGC13098 protein variant
UniRef100_Q	2	3	15.20%	138	15027	7	MGC13098 protein
UniRef100_P	30	127	17.80%	894	1E+05	6	Alpha-actinin-2
UniRef100_P	11	11	17.80%	843	93518	7	Complement component C7 precursor
UniRef100_UI	11	11	17.80%	843	93500	6	Complement component C7 precursor.
UniRef100_P	3	4	17.80%	219	24976	8	Transmembrane emp24 domain-containing protein 10 precursor

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	3	4	17.30%	225	25637	7	Full-length cDNA 5-PRIME end of clone CS0DF013YM24 of Fetal brain of Homo sapiens (Human) variant
UniRef100_P	3	4	17.80%	152	17315	5	Ubiquitin-conjugating enzyme E2 A
UniRef100_U	3	4	17.50%	154	17487	5	Ubiquitin-conjugating enzyme E2 A (EC 6.3.2.19) (Ubiquitin-protein ligase A) (Ubiquitin carrier protein A) (HR6A) (hHR6A).
UniRef100_Q	3	4	17.80%	152	17287	5	Ubiquitin-conjugating enzyme E2A isoform 1 variant
UniRef100_Q	14	19	17.70%	1117	1E+05	5	Desmoglein-2 precursor
UniRef100_Q	14	19	17.70%	1118	1E+05	5	Desmoglein 2
UniRef100_P	8	18	17.70%	525	59578	8	Histidine-rich glycoprotein precursor
UniRef100_O	5	8	17.70%	355	39518	9	Galectin-9
UniRef100_Q	5	8	20.30%	311	34691	8	Galectin-9
UniRef100_Q	5	8	19.50%	323	35858	8	Galectin 9 short isoform variant
UniRef100_Q	5	8	19.50%	323	35888	8	Lectin, galactoside-binding, soluble, 9
UniRef100_Q	6	28	17.70%	288	32728	#	60S ribosomal protein L6
UniRef100_U	6	28	18.80%	272	30905	#	PREDICTED: similar to 60S ribosomal protein L6 (TAX-responsive enhancer element-binding protein 107) (TAXREB107) (Neoplasm-related protein C140) isoform 7
UniRef100_U	6	28	18.80%	271	30777	#	PREDICTED: similar to 60S ribosomal protein L6 (TAX-responsive enhancer element-binding protein 107) (TAXREB107) (Neoplasm-related protein C140) isoform 2
UniRef100_Q	6	28	17.60%	289	32891	#	DNA-binding protein TAXREB107
UniRef100_Q	6	28	17.70%	288	32742	#	Ribosomal protein L6
UniRef100_Q	6	28	17.70%	288	32726	#	Ribosomal protein L6
UniRef100_P	15	26	17.60%	1042	1E+05	7	Superkiller viralicidic activity 2-like 2
UniRef100_P	6	15	17.60%	484	52801	5	Gasdermin domain-containing protein 1
UniRef100_Q	5	7	17.60%	250	28764	9	Shwachman-Bodian-Diamond syndrome protein
UniRef100_Q	4	7	17.60%	222	25769	6	Latexin
UniRef100_U	4	7	17.60%	222	25750	6	Latexin (Endogenous carboxypeptidase inhibitor) (ECI) (Tissue carboxypeptidase inhibitor) (TCI) (MUM).
UniRef100_Q	3	3	17.60%	205	24140	6	Protein MIS12 homolog
UniRef100_P	48	105	17.50%	3110	3E+05	6	Laminin subunit alpha-2 precursor
UniRef100_U	48	105	17.50%	3118	3E+05	6	laminin alpha 2 subunit isoform b precursor
UniRef100_U	48	105	17.50%	3123	3E+05	6	Laminin subunit alpha-2 precursor (Laminin M chain) (Merosin heavy chain).
UniRef100_U	48	105	17.50%	3122	3E+05	6	laminin alpha 2 subunit isoform a precursor
UniRef100_Q	48	105	17.50%	3122	3E+05	6	Laminin, alpha 2
UniRef100_Q	23	28	17.50%	1253	1E+05	7	Isoform 2 of Q96F07
UniRef100_U	23	28	17.40%	1256	1E+05	7	cytoplasmic FMR1 interacting protein 2
UniRef100_U	23	28	17.40%	1258	1E+05	7	cytoplasmic FMR1 interacting protein 2
UniRef100_Q	6	8	17.50%	565	65381	9	U4/U6.U5 tri-snRNP-associated protein 2
UniRef100_Q	8	14	17.50%	590	65353	5	Hypothetical protein
UniRef100_Q	6	10	17.50%	572	61277	7	Zyxin
UniRef100_U	6	10	17.20%	582	62667	8	Zyxin (Zyxin-2).
UniRef100_Q	6	10	21.50%	466	50472	8	ZYX protein

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	6	10	20.30%	493	53105	6	ESP-2
UniRef100_Q	7	9	17.50%	434	49717	7	Septin-6
UniRef100_U	7	9	17.60%	431	49309	7	Septin-6.
UniRef100_Q	7	9	13.60%	559	63143	8	MLL/SEPTIN6 fusion protein
UniRef100_Q	7	9	17.40%	438	50204	7	Septin 6 isoform E
UniRef100_Q	7	9	17.60%	431	49303	7	Septin 6
UniRef100_Q	7	9	17.80%	427	48873	7	Septin 6
UniRef100_Q	7	9	17.70%	429	49167	7	Septin 6
UniRef100_Q	4	7	17.50%	275	30277	8	COP9 signalosome complex subunit 7a
UniRef100_P	3	8	17.50%	206	23567	7	Ras-related protein Ral-A precursor
UniRef100_Q	5	7	17.50%	143	15653	9	Apolipoprotein B
UniRef100_Q	10	23	17.40%	494	56678	#	Splicing factor, arginine/serine-rich 4
UniRef100_Q	10	23	22.50%	382	44201	#	Splicing factor, arginine/serine-rich 4 variant
UniRef100_O	5	10	17.40%	432	51466	#	Cisplatin resistance-associated overexpressed protein
UniRef100_Q	5	10	29.90%	251	28926	7	CROP protein
UniRef100_Q	5	10	31.80%	236	27016	8	CROP protein
UniRef100_O	7	55	17.40%	420	46437	#	Heterogeneous nuclear ribonucleoprotein D-like
UniRef100_Q	7	55	29.90%	244	27191	9	JKTBP1delta6
UniRef100_Q	7	55	24.30%	301	33589	7	HnRNP JKTBP protein
UniRef100_Q	4	4	17.40%	420	46337	7	GDP-mannose pyrophosphorylase A
UniRef100_U	4	4	15.40%	473	52018	7	GDP-mannose pyrophosphorylase A
UniRef100_Q	4	4	17.40%	420	46351	7	CDNA FLJ10137 fis, clone HEMBA1003136, weakly similar to MANNOSE-1- PHOSPHATE GUANYLTRANSFERASE
UniRef100_Q	4	4	17.40%	420	46291	7	GDP-mannose pyrophosphorylase A
UniRef100_O	8	11	17.40%	397	43076	9	Prion protein-interacting protein
UniRef100_U	8	11	18.90%	365	40077	8	prion protein interacting protein
UniRef100_Q	8	11	31.10%	222	25009	7	Prion protein interacting protein
UniRef100_Q	8	11	33.80%	204	22890	7	Prion protein interacting protein
UniRef100_O	4	4	17.40%	253	29842	9	DnaJ homolog subfamily C member 8
UniRef100_U	4	4	16.70%	263	30829	9	DnaJ homolog subfamily C member 8 (Splicing protein spf31).
UniRef100_P	4	4	17.40%	218	23662	5	Isoform Non
UniRef100_U	3	30	17.40%	219	23367	6	Fab 48d heavy chain
UniRef100_U	3	30	16.50%	231	24660	7	Fab 412d light chain
UniRef100_O	2	2	17.40%	195	21671	5	Membrane-associated progesterone receptor component 1
UniRef100_P	3	24	17.40%	178	20252	#	60S ribosomal protein L11
UniRef100_Q	3	24	17.50%	177	20094	#	Cell growth-inhibiting protein 34
UniRef100_P	3	24	17.50%	177	20124	#	Isoform 2 of P62913
UniRef100_P	3	4	17.30%	225	25008	6	Phosphoserine phosphatase
UniRef100_Q	3	4	17.30%	225	24949	5	Phosphoserine phosphatase variant
UniRef100_Q	3	3	17.30%	225	24997	7	Ras-related protein Rab-32
UniRef100_U	3	26	17.30%	225	23908	8	FAB 2G12, heavy chain

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_O	2	7	17.30%	162	17743	5	15 kDa selenoprotein precursor
UniRef100_U	2	7	17.00%	165	17942	5	15 kDa selenoprotein isoform 1 precursor
UniRef100_P	2	2	17.30%	98	11117	5	Protein S100-A2
UniRef100_P	16	29	17.20%	1152	1E+05	5	Microtubule-associated protein 4
UniRef100_U	16	29	17.20%	1152	1E+05	5	microtubule-associated protein 4 isoform 1
UniRef100_Q	16	29	17.00%	1163	1E+05	7	Microtubule-associated protein 4 isoform 1 variant
UniRef100_P	8	26	17.20%	551	62094	8	Interferon-induced, double-stranded RNA-activated protein kinase
UniRef100_U	8	26	18.60%	510	57391	8	Interferon-induced, double-stranded RNA-activated protein kinase (EC 2.7.11.1) (Interferon-inducible RNA-dependent protein kinase) (Protein kinase RNA-activated) (PKR) (p68 kinase) (P1/eIF-2A protein kinase).
UniRef100_Q	8	26	18.50%	513	57620	8	EIF2AK2 protein
UniRef100_Q	8	26	18.60%	510	57478	8	Interferon-inducible double-stranded RNA-dependent protein kinase
UniRef100_O	4	5	17.20%	256	29481	7	Ribonuclease T2 precursor
UniRef100_Q	3	3	17.20%	163	18822	4	ADP-ribosylation factor-like protein 2-binding protein
UniRef100_Q	9	21	17.10%	783	87344	9	Nucleolar RNA helicase 2
UniRef100_P	6	12	17.10%	463	51842	7	Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl transferase) [Contains: Dipeptidyl-peptidase 1 exclusion domain chain (Dipeptidyl- peptidase I exclusion domain chain); Dipeptidyl-peptidase 1 heavy chain (Dipeptidyl-peptidase I heavy chain); Dipeptidyl-peptidase 1 light chain (Dipeptidyl-peptidase I light chain)]
UniRef100_U	6	12	17.10%	463	51854	7	Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl transferase) [Contains: Dipeptidyl-peptidase 1 exclusion domain chain (Dipeptidyl- peptidase I exclusion domain chain); Dipeptid
UniRef100_Q	6	12	17.10%	463	51902	7	Cathepsin C
UniRef100_Q	6	12	17.10%	463	51816	7	Cathepsin C
UniRef100_Q	6	12	17.10%	463	51827	7	Cathepsin C isoform a preproprotein variant
UniRef100_Q	5	12	17.10%	362	43160	9	Protein tyrosine phosphatase-like A domain containing 1
UniRef100_U	5	12	16.60%	373	44323	9	butyrate-induced transcript 1
UniRef100_U	5	12	27.70%	224	26248	6	PREDICTED: similar to butyrate-induced transcript 1
UniRef100_Q	5	12	16.60%	373	44423	9	Protein-tyrosine phosphatase-like A domain-containing protein 1
UniRef100_Q	5	12	16.80%	370	43543	8	B-ind1 protein
UniRef100_Q	5	12	17.10%	362	43126	9	CDNA FLJ90417 fis, clone NT2RP3000171, weakly similar to Mus musculus partial B-IND1 protein
UniRef100_Q	5	12	17.20%	361	42908	9	PTPLAD1 protein
UniRef100_Q	5	8	17.10%	216	25080	7	Mps one binder kinase activator-like 1B
UniRef100_U	5	8	17.30%	214	24962	7	Mps one binder kinase activator-like 1B (Mob1 homolog 1B) (Mob1 alpha) (Mob1A) (Protein Mob4B).
UniRef100_U	5	8	17.10%	216	25122	7	Mps one binder kinase activator-like 1B (Mob1 homolog 1B) (Mob1 alpha) (Mob1A) (Protein Mob4B).
UniRef100_U	5	8	17.10%	216	25008	7	Mob4B protein
UniRef100_Q	3	5	17.10%	205	23510	5	Mitotic spindle assembly checkpoint protein MAD2A

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	3	5	17.10%	205	23496	5	MAD2 mitotic arrest deficient-like 1
UniRef100_Q	3	5	17.10%	205	23526	5	MAD2-like 1 variant
UniRef100_Q	2	5	17.10%	152	16691	7	Proteolipid protein 2
UniRef100_P	3	10	17.10%	146	15799	9	Cystatin-C precursor
UniRef100_P	8	13	17.00%	601	66214	5	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform
UniRef100_Q	8	13	15.30%	667	73585	5	Protein phosphatase 2 (Formerly 2A), regulatory subunit A, beta isoform
UniRef100_Q	2	16	17.00%	212	23339	6	Ras-related protein Rab-43
UniRef100_P	70	343	16.90%	5065	6E+05	6	Epiplakin
UniRef100_Q	9	15	16.90%	726	81483	7	COPG2 protein
UniRef100_Q	9	15	14.10%	871	97622	6	Coatomer subunit gamma-2
UniRef100_P	7	19	16.90%	478	54306	6	Vitronectin precursor (Serum-spreading factor) (S-protein) (V75) [Contains: Vitronectin V65 subunit; Vitronectin V10 subunit; Somatomedin B]
UniRef100_Q	4	6	16.90%	307	33865	6	C6orf55 protein
UniRef100_U	4	6	23.60%	220	25572	9	Uncharacterized protein C6orf55 (Dopamine-responsive protein DRG-1).
UniRef100_Q	4	6	16.90%	307	33879	6	Uncharacterized protein C6orf55
UniRef100_U	3	25	16.90%	219	23573	8	HUMANIZED ANTIBODY HFE7A, HEAVY CHAIN
UniRef100_U	3	25	16.80%	220	23476	8	Huzaf antibody heavy chain
UniRef100_P	5	5	16.80%	334	36589	8	WD repeat protein 5
UniRef100_O	2	2	16.80%	190	20747	6	Dynactin subunit 6
UniRef100_Q	3	5	16.80%	179	20329	7	HD domain-containing protein 3
UniRef100_Q	3	5	16.80%	167	18820	9	CGG triplet repeat-binding protein 1
UniRef100_O	19	50	16.70%	1229	1E+05	7	SEC31 homolog A
UniRef100_U	19	50	17.40%	1181	1E+05	7	SEC31 homolog A isoform 2
UniRef100_Q	19	50	17.40%	1181	1E+05	7	ABP125
UniRef100_Q	19	50	16.80%	1220	1E+05	7	ABP130
UniRef100_Q	19	50	16.80%	1220	1E+05	7	Sec31 protein
UniRef100_Q	19	50	18.50%	1106	1E+05	7	SEC31 homolog A
UniRef100_Q	19	50	17.00%	1205	1E+05	7	SEC31 homolog A
UniRef100_Q	4	4	16.70%	455	52562	6	Bleomycin hydrolase
UniRef100_A	5	9	16.70%	365	41063	7	MHC class I antigen
UniRef100_A	5	9	22.30%	273	31760	6	MHC class I antigen
UniRef100_A	5	9	20.40%	299	34426	6	Major histocompatibility complex, class I, A
UniRef100_A	5	9	22.30%	273	31839	6	MHC class I antigen
UniRef100_Q	6	13	16.70%	365	40954	8	Actin related protein 2/3 complex subunit 1A variant
UniRef100_Q	6	13	16.50%	370	41569	8	Actin-related protein 2/3 complex subunit 1A
UniRef100_O	5	5	16.70%	348	38793	5	Arsenical pump-driving ATPase
UniRef100_U	5	5	16.00%	363	40226	5	Arsenical pump-driving ATPase (EC 3.6.3.16) (Arsenite-translocating ATPase) (Arsenical resistance ATPase) (Arsenite-transporting ATPase) (ARSA) (ASNA-I).
UniRef100_Q	4	9	16.70%	318	35964	7	Gamma-glutamyl hydrolase precursor
UniRef100_Q	5	27	16.70%	305	30841	9	Heterogeneous nuclear ribonucleoprotein A0
UniRef100_Q	3	4	16.70%	275	29572	8	Exosome complex exonuclease RRP40

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	2	2	16.70%	222	24341	6	OTTHUMP00000017168
UniRef100_U	2	2	13.50%	275	30446	9	Enoyl-CoA hydratase domain-containing protein 1.
UniRef100_U	2	2	12.90%	286	31306	8	Enoyl-CoA hydratase domain-containing protein 1.
UniRef100_U	2	2	12.20%	303	33155	8	Enoyl-CoA hydratase domain-containing protein 1.
UniRef100_Q	2	2	12.90%	286	31303	9	Uncharacterized hypothalamus protein HCDASE
UniRef100_Q	2	2	12.10%	307	33698	8	Enoyl-CoA hydratase domain-containing protein 1
UniRef100_P	2	3	16.70%	180	20140	9	Insulin-like growth factor II precursor (IGF-II) (Somatomedin A) [Contains: Insulin-like growth factor II Ala-25 Del]
UniRef100_U	2	3	16.40%	183	20423	9	Insulin-like growth factor II precursor (IGF-II) (Somatomedin A) [Contains: Insulin-like growth factor II Ala-25 Del].
UniRef100_P	2	3	16.40%	183	20477	#	Isoform 2 of P01344
UniRef100_Q	3	11	16.70%	180	19687	#	Small nuclear ribonucleoprotein polypeptide C
UniRef100_Q	9	11	16.60%	782	87973	6	Vac14 homolog
UniRef100_P	8	13	16.60%	745	83869	9	Myeloperoxidase precursor (EC 1.11.1.7) (MPO) [Contains: 89 kDa myeloperoxidase; 84 kDa myeloperoxidase; Myeloperoxidase light chain; Myeloperoxidase heavy chain]
UniRef100_P	8	13	16.00%	777	87249	9	Isoform H7 of P05164
UniRef100_P	9	11	16.60%	673	75873	6	Annexin A6
UniRef100_U	9	11	16.90%	662	74748	6	Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III) (Chromobindin-20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II).
UniRef100_U	9	11	16.70%	670	75529	6	Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III) (Chromobindin-20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II).
UniRef100_U	9	11	16.80%	667	75277	6	annexin VI isoform 2
UniRef100_Q	3	4	16.60%	314	34278	9	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial precursor
UniRef100_U	3	4	16.60%	314	34294	9	L-3-hydroxyacyl-Coenzyme A dehydrogenase precursor
UniRef100_U	3	4	13.30%	390	42123	9	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial precursor (EC 1.1.1.35) (Short chain 3-hydroxyacyl-CoA dehydrogenase) (HCDH) (Medium and short chain L-3-hydroxyacyl-coenzyme A dehydrogenase).
UniRef100_Q	3	4	13.30%	390	42123	9	Isoform 2 of Q16836
UniRef100_P	4	4	16.60%	295	34197	7	Sulfotransferase 1A1
UniRef100_U	4	4	16.60%	295	34310	8	Sulfotransferase 1A2 (EC 2.8.2.1) (Aryl sulfotransferase 2) (Phenol sulfotransferase 2) (Phenol-sulfating phenol sulfotransferase 2) (P- PST 2) (ST1A2).
UniRef100_U	4	4	16.60%	295	34165	7	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1 isoform a
UniRef100_Q	4	4	16.60%	295	34311	7	Sulfotransferase family, cytosolic, 1A, phenol-preferring, member 2
UniRef100_P	4	4	16.60%	295	34286	7	Sulfotransferase 1A2
UniRef100_Q	3	5	16.60%	205	22350	5	Dr1-associated corepressor
UniRef100_U	3	5	16.00%	212	23205	5	Dr1-associated corepressor (Dr1-associated protein 1) (Negative co- factor 2 alpha) (NC2 alpha).
UniRef100_Q	3	5	16.10%	211	23148	5	Isoform 2 of Q14919
UniRef100_P	4	10	16.60%	145	17258	#	60S ribosomal protein L26
UniRef100_Q	4	10	16.60%	145	17244	#	RPL26 protein
UniRef100_P	44	67	16.50%	3144	3E+05	6	Huntingtin

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_UI	44	67	16.50%	3142	3E+05	6	Huntingtin (Huntington disease protein) (HD protein).
UniRef100_UI	44	67	16.50%	3142	3E+05	6	Huntingtin (Huntington disease protein) (HD protein).
UniRef100_Q	16	36	16.50%	1129	1E+05	7	Regulator of nonsense transcripts 1
UniRef100_Q	16	36	16.60%	1118	1E+05	7	Isoform 2 of Q92900
UniRef100_P	11	11	16.50%	807	89421	7	Oxysterol-binding protein 1
UniRef100_P	8	16	16.50%	644	71957	7	Kininogen-1 precursor (Alpha-2-thiol proteinase inhibitor) [Contains: Kininogen-1 heavy chain; Bradykinin (Kallidin I); Lysyl-bradykinin (Kallidin II); Kininogen-1 light chain; Low molecular weight growth- promoting factor]
UniRef100_Q	8	16	24.80%	427	47901	7	Kininogen 1
UniRef100_Q	8	16	24.80%	427	47853	7	Kininogen 1 variant
UniRef100_P	8	16	24.80%	427	47883	7	Isoform LMW of P01042
UniRef100_O	4	4	16.50%	339	37840	5	Protein CIAO1
UniRef100_P	3	7	16.50%	254	28994	6	Emerin
UniRef100_Q	2	2	16.50%	182	20375	7	Histidine triad nucleotide-binding protein 3
UniRef100_Q	2	2	16.50%	182	20361	7	Histidine triad nucleotide binding protein 3
UniRef100_P	12	18	16.40%	934	1E+05	6	DNA mismatch repair protein Msh2
UniRef100_Q	12	18	17.40%	878	98262	6	MutS homolog 2 variant
UniRef100_Q	12	18	17.40%	878	98222	6	MutS homolog 2 variant
UniRef100_Q	7	11	16.40%	494	52937	5	RAN binding protein 3 transcript variant a
UniRef100_UI	7	11	14.50%	560	59465	5	Ran-binding protein 3 (RanBP3).
UniRef100_Q	7	11	16.20%	499	53411	5	Isoform 3 of Q9H6Z4
UniRef100_Q	7	11	14.40%	562	59694	5	Isoform 2 of Q9H6Z4
UniRef100_Q	7	11	14.30%	567	60210	5	Ran-binding protein 3
UniRef100_Q	2	2	16.40%	122	13332	8	UPF0366 protein C11orf67
UniRef100_P	6	7	16.30%	478	55360	7	Interferon-induced protein with tetratricopeptide repeats 1
UniRef100_Q	2	2	16.30%	294	33360	6	Metallophosphoesterase domain-containing protein 2
UniRef100_Q	2	2	17.10%	280	31777	8	Chromosome 11 open reading frame 8 variant
UniRef100_Q	3	3	16.30%	288	32790	7	Lactamase beta-2
UniRef100_Q	3	3	16.30%	288	32806	7	CGI-83 protein
UniRef100_P	4	7	16.30%	245	28180	6	Thiopurine S-methyltransferase
UniRef100_Q	4	7	16.30%	245	28233	6	Thiopurine S-methyltransferase
UniRef100_P	2	4	16.30%	147	16840	9	Ribonuclease 4 precursor
UniRef100_P	10	16	16.20%	882	97517	6	Probable transcription factor PML
UniRef100_UI	10	16	16.20%	882	97551	6	promyelocytic leukemia protein isoform 1
UniRef100_P	5	10	16.20%	394	45665	6	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short
UniRef100_UI	5	10	13.20%	484	54674	9	Neuroendocrine secretory protein 55 (NESP55) [Contains: LHAL tetrapeptide; GPIPIRRH peptide].
UniRef100_UI	5	10	8.90%	721	78734	6	Neuroendocrine secretory protein 55 (NESP55) [Contains: LHAL tetrapeptide; GPIPIRRH peptide].
UniRef100_UI	5	10	8.90%	722	78821	6	Neuroendocrine secretory protein 55 (NESP55) [Contains: LHAL tetrapeptide; GPIPIRRH peptide].

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_U	5	10	7.00%	908	97549	5	Neuroendocrine secretory protein 55 (NESP55) [Contains: LHAL tetrapeptide; GPIPIRRH peptide].
UniRef100_U	5	10	16.20%	395	45752	6	GNAS complex locus isoform f
UniRef100_Q	5	10	6.30%	1023	1E+05	5	Isoform XLas
UniRef100_Q	5	10	6.20%	1037	1E+05	5	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas
UniRef100_Q	5	10	16.90%	379	44179	6	Guanine nucleotide-binding protein G-s-alpha-3
UniRef100_P	5	10	16.80%	380	44266	6	Isoform Gnas
UniRef100_Q	4	10	16.20%	265	29774	6	EF hand domain family, member D1 variant
UniRef100_Q	4	10	18.00%	239	26928	5	EF-hand domain-containing protein 1
UniRef100_O	3	5	16.20%	148	16369	#	Endothelial differentiation-related factor 1
UniRef100_U	3	5	17.00%	141	15636	#	Endothelial differentiation-related factor 1 (EDF-1) (Multiprotein- bridging factor 1) (MBF1).
UniRef100_O	3	5	17.30%	139	15481	#	Isoform 2 of O60869
UniRef100_P	2	6	16.20%	99	10852	5	Apolipoprotein C-III precursor
UniRef100_Q	2	4	16.20%	99	10492	7	V1-3 protein
UniRef100_U	2	4	14.50%	110	11602	5	anti-glycoprotein VI immunoglobulin lambda li
UniRef100_Q	16	18	16.10%	1235	1E+05	5	STE20-like serine/threonine-protein kinase
UniRef100_P	9	13	16.10%	710	80764	6	Prolyl endopeptidase
UniRef100_Q	9	13	16.10%	710	80734	6	Prolyl endopeptidase
UniRef100_Q	9	13	16.10%	710	80700	6	Prolyl endopeptidase
UniRef100_A	6	6	16.10%	584	65163	7	Complement component 8, alpha polypeptide
UniRef100_U	6	6	16.10%	584	65063	7	Complement component C8 alpha chain precursor (Complement component 8 subunit alpha).
UniRef100_P	6	6	16.10%	584	65163	7	Complement component C8 alpha chain precursor
UniRef100_Q	5	18	16.10%	378	44468	5	Hsp90 co-chaperone Cdc37
UniRef100_Q	5	18	16.10%	378	44453	5	CDC37 protein
UniRef100_Q	5	6	16.10%	354	38210	6	Ubiquitin-conjugating enzyme E2 Z
UniRef100_Q	5	6	23.20%	246	28075	6	Isoform 2 of Q9H832
UniRef100_O	5	10	16.10%	236	25609	9	Isoform 3 of O95197
UniRef100_Q	6	19	16.00%	652	70755	8	Phosphatidylinositol-binding clathrin assembly protein
UniRef100_Q	6	19	17.00%	610	66393	9	Phosphatidylinositol binding clathrin assembly protein
UniRef100_Q	6	19	14.40%	721	77397	8	PICALM variant protein
UniRef100_Q	6	19	16.50%	632	68764	8	Isoform 2 of Q13492
UniRef100_P	8	13	16.00%	437	51557	#	U1 small nuclear ribonucleoprotein 70 kDa
UniRef100_P	10	68	16.00%	456	49168	5	Keratin, type I cytoskeletal 15
UniRef100_U	10	68	16.00%	456	49198	5	keratin 15
UniRef100_U	10	68	16.00%	456	49212	5	Keratin, type I cytoskeletal 15 (Cytokeratin-15) (CK-15) (Keratin-15) (K15).
UniRef100_Q	5	5	16.00%	393	44294	5	Hypothetical protein APG4B
UniRef100_U	5	5	12.80%	493	55446	8	PREDICTED: similar to APG4 autophagy 4 homolog B isoform b
UniRef100_U	5	5	13.50%	468	52628	9	PREDICTED: similar to APG4 autophagy 4 homolog B isoform b
UniRef100_U	5	5	13.10%	481	54301	8	PREDICTED: similar to APG4 autophagy 4 homolog B isoform a
UniRef100_U	5	5	16.60%	380	42622	6	PREDICTED: similar to APG4 autophagy 4 homolog B isoform b
UniRef100_Q	5	5	13.50%	468	52544	9	Isoform 2 of Q9Y4P1

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	5	5	16.00%	393	44309	5	Cysteine protease ATG4B
UniRef100_P	4	4	16.00%	351	40623	9	cAMP-dependent protein kinase, beta-catalytic subunit
UniRef100_Q	4	4	14.10%	398	46236	9	Protein kinase, cAMP-dependent, catalytic, beta
UniRef100_P	4	4	15.80%	355	41046	9	Isoform 7 of P22694
UniRef100_P	4	4	15.70%	357	41296	9	Isoform 6 of P22694
UniRef100_P	4	4	15.80%	354	40947	9	Isoform 5 of P22694
UniRef100_P	4	4	16.60%	338	39379	9	Isoform 4 of P22694
UniRef100_P	4	4	16.50%	339	39477	9	Isoform 3 of P22694
UniRef100_Q	4	5	16.00%	318	35231	9	Putative deoxyribose-phosphate aldolase
UniRef100_P	2	2	16.00%	268	29321	9	Ribonuclease P protein subunit p30
UniRef100_U	2	2	16.70%	258	28280	9	Ribonuclease P protein subunit p30 (EC 3.1.26.5) (RNaseP protein p30) (RNase P subunit 2).
UniRef100_O	3	5	16.00%	188	21615	#	PRA1 family protein 3
UniRef100_P	2	38	16.00%	94	10546	5	Protein S100-A1
UniRef100_Q	2	38	10.20%	147	15895	5	S100 calcium binding protein A1
UniRef100_A	13	24	15.90%	1126	1E+05	6	HLA-B associated transcript 3
UniRef100_U	13	24	15.80%	1132	1E+05	6	HLA-B associated transcript-3 isoform a
UniRef100_U	13	24	15.70%	1140	1E+05	6	HLA-B associated transcript 3
UniRef100_Q	13	24	16.60%	1077	1E+05	6	HLA-B associated transcript 3
UniRef100_Q	13	24	15.40%	1162	1E+05	6	HLA-B associated transcript 3
UniRef100_Q	13	24	15.90%	1126	1E+05	6	Hypothetical protein DKFZp686L0653
UniRef100_P	13	24	15.80%	1132	1E+05	6	Large proline-rich protein BAT3
UniRef100_O	7	10	15.90%	579	64691	7	Hunc18b2
UniRef100_U	7	10	15.50%	593	66453	7	Syntaxin-binding protein 2 (Unc-18 homolog 2) (Unc-18B) (Unc18-2).
UniRef100_Q	7	10	15.60%	590	66138	7	STXBP2 protein
UniRef100_Q	7	10	15.50%	593	66367	7	Syntaxin binding protein 2 variant
UniRef100_Q	7	10	15.50%	593	66439	7	Syntaxin-binding protein 2
UniRef100_A	6	21	15.90%	508	57090	#	RBM39 protein
UniRef100_Q	6	21	15.80%	513	57444	#	Hypothetical protein DKFZp781C0423
UniRef100_Q	6	21	15.50%	524	58657	#	RNA-binding protein 39
UniRef100_Q	6	21	15.30%	530	59380	#	RNA-binding protein 39
UniRef100_Q	6	21	22.10%	367	39818	7	Rbm39 protein
UniRef100_P	6	7	15.90%	511	56501	6	Vacuolar ATP synthase subunit B, brain isoform
UniRef100_Q	5	5	15.90%	447	51200	6	BAG family molecular chaperone regulator 5
UniRef100_U	5	5	14.50%	488	56027	6	BCL2-associated athanogene 5 isoform a
UniRef100_U	12	82	15.90%	458	49588	5	Keratin, type I cytoskeletal 13 (Cytokeratin-13) (CK-13) (Keratin-13) (K13).
UniRef100_U	12	82	15.90%	458	49558	5	keratin 13 isoform a
UniRef100_U	12	82	17.40%	420	45837	5	keratin 13 isoform b
UniRef100_U	12	82	17.40%	420	45867	5	Keratin, type I cytoskeletal 13 (Cytokeratin-13) (CK-13) (Keratin-13) (K13).
UniRef100_O	4	12	15.90%	358	38868	6	Ezrin-radixin-moesin-binding phosphoprotein 50 (EBP50) (Na(+)/H(+) exchange regulatory cofactor NHE-RF) (NHERF-1) (Regulatory cofactor of Na(+)/H(+) exchanger)
UniRef100_Q	4	9	15.90%	289	32523	5	FAM82C protein

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	4	9	9.80%	470	52118	5	CDNA FLJ10579 fis, clone NT2RP2003446
UniRef100_Q	4	9	18.70%	246	27586	5	CDNA: FLJ22310 fis, clone HRC05110
UniRef100_Q	4	9	11.70%	393	44071	5	Putative TCPTP-interacting protein
UniRef100_P	2	2	15.90%	239	26478	8	Adenylate kinase isoenzyme 2, mitochondrial
UniRef100_Q	2	2	16.40%	232	25615	8	Adenylate kinase 2
UniRef100_P	2	3	15.90%	170	19300	5	Calcineurin subunit B isoform 1
UniRef100_P	2	3	12.50%	216	24979	5	Isoform 2 of P63100
UniRef100_P	3	4	15.90%	157	17776	9	Ubiquitin-like protein 4A
UniRef100_Q	3	4	13.90%	180	20570	#	Ubiquitin-like 4
UniRef100_Q	63	72	15.80%	4544	5E+05	5	Low-density lipoprotein receptor-related protein 1 precursor
UniRef100_UI	63	72	15.80%	4544	5E+05	5	low density lipoprotein-related protein 1
UniRef100_Q	7	11	15.80%	702	80460	6	1,4-alpha-glucan branching enzyme
UniRef100_UI	7	11	15.80%	702	80540	6	1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching enzyme) (Brancher enzyme).
UniRef100_UI	7	11	15.80%	702	80474	6	glucan (1,4-alpha-), branching enzyme 1
UniRef100_O	7	10	15.80%	519	58471	5	Sorting nexin-2
UniRef100_Q	7	10	15.80%	519	58445	5	Sorting nexin 2 variant
UniRef100_Q	4	4	15.80%	342	36751	5	Methylosome protein 50 variant
UniRef100_Q	4	4	15.80%	342	36724	5	Methylosome protein 50
UniRef100_Q	9	30	15.70%	649	71425	5	Drebrin
UniRef100_UI	9	30	15.70%	649	71429	5	Drebrin (Developmentally-regulated brain protein).
UniRef100_UI	9	30	15.70%	649	71439	5	drebrin 1 isoform a
UniRef100_Q	6	7	15.70%	452	51419	8	Integrin-linked protein kinase
UniRef100_P	4	5	15.70%	369	40971	5	Deoxyhypusine synthase
UniRef100_P	3	5	15.70%	350	40097	8	Pleckstrin
UniRef100_UI	3	5	15.70%	350	40125	8	Pleckstrin (Platelet p47 protein).
UniRef100_UI	3	5	15.70%	350	40083	8	pleckstrin
UniRef100_Q	3	5	15.70%	197	21628	6	Uncharacterized protein C11orf73
UniRef100_Q	3	6	15.70%	178	18925	8	PEST proteolytic signal-containing nuclear protein
UniRef100_Q	5	8	15.60%	411	46649	5	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1
UniRef100_Q	5	8	17.60%	363	41780	6	Isoform 2 of Q969G3
UniRef100_Q	5	5	15.60%	346	39408	7	Uncharacterized protein C4orf27
UniRef100_UI	5	5	15.60%	346	39436	7	similar to CG1218-PA (LOC646058), mRNA
UniRef100_O	5	5	15.60%	366	39337	8	RNA 3'-terminal phosphate cyclase
UniRef100_O	5	12	15.60%	320	35611	6	Eukaryotic translation initiation factor 3 subunit 4
UniRef100_Q	5	12	15.60%	320	35601	6	EIF3S4 protein
UniRef100_Q	4	7	15.60%	307	34500	7	Ubiquitin fusion degradation 1-like
UniRef100_Q	4	7	14.00%	343	38725	6	Ubiquitin fusion degradation protein 1 homolog
UniRef100_Q	4	7	15.60%	288	32308	#	Mortality factor 4-like protein 2
UniRef100_Q	4	7	26.50%	170	19468	8	Mortality factor 4 like 2

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	4	7	15.60%	288	32312	#	MORF-related gene X variant
UniRef100_Q	3	3	15.60%	282	31362	5	Complement component 1 Q subcomponent-binding protein, mitochondrial precursor
UniRef100_Q	3	4	15.60%	275	30009	5	OTTHUMP00000018264
UniRef100_Q	3	4	15.60%	276	30040	5	Exosome complex exonuclease RRP43
UniRef100_Q	3	5	15.60%	199	21645	7	Chromosome 20 open reading frame 27
UniRef100_Q	3	5	17.80%	174	19291	7	Uncharacterized protein C20orf27
UniRef100_Q	3	5	24.60%	126	14249	7	Chromosome 20 open reading frame 27
UniRef100_P	4	7	15.60%	147	16550	#	Angiogenin precursor
UniRef100_Q	4	7	15.60%	147	16534	#	ANG protein
UniRef100_Q	20	32	15.50%	1504	2E+05	6	Beige-like protein variant
UniRef100_P	11	19	15.50%	882	97456	5	Epithelial-cadherin precursor (E-cadherin) (Uvomorulin) (Cadherin-1) (CAM 120/80) (CD324 antigen) [Contains: E-Cad/CTF1; E-Cad/CTF2; E- Cad/CTF3]
UniRef100_U	11	19	15.20%	903	1E+05	5	Epithelial-cadherin precursor (E-cadherin) (Uvomorulin) (Cadherin-1) (CAM 120/80) (CD324 antigen) [Contains: E-Cad/CTF1; E-Cad/CTF2; E- Cad/CTF3].
UniRef100_Q	11	19	15.20%	901	99694	5	E-cadherin
UniRef100_Q	6	8	15.50%	375	41591	8	Nucleolysin TIAR
UniRef100_U	6	8	14.80%	392	43449	8	TIA-1 related protein isoform 2
UniRef100_U	6	8	19.10%	304	34018	9	Nucleolysin TIAR (TIA-1-related protein).
UniRef100_Q	6	8	15.50%	374	41463	8	Aging-associated gene 7 protein
UniRef100_Q	5	14	15.50%	343	36918	5	RTN4 protein
UniRef100_Q	5	14	14.20%	373	40318	5	RTN4
UniRef100_P	3	3	15.50%	226	26145	8	Vacuolar ATP synthase subunit E 1
UniRef100_U	3	3	17.20%	204	23587	9	vacuolar H+ ATPase E1 isoform b
UniRef100_U	3	25	15.50%	239	25401	7	Fab X5, heavy chain
UniRef100_P	2	4	15.50%	220	24399	8	Metalloproteinase inhibitor 2 precursor
UniRef100_U	2	4	12.70%	268	29068	7	PREDICTED: similar to Metalloproteinase inhibitor 2 precursor (TIMP-2) (Tissue inhibitor of metalloproteinases 2) (CSC-21K)
UniRef100_P	5	7	15.40%	527	59756	7	Catalase
UniRef100_Q	4	11	15.40%	240	26697	5	EF-hand domain-containing protein 2
UniRef100_P	2	2	15.40%	228	25416	7	CD9 antigen
UniRef100_U	2	2	22.00%	159	17764	6	CD9 antigen (p24) (Leukocyte antigen MIC3) (Motility-related protein) (MRP-1) (Tetraspanin-29) (Tspan-29).
UniRef100_P	2	3	15.40%	117	13293	#	60S ribosomal protein L34
UniRef100_Q	2	3	15.40%	117	13129	6	Mediator of RNA polymerase II transcription, subunit 11 homolog
UniRef100_Q	2	3	13.20%	136	15301	9	Mediator of RNA polymerase II transcription subunit 11
UniRef100_Q	7	8	15.30%	523	55861	7	Probable aminopeptidase NPEPL1
UniRef100_U	7	8	15.30%	522	55774	7	Syntaxin-16 (Syn16).
UniRef100_Q	5	5	15.30%	452	47145	5	Golgi reassembly-stacking protein 2
UniRef100_Q	7	9	15.30%	412	46831	7	CDNA FLJ20030 fis, clone ADSU02156
UniRef100_Q	2	2	15.30%	216	24535	5	GINS complex subunit 3
UniRef100_U	2	2	15.10%	218	24719	5	GINS complex subunit 3 (Psf3 homolog)

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P	3	8	15.30%	203	23577	#	60S ribosomal protein L13a
UniRef100_U	3	8	15.10%	205	23358	#	similar to ribosomal protein L13a (LOC730671), mRNA
UniRef100_U	3	8	15.30%	203	23619	#	PREDICTED: similar to ribosomal protein L13a isoform 1
UniRef100_Q	3	8	15.40%	201	23375	#	RPL13A protein
UniRef100_Q	3	8	15.30%	203	23662	#	FWP004
UniRef100_Q	3	8	15.30%	203	23558	#	Ribosomal protein L13a variant
UniRef100_Q	2	2	15.30%	157	18246	8	Protein UXT
UniRef100_Q	17	22	15.20%	1443	2E+05	6	Cleavage and polyadenylation specificity factor subunit 1
UniRef100_O	10	12	15.20%	916	1E+05	5	Bifunctional protein NCOAT (Nuclear cytoplasmic O-GlcNAcase and acetyltransferase) (Meningioma-expressed antigen 5) [Includes: Beta- hexosaminidase (EC 3.2.1.52) (N-acetyl-beta-glucosaminidase) (Beta-N- acetylhexosaminidase) (Hexosaminidase C) (N-acetyl-beta-D-glucosaminidase) (O-GlcNAcase); Histone acetyltransferase (EC 2.3.1.48) (HAT)]
UniRef100_P	9	10	15.20%	689	78840	6	Thimet oligopeptidase
UniRef100_Q	9	10	15.20%	689	78824	6	Thimet oligopeptidase 1
UniRef100_P	4	6	15.20%	362	40545	7	Adenosine kinase
UniRef100_Q	4	6	15.90%	345	38703	7	Adenosine kinase
UniRef100_O	3	3	15.20%	283	30977	7	Isoform 3 of O00154
UniRef100_Q	4	6	15.10%	352	39555	5	Hypothetical protein DKFZp686E1899
UniRef100_Q	4	6	15.10%	352	39595	5	Tropomodulin-3
UniRef100_Q	4	6	15.10%	331	37485	6	Gamma-parvin
UniRef100_Q	4	6	26.70%	187	21439	6	Isoform 3 of Q9HBI0
UniRef100_Q	4	6	18.30%	273	31042	5	Isoform 2 of Q9HBI0
UniRef100_Q	3	4	15.10%	299	32674	9	Sirtuin (Silent mating type information regulation 2 homolog) 5
UniRef100_Q	3	4	14.50%	310	33881	9	NAD-dependent deacetylase sirtuin-5
UniRef100_O	15	37	15.00%	1220	1E+05	6	Eukaryotic translation initiation factor 5B
UniRef100_U	15	37	15.00%	1220	1E+05	6	Eukaryotic translation initiation factor 5B (eIF-5B) (Translation initiation factor IF-2).
UniRef100_U	15	37	15.00%	1220	1E+05	6	eukaryotic translation initiation factor 5B
UniRef100_Q	15	37	15.00%	1220	1E+05	6	Eukaryotic translation initiation factor 5B
UniRef100_O	5	5	15.00%	428	45997	5	Immunoglobulin superfamily containing leucine-rich repeat precursor
UniRef100_Q	8	16	14.90%	808	89253	5	Leucine-rich repeat flightless-interacting protein 1
UniRef100_U	8	16	15.30%	784	86438	5	leucine rich repeat (in FLII) interacting protein 1
UniRef100_Q	8	16	16.00%	752	82689	5	Isoform 3 of Q32MZ4
UniRef100_Q	8	16	15.30%	784	86404	5	Isoform 2 of Q32MZ4
UniRef100_P	6	6	14.90%	605	66035	7	Insulin-like growth factor-binding protein complex acid labile chain precursor
UniRef100_Q	6	6	14.90%	605	66067	7	Insulin-like growth factor binding protein, acid labile subunit
UniRef100_Q	2	2	14.90%	188	20481	4	Zinc finger protein 428
UniRef100_A	2	2	14.90%	175	19754	8	Hypothetical protein
UniRef100_Q	2	2	8.50%	305	34095	9	NADH-cytochrome b5 reductase isoform
UniRef100_Q	2	2	8.50%	305	34114	#	Cytochrome b5 reductase 1
UniRef100_O	9	11	14.80%	852	92903	7	Lysine-specific histone demethylase 1

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_UI	9	11	14.40%	876	95223	6	Lysine-specific histone demethylase 1 (EC 1.-.-.-) (Flavin-containing amine oxidase domain-containing protein 2) (BRAF35-HDAC complex protein BHC110).
UniRef100_O	9	11	14.40%	876	95155	6	Isoform 2 of O60341
UniRef100_Q	8	13	14.80%	622	70456	7	Phosphoglucomutase-2-like 1
UniRef100_Q	9	20	14.80%	608	68120	6	Nuclear protein localization protein 4 homolog
UniRef100_UI	9	20	14.60%	616	69360	7	Nuclear protein localization protein 4 homolog (Protein NPL4).
UniRef100_UI	9	20	14.80%	607	67987	6	Nuclear protein localization protein 4 homolog (Protein NPL4).
UniRef100_UI	9	20	14.80%	608	68183	6	nuclear protein localization 4
UniRef100_Q	9	20	14.60%	617	69461	7	Isoform 2 of Q8TAT6
UniRef100_P	8	14	14.80%	547	58994	7	Nonspecific lipid-transfer protein
UniRef100_UI	8	14	57.90%	140	15079	9	sterol carrier protein 2 isoform 2 precursor
UniRef100_P	8	14	56.60%	143	15401	9	Isoform SCP2 of P22307
UniRef100_Q	5	6	14.80%	453	50228	6	Protein prune homolog
UniRef100_Q	5	6	15.40%	435	48240	6	TcD37 homolog
UniRef100_Q	5	6	14.80%	453	50200	6	Prune homolog
UniRef100_Q	2	7	14.80%	176	18419	9	Uncharacterized protein C19orf43
UniRef100_P	20	73	14.70%	1754	2E+05	6	Collagen alpha-1(XVIII) chain precursor [Contains: Endostatin]
UniRef100_UI	20	73	17.00%	1516	2E+05	6	alpha 1 type XVIII collagen isoform 1 precursor
UniRef100_UI	20	73	14.60%	1755	2E+05	6	Collagen alpha-1(XVIII) chain precursor [Contains: Endostatin].
UniRef100_UI	20	73	17.40%	1476	2E+05	6	Collagen alpha-1(XVIII) chain precursor [Contains: Endostatin].
UniRef100_UI	20	73	19.20%	1339	1E+05	7	Collagen alpha-1(XVIII) chain precursor [Contains: Endostatin].
UniRef100_UI	20	73	19.20%	1336	1E+05	7	alpha 1 type XVIII collagen isoform 2 precursor
UniRef100_P	20	73	19.20%	1339	1E+05	7	Isoform 3 of P39060
UniRef100_P	20	73	16.90%	1519	2E+05	6	Isoform 2 of P39060
UniRef100_Q	17	18	14.70%	1564	2E+05	8	Tetratricopeptide repeat protein 37
UniRef100_Q	11	13	14.70%	1173	1E+05	7	Uncharacterized protein KIAA1033
UniRef100_Q	11	12	14.70%	1030	1E+05	6	MMS19-like protein
UniRef100_UI	11	12	14.70%	1030	1E+05	6	MMS19-like protein (hMMS19) (MET18 homolog).
UniRef100_UI	11	12	14.70%	1030	1E+05	6	MMS19-like (MET18 homolog, S. cerevisiae)
UniRef100_O	8	15	14.70%	736	81877	7	Dynamin-1-like protein
UniRef100_UI	8	15	15.20%	710	79224	7	Dynamin-1-like protein (EC 3.6.5.5) (Dynamin-like protein) (Dnm1p/Vps1p-like protein) (DVLP) (Dynamin family member proline-rich carboxyl-terminal domain less) (Dymple) (Dynamin-related protein 1) (Dynamin-like protein 4) (Dynamin-like protein IV) (HdynIV
UniRef100_UI	8	15	15.20%	710	79456	7	dynamin 1-like protein isoform 2
UniRef100_UI	8	15	15.50%	699	78061	7	dynamin 1-like protein isoform 3
UniRef100_UI	8	15	14.70%	736	81891	7	dynamin 1-like protein isoform 1
UniRef100_Q	8	15	14.40%	751	83579	8	Dynamin-like protein DYNIV-11 variant
UniRef100_O	8	15	15.20%	710	79109	7	Isoform 5 of O00429
UniRef100_O	8	15	15.50%	699	78100	7	Isoform 4 of O00429
UniRef100_O	8	15	15.20%	710	79442	7	Isoform 3 of O00429
UniRef100_O	8	15	14.90%	725	80536	7	Isoform 2 of O00429

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	6	6	14.70%	523	58315	7	Sialate O-acetylesterase precursor
UniRef100_P	5	8	14.70%	455	52949	7	Epoxide hydrolase 1
UniRef100_Q	5	8	14.70%	455	52961	7	EPHX1 protein
UniRef100_P	6	8	14.70%	443	51597	6	COP9 signalosome complex subunit 2
UniRef100_Q	6	8	14.70%	443	51570	6	COP9 constitutive photomorphogenic homolog subunit 2 variant
UniRef100_U	2	2	14.70%	184	20850	6	ADP-ribosylation factor-like 2
UniRef100_P	17	20	14.60%	1456	2E+05	7	Macrophage mannose receptor 1 precursor
UniRef100_Q	17	20	14.60%	1456	2E+05	7	Mannose receptor C type 1-like protein 1
UniRef100_Q	17	20	14.60%	1456	2E+05	7	Mannose receptor
UniRef100_P	12	15	14.60%	1107	1E+05	7	DNA polymerase delta catalytic subunit
UniRef100_U	12	15	14.60%	1107	1E+05	7	polymerase (DNA directed), delta 1, catalytic subunit 125kDa
UniRef100_Q	9	11	14.60%	759	87680	8	Cullin-4A
UniRef100_U	9	11	14.50%	763	88235	8	Cullin-4A (CUL-4A).
UniRef100_Q	9	11	16.80%	659	76821	7	Isoform 2 of Q13619
UniRef100_Q	5	8	14.60%	534	60246	5	NEDD8-activating enzyme E1 regulatory subunit
UniRef100_U	5	8	14.60%	536	60391	5	NEDD8-activating enzyme E1 regulatory subunit
UniRef100_U	5	8	14.80%	528	59447	5	NEDD8-activating enzyme E1 regulatory subunit (Amyloid protein-binding protein 1) (Amyloid beta precursor protein-binding protein 1, 59 kDa) (APP-BP1) (Protooncogene protein 1) (HPP1).
UniRef100_U	5	8	17.50%	445	50625	5	amyloid beta precursor protein-binding protein 1 isoform c
UniRef100_U	5	8	14.80%	528	59420	5	amyloid beta precursor protein-binding protein 1 isoform b
UniRef100_U	5	8	14.60%	534	60273	5	NEDD8-activating enzyme E1 regulatory subunit (Amyloid protein-binding protein 1) (Amyloid beta precursor protein-binding protein 1, 59 kDa) (APP-BP1) (Protooncogene protein 1) (HPP1).
UniRef100_Q	10	10	14.50%	975	1E+05	5	Importin-11
UniRef100_U	10	10	14.50%	974	1E+05	5	Importin-11 (Imp11) (Ran-binding protein 11) (RanBP11).
UniRef100_U	10	46	14.50%	600	60483	7	Mucin-1 precursor (MUC-1) (Polymorphic epithelial mucin) (PEM) (PEMT) (Episialin) (Tumor-associated mucin) (Carcinoma-associated mucin) (Tumor-associated epithelial membrane antigen) (EMA) (H23AG) (Peanut- reactive urinary mucin) (PUM) (Breast carcinoma-a
UniRef100_Q	5	11	14.50%	406	46649	6	Sorting nexin-6
UniRef100_Q	3	4	14.50%	304	34805	7	Hypothetical protein DKFZp666C185
UniRef100_U	3	4	14.40%	306	34925	7	PREDICTED: hypothetical protein LOC64853
UniRef100_Q	3	4	14.40%	306	34951	7	CDNA FLJ12806 fis, clone NT2RP2002235
UniRef100_Q	3	4	14.40%	306	35023	7	Uncharacterized protein C1orf80
UniRef100_Q	2	2	14.50%	234	26761	5	Syntaxin 12
UniRef100_Q	2	2	12.30%	276	31642	6	Syntaxin-12
UniRef100_Q	2	2	12.60%	269	30878	6	STX12 protein
UniRef100_Q	3	4	14.50%	179	21498	6	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase
UniRef100_U	3	4	14.50%	179	21483	6	membrane-type 1 matrix metalloproteinase cytoplasmic tail binding protein-1
UniRef100_Q	2	2	14.50%	173	19385	9	C3orf41 protein
UniRef100_Q	2	2	11.10%	226	25497	8	Glutathione S-transferase kappa 1

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	2	2	8.90%	282	31566	9	GSTK1 protein
UniRef100_P	2	2	14.50%	165	18566	5	Ubiquitin-conjugating enzyme E2 G2
UniRef100_U	2	2	17.50%	137	15614	5	ubiquitin-conjugating enzyme E2G 2 isoform 2
UniRef100_Q	2	2	18.80%	128	14098	6	Hypothetical protein DKFZp586L2318
UniRef100_Q	10	13	14.40%	963	1E+05	7	Esophageal cancer associated protein
UniRef100_Q	10	13	16.90%	824	94301	7	CDNA: FLJ21040 fis, clone CAE10642
UniRef100_Q	10	13	14.40%	963	1E+05	7	Esophageal cancer associated protein
UniRef100_Q	10	13	16.00%	869	99589	7	MGC16824 protein
UniRef100_O	7	11	14.40%	755	85853	4	HIV Tat-specific factor 1
UniRef100_P	5	5	14.40%	464	51658	7	Argininosuccinate lyase
UniRef100_U	5	5	15.20%	442	49095	6	Argininosuccinate lyase (EC 4.3.2.1) (Arginosuccinase) (ASAL).
UniRef100_U	5	5	15.00%	448	49872	6	Argininosuccinate lyase (EC 4.3.2.1) (Arginosuccinase) (ASAL).
UniRef100_U	5	5	15.30%	438	48733	6	argininosuccinate lyase isoform 3
UniRef100_U	5	5	15.10%	444	49509	6	argininosuccinate lyase isoform 2
UniRef100_P	7	11	14.30%	708	80593	6	Double-strand break repair protein MRE11A
UniRef100_P	9	52	14.30%	526	53426	9	RNA-binding protein FUS
UniRef100_Q	9	52	14.30%	526	53400	9	Fusion (Involved in t(12;16) in malignant liposarcoma)
UniRef100_Q	9	52	25.00%	300	31994	#	Fusion (Involved in t(12;16) in malignant liposarcoma) isoform a variant
UniRef100_Q	9	52	14.20%	528	53377	9	Fus-like protein
UniRef100_P	9	52	14.30%	525	53355	9	Isoform Short of P35637
UniRef100_P	5	11	14.30%	391	45374	5	Nucleosome assembly protein 1-like 1
UniRef100_Q	3	3	14.30%	217	22348	#	H/ACA ribonucleoprotein complex subunit 1
UniRef100_Q	3	3	15.60%	199	20834	#	Isoform 2 of Q9NY12
UniRef100_Q	2	4	14.30%	182	21508	7	Core-binding factor subunit beta
UniRef100_Q	2	4	13.90%	187	21991	6	Core binding factor beta isoform PEBP2B
UniRef100_Q	10	17	14.20%	950	1E+05	8	5'-3' exoribonuclease 2
UniRef100_Q	10	17	15.40%	874	99962	8	Isoform 2 of Q9H0D6
UniRef100_Q	4	11	14.20%	493	54641	5	EGF-containing fibulin-like extracellular matrix protein 1 precursor
UniRef100_U	4	11	14.90%	470	52066	5	EGF-containing fibulin-like extracellular matrix protein 1 precursor (Fibulin-3) (FIBL-3) (Fibrillin-like protein) (Extracellular protein S1-5).
UniRef100_Q	4	11	16.70%	418	46232	5	EGF-containing fibulin-like extracellular matrix protein 1 isoform b variant
UniRef100_Q	4	11	14.20%	492	54554	5	Isoform 4 of Q12805
UniRef100_Q	4	11	14.20%	492	54584	5	Isoform 3 of Q12805
UniRef100_Q	4	7	14.20%	409	45008	8	GMPR2 protein
UniRef100_U	4	7	16.70%	347	38088	9	guanosine monophosphate reductase 2 (GMPR2), transcript variant 2, mRNA
UniRef100_Q	4	7	16.70%	348	37874	7	GMP reductase 2
UniRef100_Q	4	7	18.10%	320	34597	8	Full-length cDNA clone CS0DH001YP08 of T cells (Jurkat cell line) of Homo sapiens
UniRef100_P	5	5	14.20%	373	42064	7	Glutamine synthetase
UniRef100_U	5	5	13.80%	384	43306	7	Glutamine synthetase
UniRef100_P	4	5	14.20%	339	37192	5	Lymphocyte-specific protein 1
UniRef100_Q	4	5	14.20%	339	37222	5	Lymphocyte-specific protein 1 variant

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_A	2	2	14.20%	225	24118	6	GGTL4 protein
UniRef100_U	2	2	5.60%	574	62192	7	PREDICTED: similar to Gamma-glutamyltranspeptidase 1 precursor (Gamma-glutamyltransferase 1) (CD224 antigen) isoform 1
UniRef100_U	2	2	14.70%	218	23555	6	PREDICTED: similar to gamma-glutamyltransferase 2 isoform 1
UniRef100_U	2	2	6.50%	490	53415	7	Gamma-glutamyltransferase-like protein 2.
UniRef100_U	2	2	14.10%	227	24380	5	Gamma-glutamyltransferase-like protein 4.
UniRef100_U	2	2	5.60%	569	61745	8	PREDICTED: similar to Gamma-glutamyltranspeptidase 1 precursor (Gamma-glutamyltransferase 1) (CD224 antigen) isoform 2
UniRef100_U	2	2	12.70%	252	26904	6	PREDICTED: similar to Gamma-glutamyltransferase-like protein 4 isoform 2
UniRef100_U	2	2	14.20%	225	24102	6	PREDICTED: similar to gamma-glutamyltransferase 2 isoform 3
UniRef100_Q	2	2	14.20%	225	24078	6	GGT1 protein
UniRef100_Q	2	2	14.70%	218	23589	6	GGTL4 protein
UniRef100_Q	2	2	14.20%	225	24164	5	Gamma-glutamyl transpeptidase
UniRef100_Q	2	2	12.70%	252	27049	6	Gamma-glutamyltransferase-like protein 4
UniRef100_P	2	2	14.90%	215	23152	6	Gamma-glutamyltransferase-like protein 2
UniRef100_P	2	2	5.60%	569	61410	7	Gamma-glutamyltranspeptidase 1 precursor (EC 2.3.2.2) (Gamma- glutamyltransferase 1) (GGT 1) (CD224 antigen) [Contains: Gamma- glutamyltranspeptidase 1 heavy chain; Gamma-glutamyltranspeptidase 1 light chain]
UniRef100_A	2	2	14.20%	225	24080	6	GGTL4 protein
UniRef100_P	3	14	14.20%	226	22580	#	Histone H1.5
UniRef100_Q	11	18	14.10%	1234	1E+05	6	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 3
UniRef100_U	11	18	14.60%	1190	1E+05	6	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 3 (EC 3.1.4.11) (Phosphoinositide phospholipase C) (Phospholipase C- beta-3) (PLC-beta-3).
UniRef100_Q	11	18	14.60%	1191	1E+05	6	Similar to phospholipase C, beta 3
UniRef100_Q	5	5	14.10%	524	58043	6	Serine/threonine-protein kinase PAK 2
UniRef100_Q	4	5	14.10%	376	42508	7	Chromosome 12 open reading frame 10
UniRef100_U	4	5	16.30%	325	36629	8	UPF0160 protein MYG1.
UniRef100_U	4	5	14.10%	376	42449	7	UPF0160 protein MYG1.
UniRef100_Q	4	5	16.50%	322	36363	8	C12orf10 protein
UniRef100_Q	5	5	14.10%	341	39029	6	Uncharacterized protein C9orf64
UniRef100_Q	5	23	14.10%	199	22473	7	Transgelin-3
UniRef100_U	36	53	14.00%	3075	3E+05	6	laminin, alpha 1 precursor
UniRef100_U	36	53	14.00%	3081	3E+05	6	Laminin subunit alpha-1 precursor (Laminin A chain).
UniRef100_P	13	15	14.00%	1249	1E+05	6	Tripeptidyl-peptidase 2
UniRef100_U	13	15	14.00%	1249	1E+05	6	tripeptidyl peptidase II
UniRef100_Q	13	15	13.90%	1262	1E+05	7	Tripeptidyl peptidase II
UniRef100_Q	10	28	14.00%	1043	1E+05	6	Integrator complex subunit 3
UniRef100_Q	10	28	14.00%	1042	1E+05	6	Isoform 2 of Q68E01
UniRef100_Q	8	10	14.00%	823	91131	6	Integrin beta
UniRef100_U	8	10	13.90%	825	91620	5	integrin beta 1 isoform 1C-1 precursor
UniRef100_U	8	10	14.60%	789	87446	6	integrin beta 1 isoform 1B precursor

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_UI	8	10	14.40%	801	88884	6	integrin beta 1 isoform 1D precursor
UniRef100_UI	8	10	14.00%	819	91035	5	integrin beta 1 isoform 1C-2 precursor
UniRef100_Q	8	10	14.40%	798	88415	5	Integrin, beta 1
UniRef100_Q	7	8	14.00%	537	59648	8	Stromal RNA regulating factor
UniRef100_Q	7	8	13.80%	542	60083	8	Heterogeneous nuclear ribonucleoprotein L-like
UniRef100_Q	7	8	14.80%	508	56467	8	Stromal RNA regulating factor
UniRef100_Q	3	3	14.00%	193	21472	#	Histone H2B type 2-C
UniRef100_Q	3	3	16.50%	164	18018	#	Histone H2B type 2-D
UniRef100_O	2	3	14.00%	172	19471	6	Diphosphoinositol polyphosphate phosphohydrolase 1
UniRef100_P	5	6	13.90%	418	47066	6	Beta-arrestin-1
UniRef100_UI	5	6	13.90%	418	47126	6	Beta-arrestin-1 (Arrestin beta 1).
UniRef100_P	5	6	14.10%	410	46309	6	Isoform 1B of P49407
UniRef100_A	5	9	13.90%	368	41468	8	Major histocompatibility complex class I C
UniRef100_Q	4	6	13.90%	366	40877	7	MHC class I antigen
UniRef100_Q	4	6	13.90%	366	40863	6	HLA class I histocompatibility antigen, Cw-15 alpha chain precursor
UniRef100_P	4	6	17.10%	298	34485	6	HLA-Cw*2
UniRef100_P	4	6	13.90%	366	40886	6	HLA class I histocompatibility antigen, Cw-12 alpha chain precursor
UniRef100_P	4	6	13.90%	366	40773	7	HLA class I histocompatibility antigen, Cw-8 alpha chain precursor
UniRef100_P	4	6	13.90%	366	41095	6	HLA class I histocompatibility antigen, Cw-2 alpha chain precursor
UniRef100_O	5	9	14.70%	347	38972	6	HLA-C protein
UniRef100_A	5	9	12.80%	397	44531	9	Major histocompatibility complex class I C
UniRef100_A	5	9	13.70%	372	41565	8	Major histocompatibility complex class I C
UniRef100_Q	11	14	13.80%	1019	1E+05	7	Insulin-degrading enzyme
UniRef100_Q	5	6	13.80%	607	70370	6	EPM2A-interacting protein 1
UniRef100_Q	6	6	13.80%	471	53372	7	COP9 signalosome complex subunit 1
UniRef100_UI	6	6	11.70%	555	60434	7	COP9 signalosome complex subunit 1 (Signalosome subunit 1) (SGN1) (JAB1-containing signalosome subunit 1) (G protein pathway suppressor 1) (Protein GPS1) (Protein MFH).
UniRef100_UI	6	6	12.30%	527	59050	6	G protein pathway suppressor 1 isoform 1
UniRef100_Q	6	6	11.80%	549	59818	7	Isoform 3 of Q13098
UniRef100_Q	6	6	13.70%	475	53816	7	Isoform 2 of Q13098
UniRef100_O	3	9	13.80%	390	43016	6	Homeobox protein Meis1
UniRef100_UI	3	9	13.80%	390	43001	6	Homeobox protein Meis1.
UniRef100_Q	3	9	21.90%	247	26996	6	Hypothetical protein MEIS1
UniRef100_Q	3	9	14.30%	378	41748	6	MEIS1 protein
UniRef100_P	2	3	13.80%	290	33224	8	Uncharacterized protein C21orf59
UniRef100_UI	2	3	16.30%	245	27610	7	Uncharacterized protein C21orf59.
UniRef100_Q	2	3	16.30%	245	27508	7	CDNA FLJ30766 fis, clone FEBRA2000680
UniRef100_P	2	3	13.80%	218	25712	7	Glutathione S-transferase Mu 1
UniRef100_UI	2	3	20.10%	149	17390	7	Glutathione S-transferase Mu 1 (EC 2.5.1.18) (GSTM1-1) (GST class-mu 1) (GSTM1a-1a) (GSTM1b-1b) (HB subunit 4) (GTH4).
UniRef100_Q	2	3	16.60%	181	21253	8	Glutathione S-transferase M1

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	2	3	15.40%	195	22829	5	Isoform 2 of Q03013
UniRef100_Q	2	3	13.80%	218	25561	6	Glutathione S-transferase Mu 4
UniRef100_P	24	29	13.70%	1976	2E+05	6	Myosin-10
UniRef100_Q	24	29	13.40%	2018	2E+05	6	MYH10 variant protein
UniRef100_Q	24	29	13.70%	1976	2E+05	6	Myosin, heavy chain 10, non-muscle
UniRef100_Q	24	29	13.70%	1976	2E+05	6	Myosin, heavy chain 10, non-muscle
UniRef100_P	24	29	13.50%	1997	2E+05	6	Isoform 3 of P35580
UniRef100_Q	14	31	13.70%	1268	1E+05	6	Stromal antigen 2
UniRef100_U	14	31	13.70%	1268	1E+05	6	Cohesin subunit SA-2 (Stromal antigen 2) (SCC3 homolog 2).
UniRef100_U	14	31	14.10%	1231	1E+05	5	Cohesin subunit SA-2 (Stromal antigen 2) (SCC3 homolog 2).
UniRef100_Q	14	31	14.10%	1231	1E+05	5	Cohesin subunit SA-2
UniRef100_Q	14	31	14.10%	1231	1E+05	5	Hypothetical protein DKFZp686C21148
UniRef100_Q	14	31	13.70%	1268	1E+05	6	Hypothetical protein DKFZp781H1753
UniRef100_P	7	8	13.70%	615	67818	8	Coagulation factor XII precursor (EC 3.4.21.38) (Hageman factor) (HAF) [Contains: Coagulation factor XIIa heavy chain; Beta-factor XIIa part 1; Beta-factor XIIa part 2; Coagulation factor XIIa light chain]
UniRef100_U	7	8	13.70%	615	67792	8	Coagulation factor XII precursor (EC 3.4.21.38) (Hageman factor) (HAF) [Contains: Coagulation factor XIIa heavy chain; Beta-factor XIIa part 1; Beta-factor XIIa part 2; Coagulation factor XIIa light chain].
UniRef100_Q	7	8	13.70%	615	67735	8	Coagulation factor XII-Mie
UniRef100_P	2	5	13.70%	212	24542	9	ER lumen protein retaining receptor 1
UniRef100_Q	2	5	19.30%	150	17487	7	CDNA FLJ90704 fis, clone PLACE1007296, highly similar to Human a presumptive KDEL receptor
UniRef100_P	3	4	13.70%	212	23819	8	Thymidylate kinase
UniRef100_U	3	4	17.20%	169	19032	8	PREDICTED: similar to deoxythymidylate kinase (thymidylate kinase) isoform 2
UniRef100_U	3	4	15.00%	193	21893	8	PREDICTED: similar to deoxythymidylate kinase (thymidylate kinase) isoform 3
UniRef100_U	3	4	15.40%	188	21064	9	PREDICTED: similar to deoxythymidylate kinase (thymidylate kinase) isoform 1
UniRef100_P	2	2	13.70%	117	13193	8	Transcription elongation factor SPT4
UniRef100_U	65	220	13.60%	5890	6E+05	6	AHNAK nucleoprotein isoform 1
UniRef100_P	12	35	13.60%	1094	1E+05	7	Protein transport protein Sec24C
UniRef100_U	12	35	14.30%	1042	1E+05	6	Protein transport protein Sec24C (SEC24-related protein C).
UniRef100_U	12	35	13.60%	1094	1E+05	7	SEC24-related protein C
UniRef100_Q	10	15	13.60%	1051	1E+05	6	TNPO2 variant protein
UniRef100_Q	10	15	16.10%	887	1E+05	5	Transportin 2
UniRef100_Q	8	8	13.60%	875	1E+05	5	Ubiquitin-protein ligase E3A
UniRef100_U	8	8	13.60%	875	1E+05	5	ubiquitin protein ligase E3A isoform 2
UniRef100_U	8	8	13.60%	872	1E+05	5	ubiquitin protein ligase E3A isoform 3
UniRef100_Q	8	8	14.00%	852	97968	5	CTCL tumor antigen se37-2
UniRef100_Q	8	8	13.60%	872	1E+05	5	Ubiquitin protein ligase E3A
UniRef100_Q	8	8	13.60%	872	1E+05	5	Isoform III of Q05086
UniRef100_P	4	19	13.60%	418	47366	5	26S protease regulatory subunit 6B

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_UI	4	19	13.80%	414	47018	5	PREDICTED: similar to 26S protease regulatory subunit 6B (MIP224) (MB67-interacting protein) (TAT-binding protein 7) (TBP-7)
UniRef100_Q	2	4	13.60%	250	26784	6	Parkinson disease 7 domain-containing protein 1
UniRef100_Q	2	4	15.50%	220	23298	7	CDNA FLJ34283 fis, clone FEBRA2003926, weakly similar to NonF
UniRef100_Q	2	3	13.60%	184	21850	#	U3 small nucleolar ribonucleoprotein protein IMP3
UniRef100_Q	2	5	13.60%	184	21410	9	Hypothetical protein
UniRef100_Q	2	5	5.00%	498	54284	6	Wiskott-Aldrich syndrome protein family member 2
UniRef100_P	2	2	13.60%	184	19863	5	Tumor protein D52
UniRef100_UI	2	2	11.10%	226	24485	5	Tumor protein D52 (N8 protein).
UniRef100_UI	2	2	12.00%	209	22635	5	Tumor protein D52 (N8 protein).
UniRef100_UI	2	2	10.00%	250	26480	6	Tumor protein D52 (N8 protein).
UniRef100_UI	2	2	12.10%	207	22477	5	tumor protein D52 isoform 2
UniRef100_Q	2	2	10.10%	248	26382	6	N8 protein long isoform
UniRef100_Q	2	2	11.20%	224	24327	5	Prostate and colon associated protein
UniRef100_Q	2	2	13.60%	184	19847	5	TPD52 protein
UniRef100_Q	2	2	11.30%	222	23782	6	N8 protein long isoform variant
UniRef100_P	6	7	13.50%	676	75123	6	Vitamin K-dependent protein S precursor
UniRef100_UI	6	7	13.50%	676	75073	6	protein S (alpha)
UniRef100_Q	6	7	14.00%	650	72480	6	Protein S precursor
UniRef100_Q	6	7	14.00%	650	72462	6	Protein S precursor
UniRef100_P	6	7	13.50%	651	74716	7	Beta-glucuronidase precursor
UniRef100_UI	6	7	14.70%	600	69142	7	Beta-glucuronidase precursor (EC 3.2.1.31) (Beta-G1).
UniRef100_Q	6	7	13.50%	651	74732	7	Hypothetical protein GUSB
UniRef100_P	6	7	14.70%	600	69126	7	Isoform Short of P08236
UniRef100_Q	9	22	13.50%	672	73653	9	Spermatid perinuclear RNA-binding protein
UniRef100_P	5	9	13.50%	505	54390	8	Annexin A11
UniRef100_Q	2	3	13.50%	363	39980	6	DPH2L protein
UniRef100_UI	2	3	11.10%	443	48805	8	diptheria toxin resistance protein required for diphthamide biosynthesis-like 1
UniRef100_Q	2	3	11.10%	443	48851	8	OVCA1
UniRef100_Q	2	3	11.10%	443	48833	8	Protein DPH1 homolog
UniRef100_Q	2	3	16.20%	303	33529	8	DPH1 protein
UniRef100_P	4	4	13.40%	529	56560	5	ATP synthase subunit beta, mitochondrial precursor
UniRef100_Q	4	4	16.00%	445	48113	5	Mitochondrial ATP synthase, H+ transporting F1 complex beta subunit
UniRef100_Q	7	16	13.30%	649	72752	5	GPI-anchored membrane protein 1
UniRef100_UI	7	16	13.20%	651	72930	5	GPI-anchored membrane protein 1 (GPI-anchored protein p137) (p137GPI) (Membrane component chromosome 11 surface marker 1).
UniRef100_UI	7	16	12.10%	712	78612	5	GPI-anchored membrane protein 1 (GPI-anchored protein p137) (p137GPI) (Membrane component chromosome 11 surface marker 1).
UniRef100_Q	7	16	12.10%	709	78366	5	GPI-anchored membrane protein 1
UniRef100_Q	7	16	12.40%	694	76862	5	Cytoplasmic activation/proliferation-associated protein 1
UniRef100_O	3	4	13.30%	330	37664	7	AH receptor-interacting protein

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P	4	4	13.30%	330	36295	7	Delta-aminolevulinic acid dehydratase
UniRef100_U	4	4	12.30%	359	39034	8	delta-aminolevulinic acid dehydratase isoform a
UniRef100_Q	4	4	12.30%	359	39050	8	CDNA FLJ16678 fis, clone TLIVE2002046, highly similar to DELTA- AMINOLEVULINIC ACID DEHYDRATASE
UniRef100_P	2	9	13.30%	196	23466	#	60S ribosomal protein L19
UniRef100_U	2	9	13.30%	195	23335	#	60S ribosomal protein L19.
UniRef100_Q	2	9	15.00%	173	20820	#	Ribosomal protein L19
UniRef100_Q	2	9	13.30%	196	23467	#	Ribosomal protein L19 variant
UniRef100_A	10	11	13.20%	839	94512	6	Heat shock 70 kDa protein 4-like protein
UniRef100_Q	10	11	13.20%	839	94505	6	Heat shock protein apg-1
UniRef100_O	10	11	13.20%	839	94486	6	Heat shock 70 kDa protein 4L
UniRef100_Q	6	7	13.20%	599	67098	6	CDNA FLJ16595 fis, clone TESTI4005317, highly similar to Homo sapiens rab6 GTPase activating protein
UniRef100_Q	6	7	7.90%	997	1E+05	5	Rab GTPase-activating protein 1
UniRef100_Q	4	7	13.20%	485	52723	4	Bcl-2-like 13 protein
UniRef100_Q	4	7	31.80%	201	22612	5	Isoform 1 of Q9BXK5
UniRef100_Q	4	13	13.20%	440	47535	7	C-terminal-binding protein 1
UniRef100_Q	4	13	13.50%	429	46405	7	C-terminal binding protein 1
UniRef100_Q	2	2	13.20%	310	34474	6	Protein FAM84B
UniRef100_P	2	2	13.20%	190	21879	5	Neuronal calcium sensor 1
UniRef100_Q	14	25	13.10%	1445	2E+05	6	CD109 antigen precursor
UniRef100_Q	14	25	13.20%	1428	2E+05	6	Isoform 4 of Q6YHK3
UniRef100_P	14	14	13.10%	1306	1E+05	6	Angiotensin-converting enzyme, somatic isoform precursor (EC 3.4.15.1) (Dipeptidyl carboxypeptidase I) (Kininase II) (CD143 antigen) [Contains: Angiotensin-converting enzyme, somatic isoform, soluble form]
UniRef100_Q	10	15	13.10%	981	1E+05	6	Echinoderm microtubule-associated protein-like 4
UniRef100_U	10	15	13.10%	981	1E+05	6	Echinoderm microtubule-associated protein-like 4 (EMAP-4) (Restrictedly overexpressed proliferation-associated protein) (Ropp 120).
UniRef100_Q	2	3	13.10%	329	34674	7	Serine dehydratase-like
UniRef100_P	2	3	13.10%	306	34193	7	Palmitoyl-protein thioesterase 1 precursor
UniRef100_Q	2	3	14.30%	279	30743	8	Palmitoyl-protein thioesterase 1
UniRef100_Q	3	4	13.10%	244	26856	7	Kallikrein-6 precursor
UniRef100_Q	14	21	13.00%	1288	1E+05	7	Structural maintenance of chromosomes protein 4
UniRef100_A	10	15	13.00%	808	91496	9	EIF2C2 protein
UniRef100_U	10	15	12.20%	861	97407	9	Eukaryotic translation initiation factor 2C 2 (eIF2C 2) (eIF-2C 2) (Argonaute-2) (Slicer protein) (PAZ Piwi domain protein) (PPD).
UniRef100_U	10	15	12.20%	859	97208	9	eukaryotic translation initiation factor 2C, 2
UniRef100_Q	10	15	12.30%	851	96799	9	Eukaryotic translation initiation factor 2C 2
UniRef100_O	4	4	13.00%	492	54099	6	Cytoplasmic dynein 1 light intermediate chain 2
UniRef100_Q	4	5	13.00%	455	51845	6	5'-nucleotidase domain-containing protein 1
UniRef100_Q	3	4	13.00%	423	46978	5	Exosome complex exonuclease RRP45

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	3	4	12.50%	439	48949	5	Polymyositis/scleroderma autoantigen 1
UniRef100_Q	3	4	12.10%	456	50803	5	Polymyositis/scleroderma autoantigen 1
UniRef100_P	3	3	13.00%	316	36072	6	BRCA1/BRCA2-containing complex subunit 3
UniRef100_U	3	3	13.80%	297	33814	6	BRCA1/BRCA2-containing complex subunit 3.
UniRef100_U	3	3	12.70%	322	36736	6	BRCA1/BRCA2-containing complex subunit 3.
UniRef100_Q	3	3	14.10%	291	33150	6	Novel protein
UniRef100_Q	2	2	13.00%	177	20848	9	CCDC25 protein
UniRef100_Q	2	2	11.10%	208	24479	7	Coiled-coil domain-containing protein 25
UniRef100_Q	3	4	13.00%	162	18410	8	Riboflavin kinase
UniRef100_U	3	4	13.00%	162	18392	8	Riboflavin kinase (EC 2.7.1.26) (ATP:riboflavin 5'-phosphotransferase) (Flavokinase).
UniRef100_Q	2	3	13.00%	146	16634	5	Zinc finger and BTB domain containing 8 opposite strand
UniRef100_U	2	3	17.00%	112	13075	5	UPI0000D612C8 UniRef100 entry
UniRef100_U	2	3	14.00%	136	15579	5	PREDICTED: similar to zinc finger and BTB domain containing 8 opposite strand
UniRef100_Q	2	3	10.60%	179	20675	5	Zinc finger and BTB domain-containing opposite strand protein 8
UniRef100_Q	49	98	12.90%	5183	6E+05	6	Zinc finger UBR1-type protein 1
UniRef100_Q	20	63	12.90%	1912	2E+05	6	Chromodomain helicase-DNA-binding protein 4
UniRef100_U	20	63	12.70%	1940	2E+05	6	Chromodomain helicase-DNA-binding protein 4 (EC 3.6.1.-) (ATP- dependent helicase CHD4) (CHD-4) (Mi-2 autoantigen 218 kDa protein) (Mi2-beta).
UniRef100_U	20	63	12.90%	1912	2E+05	6	chromodomain helicase DNA binding protein 4
UniRef100_Q	20	63	12.70%	1940	2E+05	6	Isoform 2 of Q14839
UniRef100_A	5	6	12.90%	595	68114	7	Guanylate binding protein 3
UniRef100_U	5	6	13.70%	563	64167	6	Guanylate-binding protein 3 (GTP-binding protein 3) (Guanine nucleotide-binding protein 3) (GBP-3).
UniRef100_Q	5	6	13.70%	563	64180	6	Guanylate-binding protein 3
UniRef100_Q	2	2	12.90%	287	33245	8	CCNY protein
UniRef100_Q	2	2	11.70%	316	36504	8	Isoform 2 of Q8ND76
UniRef100_Q	2	2	10.90%	341	39337	7	Cyclin fold protein 1
UniRef100_Q	2	2	10.90%	341	39403	7	Cyclin Y
UniRef100_Q	2	5	12.90%	194	21569	7	Ras-related protein Rab-31
UniRef100_U	2	5	12.80%	195	21700	7	RAB31, member RAS oncogene family
UniRef100_Q	2	5	12.80%	195	21686	7	RAB31, member RAS oncogene family variant
UniRef100_Q	18	20	12.80%	1796	2E+05	5	Collagen alpha-1(XIV) chain precursor
UniRef100_Q	18	20	12.90%	1780	2E+05	5	Isoform 2 of Q05707
UniRef100_Q	10	10	12.80%	975	1E+05	6	E3 ubiquitin-protein ligase BRE1A
UniRef100_U	10	10	12.80%	977	1E+05	6	Ubiquitin-protein ligase BRE1A (EC 6.3.2.-) (BRE1-A) (hBRE1) (RING finger protein 20).
UniRef100_P	10	14	12.80%	935	1E+05	7	C-1-tetrahydrofolate synthase, cytoplasmic (C1-THF synthase) [Includes: Methylenetetrahydrofolate dehydrogenase (EC 1.5.1.5); Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9); Formyltetrahydrofolate synthetase (EC 6.3.4.3)]
UniRef100_U	10	14	12.80%	935	1E+05	7	methylenetetrahydrofolate dehydrogenase 1

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_U	10	14	12.80%	935	1E+05	7	C-1-tetrahydrofolate synthase, cytoplasmic (C1-THF synthase) [Includes: Methylenetetrahydrofolate dehydrogenase (EC 1.5.1.5); Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9); Formyltetrahydrofolate synthetase (EC 6.3.4.3)].
UniRef100_P	6	16	12.80%	687	77329	5	Protein-glutamine gamma-glutamyltransferase 2 (EC 2.3.2.13) (Tissue transglutaminase) (TGase C) (TGC) (TG(C))
UniRef100_P	9	58	12.80%	643	71028	6	Heat shock 70 kDa protein 6
UniRef100_Q	9	58	12.80%	643	71004	6	Heat shock 70kDa protein 6 (HSP70B') variant
UniRef100_Q	4	6	12.80%	602	69992	8	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform
UniRef100_Q	4	6	13.50%	570	66181	8	Isoform Delta
UniRef100_O	4	7	12.80%	475	51841	8	U3 small nucleolar RNA-interacting protein 2
UniRef100_P	4	4	12.80%	398	43920	9	Beta-1,4-galactosyltransferase 1 (EC 2.4.1.-) (Beta-1,4-GalTase 1) (Beta4Gal-T1) (b4Gal-T1) (UDP-galactose:beta-N-acetylglucosamine beta- 1,4-galactosyltransferase 1) (UDP-Gal:beta-GlcNAc beta-1,4- galactosyltransferase 1) [Includes: Lactose synthase A protein (EC 2.4.1.22); N-acetyllactosamine synthase (EC 2.4.1.90) (Nal synthetase); Beta-N-acetylglucosaminylglycopeptide beta-1,4- galactosyltransferase (EC 2.4.1.38); Beta-N-acetylglucosaminyl- glycolipid beta-1,4-galactosyltransferase (EC 2.4.1.-)]
UniRef100_Q	2	5	12.80%	312	34734	#	PPP1R10 protein
UniRef100_Q	2	5	4.30%	940	99058	9	Serine/threonine-protein phosphatase 1 regulatory subunit 10
UniRef100_Q	9	59	12.70%	535	57810	7	Keratin 6L
UniRef100_Q	9	59	12.70%	535	57836	7	Keratin 6L
UniRef100_Q	9	59	12.70%	535	57776	7	Keratin 6L
UniRef100_P	3	4	12.70%	220	23292	8	Claudin-6
UniRef100_U	3	4	12.70%	220	23278	8	claudin 6
UniRef100_Q	8	23	12.60%	506	56921	5	CDK5 regulatory subunit-associated protein 3
UniRef100_U	8	23	12.60%	507	56947	5	CDK5 regulatory subunit-associated protein 3 (CDK5 activator-binding protein C53) (HSF-27 protein).
UniRef100_Q	4	4	12.60%	476	55172	6	Vacuolar proton pump subunit SFD alpha isoform
UniRef100_Q	4	4	12.90%	465	54151	7	Isoform 2 of Q9UI12
UniRef100_Q	4	4	12.40%	483	55883	7	Vacuolar ATP synthase subunit H
UniRef100_P	3	4	12.60%	293	33310	7	Caspase-6 precursor (EC 3.4.22.59) (CASP-6) (Apoptotic protease Mch-2) [Contains: Caspase-6 subunit p18; Caspase-6 subunit p11]
UniRef100_P	2	2	12.60%	231	25953	6	Ribosyldihydronicotinamide dehydrogenase [quinone]
UniRef100_Q	2	2	15.00%	193	21537	7	NAD(P)H dehydrogenase, quinone 2
UniRef100_Q	2	2	12.60%	231	25919	6	NAD(P)H dehydrogenase, quinone 2
UniRef100_Q	11	17	12.50%	1176	1E+05	7	Leucyl-tRNA synthetase, cytoplasmic
UniRef100_Q	4	7	12.50%	368	40781	6	Serine/threonine kinase 24
UniRef100_Q	4	7	10.40%	443	49308	6	Serine/threonine-protein kinase 24
UniRef100_Q	4	7	10.70%	431	47941	5	Serine/threonine kinase 24
UniRef100_Q	4	7	10.70%	431	47913	5	Serine/threonine kinase 24
UniRef100_O	3	3	12.50%	313	34063	5	Small glutamine-rich tetratricopeptide repeat-containing protein A
UniRef100_Q	2	5	12.50%	287	32448	9	Kinesin family member 2C

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_UI	2	5	5.00%	725	81313	8	kinesin family member 2C
UniRef100_Q	2	5	5.00%	725	81313	8	Kinesin-like protein KIF2C
UniRef100_Q	2	5	10.70%	336	37922	9	Kinesin family member 2C
UniRef100_P	23	36	12.40%	2137	2E+05	5	Spectrin beta chain, erythrocyte
UniRef100_UI	23	36	11.40%	2332	3E+05	5	Spectrin beta chain, erythrocyte (Beta-I spectrin).
UniRef100_UI	23	36	12.40%	2137	2E+05	5	spectrin beta isoform b
UniRef100_Q	23	36	11.40%	2332	3E+05	5	Spectrin, beta, erythrocytic (Includes spherocytosis, clinical type I) variant
UniRef100_P	23	36	11.40%	2328	3E+05	5	Isoform 2 of P11277
UniRef100_Q	7	10	12.40%	580	65697	6	Negative elongation factor B
UniRef100_P	3	3	12.40%	427	48542	8	Kallistatin precursor
UniRef100_Q	2	4	12.40%	194	21855	8	Ras-related protein Rab-22A
UniRef100_P	8	20	12.30%	1023	1E+05	6	Sodium/potassium-transporting ATPase alpha-1 chain precursor (EC 3.6.3.9) (Sodium pump 1) (Na(+)/K(+) ATPase 1)
UniRef100_Q	5	7	12.30%	673	71713	7	Vasorin precursor
UniRef100_UI	5	7	13.70%	608	64060	7	Vasorin precursor (Protein Slit-like 2).
UniRef100_P	3	3	12.30%	235	26458	6	N-terminal acetyltransferase complex ARD1 subunit homolog A
UniRef100_Q	15	39	12.20%	1600	2E+05	5	Eukaryotic translation initiation factor 4 gamma 1
UniRef100_UI	15	39	12.00%	1624	2E+05	5	Eukaryotic translation initiation factor 4 gamma 1 (eIF-4-gamma 1) (eIF-4G1) (eIF-4G 1) (p220).
UniRef100_UI	15	39	12.90%	1512	2E+05	5	Eukaryotic translation initiation factor 4 gamma 1 (eIF-4-gamma 1) (eIF-4G1) (eIF-4G 1) (p220).
UniRef100_UI	15	39	12.20%	1599	2E+05	5	Eukaryotic translation initiation factor 4 gamma 1 (eIF-4-gamma 1) (eIF-4G1) (eIF-4G 1) (p220).
UniRef100_UI	15	39	12.90%	1512	2E+05	5	eukaryotic translation initiation factor 4 gamma, 1 isoform 2
UniRef100_UI	15	39	13.60%	1435	2E+05	5	eukaryotic translation initiation factor 4 gamma, 1 isoform 3
UniRef100_UI	15	39	12.20%	1599	2E+05	5	eukaryotic translation initiation factor 4 gamma, 1 isoform 1
UniRef100_UI	15	39	13.90%	1403	2E+05	5	eukaryotic translation initiation factor 4 gamma, 1 isoform 4
UniRef100_UI	15	39	12.20%	1600	2E+05	5	Eukaryotic translation initiation factor 4 gamma 1 (eIF-4-gamma 1) (eIF-4G1) (eIF-4G 1) (p220).
UniRef100_Q	15	39	12.00%	1624	2E+05	5	EIF4G1 variant protein
UniRef100_Q	15	39	13.90%	1404	2E+05	5	Isoform E of Q04637
UniRef100_Q	15	39	13.60%	1436	2E+05	5	Isoform D of Q04637
UniRef100_Q	15	39	12.90%	1513	2E+05	5	Isoform C of Q04637
UniRef100_Q	15	39	12.50%	1560	2E+05	5	Isoform B of Q04637
UniRef100_P	7	10	12.20%	707	78427	6	Matrix metalloproteinase-9 precursor (EC 3.4.24.35) (MMP-9) (92 kDa type IV collagenase) (92 kDa gelatinase) (Gelatinase B) (GELB) [Contains: 67 kDa matrix metalloproteinase-9; 82 kDa matrix metalloproteinase-9]
UniRef100_Q	6	10	12.20%	681	75585	7	RNA-binding protein 35A
UniRef100_UI	6	10	16.10%	517	57696	7	RNA-binding protein 35A (RNA-binding motif protein 35A).
UniRef100_UI	6	10	12.30%	677	75084	7	RNA binding motif protein 35A isoform 2
UniRef100_Q	6	10	12.50%	663	73574	7	Isoform 4 of Q6NXG1

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	6	10	12.30%	677	75144	7	Isoform 3 of Q6NXG1
UniRef100_Q	6	10	13.70%	608	67665	7	Isoform 2 of Q6NXG1
UniRef100_O	4	9	12.20%	624	70833	7	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthetase 1 (PAPS synthetase 1) (PAPSS 1) (Sulfurylase kinase 1) (SK1) (SK 1) [Includes: Sulfate adenylyltransferase (EC 2.7.7.4) (Sulfate adenylate transferase) (SAT) (ATP-sulfurylase); Adenylyl-sulfate kinase (EC 2.7.1.25) (Adenylylsulfate 3'-phosphotransferase) (APS kinase) (Adenosine-5'-phosphosulfate 3'-phosphotransferase) (3'- phosphoadenosine-5'-phosphosulfate synthetase)]
UniRef100_Q	4	9	13.30%	571	64507	7	Hypothetical protein
UniRef100_Q	5	9	12.20%	534	60627	7	EH domain-containing protein 1
UniRef100_O	8	66	12.20%	551	59504	8	Keratin-75
UniRef100_U	8	66	12.20%	551	59560	8	cytokeratin type II
UniRef100_Q	8	66	12.20%	551	59530	8	Cytokeratin
UniRef100_P	2	2	12.20%	245	25774	8	Complement C1q subcomponent subunit C precursor
UniRef100_Q	2	2	12.20%	188	22079	5	Isoform 3 of Q9NZI2
UniRef100_Q	26	47	12.10%	2547	3E+05	6	Probable ubiquitin carboxyl-terminal hydrolase FAF-X
UniRef100_U	26	47	12.10%	2563	3E+05	6	Probable ubiquitin carboxyl-terminal hydrolase FAF-X (EC 3.1.2.15) (Ubiquitin thioesterase FAF-X) (Ubiquitin-specific-processing protease FAF-X) (Deubiquitinating enzyme FAF-X) (Fat facets protein-related, X- linked) (Ubiquitin-specific protease 9, X chro
UniRef100_U	26	47	12.10%	2564	3E+05	6	Probable ubiquitin carboxyl-terminal hydrolase FAF-X (EC 3.1.2.15) (Ubiquitin thioesterase FAF-X) (Ubiquitin-specific-processing protease FAF-X) (Deubiquitinating enzyme FAF-X) (Fat facets protein-related, X- linked) (Ubiquitin-specific protease 9, X chro
UniRef100_U	26	47	12.10%	2554	3E+05	6	ubiquitin specific protease 9, X-linked isoform 4
UniRef100_U	26	47	12.00%	2570	3E+05	6	ubiquitin specific protease 9, X-linked isoform 3
UniRef100_Q	26	47	12.10%	2563	3E+05	6	Isoform Long of Q93008
UniRef100_Q	18	36	12.10%	1972	2E+05	5	Tumor suppressor p53-binding protein 1
UniRef100_U	18	36	12.40%	1922	2E+05	5	Tumor suppressor p53-binding protein 1 (p53-binding protein 1) (p53BP1) (53BP1).
UniRef100_P	9	12	12.10%	963	1E+05	7	Kinesin heavy chain
UniRef100_U	9	12	12.10%	963	1E+05	7	Kinesin heavy chain (Ubiquitous kinesin heavy chain) (UKHC).
UniRef100_O	3	3	12.10%	380	41796	9	Cytosolic acyl coenzyme A thioester hydrolase
UniRef100_O	3	3	14.00%	329	36568	8	Isoform 6 of O00154
UniRef100_O	3	3	13.60%	338	37420	7	Isoform 4 of O00154
UniRef100_O	3	4	12.10%	297	33010	8	Down syndrome critical region protein 3
UniRef100_P	2	2	12.10%	256	27693	8	Thioredoxin-dependent peroxide reductase, mitochondrial precursor
UniRef100_U	2	2	13.00%	238	25889	8	Thioredoxin-dependent peroxide reductase, mitochondrial precursor (EC 1.11.1.15) (Peroxiredoxin-3) (PRX III) (Antioxidant protein 1) (AOP-1) (Protein MER5 homolog) (HBC189).
UniRef100_U	2	2	13.00%	238	25839	8	peroxiredoxin 3 isoform b
UniRef100_Q	2	2	12.10%	256	27625	8	Peroxiredoxin 3 isoform a variant
UniRef100_Q	14	15	12.00%	1354	2E+05	6	Rho-associated protein kinase 1
UniRef100_U	14	15	12.00%	1354	2E+05	6	Rho-associated protein kinase 1 (EC 2.7.11.1) (Rho-associated, coiled- coil-containing protein kinase 1) (p160 ROCK-1) (p160ROCK) (Renal carcinoma antigen NY-REN-35).

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P	9	17	12.00%	952	1E+05	6	Lysosomal alpha-glucosidase precursor (EC 3.2.1.20) (Acid maltase) (Aglucosidase alfa) [Contains: 76 kDa lysosomal alpha-glucosidase; 70 kDa lysosomal alpha-glucosidase]
UniRef100_Q	3	4	12.00%	499	55456	6	U4/U6 small nuclear ribonucleoprotein Prp31
UniRef100_U	3	4	12.00%	499	55442	6	pre-mRNA processing factor 31 homolog
UniRef100_P	3	4	12.00%	359	40569	5	Tropomodulin-1
UniRef100_Q	3	4	18.50%	232	26014	9	Tropomodulin 1
UniRef100_P	2	3	12.00%	249	28380	9	Transcription initiation factor IIF subunit beta
UniRef100_Q	7	10	11.90%	670	75407	#	ATP-dependent RNA helicase DDX18
UniRef100_P	2	2	11.90%	218	25675	7	Glutathione S-transferase Mu 5
UniRef100_O	2	16	11.90%	219	24267	5	Ras-related protein Rab-3D
UniRef100_A	3	5	11.90%	201	23072	#	Ribosomal protein L10
UniRef100_U	3	5	17.40%	138	15774	#	PREDICTED: similar to ribosomal protein L10
UniRef100_U	3	5	10.20%	235	25211	#	PREDICTED: similar to ribosomal protein L10
UniRef100_U	3	5	11.20%	214	24627	#	PREDICTED: similar to ribosomal protein L10 isoform 1
UniRef100_Q	3	5	11.20%	214	24604	#	60S ribosomal protein L10
UniRef100_Q	3	5	10.40%	230	26593	#	Ribosomal protein L10
UniRef100_Q	3	5	11.20%	214	24543	#	Ribosomal protein L10 variant
UniRef100_P	3	5	11.20%	214	24577	#	60S ribosomal protein L10
UniRef100_P	2	3	11.90%	194	20863	#	Histone H1.0 (Histone H1(0))
UniRef100_P	5	7	11.80%	536	59835	7	Proto-oncogene tyrosine-protein kinase Src
UniRef100_Q	5	7	25.10%	251	28721	6	CDNA FLJ14219 fis, clone NT2RP3003800, highly similar to Rattus norvegicus tyrosine protein kinase pp60-c-src mRNA
UniRef100_Q	5	7	11.60%	542	60589	8	V-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog
UniRef100_P	3	6	11.80%	340	38044	9	DnaJ homolog subfamily B member 1
UniRef100_Q	3	6	11.80%	340	38010	9	DNAJB1 protein
UniRef100_Q	3	19	11.80%	272	31264	#	Splicing factor, arginine/serine-rich 5
UniRef100_Q	3	19	9.80%	326	37254	#	CS0DF038YO05 variant
UniRef100_Q	3	6	11.80%	237	26833	7	Oligoribonuclease, mitochondrial precursor
UniRef100_U	3	6	11.80%	237	26861	7	small fragment nuclease
UniRef100_Q	16	30	11.70%	1621	2E+05	4	Nestin
UniRef100_P	5	6	11.70%	592	67568	5	Calnexin precursor
UniRef100_P	4	6	11.70%	435	49967	6	Tyrosine-protein phosphatase non-receptor type 1
UniRef100_P	22	28	11.60%	2491	3E+05	6	Cation-independent mannose-6-phosphate receptor precursor
UniRef100_U	22	28	11.60%	2491	3E+05	6	Cation-independent mannose-6-phosphate receptor precursor (CI Man-6-P receptor) (CI-MPR) (M6PR) (Insulin-like growth factor 2 receptor) (Insulin-like growth factor II receptor) (IGF-II receptor) (M6P/IGF2 receptor) (M6P/IGF2R) (300 kDa mannose 6-phosphate
UniRef100_Q	16	32	11.60%	1821	2E+05	5	Latent-transforming growth factor beta-binding protein 2 precursor
UniRef100_U	16	32	11.60%	1821	2E+05	5	latent transforming growth factor beta binding protein 2
UniRef100_Q	16	32	11.60%	1821	2E+05	5	Latent transforming growth factor beta binding protein 2
UniRef100_Q	5	30	11.60%	551	59210	7	Cleavage and polyadenylation specificity factor 6
UniRef100_U	5	30	11.60%	551	59209	7	cleavage and polyadenylation specific factor 6, 68 kD subunit

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	5	30	13.40%	478	52326	6	Isoform 3 of Q16630
UniRef100_Q	5	30	10.90%	588	63471	8	Isoform 2 of Q16630
UniRef100_Q	2	4	11.60%	249	26525	#	Chromosome 1 open reading frame 77
UniRef100_UI	2	4	13.00%	223	23661	#	Uncharacterized protein C1orf77.
UniRef100_Q	2	4	11.70%	248	26397	#	Uncharacterized protein C1orf77
UniRef100_Q	2	4	14.40%	202	21918	#	Chromosome 1 open reading frame 77
UniRef100_Q	2	3	11.60%	207	22913	7	Ubiquitin-conjugating enzyme E2 E3
UniRef100_UI	20	39	11.50%	2454	3E+05	6	PREDICTED: similar to Ubiquitin carboxyl-terminal hydrolase 24 (Ubiquitin thioesterase 24) (Ubiquitin-specific-processing protease 24) (Deubiquitinating enzyme 24) isoform 5
UniRef100_Q	4	7	11.50%	522	59070	5	Sorting nexin-1
UniRef100_UI	4	7	13.00%	460	52225	6	Sorting nexin-1.
UniRef100_UI	4	7	12.70%	473	53189	5	Sorting nexin-1.
UniRef100_UI	4	7	11.50%	521	58955	5	Sorting nexin-1.
UniRef100_UI	4	7	12.70%	474	53304	5	sorting nexin 1 isoform c
UniRef100_Q	4	7	13.90%	432	50099	7	Sorting nexin 1 isoform a variant
UniRef100_Q	4	7	11.50%	522	59012	5	Sorting nexin 1 isoform a variant
UniRef100_Q	4	7	13.10%	457	51813	6	Isoform 1A of Q13596
UniRef100_Q	5	6	11.50%	521	58688	6	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform
UniRef100_Q	5	6	11.70%	511	57659	6	Serine/threonine protein phosphatase
UniRef100_Q	3	4	11.50%	243	26224	8	Collagen triple helix repeat-containing protein 1 precursor
UniRef100_UI	3	4	12.20%	229	24770	8	Collagen triple helix repeat-containing protein 1 precursor (NMTC1 protein).
UniRef100_Q	2	5	11.50%	183	20745	5	Ras-related protein Rap-2c precursor
UniRef100_Q	9	10	11.40%	1159	1E+05	7	Uncharacterized protein KIAA0196
UniRef100_UI	9	10	11.40%	1161	1E+05	7	KIAA0196 (KIAA0196), mRNA
UniRef100_P	7	14	11.40%	900	1E+05	6	Methionyl-tRNA synthetase, cytoplasmic
UniRef100_P	3	3	11.40%	368	40968	8	mRNA-associated protein mrnp 41
UniRef100_Q	3	3	11.90%	352	39479	8	Migration-inducing gene 14
UniRef100_Q	2	2	11.40%	297	34499	5	Hypothetical protein DKFZp686M05248
UniRef100_Q	2	2	11.40%	299	34529	5	Isoform 2 of Q7LG56
UniRef100_Q	2	2	9.70%	351	40737	5	Ribonucleoside-diphosphate reductase M2 subunit B
UniRef100_Q	2	2	11.40%	272	28235	6	Exosome component 6
UniRef100_P	14	22	11.30%	1482	2E+05	6	Pregnancy zone protein precursor
UniRef100_UI	14	22	11.30%	1482	2E+05	6	Pregnancy zone protein precursor.
UniRef100_Q	11	20	11.30%	1328	1E+05	9	Myb-binding protein 1A
UniRef100_Q	11	20	11.30%	1332	1E+05	9	Isoform 2 of Q9BQG0
UniRef100_P	5	5	11.30%	538	60249	5	Importin alpha-1 subunit
UniRef100_UI	5	5	13.60%	450	49646	5	IMPORTIN ALPHA-1 SUBUNIT
UniRef100_UI	5	5	11.30%	538	60222	5	Importin alpha-1 subunit (Karyopherin alpha-1 subunit) (SRP1-beta) (RAG cohort protein 2) (Nucleoprotein interactor 1) (NPI-1).
UniRef100_Q	5	5	11.30%	538	60309	5	Karyopherin alpha 1
UniRef100_P	8	12	11.20%	967	1E+05	6	Aminopeptidase N

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_U	8	12	11.20%	967	1E+05	5	membrane alanine aminopeptidase precursor
UniRef100_Q	8	12	11.10%	977	1E+05	6	Membrane alanine aminopeptidase variant
UniRef100_Q	6	14	11.20%	623	69918	6	Xaa-Pro aminopeptidase 1
UniRef100_P	2	2	11.20%	331	37579	7	5'-AMP-activated protein kinase subunit gamma-1
UniRef100_Q	2	2	11.20%	276	31458	9	Cytochrome b5 reductase 2
UniRef100_U	2	2	13.10%	237	27043	8	cytochrome b5 reductase b5R.2
UniRef100_Q	2	2	11.20%	276	31562	9	Cytochrome b5 reductase b5R.2
UniRef100_Q	2	2	11.50%	270	30658	7	Hypothetical protein DKFZp434A149
UniRef100_Q	2	2	13.10%	237	27044	8	CYB5R2 protein
UniRef100_Q	2	4	11.20%	242	26930	7	COMMD7 protein
UniRef100_U	2	4	13.50%	200	22600	7	COMM domain containing 7
UniRef100_Q	2	4	13.50%	200	22540	6	COMM domain-containing protein 7
UniRef100_O	14	32	11.10%	1756	2E+05	6	Periplakin
UniRef100_U	14	32	11.10%	1756	2E+05	6	periplakin
UniRef100_U	14	32	11.10%	1756	2E+05	6	Periplakin (195 kDa cornified envelope precursor protein) (190 kDa paraneoplastic pemphigus antigen).
UniRef100_Q	14	32	11.10%	1756	2E+05	6	Periplakin
UniRef100_Q	5	8	11.10%	540	56528	6	Mitochondrial antiviral-signaling protein
UniRef100_U	5	8	14.90%	403	42827	7	Mitochondrial antiviral-signaling protein (Interferon-beta promoter stimulator protein 1) (IPS-1) (Virus-induced-signaling adapter) (CARD adapter inducing interferon-beta) (Cardif) (Putative NF-kappa-B- activating protein 031N).
UniRef100_Q	5	12	11.10%	422	48177	7	Keratin 23
UniRef100_Q	5	12	11.10%	422	48131	7	Keratin, type I cytoskeletal 23
UniRef100_P	3	3	11.10%	423	46656	6	Mannose-6-phosphate isomerase
UniRef100_P	3	3	13.00%	362	39834	5	Isoform 2 of P34949
UniRef100_P	4	6	11.10%	379	44409	5	Protein farnesyltransferase/geranylgeranyltransferase type I alpha subunit
UniRef100_U	4	6	13.50%	312	36493	5	farnesyltransferase, CAAX box, alpha isoform c
UniRef100_U	4	6	14.60%	288	34729	6	farnesyltransferase, CAAX box, alpha isoform b
UniRef100_Q	2	2	11.10%	180	19761	7	Coiled-coil domain-containing protein 115
UniRef100_P	4	4	11.00%	499	56879	6	Serine/threonine-protein phosphatase 5
UniRef100_Q	4	4	11.40%	484	55096	6	PPP5C protein
UniRef100_Q	4	6	11.00%	447	49824	9	CDNA FLJ90138 fis, clone HEMBB1000905, weakly similar to TRANSCRIPTIONAL REPRESSOR RCO-1
UniRef100_Q	4	6	11.00%	447	49798	9	Transducin beta-like 2 protein
UniRef100_P	3	3	11.00%	400	46059	8	2'-5'-oligoadenylate synthetase 1 (EC 2.7.7.-) ((2-5')oligo(A) synthetase 1)
UniRef100_U	3	3	11.50%	381	43747	9	2',5'-oligoadenylate synthetase 1 isoform 3
UniRef100_U	3	3	9.60%	459	52042	9	2',5'-oligoadenylate synthetase 1 isoform 3
UniRef100_U	3	3	10.60%	414	47408	9	2''",5''"-oligoadenylate synthetase 1 isoform 3
UniRef100_U	3	3	11.00%	400	46029	8	2''",5''"-oligoadenylate synthetase 1 isoform 1
UniRef100_Q	3	3	12.10%	364	41740	9	2',5'-oligoadenylate synthetase 1, 40/46kDa
UniRef100_Q	3	3	12.10%	364	41701	9	2',5'-oligoadenylate synthetase 1, 40/46kDa

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	3	3	11.50%	382	43944	9	2'-5' oligoadenylate synthetase OAS1p44
UniRef100_Q	3	3	12.10%	364	41770	9	2',5'-oligoadenylate synthetase 1, 40/46kDa
UniRef100_Q	3	3	11.90%	371	42464	9	2',5'-oligoadenylate synthetase 1, isoform E16 variant
UniRef100_Q	3	3	9.60%	459	52166	9	2'-5' oligoadenylate synthetase 1 p52 isoform
UniRef100_Q	3	3	10.60%	414	47537	9	2'-5' oligoadenylate synthetase 1 p48 isoform
UniRef100_Q	3	3	11.00%	400	46004	8	2'-5' oligoadenylate synthetase
UniRef100_Q	2	2	11.00%	154	18280	7	AP-1 complex subunit sigma-3
UniRef100_U	2	2	11.00%	154	18477	6	adaptor-related protein complex 1, sigma 3 subunit
UniRef100_Q	2	2	16.30%	104	12655	#	Isoform 3 of Q96PC3
UniRef100_Q	2	2	10.40%	164	19445	8	Isoform 2 of Q96PC3
UniRef100_P	10	29	10.90%	744	82560	7	Vesicle-fusing ATPase
UniRef100_U	10	29	11.00%	739	82092	7	Vesicle-fusing ATPase (EC 3.6.4.6) (Vesicular-fusion protein NSF) (N- ethylmaleimide sensitive fusion protein) (NEM-sensitive fusion protein).
UniRef100_O	2	3	10.90%	313	34404	8	Interferon-inducible double stranded RNA-dependent protein kinase activator A
UniRef100_O	2	3	11.30%	302	33123	8	Isoform 2 of O75569
UniRef100_P	26	39	10.80%	2863	3E+05	6	Lipopolysaccharide-responsive and beige-like anchor protein
UniRef100_U	26	39	10.80%	2863	3E+05	6	Lipopolysaccharide-responsive and beige-like anchor protein (CDC4-like protein) (Beige-like protein).
UniRef100_U	26	39	10.80%	2863	3E+05	6	Lipopolysaccharide-responsive and beige-like anchor protein (CDC4-like protein) (Beige-like protein).
UniRef100_Q	26	38	10.80%	2851	3E+05	6	Beige-like protein
UniRef100_Q	11	14	10.80%	1589	2E+05	8	Sterile alpha motif domain-containing protein 9
UniRef100_Q	7	11	10.80%	944	1E+05	6	UNC45 homolog A
UniRef100_Q	7	11	11.00%	929	1E+05	6	Isoform 2 of Q9H3U1
UniRef100_O	4	14	10.80%	527	58022	6	Serine/threonine-protein kinase OSR1
UniRef100_Q	2	2	10.80%	277	30720	9	Lysophospholipase-like protein
UniRef100_U	2	2	9.60%	313	34305	7	Monoglyceride lipase (EC 3.1.1.23) (MGL) (HU-K5) (Lysophospholipase homolog) (Lysophospholipase-like).
UniRef100_Q	2	2	9.90%	303	33261	7	Monoglyceride lipase
UniRef100_P	2	16	10.80%	203	22774	9	Ras-related protein Rab-13
UniRef100_U	2	16	10.80%	203	22745	9	UPI0000D62205 UniRef100 entry
UniRef100_O	19	21	10.70%	2243	3E+05	7	DnaJ homolog subfamily C member 13
UniRef100_Q	19	21	10.70%	2243	3E+05	7	DnaJ domain-containing protein RME-8
UniRef100_O	4	6	10.70%	522	58449	7	U4/U6 small nuclear ribonucleoprotein Prp4
UniRef100_Q	4	6	10.70%	521	58307	7	PRPF4 protein
UniRef100_Q	4	6	10.70%	521	58321	7	PRP4 pre-mRNA processing factor 4 homolog
UniRef100_Q	4	6	10.40%	537	60022	8	PRPF4 protein variant
UniRef100_A	4	7	10.70%	366	40991	6	MHC class I antigen
UniRef100_O	3	3	10.70%	338	40042	#	P40
UniRef100_U	3	3	10.70%	338	39947	9	P40
UniRef100_U	3	3	10.70%	338	40040	#	UPI000013F1EA UniRef100 entry

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_UI	3	3	10.70%	338	39996	9	P40
UniRef100_Q	3	3	10.70%	338	40056	#	Hypothetical protein ORF1
UniRef100_Q	3	3	10.70%	338	40060	9	Hypothetical protein
UniRef100_Q	3	3	10.70%	338	40086	#	Hypothetical protein
UniRef100_Q	3	3	10.70%	338	40084	#	ORF1 codes for a 40 kDa product
UniRef100_O	3	3	10.70%	338	40054	#	P40
UniRef100_O	3	3	10.70%	338	39982	9	P40
UniRef100_O	3	3	10.70%	338	40056	#	P40
UniRef100_O	3	3	10.70%	338	39982	#	P40
UniRef100_O	3	3	10.70%	338	40028	#	P40
UniRef100_O	3	3	10.70%	338	39947	9	P40
UniRef100_O	3	3	10.70%	338	40098	9	P40
UniRef100_O	3	5	10.70%	335	37432	5	Thioredoxin-like protein 2
UniRef100_Q	2	2	10.70%	308	33850	7	SVH-B
UniRef100_Q	2	2	10.70%	308	33840	7	ARMC10 protein
UniRef100_Q	2	2	9.60%	343	37540	7	CDNA PSEC0198 fis, clone HEMBA1001552, highly similar to SVH protein
UniRef100_Q	2	2	13.30%	249	27390	8	SVH-D
UniRef100_Q	2	2	11.60%	284	31080	7	SVH-C
UniRef100_Q	2	2	10.70%	243	27939	4	RWD domain-containing protein 1
UniRef100_Q	2	2	10.70%	233	26057	5	UPF0368 protein Cxorf26
UniRef100_Q	2	2	10.70%	224	25320	8	HCCA3 protein
UniRef100_Q	2	2	9.40%	256	28616	8	HDCMC29P
UniRef100_Q	2	2	9.10%	264	29396	7	Tumor necrosis factor superfamily, member 5-induced protein 1
UniRef100_Q	6	7	10.60%	650	73954	5	FAS-associated factor 1
UniRef100_Q	2	2	10.60%	454	51103	6	Uncharacterized protein C1orf27
UniRef100_UI	2	2	10.50%	456	51333	6	Putative LAG1-interacting protein
UniRef100_Q	2	2	14.30%	335	37773	8	CDNA FLJ20505 fis, clone KAT09459
UniRef100_Q	3	3	10.60%	397	45139	6	CLINT
UniRef100_UI	3	3	11.60%	363	41471	7	Beta-parvin (Affixin).
UniRef100_UI	3	3	10.60%	397	45117	6	Beta-parvin (Affixin).
UniRef100_UI	3	3	10.60%	397	45183	6	parvin, beta isoform a
UniRef100_Q	3	3	11.50%	364	41714	7	Beta-parvin
UniRef100_O	3	3	10.60%	341	37646	5	CD2 antigen cytoplasmic tail-binding protein 2
UniRef100_Q	8	11	10.50%	929	1E+05	6	Adipocyte-derived leucine aminopeptidase precursor
UniRef100_UI	8	11	10.40%	941	1E+05	7	type 1 tumor necrosis factor receptor shedding aminopeptidase regulator isoform b
UniRef100_Q	8	11	10.50%	936	1E+05	6	Isoform 2 of Q9NZ08
UniRef100_P	8	14	10.50%	920	1E+05	5	Ubiquitin carboxyl-terminal hydrolase 11
UniRef100_UI	8	14	10.10%	963	1E+05	6	ubiquitin specific protease 11
UniRef100_Q	8	14	10.50%	923	1E+05	5	USP11 protein
UniRef100_O	6	8	10.50%	668	75023	#	Metastasis-associated protein MTA2
UniRef100_Q	6	6	10.50%	561	59220	5	Ubiquilin 1

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	6	6	10.00%	589	62519	5	Ubiquilin-1
UniRef100_P	3	5	10.50%	478	52892	6	Methionine aminopeptidase 2
UniRef100_A	2	3	10.50%	277	31152	9	Chromosome 20 open reading frame 43
UniRef100_U	2	3	10.10%	287	31935	8	Uncharacterized protein C20orf43.
UniRef100_U	2	3	9.50%	306	33887	9	Uncharacterized protein C20orf43.
UniRef100_Q	2	3	10.10%	287	31903	8	Isoform 2 of Q9BY42
UniRef100_Q	2	3	9.50%	306	33855	9	Uncharacterized protein C20orf43
UniRef100_Q	2	5	10.50%	181	20874	8	Retinol binding protein 7, cellular
UniRef100_Q	2	5	14.20%	134	15536	8	Retinoid-binding protein 7
UniRef100_Q	2	5	8.40%	225	25846	#	RBP7 protein
UniRef100_A	8	34	10.40%	875	1E+05	6	Arsenate resistance protein ARS2
UniRef100_U	8	34	10.30%	884	1E+05	6	Arsenite-resistance protein 2.
UniRef100_Q	8	34	10.40%	872	1E+05	6	Isoform B of Q9BXP5
UniRef100_Q	8	34	10.40%	876	1E+05	6	Arsenite-resistance protein 2
UniRef100_Q	8	34	11.50%	788	89187	6	Arsenite-resistant protein ASR2
UniRef100_Q	8	34	11.20%	812	92194	6	ARS2 protein
UniRef100_Q	8	34	10.40%	871	1E+05	6	ARS2 protein
UniRef100_A	8	34	11.40%	796	90251	6	Arsenate resistance protein ARS2
UniRef100_Q	4	7	10.40%	644	74404	6	Tubulin--tyrosine ligase-like protein 12
UniRef100_O	6	8	10.40%	608	67455	7	Mitochondrial precursor proteins import receptor
UniRef100_Q	6	8	10.40%	607	67398	7	Translocase of outer mitochondrial membrane 70 homolog A
UniRef100_A	5	9	10.40%	481	53603	6	Nuclear interacting partner of anaplastic lymphoma kinase
UniRef100_U	5	9	11.60%	430	47710	5	Nuclear-interacting partner of ALK (Nuclear-interacting partner of anaplastic lymphoma kinase) (hNIPA) (Zinc finger C3HC-type protein 1).
UniRef100_U	5	9	10.00%	501	55200	6	Nuclear-interacting partner of ALK (Nuclear-interacting partner of anaplastic lymphoma kinase) (hNIPA) (Zinc finger C3HC-type protein 1).
UniRef100_U	5	9	10.40%	480	53498	6	Nuclear-interacting partner of ALK (Nuclear-interacting partner of anaplastic lymphoma kinase) (hNIPA) (Zinc finger C3HC-type protein 1).
UniRef100_Q	5	9	11.60%	431	47771	5	Isoform 3 of Q86WB0
UniRef100_Q	5	9	10.40%	481	53559	6	Isoform 2 of Q86WB0
UniRef100_Q	5	9	10.00%	502	55262	6	Nuclear-interacting partner of ALK
UniRef100_Q	2	4	10.40%	309	35776	7	L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase
UniRef100_Q	3	3	10.40%	269	31431	5	Protein arginine N-methyltransferase 4 variant
UniRef100_U	3	3	8.40%	334	38836	6	Protein arginine N-methyltransferase 8 (EC 2.1.1.-) (Heterogeneous nuclear ribonucleoprotein methyltransferase-like protein 4).
UniRef100_Q	3	3	7.10%	394	45291	7	Protein arginine N-methyltransferase 8
UniRef100_Q	2	3	10.40%	270	30063	8	Uncharacterized protein C12orf5
UniRef100_P	6	13	10.30%	911	1E+05	5	Band 3 anion transport protein
UniRef100_Q	6	13	10.30%	911	1E+05	5	Solute carrier family 4, anion exchanger, member 1
UniRef100_Q	6	13	10.30%	911	1E+05	5	Solute carrier family 4 anion exchanger member 1 variant
UniRef100_Q	4	4	10.30%	715	80489	6	Adseverin

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	4	4	12.80%	580	65357	8	Isoform 2 of Q9Y6U3
UniRef100_Q	2	2	10.30%	418	46982	7	CDNA: FLJ23330 fis, clone HEP12654
UniRef100_Q	2	2	10.30%	418	46939	7	AP-3 complex subunit mu-1
UniRef100_P	3	6	10.30%	407	45836	#	Myeloid cell nuclear differentiation antigen
UniRef100_Q	3	6	13.50%	310	34981	#	Hypothetical protein
UniRef100_Q	6	40	10.30%	406	45518	6	TUBAL3 protein
UniRef100_U	6	40	9.40%	446	49908	6	tubulin, alpha-like 3
UniRef100_Q	6	40	9.40%	446	49909	6	Tubulin alpha chain-like 3
UniRef100_Q	2	2	10.30%	339	37760	8	Hypothetical protein
UniRef100_U	2	2	8.40%	417	46338	7	Actin-related protein 10 (hARP11).
UniRef100_Q	2	2	8.40%	417	46307	7	Actin-related protein 10
UniRef100_Q	2	2	8.40%	417	46207	7	Uncharacterized hypothalamus protein HARP11 variant
UniRef100_Q	2	2	8.40%	417	46308	7	Uncharacterized hypothalamus protein HARP11 variant
UniRef100_Q	2	2	10.30%	329	36568	5	HSPC142 protein
UniRef100_U	2	2	9.20%	369	41362	6	CDNA FLJ20571 fis, clone REC01040 (HSPC142 protein) (Hypothetical protein DKFZp564N2378).
UniRef100_U	2	2	10.30%	329	36427	5	CDNA FLJ20571 fis, clone REC01040 (HSPC142 protein) (Hypothetical protein DKFZp564N2378).
UniRef100_Q	2	2	9.30%	367	41268	5	HSPC142
UniRef100_Q	2	2	10.30%	329	36560	5	CDNA FLJ20571 fis, clone REC01040
UniRef100_Q	2	2	10.30%	330	36247	5	Hypothetical protein DKFZp547P162
UniRef100_Q	2	2	8.10%	419	45899	5	Probable oxidoreductase KIAA1576
UniRef100_A	2	3	10.30%	273	29519	9	Chemokine (C-X-C motif) ligand 16
UniRef100_U	2	3	10.30%	273	29535	9	chemokine (C-X-C motif) ligand 16
UniRef100_Q	2	3	11.00%	254	27607	9	Small inducible cytokine B16 precursor
UniRef100_Q	3	5	10.30%	263	28957	6	Proteasome (Prosome, macropain) inhibitor subunit 1
UniRef100_U	3	5	16.40%	165	18335	6	Proteasome inhibitor PI31 subunit (hPI31).
UniRef100_U	3	5	10.00%	271	29773	6	proteasome inhibitor subunit 1 isoform 1
UniRef100_U	3	5	12.20%	222	24393	#	Proteasome inhibitor PI31 subunit (hPI31).
UniRef100_Q	3	5	10.00%	271	29817	6	Proteasome inhibitor PI31 subunit
UniRef100_Q	2	2	10.30%	213	22487	#	Histone H1x
UniRef100_O	10	10	10.20%	1717	2E+05	7	DNA-directed RNA polymerase I largest subunit
UniRef100_O	5	10	10.20%	683	77529	#	U4/U6 small nuclear ribonucleoprotein Prp3
UniRef100_Q	5	10	10.20%	683	77441	#	PRP3 pre-mRNA processing factor 3 homolog
UniRef100_Q	4	18	10.20%	443	48227	9	KH domain-containing, RNA-binding, signal transduction-associated protein 1
UniRef100_Q	4	18	11.10%	404	44027	7	Isoform 3 of Q07666
UniRef100_Q	2	2	10.20%	285	32815	5	CAF1
UniRef100_U	2	2	11.90%	244	28228	5	CCR4-NOT transcription complex, subunit 7 isoform 2
UniRef100_Q	2	2	10.20%	285	32745	5	CCR4-NOT transcription complex subunit 7
UniRef100_Q	2	2	11.80%	246	28364	5	CNOT7 protein
UniRef100_P	10	21	10.10%	1226	1E+05	9	Double-stranded RNA-specific adenosine deaminase

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	10	21	10.00%	1244	1E+05	9	Adenosine deaminase, RNA-specific isoform ADAR-a variant
UniRef100_P	10	21	10.50%	1181	1E+05	9	Isoform 3 of P55265
UniRef100_P	10	21	10.30%	1200	1E+05	9	Isoform 2 of P55265
UniRef100_Q	7	7	10.10%	895	97581	9	Dystroglycan precursor (Dystrophin-associated glycoprotein 1) [Contains: Alpha-dystroglycan (Alpha-DG); Beta-dystroglycan (Beta- DG)]
UniRef100_U	7	7	10.10%	895	97441	9	Dystroglycan precursor (Dystrophin-associated glycoprotein 1) [Contains: Alpha-dystroglycan (Alpha-DG); Beta-dystroglycan (Beta- DG)].
UniRef100_Q	7	7	10.10%	895	97541	9	Dystroglycan 1
UniRef100_P	4	6	10.10%	386	42961	8	Nucleolysin TIA-1 isoform p40 (RNA-binding protein TIA-1) (p40-TIA-1) [Contains: Nucleolysin TIA-1 isoform p15 (p15-TIA-1)]
UniRef100_U	4	6	10.10%	386	42962	8	TIA1 protein isoform 2
UniRef100_Q	4	6	8.40%	464	51330	8	TIA1 protein variant
UniRef100_Q	4	6	10.10%	386	42963	8	Hypothetical protein TIA1
UniRef100_P	4	6	10.40%	375	41800	8	Isoform Short of P31483
UniRef100_Q	3	5	10.10%	366	40691	6	TFG protein
UniRef100_Q	3	5	9.20%	400	43448	5	TRK-fused gene
UniRef100_Q	3	5	9.20%	400	43434	5	Protein TFG
UniRef100_Q	3	5	4.60%	803	88671	6	TRK-fused gene/anaplastic large cell lymphoma kinase extra long form
UniRef100_Q	3	5	9.30%	396	43006	5	Putative MAPK activating protein
UniRef100_Q	4	4	10.10%	327	36504	5	UPF0363 protein C7orf20
UniRef100_O	2	2	10.10%	258	29662	9	Axonemal dynein light intermediate polypeptide 1
UniRef100_U	2	2	9.30%	280	31848	9	dynein, axonemal, light intermediate chain 1
UniRef100_Q	2	2	9.30%	280	31859	9	Hypothetical protein DKFZp686M1712
UniRef100_P	2	2	10.10%	237	26091	8	Ribose-5-phosphate isomerase
UniRef100_O	2	4	10.10%	198	23003	8	Tumor necrosis factor, alpha-induced protein 8
UniRef100_U	2	4	10.50%	190	22106	9	tumor necrosis factor, alpha-induced protein 8 isoform b
UniRef100_Q	2	4	10.60%	188	21877	9	TNF-induced protein GG2-1
UniRef100_Q	2	4	10.50%	190	22047	9	MDC-3.13 isoform 1
UniRef100_Q	21	68	10.00%	2671	3E+05	7	GCN1-like protein 1
UniRef100_U	21	68	10.00%	2671	3E+05	7	GCN1 general control of amino-acid synthesis 1-like 1
UniRef100_Q	12	27	10.00%	1105	1E+05	6	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1
UniRef100_U	12	27	10.00%	1105	1E+05	6	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin c1
UniRef100_Q	12	27	10.00%	1105	1E+05	6	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1
UniRef100_Q	6	12	10.00%	856	95739	7	Heterogeneous nuclear ribonucleoprotein U-like protein 1
UniRef100_Q	6	12	11.40%	756	84794	9	Isoform 4 of Q9BUJ2
UniRef100_Q	6	12	10.70%	804	90292	7	Isoform 2 of Q9BUJ2
UniRef100_Q	6	21	10.00%	639	68330	9	Splicing factor 1
UniRef100_U	6	21	8.40%	764	80370	9	Splicing factor 1 (Zinc finger protein 162) (Transcription factor ZFM1) (Zinc finger gene in MEN1 locus) (Mammalian branch point-binding protein mBBP) (BBP).

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_U	6	21	10.30%	624	67309	9	Splicing factor 1 (Zinc finger protein 162) (Transcription factor ZFM1) (Zinc finger gene in MEN1 locus) (Mammalian branch point-binding protein mBBP) (BBP).
UniRef100_Q	6	21	11.20%	571	61889	9	Isoform 6 of Q15637
UniRef100_Q	6	21	8.40%	764	80621	#	Isoform 5 of Q15637
UniRef100_Q	6	21	11.70%	548	59712	#	Isoform 4 of Q15637
UniRef100_Q	6	21	10.30%	623	67277	9	Isoform 3 of Q15637
UniRef100_Q	6	21	10.00%	638	68633	9	Isoform 2 of Q15637
UniRef100_Q	7	28	10.00%	578	61802	6	Keratin 77
UniRef100_U	7	28	10.00%	578	61901	6	Keratin, type II cytoskeletal 1b (Keratin-77).
UniRef100_U	7	28	10.00%	578	61801	6	keratin 1B
UniRef100_P	3	3	10.00%	481	53384	7	Lipopolysaccharide-binding protein precursor
UniRef100_Q	3	3	10.10%	477	52934	7	LBP protein
UniRef100_Q	3	5	10.00%	260	28860	7	Hydroxyacylglutathione hydrolase
UniRef100_Q	2	2	10.00%	201	22255	8	Ubiquitin-conjugating enzyme E2 E2
UniRef100_Q	12	22	9.90%	1948	2E+05	7	Receptor-type tyrosine-protein phosphatase S precursor
UniRef100_U	12	22	10.00%	1928	2E+05	7	Receptor-type tyrosine-protein phosphatase S precursor (EC 3.1.3.48) (R-PTP-S) (Protein-tyrosine phosphatase sigma) (R-PTP-sigma).
UniRef100_U	12	22	9.90%	1948	2E+05	7	protein tyrosine phosphatase, receptor type, sigma isoform 1 precursor
UniRef100_U	12	22	9.90%	1939	2E+05	7	Receptor-type tyrosine-protein phosphatase S precursor (EC 3.1.3.48) (R-PTP-S) (Protein-tyrosine phosphatase sigma) (R-PTP-sigma).
UniRef100_U	12	22	9.90%	1948	2E+05	7	Receptor-type tyrosine-protein phosphatase S precursor (EC 3.1.3.48) (R-PTP-S) (Protein-tyrosine phosphatase sigma) (R-PTP-sigma).
UniRef100_U	12	22	10.10%	1910	2E+05	7	protein tyrosine phosphatase, receptor type, sigma isoform 2 precursor
UniRef100_Q	12	22	9.90%	1939	2E+05	7	Isoform PTPS
UniRef100_Q	12	22	10.00%	1928	2E+05	7	Isoform PTPS
UniRef100_Q	12	22	9.90%	1939	2E+05	7	Isoform PTPS
UniRef100_O	5	8	9.90%	786	86489	7	Loss of heterozygosity 11 chromosomal region 2 gene A protein
UniRef100_O	5	8	29.30%	266	29235	5	Isoform 4 of O00534
UniRef100_O	5	8	18.80%	415	45923	5	Isoform 3 of O00534
UniRef100_O	5	8	18.30%	426	47049	5	Isoform 2 of O00534
UniRef100_Q	6	7	9.90%	680	77861	7	Pleckstrin homology domain-containing family C member 1
UniRef100_Q	6	7	10.60%	633	72397	8	Isoform 2 of Q96AC1
UniRef100_P	3	3	9.90%	392	42272	7	Galactokinase
UniRef100_U	3	3	9.70%	402	42804	8	Galactokinase (EC 2.7.1.6) (Galactose kinase).
UniRef100_Q	3	3	9.80%	396	42952	7	CDNA FLJ26554 fis, clone LNF01773, highly similar to Galactokinase
UniRef100_P	2	3	9.90%	212	22763	8	Peptidyl-prolyl cis-trans isomerase C
UniRef100_O	9	21	9.80%	1052	1E+05	8	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5
UniRef100_U	9	21	9.80%	1052	1E+05	8	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin a5
UniRef100_Q	6	12	9.80%	938	1E+05	7	ATP-dependent RNA helicase DDX42
UniRef100_U	6	12	9.80%	938	1E+05	7	DEAD box polypeptide 42 protein

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	6	12	11.20%	819	90068	8	Isoform 2 of Q86XP3
UniRef100_Q	4	7	9.80%	564	62329	7	Bifunctional coenzyme A synthase (CoA synthase) (NBP) (POV-2) [Includes: Phosphopantetheine adenylyltransferase (EC 2.7.7.3) (Pantetheine-phosphate adenylyltransferase) (PPAT) (Dephospho-CoA pyrophosphorylase); Dephospho-CoA kinase (EC 2.7.1.24) (DPCK) (Dephosphocoenzyme A kinase) (DPCOAK)]
UniRef100_P	3	4	9.80%	419	46374	7	Fumarylacetoacetase
UniRef100_P	3	3	9.80%	377	40737	5	26S proteasome non-ATPase regulatory subunit 4
UniRef100_Q	3	3	9.70%	380	41079	5	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 4
UniRef100_Q	3	4	9.80%	287	32408	9	ATAD1 protein
UniRef100_Q	3	4	7.80%	361	40744	7	ATPase family AAA domain-containing protein 1
UniRef100_P	10	21	9.70%	1464	1E+05	6	Collagen alpha-1(I) chain precursor
UniRef100_Q	7	11	9.70%	1007	1E+05	#	Serine/threonine-protein kinase PRP4 homolog
UniRef100_Q	7	11	9.70%	1007	1E+05	#	PRP4 pre-mRNA processing factor 4 homolog B
UniRef100_Q	7	11	9.70%	1007	1E+05	#	PRP4 pre-mRNA processing factor 4 homolog B
UniRef100_Q	4	4	9.70%	627	70730	9	Signal recognition particle 68 kDa protein
UniRef100_U	4	4	10.20%	596	67388	9	Signal recognition particle 68 kDa protein (SRP68).
UniRef100_Q	4	4	10.20%	596	67304	9	Isoform 2 of Q9UHB9
UniRef100_Q	2	2	9.70%	279	31920	9	Nicotinamide nucleotide adenylyltransferase 1 variant
UniRef100_Q	2	2	9.70%	279	31932	9	Nicotinamide mononucleotide adenylyltransferase 1
UniRef100_Q	2	3	9.70%	259	29345	9	Vesicle transport protein USE1
UniRef100_U	2	3	17.10%	146	16509	9	Vesicle transport protein USE1 (USE1-like protein) (Putative MAPK- activating protein PM26) (Protein p31).
UniRef100_U	2	3	9.70%	259	29369	9	Vesicle transport protein USE1 (USE1-like protein) (Putative MAPK- activating protein PM26) (Protein p31).
UniRef100_Q	2	3	18.50%	135	15063	8	Isoform 3 of Q9NZ43
UniRef100_Q	2	3	17.10%	146	16511	9	Isoform 2 of Q9NZ43
UniRef100_P	14	42	9.60%	2035	2E+05	8	Host cell factor (HCF) (HCF-1) (C1 factor) (VP16 accessory protein) (VCAF) (CFF) [Contains: HCF N-terminal chain 1; HCF N-terminal chain 2; HCF N-terminal chain 3; HCF N-terminal chain 4; HCF N-terminal chain 5; HCF N-terminal chain 6; HCF C-terminal chain 1; HCF C- terminal chain 2; HCF C-terminal chain 3; HCF C-terminal chain 4; HCF C-terminal chain 5; HCF C-terminal chain 6]
UniRef100_U	14	42	9.90%	1966	2E+05	8	Host cell factor (HCF) (HCF-1) (C1 factor) (VP16 accessory protein) (VCAF) (CFF) [Contains: HCF N-terminal chain 1; HCF N-terminal chain 2; HCF N-terminal chain 3; HCF N-terminal chain 4; HCF N-terminal chain 5; HCF N-terminal chain 6; HCF C-terminal chai
UniRef100_U	14	42	9.60%	2035	2E+05	8	host cell factor 1
UniRef100_P	14	42	9.90%	1966	2E+05	8	Isoform 2 of P51610
UniRef100_Q	9	16	9.60%	1804	2E+05	5	KIAA1327 protein
UniRef100_Q	8	9	9.60%	1130	1E+05	4	Proline-, glutamic acid- and leucine-rich protein 1
UniRef100_U	8	9	10.40%	1042	1E+05	4	PELP1_HUMAN Isoform 2 of Q8IZL8 - Homo sapiens (Human)
UniRef100_U	8	9	8.50%	1272	1E+05	4	PELP1_HUMAN Isoform 2 of Q8IZL8 - Homo sapiens (Human)
UniRef100_U	8	9	9.60%	1130	1E+05	4	proline-, glutamic acid-, leucine-rich protein 1

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	8	9	8.50%	1275	1E+05	4	Isoform 2 of Q8IZL8
UniRef100_P	5	5	9.60%	753	84152	6	Neuroendocrine convertase 1 precursor
UniRef100_P	5	8	9.60%	688	76685	5	Complement C1s subcomponent precursor (EC 3.4.21.42) (C1 esterase) [Contains: Complement C1s subcomponent heavy chain; Complement C1s subcomponent light chain]
UniRef100_Q	3	4	9.60%	499	56369	7	Calcium/calmodulin-dependent protein kinase type II delta chain
UniRef100_Q	3	4	10.00%	478	54128	7	Isoform Delta 6 of Q13557
UniRef100_Q	3	4	9.40%	512	57773	7	Isoform Delta 9 of Q13557
UniRef100_Q	3	4	9.60%	498	56298	7	Isoform Delta 11 of Q13557
UniRef100_Q	4	14	9.60%	471	52050	8	Cleavage and polyadenylation specificity factor 7
UniRef100_Q	4	14	9.70%	462	51096	8	Isoform 2 of Q8N684
UniRef100_Q	4	5	9.60%	457	49845	8	PDZ and LIM domain protein 7
UniRef100_O	8	8	9.50%	1197	1E+05	9	Structural maintenance of chromosomes protein 2
UniRef100_U	8	8	9.50%	1195	1E+05	9	Structural maintenance of chromosomes protein 2 (Chromosome-associated protein E) (hCAP-E) (XCAP-E homolog).
UniRef100_Q	8	8	9.50%	1197	1E+05	8	SMC2 protein
UniRef100_Q	5	11	9.50%	751	83868	8	Periodontal ligament-specific periostin
UniRef100_Q	5	11	8.80%	808	90143	8	Periostin, osteoblast specific factor
UniRef100_O	2	5	9.50%	338	38274	6	Activator of 90 kDa heat shock protein ATPase homolog 1
UniRef100_P	2	2	9.50%	274	30727	6	Glutamate--cysteine ligase regulatory subunit
UniRef100_Q	2	2	9.50%	222	25073	5	Charged multivesicular body protein 3
UniRef100_U	2	2	13.50%	156	17326	5	vacuolar protein sorting 24 isoform 2
UniRef100_P	2	5	9.50%	220	24935	9	Synaptobrevin-like protein 1
UniRef100_Q	2	5	30.90%	68	7707	9	SYBL1
UniRef100_P	2	5	8.10%	260	30217	8	Isoform 2 of P51809
UniRef100_Q	12	17	9.40%	1849	2E+05	6	Brefeldin A-inhibited guanine nucleotide-exchange protein 1
UniRef100_Q	6	9	9.40%	958	1E+05	7	Exosome complex exonuclease RRP44
UniRef100_U	6	9	9.40%	960	1E+05	7	Exosome complex exonuclease RRP44 (EC 3.1.13.-) (Ribosomal RNA- processing protein 44) (DIS3 protein homolog).
UniRef100_U	6	9	9.40%	958	1E+05	7	KIAA1008
UniRef100_P	9	12	9.40%	934	1E+05	7	Complement component C6 precursor
UniRef100_U	9	12	9.40%	934	1E+05	7	Complement component C6 precursor.
UniRef100_P	5	7	9.40%	848	93361	5	Neural cell adhesion molecule 1, 140 kDa isoform precursor
UniRef100_U	5	7	9.30%	858	94574	5	neural cell adhesion molecule 1 isoform 2
UniRef100_Q	5	7	9.30%	858	94601	5	Neural cell adhesion molecule 1
UniRef100_Q	6	6	9.40%	832	91238	7	Transducin beta-like 3 variant
UniRef100_Q	6	6	9.70%	808	89035	7	TBL3 protein (Transducin (Beta)-like 3)
UniRef100_Q	6	6	9.70%	808	88936	7	Transducin (Beta)-like 3

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P	5	9	9.40%	770	86943	5	Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer disease amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease nexin-II) (PN-II) (APPI) (PreA4) [Contains: Soluble APP-alpha (S-APP- alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59)) (AICD-59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57) (Amyloid intracellular domain 57) (AID(57)) (AICD-57); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain 50) (AID(50)) (AICD-50); C31]
UniRef100_Q	5	9	9.60%	751	84819	5	Amyloid beta (A4) protein
UniRef100_P	5	9	9.60%	752	85040	5	Isoform L
UniRef100_P	5	9	9.80%	733	82916	5	Isoform L
UniRef100_P	5	9	10.10%	714	80769	5	Isoform APP714 of P05067
UniRef100_P	5	9	10.30%	696	78866	5	Isoform L
UniRef100_P	5	9	10.40%	695	78663	5	Isoform APP695 of P05067
UniRef100_P	5	9	10.60%	677	76760	5	Isoform L
UniRef100_Q	7	9	9.40%	802	85113	7	Aldehyde dehydrogenase family 16 member A1
UniRef100_U	7	9	9.40%	802	85127	7	aldehyde dehydrogenase 16 family, member A1
UniRef100_O	5	9	9.40%	720	80420	8	Long-chain-fatty-acid--CoA ligase 3
UniRef100_P	5	7	9.40%	561	64970	6	Cytosolic purine 5'-nucleotidase
UniRef100_P	2	2	9.40%	342	38926	6	WD repeat protein 68
UniRef100_U	2	2	9.40%	341	38855	6	WD repeat protein 68 (WD repeat protein An11 homolog).
UniRef100_O	2	2	9.40%	255	29176	5	Syntaxin-6
UniRef100_O	6	10	9.30%	1005	1E+05	5	Band 4.1-like protein 2
UniRef100_O	6	6	9.30%	785	87117	7	AP-1 complex subunit gamma-2
UniRef100_P	2	4	9.30%	430	46626	7	Pre-B-cell leukemia transcription factor 1
UniRef100_Q	2	4	11.50%	347	38427	8	Pre-B-cell leukemia transcription factor 1
UniRef100_Q	16	16	9.20%	2346	3E+05	6	Acetyl-CoA carboxylase 1 (EC 6.4.1.2) (ACC-alpha) [Includes: Biotin carboxylase (EC 6.3.4.14)]
UniRef100_U	16	16	9.00%	2383	3E+05	7	acetyl-Coenzyme A carboxylase alpha isoform 1
UniRef100_Q	9	18	9.20%	1275	1E+05	6	STAG1 variant protein
UniRef100_U	9	18	9.30%	1258	1E+05	6	stromal antigen 1
UniRef100_Q	9	18	9.30%	1258	1E+05	6	Cohesin subunit SA-1
UniRef100_Q	9	18	9.60%	1221	1E+05	6	STAG1 protein
UniRef100_Q	5	14	9.20%	633	68448	5	GSPT1 protein
UniRef100_P	4	7	9.20%	599	67314	8	ATP-binding cassette sub-family E member 1
UniRef100_O	3	4	9.20%	444	49302	7	Vacuolar protein sorting-associating protein 4B (Suppressor of K(+) transport growth defect 1)
UniRef100_Q	2	2	9.20%	238	27166	4	Ubiquitin-conjugating enzyme E2 R2
UniRef100_Q	6	9	9.10%	639	71451	6	CD2-associated protein
UniRef100_U	6	9	9.10%	639	71433	6	CD2-associated protein (Cas ligand with multiple SH3 domains) (Adapter protein CMS).
UniRef100_P	10	33	9.00%	1360	2E+05	7	DNA mismatch repair protein MSH6
UniRef100_Q	7	7	9.00%	879	98556	7	Prostaglandin F2 receptor negative regulator precursor

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	5	5	9.00%	698	78214	6	Adducin 3 isoform a variant
UniRef100_Q	5	5	8.90%	706	79155	6	Gamma-adducin
UniRef100_Q	5	5	9.30%	674	75671	7	Adducin 3
UniRef100_Q	3	5	9.00%	401	44962	6	Splicing factor 45
UniRef100_Q	2	3	9.00%	334	38379	6	Leucine carboxyl methyltransferase 1
UniRef100_U	2	3	8.40%	357	41116	8	Leucine carboxyl methyltransferase 1 (EC 2.1.1.-) (Protein-leucine O- methyltransferase).
UniRef100_U	2	3	8.90%	338	38834	7	Leucine carboxyl methyltransferase 1 (EC 2.1.1.-) (Protein-leucine O- methyltransferase).
UniRef100_U	2	3	10.70%	281	32456	7	Leucine carboxyl methyltransferase 1 (EC 2.1.1.-) (Protein-leucine O- methyltransferase).
UniRef100_U	2	3	10.80%	279	32172	6	leucine carboxyl methyltransferase 1 isoform b
UniRef100_Q	2	3	8.40%	357	41106	7	Isoform 2 of Q9UIC8
UniRef100_P	2	3	9.00%	323	35709	9	Tumor-associated calcium signal transducer 2 precursor
UniRef100_U	2	3	9.00%	323	35723	9	tumor-associated calcium signal transducer 2 precursor
UniRef100_Q	2	3	9.00%	323	35709	9	Tumor-associated calcium signal transducer 2
UniRef100_Q	2	3	9.00%	323	35767	9	TACSTD2 protein
UniRef100_Q	2	3	9.00%	201	21227	9	Cardiotrophin-1
UniRef100_Q	2	3	9.00%	200	21098	9	Cardiotrophin 1
UniRef100_O	9	9	8.90%	1309	1E+05	6	Putative eukaryotic translation initiation factor 3 subunit
UniRef100_Q	4	5	8.90%	660	71801	7	OGFR protein
UniRef100_U	4	5	11.50%	514	54396	6	Opioid growth factor receptor (OGFr) (Zeta-type opioid receptor) (7-60 protein).
UniRef100_U	4	5	9.00%	659	71779	5	Opioid growth factor receptor (OGFr) (Zeta-type opioid receptor) (7-60 protein).
UniRef100_U	4	5	9.40%	625	67195	5	Opioid growth factor receptor (OGFr) (Zeta-type opioid receptor) (7-60 protein).
UniRef100_Q	4	5	9.00%	657	71424	5	Isoform 2 of Q9NZT2
UniRef100_Q	4	5	8.70%	677	73325	5	Opioid growth factor receptor
UniRef100_Q	4	5	11.50%	513	54097	6	OGFR protein
UniRef100_P	4	5	8.90%	638	69811	9	Signal recognition particle receptor subunit alpha
UniRef100_U	4	5	8.90%	640	69982	9	Signal recognition particle receptor subunit alpha (SR-alpha) (Docking protein alpha) (DP-alpha).
UniRef100_Q	4	5	8.90%	638	69894	9	SRPR protein
UniRef100_Q	4	13	8.90%	563	65145	5	Catenin, beta like 1
UniRef100_U	4	13	8.80%	568	65751	5	Beta-catenin-like protein 1 (Nuclear-associated protein) (NAP) (Testis development protein NYD-SP19).
UniRef100_Q	4	13	16.10%	311	36103	7	Isoform 3 of Q8WYA6
UniRef100_Q	4	13	13.30%	376	43392	6	Isoform 2 of Q8WYA6
UniRef100_Q	4	13	8.90%	563	65173	5	Beta-catenin-like protein 1
UniRef100_Q	5	11	8.90%	571	59481	9	Interferon regulatory factor 2 binding protein 2
UniRef100_Q	5	11	8.70%	587	61025	9	Interferon regulatory factor 2-binding protein 2
UniRef100_Q	4	7	8.80%	900	96749	6	Nuclear factor NF-kappa-B p100 subunit (DNA-binding factor KBF2) (H2TF1) (Lymphocyte translocation chromosome 10) (Oncogene Lyt-10) (Lyt10) [Contains: Nuclear factor NF-kappa-B p52 subunit]

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_U	4	7	8.50%	930	1E+05	7	Nuclear factor NF-kappa-B p100 subunit (DNA-binding factor KBF2) (H2TF1) (Lymphocyte translocation chromosome 10) (Oncogene Lyt-10) (Lyt10) [Contains: Nuclear factor NF-kappa-B p52 subunit].
UniRef100_U	4	7	8.80%	899	96678	6	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 isoform b
UniRef100_P	5	10	8.80%	760	84871	7	Transferrin receptor protein 1
UniRef100_U	5	10	8.80%	760	84901	7	transferrin receptor
UniRef100_Q	4	7	8.80%	577	64283	9	Inter-alpha (Globulin) inhibitor H5
UniRef100_U	4	7	6.90%	742	82105	8	inter-alpha trypsin inhibitor heavy chain precursor 5 isoform 2
UniRef100_U	4	7	5.30%	956	1E+05	8	inter-alpha trypsin inhibitor heavy chain precursor 5 isoform 1
UniRef100_Q	4	7	5.40%	942	1E+05	8	CDNA FLJ14469 fis, clone MAMMA1000897, weakly similar to INTER-ALPHA- TRYPSIN INHIBITOR HEAVY CHAIN H3
UniRef100_Q	4	7	6.20%	824	91175	8	KIAA1953 protein
UniRef100_Q	4	7	5.40%	942	1E+05	8	Inter-alpha trypsin inhibitor heavy chain 5
UniRef100_Q	4	7	7.30%	694	77401	9	LLLL311
UniRef100_Q	4	7	11.10%	460	51045	9	Hypothetical protein DKFZp686F0145
UniRef100_Q	4	7	5.30%	956	1E+05	8	Inter-alpha inhibitor H5
UniRef100_Q	4	7	6.90%	742	82165	8	Inter-alpha (Globulin) inhibitor H5
UniRef100_Q	3	3	8.80%	411	44743	9	Glycerol-3-phosphate dehydrogenase 1-like protein
UniRef100_Q	3	3	13.90%	259	28446	7	GPD1L protein
UniRef100_Q	3	3	10.30%	351	38419	7	Glycerol-3-phosphate dehydrogenase 1-like
UniRef100_Q	2	2	8.80%	318	35185	7	Ubiquitin-conjugating enzyme E2, J1 variant
UniRef100_Q	2	2	8.80%	318	35199	7	Ubiquitin-conjugating enzyme E2 J1
UniRef100_Q	2	2	8.80%	296	32079	9	LSM14 homolog B
UniRef100_Q	2	2	6.80%	385	42021	9	Isoform 2 of Q9BX40
UniRef100_Q	2	2	6.80%	385	42071	#	LSM14 protein homolog B
UniRef100_Q	2	2	11.70%	223	23822	#	LSM14 homolog B
UniRef100_P	3	3	8.80%	240	25851	7	Extracellular superoxide dismutase [Cu-Zn] precursor
UniRef100_P	2	3	8.80%	239	25358	5	Proteasome subunit beta type 6 precursor
UniRef100_Q	2	3	8.80%	147	15911	5	Protein phosphatase 1 regulatory subunit 14B
UniRef100_Q	48	70	8.70%	6885	8E+05	5	Nesprin-2
UniRef100_Q	48	70	8.70%	6907	8E+05	5	Isoform 2 of Q8WXH0
UniRef100_Q	10	15	8.70%	1104	1E+05	6	Protein FAM62A
UniRef100_Q	10	15	8.60%	1114	1E+05	6	Isoform 2 of Q9BSJ8
UniRef100_Q	5	7	8.70%	782	86042	7	Uncharacterized protein C11orf2
UniRef100_Q	6	32	8.70%	505	58264	5	Heat shock protein 90Bd
UniRef100_Q	4	6	8.70%	517	56760	6	Copine I variant
UniRef100_Q	4	6	8.40%	537	59059	6	Copine-1
UniRef100_Q	2	6	8.70%	229	25764	9	Uncharacterized protein C10orf58 precursor
UniRef100_U	2	6	8.70%	229	25750	9	hypothetical protein LOC84293
UniRef100_Q	2	2	8.70%	172	18322	8	Cyclin-L1
UniRef100_Q	2	2	6.50%	232	25408	9	Isoform 4 of Q9UK58

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	2	2	2.90%	526	59634	#	Cyclin-L1
UniRef100_Q	39	49	8.60%	5635	6E+05	7	Hemicentin-1 precursor
UniRef100_U	39	49	8.60%	5633	6E+05	7	Hemicentin-1 precursor (Fibulin-6) (FIBL-6).
UniRef100_Q	12	17	8.60%	1726	2E+05	5	Transcription elongation factor SPT6
UniRef100_U	12	17	8.60%	1728	2E+05	5	Transcription elongation factor SPT6 (hSPT6) (Tat-cotransactivator 2 protein) (Tat-CT2 protein).
UniRef100_Q	9	12	8.60%	1297	1E+05	9	RRP12-like protein
UniRef100_U	9	12	8.60%	1297	1E+05	9	ribosomal RNA processing 12 homolog
UniRef100_Q	11	45	8.60%	955	1E+05	#	Thyroid hormone receptor-associated protein 3
UniRef100_U	11	45	8.60%	955	1E+05	#	thyroid hormone receptor associated protein 3
UniRef100_O	7	16	8.60%	941	1E+05	8	Pre-mRNA-processing factor 6
UniRef100_A	5	16	8.60%	686	74262	7	Long form collapsin response mediator protein 1
UniRef100_Q	5	16	10.30%	572	62184	7	Dihydropyrimidinase-related protein 1
UniRef100_Q	6	33	8.60%	700	73745	#	Nucleolar and coiled-body phosphoprotein 1
UniRef100_P	3	4	8.60%	595	67561	8	Tyrosine-protein phosphatase non-receptor type 6
UniRef100_U	3	4	8.20%	624	70131	8	Tyrosine-protein phosphatase non-receptor type 6 (EC 3.1.3.48) (Protein-tyrosine phosphatase 1C) (PTP-1C) (Hematopoietic cell protein-tyrosine phosphatase) (SH-PTP1) (Protein-tyrosine phosphatase SHP-1).
UniRef100_Q	3	4	8.20%	624	70117	8	70 kDa SHP-1L protein
UniRef100_Q	3	4	8.50%	597	67719	8	Protein tyrosine phosphatase, non-receptor type 6
UniRef100_Q	3	4	8.60%	595	67609	8	Protein tyrosine phosphatase, non-receptor type 6 isoform 1 variant
UniRef100_P	3	4	9.20%	556	63125	7	Isoform 3 of P29350
UniRef100_Q	4	7	8.60%	570	65077	8	Vacuolar protein sorting-associated protein 45
UniRef100_O	3	8	8.60%	467	53130	5	Interferon regulatory factor 6
UniRef100_Q	2	2	8.60%	452	50240	7	Translation initiation factor eIF-2B subunit gamma
UniRef100_Q	2	2	8.60%	361	40822	5	NudC domain-containing protein 3
UniRef100_Q	2	5	8.60%	339	37464	5	TERF2IP protein
UniRef100_Q	2	5	7.30%	399	44260	5	Telomeric repeat-binding factor 2-interacting protein 1
UniRef100_U	10	13	8.50%	1435	2E+05	8	CDNA FLJ14303 fis, clone PLACE2000132.
UniRef100_Q	8	14	8.50%	1128	1E+05	7	Nck-associated protein 1
UniRef100_U	8	14	8.50%	1134	1E+05	7	NCK-associated protein 1 isoform 2
UniRef100_O	7	10	8.50%	1037	1E+05	5	Importin-8
UniRef100_U	7	10	8.50%	1037	1E+05	5	importin 8
UniRef100_Q	4	12	8.50%	550	61636	5	Src substrate cortactin
UniRef100_U	4	12	8.50%	551	61762	5	Src substrate cortactin (Amplaxin) (Oncogene EMS1).
UniRef100_U	4	12	8.50%	550	61586	5	cortactin isoform a
UniRef100_Q	4	12	9.20%	513	57467	5	Cortactin
UniRef100_Q	4	12	8.50%	550	61558	5	Cortactin isoform a variant
UniRef100_Q	2	3	8.50%	470	53687	9	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	2	3	8.30%	483	55016	9	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 3
UniRef100_Q	2	2	8.50%	387	43603	5	Protein TSSC1
UniRef100_P	2	2	8.50%	353	41467	6	Guanine nucleotide-binding protein G(q) subunit alpha
UniRef100_Q	2	2	8.40%	359	42142	6	Guanine nucleotide binding protein (G protein), q polypeptide
UniRef100_P	2	4	8.50%	351	38990	6	Translation initiation factor eIF-2B subunit beta
UniRef100_Q	2	4	8.50%	351	39004	6	Eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa
UniRef100_Q	14	15	8.40%	2214	2E+05	6	Sortilin-related receptor precursor
UniRef100_Q	7	7	8.40%	1299	1E+05	6	Tenascin-N precursor
UniRef100_Q	6	34	8.40%	699	73603	#	Nucleolar phosphoprotein p130
UniRef100_U	6	34	8.40%	699	73720	#	nucleolar and coiled-body phosphoprotein 1
UniRef100_Q	6	34	8.30%	709	74747	#	Isoform Beta of Q14978
UniRef100_P	3	5	8.40%	359	42123	6	Guanine nucleotide-binding protein subunit alpha-11 (G alpha-11) (Guanine nucleotide-binding protein G(y) subunit alpha)
UniRef100_Q	3	5	8.40%	357	41891	6	Guanine nucleotide-binding protein G, alpha subunit variant
UniRef100_P	2	5	8.40%	333	37564	5	Cathepsin L precursor (EC 3.4.22.15) (Major excreted protein) (MEP) [Contains: Cathepsin L heavy chain; Cathepsin L light chain]
UniRef100_Q	2	2	8.40%	299	34593	5	Leucine zipper transcription factor-like protein 1
UniRef100_U	2	2	8.40%	298	34461	5	leucine zipper transcription factor-like 1
UniRef100_Q	2	2	8.40%	299	34591	5	Leucine zipper transcription factor-like 1
UniRef100_Q	2	2	8.40%	299	34592	5	Leucine zipper transcription factor-like 1
UniRef100_P	3	6	8.40%	274	30868	9	NAD(P)H dehydrogenase [quinone] 1 (EC 1.6.5.2) (Quinone reductase 1) (NAD(P)H:quinone oxidoreductase 1)
UniRef100_U	3	6	9.70%	236	26365	9	NAD(P)H menadione oxidoreductase 1, dioxin-inducible isoform c
UniRef100_Q	3	6	9.60%	240	26922	9	Hypothetical protein
UniRef100_Q	11	17	8.30%	1626	2E+05	8	DNA topoisomerase 2-beta
UniRef100_Q	11	17	8.40%	1598	2E+05	8	DNA topoisomerase II beta
UniRef100_Q	11	17	8.30%	1621	2E+05	8	Isoform Beta
UniRef100_Q	12	20	8.30%	1372	2E+05	8	CDNA FLJ46776 fis, clone TRACH3026650, highly similar to Actin cross- linking family protein 7
UniRef100_O	8	9	8.30%	1001	1E+05	6	E3 ubiquitin-protein ligase BRE1B
UniRef100_U	8	9	9.90%	838	94796	6	Ubiquitin-protein ligase BRE1B (EC 6.3.2.-) (BRE1-B) (RING finger protein 40) (95 kDa retinoblastoma-associated protein) (RBP95).
UniRef100_U	8	9	8.30%	1001	1E+05	6	Ubiquitin-protein ligase BRE1B (EC 6.3.2.-) (BRE1-B) (RING finger protein 40) (95 kDa retinoblastoma-associated protein) (RBP95).
UniRef100_O	8	9	9.90%	838	94824	6	Isoform 3 of O75150
UniRef100_O	6	8	8.30%	963	1E+05	5	Importin-13
UniRef100_U	6	8	8.30%	963	1E+05	5	importin 13
UniRef100_O	5	6	8.30%	923	1E+05	6	Neuropilin-1 precursor
UniRef100_Q	5	6	8.50%	906	1E+05	6	Neuropilin-1
UniRef100_Q	5	6	8.30%	923	1E+05	6	Hypothetical protein DKFZp781F1414

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q!	5	6	8.30%	923	1E+05	6	Neuropilin 1
UniRef100_Q!	5	6	10.50%	735	81990	6	Neuropilin 1
UniRef100_Q!	5	6	8.70%	890	99694	6	Neuropilin-1 variant
UniRef100_P3	3	8	8.30%	576	62608	9	Coilin
UniRef100_O7	3	4	8.30%	459	50925	5	Zinc-finger protein ZPR1
UniRef100_Q	2	3	8.30%	396	44244	5	Wilms' tumor 1-associating protein (WT1-associated protein) (Putative pre-mRNA-splicing regulator female-lethal(2D) homolog)
UniRef100_Q4	3	5	8.30%	336	39155	7	Vacuolar protein sorting-associated protein 26B
UniRef100_A2	11	15	8.20%	1479	2E+05	9	CLASP1 protein
UniRef100_Q7	11	15	8.10%	1494	2E+05	9	Isoform 3 of Q7Z460
UniRef100_Q7	11	15	8.20%	1471	2E+05	9	Isoform 2 of Q7Z460
UniRef100_Q7	11	15	7.90%	1538	2E+05	9	CLIP-associating protein 1
UniRef100_P4	6	8	8.20%	1011	1E+05	6	Ubiquitin-activating enzyme E1 homolog
UniRef100_UI	6	8	8.20%	1009	1E+05	6	Ubiquitin-activating enzyme E1 homolog (D8).
UniRef100_Q9	6	8	8.20%	1012	1E+05	6	Ubiquitin-activating enzyme E1-like
UniRef100_Q!	4	4	8.20%	600	63740	5	Ataxin-1 ubiquitin-like interacting protein variant
UniRef100_Q9	4	4	8.20%	601	63853	5	Ubiquilin-4
UniRef100_Q7	2	2	8.20%	257	29405	7	BTB/POZ domain-containing protein KCTD1
UniRef100_P5	5	5	8.10%	925	1E+05	5	Nuclear pore complex protein Nup107
UniRef100_Q	3	7	8.10%	720	79119	6	WD repeat protein 43
UniRef100_UI	3	7	8.10%	720	79154	6	WD repeat protein 43.
UniRef100_Q8	4	10	8.10%	631	70902	9	ZFR protein
UniRef100_UI	4	10	4.80%	1055	1E+05	9	zinc finger RNA binding protein
UniRef100_UI	4	10	4.70%	1074	1E+05	9	zinc finger RNA binding protein
UniRef100_UI	4	10	4.70%	1074	1E+05	9	zinc finger RNA binding protein
UniRef100_Q9	4	10	4.80%	1057	1E+05	9	Zinc finger RNA-binding protein
UniRef100_P1	3	7	8.10%	480	52222	7	Uridine 5'-monophosphate synthase (UMP synthase) [Includes: Orotate phosphoribosyltransferase (EC 2.4.2.10) (OPRTase); Orotidine 5'- phosphate decarboxylase (EC 4.1.1.23) (OMPdecase)]
UniRef100_Q	3	6	8.10%	407	42153	5	Adhesion-regulating molecule 1 precursor
UniRef100_UI	3	6	8.50%	387	40237	5	Adhesion-regulating molecule 1 precursor (110 kDa cell membrane glycoprotein) (Gp110).
UniRef100_Q6	2	2	8.10%	357	40514	7	Protein FAM45B
UniRef100_Q8	2	2	8.10%	357	40513	7	Protein FAM45A
UniRef100_Q!	2	4	8.10%	344	38122	8	WD repeat domain phosphoinositide-interacting protein 3
UniRef100_Q4	2	2	8.10%	260	29643	7	BTB/POZ domain-containing protein KCTD21
UniRef100_P3	4	4	8.00%	622	69195	6	Phosphoenolpyruvate carboxykinase, cytosolic [GTP]
UniRef100_UI	4	4	8.00%	622	69195	6	cytosolic phosphoenolpyruvate carboxykinase 1
UniRef100_O	2	7	8.00%	563	61248	7	Tripeptidyl-peptidase 1 precursor
UniRef100_UI	2	7	8.10%	555	60357	6	Tripeptidyl-peptidase 1 precursor (EC 3.4.14.9) (Tripeptidyl-peptidase I) (TPP-1) (TPP-I) (Tripeptidyl aminopeptidase) (Lysosomal pepstatin insensitive protease) (LPIC) (Cell growth-inhibiting gene 1 protein).

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	2	7	8.00%	563	61213	7	Tripeptidyl-peptidase I variant
UniRef100_O	2	7	8.10%	556	60458	6	Isoform 3 of O14773
UniRef100_P	3	3	8.00%	514	58777	6	Seryl-tRNA synthetase, cytoplasmic
UniRef100_U	3	3	7.60%	536	61285	7	Seryl-tRNA synthetase, cytoplasmic (EC 6.1.1.11) (Serine--tRNA ligase) (SerRS).
UniRef100_Q	3	3	7.60%	536	61313	7	Seryl-tRNA synthetase
UniRef100_Q	3	3	8.00%	514	58690	6	Seryl-tRNA synthetase variant
UniRef100_Q	3	3	8.00%	511	58407	6	SARS protein
UniRef100_Q	2	2	8.00%	314	35864	5	Autophagy-related protein 3
UniRef100_Q	2	3	8.00%	225	25697	9	Thymocyte nuclear protein 1
UniRef100_A	15	16	7.90%	2394	3E+05	7	DKFZP586J0619 protein
UniRef100_U	15	16	8.00%	2381	3E+05	7	integrator complex subunit 1
UniRef100_U	15	16	9.00%	2122	2E+05	6	CDNA FLJ46511 fis, clone THYMU3031868.
UniRef100_Q	15	16	8.70%	2190	2E+05	6	Integrator complex subunit 1
UniRef100_A	15	16	7.90%	2408	3E+05	7	DKFZP586J0619 protein
UniRef100_O	6	7	7.90%	1119	1E+05	6	Cullin-associated NEDD8-dissociated protein 2
UniRef100_U	6	7	7.90%	1119	1E+05	6	TBP-interacting protein
UniRef100_P	5	8	7.90%	851	97916	6	Signal transducer and activator of transcription 2
UniRef100_Q	4	8	7.90%	851	91174	6	Ankyrin repeat domain-containing protein 25
UniRef100_Q	4	8	8.00%	841	90044	6	Isoform 3 of Q63ZY3
UniRef100_P	3	4	7.90%	660	73882	6	72 kDa type IV collagenase precursor
UniRef100_P	4	5	7.90%	570	65336	9	Cytochrome b-245 heavy chain (p22 phagocyte B-cytochrome) (Neutrophil cytochrome b 91 kDa polypeptide) (CGD91-phox) (gp91-phox) (gp91-1) (Heme-binding membrane glycoprotein gp91phox) (Cytochrome b(558) subunit beta)
UniRef100_Q	3	3	7.90%	545	62135	9	HSR1 protein
UniRef100_Q	3	3	7.10%	607	68661	6	Guanine nucleotide binding protein-like 1
UniRef100_O	3	8	7.90%	484	54396	5	Isoform 7 of O60271
UniRef100_P	3	7	7.90%	431	49223	6	Eukaryotic translation initiation factor 5
UniRef100_Q	3	7	7.90%	431	49152	6	EIF5 protein
UniRef100_P	2	2	7.90%	382	43942	8	Vacuolar ATP synthase subunit C
UniRef100_U	2	2	8.20%	364	41871	7	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1 isoform B
UniRef100_P	2	2	7.90%	382	42448	5	Protein phosphatase 2C isoform alpha
UniRef100_P	2	2	9.30%	324	35958	6	Isoform Alpha
UniRef100_Q	2	2	7.90%	280	31236	6	FHL3 protein
UniRef100_Q	2	2	7.90%	280	31282	6	LIM-only protein FHL3
UniRef100_Q	2	2	7.90%	280	31192	6	Four and a half LIM domains 3
UniRef100_Q	2	2	12.80%	172	18918	8	FHL3 protein
UniRef100_U	20	27	7.80%	3056	4E+05	7	Serine-protein kinase ATM (EC 2.7.11.1) (Ataxia telangiectasia mutated) (A-T, mutated).
UniRef100_U	20	27	7.80%	3056	4E+05	7	Serine-protein kinase ATM (EC 2.7.11.1) (Ataxia telangiectasia mutated) (A-T, mutated).
UniRef100_U	20	27	7.80%	3056	4E+05	7	ataxia telangiectasia mutated protein isoform 1
UniRef100_Q	15	31	7.80%	2127	2E+05	7	Hypothetical protein DKFZp686E0722
UniRef100_U	15	31	6.90%	2376	3E+05	7	CCR4-NOT transcription complex, subunit 1 isoform a

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	2	3	7.80%	523	56579	6	Cytoplasmic dynein 1 light intermediate chain 1
UniRef100_UI	2	3	7.80%	523	56627	7	dynein light chain-A
UniRef100_Q	3	8	7.80%	359	41815	8	B aggressive lymphoma gene variant
UniRef100_UI	3	8	3.30%	854	96283	8	poly (ADP-ribose) polymerase family, member 9
UniRef100_Q	3	8	3.40%	819	92272	8	Isoform 2 of Q8IXQ6
UniRef100_Q	3	8	3.30%	854	96343	8	Poly [ADP-ribose] polymerase 9
UniRef100_Q	2	2	7.80%	357	39311	8	WD repeat protein 57
UniRef100_Q	2	2	7.80%	333	37805	5	SGT1, suppressor of G2 allele of SKP1
UniRef100_Q	2	2	7.10%	365	41024	5	Suppressor of G2 allele of SKP1 homolog
UniRef100_P	10	16	7.70%	1647	2E+05	8	Probable global transcription activator SNF2L4
UniRef100_Q	10	16	7.50%	1679	2E+05	8	SMARCA4 isoform 2
UniRef100_Q	4	7	7.70%	807	91680	8	ATP-binding cassette, sub-family F (GCN20), member 1
UniRef100_Q	4	7	7.30%	845	95926	7	ATP-binding cassette sub-family F member 1
UniRef100_P	5	6	7.70%	607	68569	6	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit precursor
UniRef100_Q	5	6	8.30%	568	64582	7	Similar to ribophorin I
UniRef100_Q	5	6	7.70%	607	68607	6	RPN1 protein
UniRef100_Q	5	6	7.70%	607	68580	6	Ribophorin I variant
UniRef100_Q	3	6	7.70%	532	59681	9	Growth factor receptor-bound protein 7
UniRef100_Q	2	7	7.70%	492	54341	6	Dipeptidyl-peptidase 7
UniRef100_UI	2	7	6.80%	556	60414	8	PREDICTED: similar to Dipeptidyl-peptidase 2 precursor (Dipeptidyl-peptidase II) (DPP II) (Dipeptidyl aminopeptidase II) (Quiescent cell proline dipeptidase) (Dipeptidyl peptidase 7)
UniRef100_Q	2	7	7.70%	492	54327	6	Dipeptidyl-peptidase 2 precursor
UniRef100_P	2	2	7.70%	379	43363	7	Galactose-1-phosphate uridylyltransferase
UniRef100_UI	2	2	24.20%	120	13391	8	Interleukin-11 receptor alpha chain precursor (IL-11R-alpha) (IL- 11RA).
UniRef100_Q	2	2	17.90%	162	18315	8	CDNA FLJ38707 fis, clone KIDNE2002839, highly similar to GALACTOSE-1- PHOSPHATE URIDYLYLTRANSFERASE
UniRef100_Q	2	2	7.70%	379	43364	7	Galactose-1-phosphate uridylyltransferase
UniRef100_Q	3	8	7.70%	392	42907	7	Integrin-linked kinase-associated serine/threonine phosphatase 2C
UniRef100_P	2	2	7.70%	261	28993	7	Endoplasmic reticulum protein ERp29 precursor
UniRef100_Q	2	4	7.70%	209	23138	6	Pyroglutamyl-peptidase 1
UniRef100_A	2	4	7.60%	539	58499	9	Wolf-Hirschhorn syndrome candidate 2
UniRef100_Q	2	4	7.80%	528	57277	9	Isoform 2 of Q9H3P2
UniRef100_Q	2	4	7.80%	528	57349	9	Wolf-Hirschhorn syndrome candidate 2 protein variant
UniRef100_Q	2	2	7.60%	421	47328	7	Phosphatidylinositol-4-phosphate 5-kinase type II gamma
UniRef100_UI	2	2	7.60%	421	47300	7	phosphatidylinositol-4-phosphate 5-kinase, type II, gamma
UniRef100_Q	2	2	14.40%	222	25000	6	CDNA: FLJ22055 fis, clone HEP09645
UniRef100_P	2	3	7.60%	355	39749	5	Serum paraoxonase/arylesterase 1
UniRef100_Q	2	3	7.60%	355	39731	5	Paraoxonase 1
UniRef100_Q	2	3	7.60%	263	28343	8	Hypothetical protein
UniRef100_UI	2	3	10.30%	194	21952	6	Adaptin ear-binding coat-associated protein 2 (NECAP-2).
UniRef100_Q	2	3	11.60%	172	19419	7	Isoform 3 of Q9NVZ3

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	2	3	7.30%	273	29464	8	Isoform 2 of Q9NVZ3
UniRef100_Q	2	3	7.60%	263	28339	8	Adaptin ear-binding coat-associated protein 2
UniRef100_Q	6	7	7.50%	1031	1E+05	9	Probable ATP-dependent RNA helicase DDX46
UniRef100_UI	6	7	7.50%	1032	1E+05	9	Probable ATP-dependent RNA helicase DDX46 (EC 3.6.1.-) (DEAD box protein 46) (PRP5 homolog).
UniRef100_UI	6	7	7.50%	1033	1E+05	9	Probable ATP-dependent RNA helicase DDX46 (EC 3.6.1.-) (DEAD box protein 46) (PRP5 homolog).
UniRef100_Q	4	12	7.50%	684	77470	6	Cleavage and polyadenylation specific factor 3, 73kDa variant
UniRef100_Q	4	12	7.50%	684	77486	6	Cleavage and polyadenylation specificity factor subunit 3
UniRef100_Q	4	5	7.50%	590	66247	5	Negative elongation factor C/D
UniRef100_Q	4	5	7.60%	581	65479	5	Isoform NELF
UniRef100_O	3	8	7.50%	521	56502	9	Regulator of differentiation 1
UniRef100_Q	3	8	7.40%	524	56821	9	ROD1 regulator of differentiation 1
UniRef100_Q	3	8	7.10%	552	59690	9	ROD1 regulator of differentiation 1
UniRef100_O	3	8	6.40%	614	66234	#	Isoform 2 of O95758
UniRef100_P	2	2	7.50%	347	38178	7	Leucine-rich alpha-2-glycoprotein precursor
UniRef100_Q	2	2	7.50%	347	38168	7	Leucine-rich alpha-2-glycoprotein
UniRef100_Q	2	4	7.50%	281	31982	6	Microtubule-associated protein RP/EB family member 3
UniRef100_Q	2	4	7.90%	266	30380	5	Isoform 2 of Q9UPY8
UniRef100_Q	2	2	7.50%	187	20578	6	Uncharacterized protein C9orf103
UniRef100_P	6	6	7.40%	1257	1E+05	6	Neural cell adhesion molecule L1 precursor
UniRef100_UI	6	6	7.40%	1253	1E+05	6	Neural cell adhesion molecule L1 precursor (N-CAM L1) (CD171 antigen).
UniRef100_UI	6	6	7.40%	1257	1E+05	6	Neural cell adhesion molecule L1 precursor (N-CAM L1) (CD171 antigen).
UniRef100_UI	6	6	7.50%	1248	1E+05	6	Neural cell adhesion molecule L1 precursor (N-CAM L1) (CD171 antigen).
UniRef100_P	6	6	7.40%	1253	1E+05	6	Isoform 2 of P32004
UniRef100_P	5	14	7.40%	1026	1E+05	6	Neurofilament heavy polypeptide
UniRef100_UI	5	14	7.50%	1020	1E+05	6	neurofilament, heavy polypeptide 200kDa
UniRef100_O	7	7	7.40%	981	1E+05	5	Calsyntenin-1 precursor
UniRef100_UI	7	7	7.60%	962	1E+05	5	Calsyntenin-1 precursor.
UniRef100_Q	7	7	7.50%	971	1E+05	5	Calsyntenin 1
UniRef100_Q	7	7	7.50%	971	1E+05	5	Non-classical cadherin XB31alpha1
UniRef100_Q	7	7	7.50%	971	1E+05	5	Alcadein alpha-1
UniRef100_Q	7	7	9.30%	782	88040	5	Calsyntenin 1
UniRef100_O	2	4	7.40%	337	38223	9	Zinc finger Ran-binding domain-containing protein 2
UniRef100_UI	2	4	7.40%	336	38136	9	Zinc finger Ran-binding domain-containing protein 2 (Zinc finger protein 265) (Zinc finger, splicing).
UniRef100_Q	2	4	7.60%	330	37404	#	Zinc finger, RAN-binding domain containing 2
UniRef100_Q	2	4	7.80%	320	36318	#	Zinc finger, RAN-binding domain containing 2
UniRef100_Q	2	4	7.90%	316	36032	#	Zinc finger protein 265 isoform 1 variant
UniRef100_Q	2	4	7.60%	330	37332	#	Zinc finger protein 265 isoform 1 variant
UniRef100_O	2	4	8.00%	311	35304	9	Isoform ZIS

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	2	4	7.40%	312	33241	5	Transcriptional activator protein Pur-beta
UniRef100_P	7	8	7.30%	1028	1E+05	5	Collagen alpha-1(VI) chain precursor
UniRef100_A	4	5	7.30%	875	1E+05	7	Hypothetical protein
UniRef100_Q	4	5	7.50%	852	98441	6	CDNA FLJ13089 fis, clone NT2RP3002108, weakly similar to DEC1 PROTEIN
UniRef100_Q	4	5	6.60%	972	1E+05	7	P120
UniRef100_Q	4	5	7.40%	863	99635	6	Hypothetical protein DKFZp686H03169
UniRef100_Q	4	5	6.60%	972	1E+05	7	Uncharacterized protein C12orf30
UniRef100_Q	4	4	7.30%	901	99962	5	Desmocollin-2 precursor
UniRef100_Q	4	4	8.70%	758	83789	5	Hypothetical protein DKFZp686P18250
UniRef100_Q	4	4	7.80%	847	93769	6	Isoform 2B of Q02487
UniRef100_Q	3	3	7.30%	726	79444	6	NHL repeat-containing protein 2
UniRef100_O	2	2	7.30%	426	48112	7	Serine/threonine-protein kinase 25
UniRef100_Q	2	2	7.50%	416	46529	5	Serine/threonine-protein kinase MST4
UniRef100_Q	2	2	10.60%	293	32883	7	CDNA FLJ20549 fis, clone KAT11561
UniRef100_Q	2	2	7.30%	426	48113	7	STK25 protein
UniRef100_Q	2	2	9.10%	339	37770	6	CDNA FLJ90626 fis, clone PLACE1003135, weakly similar to SPORULATION- SPECIFIC PROTEIN 1
UniRef100_Q	2	2	7.90%	392	43868	5	CDNA FLJ90669 fis, clone PLACE1005519, moderately similar to Homo sapiens STE20-like kinase 3 (mst-3) mRNA
UniRef100_Q	2	2	10.80%	287	32196	8	Hypothetical protein DKFZp686J1430
UniRef100_Q	2	2	7.50%	416	46530	5	Serine/threonine protein kinase MST4
UniRef100_O	2	2	7.30%	412	45746	7	DnaJ homolog subfamily A member 2
UniRef100_P	2	2	7.30%	381	42020	5	Pentraxin-related protein PTX3 precursor
UniRef100_Q	2	2	7.30%	381	41976	5	Pentaxin-related protein PTX3
UniRef100_Q	2	2	7.30%	329	37534	8	GTPase IMAP family member 4
UniRef100_O	2	2	7.30%	316	35539	8	Galectin-8
UniRef100_U	2	2	7.70%	300	33985	9	Galectin-8 (Gal-8) (Prostate carcinoma tumor antigen 1) (PCTA-1) (Po66 carbohydrate-binding protein) (Po66-CBP).
UniRef100_U	2	2	6.40%	359	40541	8	Galectin-8 (Gal-8) (Prostate carcinoma tumor antigen 1) (PCTA-1) (Po66 carbohydrate-binding protein) (Po66-CBP).
UniRef100_Q	2	2	6.40%	359	40363	9	Colorectal carcinoma-derived galectin-8 variant II
UniRef100_Q	2	2	7.70%	300	33739	9	Lymphocyte/NHL galectin-8 short isoform
UniRef100_Q	2	2	6.40%	359	40151	9	Lymphocyte/NHL galectin-8 long isoform
UniRef100_Q	2	2	7.30%	317	35808	8	Lectin, galactoside-binding, soluble, 8
UniRef100_Q	2	2	6.40%	359	40397	9	Lectin, galactoside-binding, soluble, 8
UniRef100_O	2	2	6.40%	359	40336	7	Isoform 3 of O00214
UniRef100_O	2	2	6.40%	358	40128	9	Isoform 2 of O00214
UniRef100_Q	3	6	7.20%	567	62681	8	Hypothetical protein
UniRef100_Q	3	6	5.00%	822	92001	7	General transcription factor 3C polypeptide 4
UniRef100_Q	3	6	5.00%	822	91982	7	General transcription factor IIIC, polypeptide 4, 90kDa
UniRef100_Q	2	2	7.20%	377	41968	7	Hypothetical protein NIF3L1

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	2	2	7.70%	350	38984	6	NIF3-like protein 1
UniRef100_Q	2	2	8.10%	332	37029	7	Hypothetical protein DKFZp762L015
UniRef100_O	2	3	7.20%	290	32113	7	Pirin
UniRef100_Q	2	3	7.20%	290	32157	7	PIR protein
UniRef100_P	2	3	7.20%	251	26886	#	Azurocidin precursor
UniRef100_Q	6	15	7.10%	1274	1E+05	6	Symplekin
UniRef100_Q	5	5	7.10%	1049	1E+05	5	Desmoglein-1 precursor
UniRef100_UI	5	5	7.10%	1049	1E+05	5	desmoglein 1 preproprotein
UniRef100_Q	2	3	7.10%	538	60647	7	CWF19-like protein 1
UniRef100_Q	2	3	7.10%	538	60619	7	CDNA FLJ10998 fis, clone PLACE1002465
UniRef100_Q	3	3	7.10%	507	58579	8	SEPT10 protein
UniRef100_UI	3	3	6.60%	547	63282	7	Septin-10.
UniRef100_UI	3	3	6.90%	519	60191	7	Septin-10.
UniRef100_Q	3	3	7.90%	454	52593	7	Isoform 2 of Q9P0V9
UniRef100_Q	3	3	7.00%	517	59982	7	Septin-10
UniRef100_Q	2	5	7.10%	476	51856	8	Abl-interactor 1 variant
UniRef100_UI	2	5	8.70%	393	43267	6	Abl interactor 1 (Abelson interactor 1) (Abi-1) (Spectrin SH3 domain- binding protein 1) (Eps8 SH3 domain-binding protein) (Eps8-binding protein) (e3B1) (Nap1-binding protein) (Nap1BP) (Abl-binding protein 4) (AblBP4).
UniRef100_UI	2	5	8.10%	422	46359	6	Abl interactor 1 (Abelson interactor 1) (Abi-1) (Spectrin SH3 domain- binding protein 1) (Eps8 SH3 domain-binding protein) (Eps8-binding protein) (e3B1) (Nap1-binding protein) (Nap1BP) (Abl-binding protein 4) (AblBP4).
UniRef100_UI	2	5	7.10%	476	51829	7	Abl interactor 1 (Abelson interactor 1) (Abi-1) (Spectrin SH3 domain- binding protein 1) (Eps8 SH3 domain-binding protein) (Eps8-binding protein) (e3B1) (Nap1-binding protein) (Nap1BP) (Abl-binding protein 4) (AblBP4).
UniRef100_UI	2	5	7.10%	481	52441	7	Abl interactor 1 (Abelson interactor 1) (Abi-1) (Spectrin SH3 domain- binding protein 1) (Eps8 SH3 domain-binding protein) (Eps8-binding protein) (e3B1) (Nap1-binding protein) (Nap1BP) (Abl-binding protein 4) (AblBP4).
UniRef100_UI	2	5	6.70%	508	55054	6	Abl interactor 1 (Abelson interactor 1) (Abi-1) (Spectrin SH3 domain- binding protein 1) (Eps8 SH3 domain-binding protein) (Eps8-binding protein) (e3B1) (Nap1-binding protein) (Nap1BP) (Abl-binding protein 4) (AblBP4).
UniRef100_UI	2	5	7.20%	475	51770	7	Abl interactor 1 (Abelson interactor 1) (Abi-1) (Spectrin SH3 domain- binding protein 1) (Eps8 SH3 domain-binding protein) (Eps8-binding protein) (e3B1) (Nap1-binding protein) (Nap1BP) (Abl-binding protein 4) (AblBP4).
UniRef100_Q	2	5	8.70%	393	43309	6	Isoform 8 of Q8IZP0
UniRef100_Q	2	5	8.10%	422	46386	6	Isoform 7 of Q8IZP0
UniRef100_Q	2	5	8.80%	388	42668	6	Isoform 10 of Q8IZP0
UniRef100_Q	2	5	6.70%	508	55081	7	Abl interactor 1
UniRef100_Q	2	5	7.10%	476	51841	7	Spectrin SH3 domain binding protein 1
UniRef100_Q	2	5	7.50%	452	49376	7	Spectrin SH3 domain binding protein 1
UniRef100_Q	2	5	7.60%	446	48678	7	Spectrin SH3 domain binding protein 1

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	2	5	7.10%	480	52397	7	Spectrin SH3 domain binding protein 1
UniRef100_Q	2	5	7.10%	481	52468	7	Spectrin SH3 domain binding protein 1
UniRef100_O	3	3	7.10%	438	49754	6	Epsilon-sarcoglycan precursor
UniRef100_U	3	3	6.70%	462	52646	7	Epsilon-sarcoglycan precursor (Epsilon-SG).
UniRef100_Q	3	3	7.10%	437	49864	7	Sarcoglycan, epsilon
UniRef100_Q	3	3	7.10%	437	49881	7	Mutant epsilon-sarcoglycan
UniRef100_Q	3	3	7.30%	427	48574	6	Brain epsilon-sarcoglycan
UniRef100_O	3	3	7.50%	413	47011	6	Isoform SGCE
UniRef100_Q	4	5	7.00%	886	1E+05	5	General transcription factor 3C polypeptide 3
UniRef100_Q	2	5	7.00%	385	44141	6	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1
UniRef100_U	2	5	6.90%	393	44913	6	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1 (Integrase interactor 1 protein) (hSNF5) (BAF47).
UniRef100_Q	2	5	6.90%	394	45051	6	CDNA FLJ13963 fis, clone Y79AA1001299, highly similar to Homo sapiens integrase interactor 1b protein
UniRef100_Q	2	5	33.80%	80	9094	7	Integrase interactor 1 protein isoform D
UniRef100_Q	2	5	30.30%	89	10077	9	Integrase interactor 1 protein isoform E
UniRef100_Q	2	5	7.20%	376	43158	6	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1
UniRef100_P	2	2	7.00%	256	27807	8	Myeloblastin precursor
UniRef100_Q	2	2	7.60%	237	25885	8	Proteinase 3 precursor
UniRef100_Q	2	2	7.00%	256	27821	8	Proteinase 3
UniRef100_A	6	10	6.90%	1052	1E+05	6	Ubiquitin-activating enzyme E1-like protein 2
UniRef100_U	6	10	6.90%	1052	1E+05	6	ubiquitin-activating enzyme E1-like 2
UniRef100_A	5	7	6.90%	1043	1E+05	7	Tight junction protein 2
UniRef100_U	5	7	6.10%	1190	1E+05	7	tight junction protein 2 (zona occludens 2) isoform 1
UniRef100_Q	5	7	7.30%	993	1E+05	8	Isoform A3 of Q9UDY2
UniRef100_Q	5	7	7.10%	1019	1E+05	7	Isoform C2 of Q9UDY2
UniRef100_Q	5	7	6.20%	1167	1E+05	7	Isoform C1 of Q9UDY2
UniRef100_Q	5	7	6.90%	1042	1E+05	7	Isoform A2 of Q9UDY2
UniRef100_Q	5	7	6.10%	1190	1E+05	7	Tight junction protein ZO-2
UniRef100_Q	5	7	7.30%	993	1E+05	8	Tight junction protein 2
UniRef100_Q	4	6	6.90%	1059	1E+05	7	Microtubule-associated protein 1S
UniRef100_Q	4	6	10.90%	672	70686	9	CDNA FLJ10669 fis, clone NT2RP2006275, weakly similar to MICROTUBULE- ASSOCIATED PROTEIN 1B
UniRef100_Q	4	6	7.60%	962	1E+05	8	MAP1S protein
UniRef100_Q	4	6	19.80%	369	39002	7	MAP1S protein
UniRef100_Q	4	6	9.10%	806	85041	9	MAP1S protein
UniRef100_Q	4	6	10.90%	672	70686	9	OK/SW-cl.100 protein
UniRef100_Q	4	6	6.90%	1059	1E+05	7	VCY2 interacting protein-1
UniRef100_Q	4	6	6.90%	1061	1E+05	7	Hypothetical protein DKFZp761H0722

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	4	6	6.90%	1061	1E+05	7	Microtubule-associated protein 1S
UniRef100_Q	3	6	6.90%	671	74317	8	Hepatoma-derived growth factor 2
UniRef100_U	3	6	6.80%	676	74816	7	hepatoma-derived growth factor-related protein 2 isoform 1
UniRef100_Q	3	6	6.90%	670	74230	8	Hepatoma-derived growth factor-related protein 2
UniRef100_P	4	5	6.90%	638	71370	8	Plasma kallikrein precursor (EC 3.4.21.34) (Plasma prekallikrein) (Kininogenin) (Fletcher factor) [Contains: Plasma kallikrein heavy chain; Plasma kallikrein light chain]
UniRef100_U	4	5	6.90%	641	71726	8	Plasma kallikrein precursor (EC 3.4.21.34) (Plasma prekallikrein) (Kininogenin) (Fletcher factor) [Contains: Plasma kallikrein heavy chain; Plasma kallikrein light chain].
UniRef100_Q	4	5	6.90%	638	71343	8	Hypothetical protein KLKB1
UniRef100_Q	4	5	6.90%	638	71342	8	Kallikrein B, plasma (Fletcher factor) 1
UniRef100_O	3	6	6.90%	577	63182	9	Double-stranded RNA-binding protein Staufen homolog 1
UniRef100_Q	3	6	8.10%	494	54709	#	Staufen, RNA binding protein, homolog 1
UniRef100_Q	3	6	8.00%	502	55635	#	Staufen, RNA binding protein, homolog 1
UniRef100_O	3	6	8.10%	496	54934	#	Isoform Short of O95793
UniRef100_Q	3	6	6.90%	436	48963	8	Enigma homolog
UniRef100_U	3	6	6.20%	487	53135	8	PDZ and LIM domain 5 isoform b
UniRef100_U	3	6	5.00%	596	64002	8	PDZ and LIM domain 5 isoform a
UniRef100_Q	3	6	5.00%	596	63972	8	PDZ and LIM domain protein 5
UniRef100_Q	3	6	5.00%	596	64028	8	L9
UniRef100_Q	2	6	6.90%	291	32315	8	RALY-like protein isoform 1
UniRef100_U	2	6	7.00%	286	31701	8	RALY-like protein isoform 1 (RALY-like protein isoform 2).
UniRef100_Q	2	6	6.90%	291	32331	8	LOC138046 protein
UniRef100_P	2	4	6.90%	288	31731	8	Erythrocyte band 7 integral membrane protein
UniRef100_Q	2	4	16.30%	123	13475	8	Stomatin
UniRef100_P	18	40	6.80%	3396	4E+05	5	Versican core protein precursor
UniRef100_Q	18	40	6.70%	3410	4E+05	5	Chondroitin sulfate proteoglycan 2 (Versican) variant
UniRef100_P	18	40	6.80%	3370	4E+05	5	Isoform Vint of P13611
UniRef100_P	18	40	9.50%	2409	3E+05	5	Isoform V1 of P13611
UniRef100_Q	14	39	6.80%	2542	3E+05	6	Talin-2
UniRef100_U	14	39	6.80%	2544	3E+05	6	Talin-2.
UniRef100_U	14	39	6.80%	2542	3E+05	6	Talin-2.
UniRef100_A	4	4	6.80%	902	1E+05	8	Zinc finger CCCH type, antiviral 1
UniRef100_U	4	4	6.80%	902	1E+05	8	Zinc finger CCCH type antiviral protein 1 (Zinc finger CCCH domain- containing protein 2).
UniRef100_Q	4	4	6.80%	902	1E+05	8	Zinc finger CCCH type antiviral protein 1
UniRef100_P	2	2	6.80%	322	34735	7	Arginase-1
UniRef100_U	2	2	9.30%	237	25485	8	Arginase-1 (EC 3.5.3.1) (Type I arginase) (Liver-type arginase).
UniRef100_Q	2	2	9.30%	236	25356	9	Arginase, liver
UniRef100_P	2	2	6.70%	330	35664	7	Isoform 2 of P05089
UniRef100_P	6	8	6.70%	1366	1E+05	9	Collagen alpha-2(I) chain precursor
UniRef100_U	6	8	6.70%	1366	1E+05	9	alpha 2 type I collagen
UniRef100_Q	3	3	6.70%	659	72996	5	Protein phosphatase Slingshot homolog 3

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_UI	3	3	6.70%	659	72936	5	slingshot homolog 3
UniRef100_A(	3	3	6.70%	598	65990	9	Insulin-like growth factor 2 mRNA binding protein 2
UniRef100_Q!	3	3	7.20%	556	61843	8	Insulin-like growth factor 2 mRNA-binding protein 2
UniRef100_P1	4	228	6.70%	534	57285	7	Keratin, type II cytoskeletal 4
UniRef100_UI	4	228	6.10%	594	63911	8	keratin 4
UniRef100_UI	4	228	6.90%	520	56144	7	Keratin, type II cytoskeletal 4 (Cytokeratin-4) (CK-4) (Keratin-4) (K4).
UniRef100_O(	2	12	6.70%	492	53818	5	Target of Myb protein 1
UniRef100_Q8	2	12	6.70%	493	53875	5	Target of myb1
UniRef100_Q!	2	3	6.70%	460	52337	7	Dynactin subunit 4
UniRef100_Q8	2	5	6.70%	464	48525	5	Proline-rich coiled-coil protein 1
UniRef100_UI	2	5	6.70%	466	48637	6	proline-rich coiled-coil 1
UniRef100_UI	2	5	10.20%	304	32825	6	proline-rich coiled-coil 1
UniRef100_Q!	2	5	7.00%	445	46701	6	CDNA FLJ32875 fis, clone TESTI2004031
UniRef100_Q8	2	5	10.20%	305	32896	6	FLJ00410 protein
UniRef100_Q8	2	5	6.70%	462	48907	5	Hypothetical protein
UniRef100_Q8	2	3	6.70%	312	37477	#	PRP38 pre-mRNA processing factor 38 domain-containing protein A
UniRef100_Q!	2	3	8.90%	236	28732	#	CDNA FLJ14936 fis, clone PLACE1010194, weakly similar to SPLICING FACTOR, ARGININE/SERINE-RICH 2
UniRef100_P(	2	2	6.70%	255	28837	#	Cathepsin G precursor
UniRef100_O	11	13	6.60%	2285	2E+05	7	AT-rich interactive domain-containing protein 1A
UniRef100_O	11	13	7.30%	2068	2E+05	7	Isoform 2 of O14497
UniRef100_Q!	7	7	6.60%	1393	2E+05	6	Rab3 GTPase-activating protein non-catalytic subunit
UniRef100_UI	7	7	6.60%	1393	2E+05	6	Rab3 GTPase-activating protein non-catalytic subunit (Rab3 GTPase- activating protein 150 kDa subunit) (Rab3-GAP p150) (Rab3-GAP regulatory subunit) (RAB3-GAP150) (RGAP-iso).
UniRef100_Q!	7	8	6.60%	1272	1E+05	6	Regulator of nonsense transcripts 2
UniRef100_Q	5	8	6.60%	1158	1E+05	5	Aortic carboxypeptidase-like protein ACLP
UniRef100_Q8	5	8	6.60%	1158	1E+05	5	AE binding protein 1
UniRef100_Q7	5	8	9.10%	845	96173	5	AEBP1
UniRef100_Q(	5	8	10.50%	733	81996	5	CDNA FLJ45634 fis, clone CHONS2002829, moderately similar to Homo sapiens adipocyte enhancer binding protein 1
UniRef100_Q!	5	8	6.60%	1172	1E+05	5	AE-binding protein 1
UniRef100_Q!	4	7	6.60%	717	81614	7	Pinin
UniRef100_UI	4	7	6.60%	717	81628	7	Pinin (140 kDa nuclear and cell adhesion-related phosphoprotein) (Domain-rich serine protein) (DRS-protein) (DRSP) (Melanoma metastasis clone A protein) (Desmosome-associated protein) (SR-like protein) (Nuclear protein SDK3).
UniRef100_Q!	4	7	8.00%	584	67005	6	Isoform 2 of Q9H307
UniRef100_O!	2	2	6.60%	621	71479	6	F-box only protein 21
UniRef100_Q8	2	2	8.60%	477	55831	6	FBXO21 protein
UniRef100_Q4	2	2	7.60%	537	62516	6	FBXO21 protein
UniRef100_O!	2	2	6.50%	628	72270	6	Isoform 2 of O94952
UniRef100_Q	4	5	6.60%	482	55103	6	Histone deacetylase 1

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_UI	8	15	6.50%	1593	2E+05	8	THO complex 2 isoform 1
UniRef100_Q	3	4	6.50%	795	87157	6	Phospholipase A-2-activating protein
UniRef100_UI	3	4	7.00%	738	80827	6	phospholipase A2-activating protein isoform 2
UniRef100_A	3	9	6.50%	689	73612	7	Zinc finger protein 185
UniRef100_UI	3	9	13.80%	327	34954	5	Zinc finger protein 185 (LIM domain protein ZNF185) (P1-A).
UniRef100_UI	3	9	10.00%	452	48621	5	Zinc finger protein 185 (LIM domain protein ZNF185) (P1-A).
UniRef100_Q	3	9	13.80%	327	34982	6	CDNA FLJ37939 fis, clone CTONG2007613, highly similar to ZINC FINGER PROTEIN 185
UniRef100_Q	3	9	9.60%	471	49933	6	Hypothetical protein DKFZp686B22130
UniRef100_O	3	9	9.80%	457	49187	5	Zinc finger protein 185
UniRef100_Q	2	2	6.50%	601	68352	6	Cdc42-interacting protein 4
UniRef100_Q	2	2	11.40%	341	39583	8	Isoform 5 of Q15642
UniRef100_Q	2	2	8.60%	456	52700	7	Isoform 4 of Q15642
UniRef100_Q	2	2	6.60%	593	67603	6	Isoform 3 of Q15642
UniRef100_Q	2	2	7.20%	545	62592	5	Isoform 2 of Q15642
UniRef100_Q	2	5	6.50%	568	63070	9	MSTP089
UniRef100_UI	2	5	6.10%	608	67707	9	eukaryotic translation initiation factor 2A
UniRef100_UI	2	5	6.30%	585	64990	9	eukaryotic translation initiation factor 2A
UniRef100_Q	2	5	6.10%	609	67851	9	Eukaryotic translation initiation factor 2A 65 kDa
UniRef100_Q	2	5	6.30%	585	64986	9	CDNA FLJ14450 fis, clone HEMBB1001736, weakly similar to EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9
UniRef100_Q	2	5	6.30%	585	64989	9	Eukaryotic translation initiation factor 2A, 65kDa
UniRef100_Q	2	5	6.30%	585	65060	9	Eukaryotic translation initiation factor 2A
UniRef100_Q	2	2	6.50%	292	34068	6	DCN1-like protein 4
UniRef100_Q	2	2	7.40%	257	29984	6	Isoform 2 of Q92564
UniRef100_A	2	2	6.50%	261	28554	9	Hypothetical protein
UniRef100_UI	2	2	5.00%	340	36992	9	muscleblind-like 1 isoform f
UniRef100_Q	2	2	5.60%	302	33050	9	Isoform EXP35 of Q9NR56
UniRef100_Q	2	2	4.60%	370	39831	9	Isoform EXP40 of Q9NR56
UniRef100_Q	2	2	4.40%	388	41817	9	Muscleblind-like protein 1
UniRef100_Q	2	2	5.40%	314	34211	9	36 kDa muscleblind protein EXP36
UniRef100_Q	2	2	4.50%	382	40992	9	Muscleblind 41kD isoform
UniRef100_Q	2	2	5.00%	341	37063	9	Muscleblind-like protein EXP40s
UniRef100_Q	2	2	5.00%	342	37074	9	Muscleblind-like protein EXP41s
UniRef100_Q	2	2	4.60%	367	39334	9	Isoform 2 of Q5VZF2
UniRef100_Q	2	2	4.60%	373	40518	8	Muscleblind-like protein 2
UniRef100_O	2	2	6.70%	255	28141	9	Zinc finger protein
UniRef100_A	2	2	4.70%	361	39356	8	Muscleblind-like 2
UniRef100_Q	11	13	6.40%	2054	2E+05	6	Myosin-XVIIIa
UniRef100_UI	11	13	6.50%	2005	2E+05	6	TGFB1-induced anti-apoptotic factor 1 (12 kDa TGF-beta1-induced antiapoptotic factor).
UniRef100_UI	11	13	6.40%	2057	2E+05	6	TGFB1-induced anti-apoptotic factor 1 (12 kDa TGF-beta1-induced antiapoptotic factor).
UniRef100_UI	11	13	6.40%	2042	2E+05	6	TGFB1-induced anti-apoptotic factor 1 (12 kDa TGF-beta1-induced antiapoptotic factor).

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	11	13	6.40%	2039	2E+05	6	Isoform 4 of Q92614
UniRef100_Q	11	13	6.50%	2002	2E+05	6	Isoform 3 of Q92614
UniRef100_Q	9	23	6.40%	1781	2E+05	4	A-kinase anchor protein 12
UniRef100_Q	9	23	6.80%	1678	2E+05	4	Hypothetical protein DKFZp686O0331
UniRef100_Q	9	23	6.80%	1684	2E+05	4	A kinase (PRKA) anchor protein (Gravin) 12
UniRef100_Q	9	23	6.40%	1782	2E+05	4	A kinase (PRKA) anchor protein (Gravin) 12
UniRef100_Q	9	23	6.40%	1791	2E+05	4	AKAP12 variant protein
UniRef100_Q	9	23	6.80%	1683	2E+05	4	Isoform 2 of Q02952
UniRef100_Q	4	6	6.40%	999	1E+05	5	Oxygen regulated protein variant
UniRef100_Q	4	6	6.40%	999	1E+05	5	150 kDa oxygen-regulated protein precursor
UniRef100_A	5	8	6.40%	839	97000	7	Vav 2 oncogene
UniRef100_U	5	8	6.40%	840	97202	7	Protein vav-2.
UniRef100_U	5	8	6.10%	879	1E+05	7	Protein vav-2.
UniRef100_Q	5	8	6.20%	878	1E+05	7	Vav 2 oncogene
UniRef100_Q	5	8	6.20%	868	1E+05	7	Vav 2 oncogene
UniRef100_Q	5	8	6.40%	839	97032	7	Vav 2 oncogene
UniRef100_P	5	8	6.20%	878	1E+05	7	Protein vav-2
UniRef100_P	3	4	6.40%	677	76091	7	Beta-galactosidase precursor
UniRef100_U	3	4	6.40%	677	76075	7	galactosidase, beta 1 isoform a
UniRef100_U	3	4	6.40%	677	76038	7	Beta-galactosidase-related protein precursor (Beta-galactosidase-like protein) (S-Gal) (Elastin-binding protein) (EBP).
UniRef100_Q	3	4	6.40%	677	76110	6	Galactosidase, beta 1 variant
UniRef100_Q	3	4	6.40%	677	76069	7	Galactosidase, beta 1 variant
UniRef100_P	3	4	6.40%	661	75511	6	Coagulation factor XIII B chain precursor
UniRef100_Q	2	3	6.40%	629	73986	6	PRPF39 protein
UniRef100_Q	2	3	6.40%	629	73887	6	Pre-mRNA-processing factor 39
UniRef100_P	4	6	6.40%	543	60801	7	Proto-oncogene tyrosine-protein kinase Yes
UniRef100_Q	4	8	6.40%	545	60234	#	Hypothetical protein DKFZP564A2416
UniRef100_U	4	8	6.40%	546	60362	#	DNA polymerase-transactivated protein 6 (DNAPTP6), mRNA
UniRef100_U	4	8	7.30%	477	52812	#	DNA polymerase-transactivated protein 6 (DNAPTP6), mRNA
UniRef100_Q	4	8	6.30%	558	61759	#	CDNA FLJ11202 fis, clone PLACE1007746
UniRef100_Q	4	8	7.20%	488	54050	#	DNAPTP6 protein
UniRef100_Q	2	2	6.40%	486	56194	7	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit alpha isoform
UniRef100_Q	8	12	6.30%	1619	2E+05	7	Laminin, gamma 3
UniRef100_U	8	12	6.40%	1589	2E+05	7	Laminin subunit gamma-3 precursor (Laminin 12 gamma 3 subunit).
UniRef100_U	8	12	6.50%	1575	2E+05	7	laminin, gamma 3 precursor
UniRef100_Q	8	12	6.40%	1587	2E+05	7	Laminin, gamma 3
UniRef100_P	5	6	6.30%	917	1E+05	6	Hexokinase-2
UniRef100_U	5	6	6.40%	902	1E+05	6	Hexokinase-2
UniRef100_Q	5	6	6.50%	889	98916	6	Hypothetical protein DKFZp686M1669
UniRef100_P	3	4	6.30%	607	66403	5	Rap1 GTPase-GDP dissociation stimulator 1

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_UI	3	4	7.40%	515	56404	5	Rap1 GTPase-GDP dissociation stimulator 1 (SMG P21 stimulatory GDP/GTP exchange protein) (SMG GDS protein) (Exchange factor smgGDS).
UniRef100_UI	3	4	6.20%	608	66388	5	Rap1 GTPase-GDP dissociation stimulator 1 (SMG P21 stimulatory GDP/GTP exchange protein) (SMG GDS protein) (Exchange factor smgGDS).
UniRef100_Q	3	4	6.30%	607	66331	5	RAP1, GTP-GDP dissociation stimulator 1
UniRef100_Q	3	4	7.40%	516	56488	5	GTP-GDP dissociation stimulator 1 isoform A
UniRef100_Q	3	4	6.20%	608	66316	5	RAP1, GTP-GDP dissociation stimulator 1
UniRef100_Q	3	4	6.80%	558	61037	5	RAP1GDS1 protein
UniRef100_Q	3	4	6.80%	559	61108	5	RAP1GDS1 protein
UniRef100_P	3	4	6.80%	558	61123	6	Isoform 2 of P52306
UniRef100_O	2	2	6.30%	538	59232	7	Eyes absent homolog 2
UniRef100_UI	2	2	6.70%	507	55589	7	Eyes absent homolog 2 (EC 3.1.3.48).
UniRef100_Q	2	2	6.60%	514	56703	7	Eyes absent homolog 2
UniRef100_Q	2	2	6.70%	508	55719	7	Eyes absent homolog 2
UniRef100_O	2	2	6.60%	514	56689	7	Isoform 2 of O00167
UniRef100_O	2	2	6.30%	331	36522	5	DNA fragmentation factor subunit alpha
UniRef100_Q	2	2	7.80%	268	29411	5	DNAation factor, 45kDa, alpha polypeptide
UniRef100_Q	2	2	6.30%	331	36594	5	DNAation factor, 45kDa, alpha polypeptide isoform 1 variant
UniRef100_UI	29	40	6.20%	5497	6E+05	6	dystonin isoform 1
UniRef100_Q	6	10	6.20%	1337	2E+05	8	SCC-112 protein
UniRef100_UI	6	10	6.40%	1302	1E+05	8	SCC-112 protein
UniRef100_Q	6	10	6.40%	1297	1E+05	8	SCC-112
UniRef100_Q	6	10	6.40%	1297	1E+05	8	Hypothetical protein DKFZp686B19246
UniRef100_O	5	13	6.20%	1078	1E+05	8	Protein transport protein Sec24A
UniRef100_UI	5	13	6.20%	1077	1E+05	8	Protein transport protein Sec24A (SEC24-related protein A)
UniRef100_UI	5	13	6.10%	1093	1E+05	8	SEC24 related gene family, member A
UniRef100_Q	4	5	6.20%	1024	1E+05	6	Myosin phosphatase Rho-interacting protein
UniRef100_UI	4	5	6.20%	1025	1E+05	6	myosin phosphatase-Rho interacting protein isoform 2
UniRef100_UI	4	5	6.20%	1038	1E+05	6	myosin phosphatase-Rho interacting protein isoform 1
UniRef100_Q	4	5	6.20%	1037	1E+05	6	Isoform 2 of Q6WCQ1
UniRef100_Q	4	4	6.20%	1023	1E+05	6	Transmembrane protein 132A
UniRef100_UI	4	4	8.10%	774	83021	5	transmembrane protein 132A isoform a
UniRef100_Q	4	4	8.10%	774	83181	5	CDNA FLJ20539 fis, clone KAT11311
UniRef100_Q	4	4	9.90%	639	68405	5	CDNA FLJ13515 fis, clone PLACE1005595
UniRef100_Q	2	3	6.20%	368	41149	#	F-box only protein 28
UniRef100_P	3	3	6.10%	792	90070	7	Ribonucleoside-diphosphate reductase large subunit
UniRef100_P	3	4	6.10%	737	83786	6	Glycogen [starch] synthase, muscle
UniRef100_Q	3	4	6.70%	673	76483	7	GYS1 protein
UniRef100_Q	3	4	6.10%	737	83858	6	Glycogen synthase 1 (Muscle) variant
UniRef100_A	3	4	6.10%	560	62643	7	Glycoprotein (Transmembrane) nmb
UniRef100_Q	3	4	5.90%	572	63923	7	Transmembrane glycoprotein NMB precursor

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	3	4	6.10%	544	61555	6	Lariat debranching enzyme
UniRef100_Q	3	3	6.10%	524	61061	7	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform
UniRef100_U	3	3	8.20%	388	45892	7	Serine/threonine-protein phosphatase 2A 56 kD
UniRef100_U	3	3	8.20%	392	45803	6	SERINE/THREONINE-PROTEIN PHOSPHATASE 2A 56 KD
UniRef100_Q	3	3	6.70%	475	55556	7	PP2A B56 gamma 2
UniRef100_Q	3	3	7.30%	439	51563	7	PP2A B56 gamma 1
UniRef100_Q	3	3	8.30%	384	44878	7	Protein phosphatase 2, regulatory subunit B', gamma isoform
UniRef100_Q	3	3	6.20%	514	59956	7	PP2A B56 gamma 3
UniRef100_Q	3	3	5.90%	540	62755	9	CDNA FLJ16473 fis, clone BRHIP3026052, highly similar to Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit, gamma isoform
UniRef100_Q	3	3	6.60%	485	56661	7	Isoform Gamma
UniRef100_Q	3	3	7.10%	449	52625	7	Isoform Gamma
UniRef100_Q	2	3	6.10%	445	52624	6	UBX domain-containing protein 8
UniRef100_O	2	2	6.10%	393	45374	9	Protein KIN homolog
UniRef100_U	2	2	6.10%	396	45372	5	apolipoprotein A-IV precursor
UniRef100_P	3	8	6.00%	929	1E+05	6	RNA-binding protein 10
UniRef100_Q	3	8	6.00%	930	1E+05	6	RNA binding motif protein 10
UniRef100_Q	3	8	5.60%	995	1E+05	6	Hypothetical protein DKFZp686E2459
UniRef100_Q	3	3	6.00%	646	73575	7	Peptidylprolyl isomerase domain and WD repeat-containing protein 1
UniRef100_O	2	3	6.00%	250	28613	9	Golgi SNAP receptor complex member 1
UniRef100_U	2	3	6.00%	248	28293	9	golgi SNAP receptor complex member 1 isoform 2
UniRef100_U	2	3	8.10%	185	21214	#	golgi SNAP receptor complex member 1 isoform 3
UniRef100_U	2	3	8.60%	174	19969	9	Golgi SNAP receptor complex member 1 (28 kDa Golgi SNARE protein) (28 kDa cis-Golgi SNARE p28) (GOS-28).
UniRef100_Q	2	3	8.60%	175	20068	9	GOSR1 protein
UniRef100_Q	2	3	6.00%	248	28336	9	Golgi SNAP receptor complex member 1
UniRef100_Q	7	7	5.90%	1717	2E+05	6	SF21 protein
UniRef100_U	7	7	5.90%	1717	2E+05	6	MON2 homolog
UniRef100_Q	7	7	5.80%	1736	2E+05	6	Protein MON2 homolog
UniRef100_Q	8	12	5.90%	1681	2E+05	7	Hypothetical protein DKFZp434I0113
UniRef100_U	8	12	5.80%	1706	2E+05	7	PREDICTED: similar to c11.1 CG12132-PA isoform 11
UniRef100_U	8	12	5.90%	1681	2E+05	7	CDNA FLJ35542 fis, clone SPLEN2002917.
UniRef100_O	3	5	5.90%	711	79188	8	Long-chain-fatty-acid--CoA ligase 4
UniRef100_Q	3	5	6.30%	670	74422	8	Acyl-CoA synthetase 4
UniRef100_Q	3	21	5.90%	511	55891	7	Keratin-72
UniRef100_Q	3	21	5.90%	510	55749	7	Keratin protein K6irs
UniRef100_Q	3	21	5.90%	511	55877	7	Keratin protein K6irs
UniRef100_Q	3	21	7.50%	398	44698	5	CDNA FLJ35741 fis, clone TESTI2004163, moderately similar to Mus musculus type II cytokeratin
UniRef100_Q	2	4	5.90%	408	45885	6	Aminoacylase-1
UniRef100_Q	17	38	5.80%	3259	4E+05	5	Golgin subfamily B member 1

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_U	17	38	5.80%	3259	4E+05	5	golgi autoantigen, golgin subfamily b, macrogolgin (with transmembrane signal), 1
UniRef100_O	3	3	5.80%	926	1E+05	6	Peripheral plasma membrane protein CASK
UniRef100_U	3	3	6.40%	842	95764	7	Peripheral plasma membrane protein CASK (EC 2.7.11.1) (hCASK) (Calcium/calmodulin-dependent serine protein kinase) (Lin-2 homolog).
UniRef100_U	3	3	6.30%	859	97676	7	Peripheral plasma membrane protein CASK (EC 2.7.11.1) (hCASK) (Calcium/calmodulin-dependent serine protein kinase) (Lin-2 homolog).
UniRef100_U	3	3	5.90%	921	1E+05	7	Peripheral plasma membrane protein CASK (EC 2.7.11.1) (hCASK) (Calcium/calmodulin-dependent serine protein kinase) (Lin-2 homolog).
UniRef100_U	3	3	5.90%	921	1E+05	7	calcium/calmodulin-dependent serine protein kinase (MAGUK family)
UniRef100_O	3	3	5.90%	909	1E+05	6	Isoform 6 of O14936
UniRef100_O	3	3	6.00%	898	1E+05	6	Isoform 4 of O14936
UniRef100_O	3	3	6.00%	897	1E+05	6	Isoform 3 of O14936
UniRef100_O	3	3	5.90%	921	1E+05	7	Isoform 2 of O14936
UniRef100_Q	5	9	5.80%	913	1E+05	#	Serine/arginine repetitive matrix 1
UniRef100_Q	5	9	5.90%	902	1E+05	#	Isoform 2 of Q8IYB3
UniRef100_Q	5	9	5.90%	904	1E+05	#	Serine/arginine repetitive matrix protein 1
UniRef100_Q	3	3	5.80%	719	81124	6	Nucleolar protein 11
UniRef100_Q	16	28	5.80%	586	68186	5	Spectrin, alpha, erythrocytic 1 human alpha 1-584 spectrin
UniRef100_Q	2	2	5.80%	479	51359	5	PVRL2 protein
UniRef100_Q	2	2	6.20%	449	48152	5	Polio virus related protein 2, alpha isoform
UniRef100_Q	2	2	5.20%	538	57742	5	Poliovirus receptor-related protein 2 precursor
UniRef100_Q	2	4	5.80%	434	50144	8	tRNA-nucleotidyltransferase 1, mitochondrial precursor
UniRef100_U	2	4	6.00%	414	47829	9	tRNA-nucleotidyltransferase 1, mitochondrial precursor (EC 2.7.7.25) (Mitochondrial tRNA nucleotidyl transferase, CCA-adding) (mt tRNA adenylyltransferase) (mt tRNA CCA-pyrophosphorylase) (mt tRNA CCA- diphosphorylase) (mt CCA-adding enzyme).
UniRef100_U	2	4	5.80%	434	50128	8	tRNA-nucleotidyltransferase 1, mitochondrial precursor (EC 2.7.7.25) (Mitochondrial tRNA nucleotidyl transferase, CCA-adding) (mt tRNA adenylyltransferase) (mt tRNA CCA-pyrophosphorylase) (mt tRNA CCA- diphosphorylase) (mt CCA-adding enzyme).
UniRef100_Q	2	4	6.00%	414	47845	9	Isoform 2 of Q96Q11
UniRef100_Q	2	3	5.80%	328	36437	8	ATP synthase mitochondrial F1 complex assembly factor 1
UniRef100_U	2	3	7.30%	260	28658	9	ATP synthase mitochondrial F1 complex assembly factor 1 isoform 2 precursor
UniRef100_Q	2	3	5.80%	328	36407	8	CDNA: FLJ22351 fis, clone HRC06325
UniRef100_Q	2	3	5.80%	328	35816	8	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial precursor
UniRef100_Q	2	2	5.80%	309	35171	8	Fructosamine-3-kinase
UniRef100_Q	9	11	5.70%	2236	2E+05	7	AT-rich interactive domain-containing protein 1B
UniRef100_U	9	11	5.70%	2249	2E+05	7	AT-rich interactive domain-containing protein 1B (ARID domain- containing protein 1B) (Osa homolog 2) (hOsa2) (p250R) (BRG1-binding protein hELD/OSA1) (BRG1-associated factor 250b) (BAF250B).
UniRef100_U	9	11	7.40%	1736	2E+05	6	AT-rich interactive domain-containing protein 1B (ARID domain- containing protein 1B) (Osa homolog 2) (hOsa2) (p250R) (BRG1-binding protein hELD/OSA1) (BRG1-associated factor 250b) (BAF250B).

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_U	9	11	5.90%	2178	2E+05	7	AT rich interactive domain 1B (SWI1-like) isoform 3
UniRef100_Q	9	11	5.60%	2289	2E+05	7	Isoform 3 of Q8NFD5
UniRef100_Q	9	11	5.70%	2249	2E+05	7	Isoform 2 of Q8NFD5
UniRef100_O	3	4	5.70%	902	98829	6	10-formyltetrahydrofolate dehydrogenase
UniRef100_Q	3	4	10.10%	505	55394	5	ALDH1L1 protein
UniRef100_Q	3	4	5.30%	954	1E+05	6	Aldehyde dehydrogenase 1 family, member L1 variant
UniRef100_Q	3	4	5.70%	902	98857	6	Formyltetrahydrofolate dehydrogenase isoform a variant
UniRef100_O	2	4	5.70%	671	74606	9	Signal recognition particle 72 kDa protein
UniRef100_Q	3	4	5.70%	597	68436	7	Tyrosine-protein phosphatase non-receptor type 11
UniRef100_Q	3	4	7.40%	460	52828	7	Isoform 3 of Q06124
UniRef100_Q	3	4	5.70%	593	68011	7	Isoform 2 of Q06124
UniRef100_Q	3	4	5.70%	582	66899	#	La-related protein 7
UniRef100_Q	3	4	15.40%	214	24488	9	Isoform 2 of Q4G0J3
UniRef100_O	2	7	5.70%	548	63973	6	Eukaryotic translation initiation factor 3 subunit 7
UniRef100_Q	2	2	5.70%	524	58852	6	Hypothetical protein FLJ20071
UniRef100_U	2	2	4.50%	669	75935	6	dymeclin
UniRef100_Q	2	2	7.10%	424	47994	7	CDNA FLJ20071 fis, clone COL01887
UniRef100_Q	2	2	4.50%	669	75936	6	Dymeclin
UniRef100_Q	2	2	5.70%	510	55382	5	Poliovirus receptor-related protein 4
UniRef100_Q	2	2	5.70%	510	55454	5	Nectin 4
UniRef100_P	2	3	5.70%	333	38388	6	Eukaryotic translation initiation factor 2 subunit 2
UniRef100_U	2	3	5.80%	327	37787	6	PREDICTED: similar to Eukaryotic translation initiation factor 2 subunit 2 (Eukaryotic translation initiation factor 2 beta subunit) (eIF-2-beta)
UniRef100_Q	2	3	8.90%	214	24575	9	EIF2S2 protein
UniRef100_P	13	21	5.60%	1972	2E+05	6	Myosin-11
UniRef100_Q	13	21	5.60%	1979	2E+05	6	Smooth muscle myosin heavy chain isoform SM1
UniRef100_Q	13	21	5.70%	1945	2E+05	6	Smooth muscle myosin heavy chain isoform SM2
UniRef100_Q	13	21	5.70%	1938	2E+05	6	Myosin, heavy chain 11, smooth muscle
UniRef100_Q	10	20	5.60%	2060	2E+05	4	Hypothetical protein DKFZp686K06110
UniRef100_O	4	6	5.60%	1032	1E+05	7	Protein transport protein Sec24D
UniRef100_U	4	6	5.60%	1032	1E+05	7	Protein transport protein Sec24D (SEC24-related protein D).
UniRef100_Q	4	6	5.60%	1033	1E+05	7	SEC24 related gene family, member D
UniRef100_Q	4	6	14.80%	393	43969	6	SEC24D protein
UniRef100_O	4	14	5.60%	957	1E+05	8	Pre-mRNA-processing factor 40 homolog A
UniRef100_U	4	14	5.50%	974	1E+05	8	PREDICTED: similar to Pre-mRNA-processing factor 40 homolog A (Formin-binding protein 3) (Huntingtin yeast partner A) (Huntingtin-interacting protein HYPA/FBP11) (Fas ligand-associated factor 1) (NY-REN-6 antigen) isoform 1
UniRef100_U	4	14	6.50%	827	95332	8	Pre-mRNA-processing factor 40 homolog A (Formin-binding protein 3) (Formin-binding protein 11) (Huntingtin-interacting protein HYPA) (Huntingtin yeast partner A) (Fas ligand-associated factor 1) (NY-REN- 6 antigen).
UniRef100_O	4	14	5.80%	939	1E+05	7	Isoform 3 of O75400

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_O	4	14	5.90%	915	1E+05	8	Isoform 2 of O75400
UniRef100_Q	2	2	5.60%	832	94133	7	KIAA1274
UniRef100_U	2	2	5.50%	856	96754	7	KIAA1274
UniRef100_Q	2	2	5.50%	861	97356	7	Protein KIAA1274
UniRef100_Q	4	7	5.60%	802	92251	8	Cell division cycle 5-like protein
UniRef100_Q	2	3	5.60%	710	78418	7	Hypothetical protein DKFZp686I1650
UniRef100_Q	2	3	4.20%	951	1E+05	8	WD repeat protein 36
UniRef100_A	2	2	5.60%	478	53226	9	Hypothetical protein
UniRef100_O	2	2	3.60%	754	84959	7	Nibrin
UniRef100_P	3	4	5.60%	447	51692	6	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform
UniRef100_U	3	4	5.60%	448	52925	8	Dedicator of cytokinesis protein 5.
UniRef100_Q	3	4	5.60%	448	52953	8	CDNA FLJ26613 fis, clone MPB05565, highly similar to Serine/threonine protein phosphatase 2A, 55 kDa regulatory subunit B, alpha isoform
UniRef100_Q	3	4	5.60%	447	51648	6	Lung cancer-related protein 9
UniRef100_Q	2	3	5.60%	394	44403	5	RNA U small nuclear RNA export adapter protein
UniRef100_P	13	33	5.50%	3433	4E+05	5	Utrophin
UniRef100_U	13	33	5.50%	3433	4E+05	5	Utrophin (Dystrophin-related protein 1) (DRP1) (DRP).
UniRef100_Q	13	33	5.50%	3433	4E+05	5	Utrophin
UniRef100_Q	10	16	5.50%	2570	3E+05	7	FEX1
UniRef100_U	10	16	5.50%	2570	3E+05	7	stabilin 1 precursor
UniRef100_Q	10	16	5.50%	2570	3E+05	7	Stabilin-1 precursor
UniRef100_P	8	13	5.50%	1531	2E+05	9	DNA topoisomerase 2-alpha
UniRef100_U	8	13	5.40%	1568	2E+05	9	TOP2A_HUMAN Isoform 2 of P11388 - Homo sapiens (Human)
UniRef100_P	8	13	5.20%	1612	2E+05	9	Isoform 4 of P11388
UniRef100_P	8	13	5.40%	1567	2E+05	9	Isoform 3 of P11388
UniRef100_P	8	13	5.40%	1557	2E+05	9	Isoform 2 of P11388
UniRef100_Q	2	2	5.50%	763	86647	5	COG4 protein
UniRef100_U	2	2	5.30%	789	89501	5	component of oligomeric golgi complex 4
UniRef100_U	2	2	6.00%	695	78862	5	Conserved oligomeric Golgi complex component 4.
UniRef100_Q	2	2	5.40%	785	89095	5	Conserved oligomeric Golgi complex component 4
UniRef100_Q	2	2	6.00%	695	78969	5	CDNA FLJ39238 fis, clone OCBBF2007946
UniRef100_Q	3	3	5.50%	709	79664	5	DCC-interacting protein 13 alpha
UniRef100_Q	2	2	5.50%	603	69932	8	Myotubularin
UniRef100_U	2	2	5.50%	605	70104	8	Myotubularin (EC 3.1.3.48).
UniRef100_U	2	2	5.50%	602	69804	8	Myotubularin (EC 3.1.3.48).
UniRef100_Q	3	13	5.50%	508	57564	8	Phenylalanyl-tRNA synthetase alpha chain
UniRef100_P	2	3	5.50%	452	50909	9	Isocitrate dehydrogenase [NADP], mitochondrial precursor (EC 1.1.1.42) (Oxalosuccinate decarboxylase) (IDH) (NADP(+)-specific ICDH)
UniRef100_Q	2	3	5.50%	452	50910	9	Isocitrate dehydrogenase 2 (NADP+), mitochondrial variant
UniRef100_Q	5	6	5.40%	1057	1E+05	6	Probable E3 ubiquitin-protein ligase HERC4
UniRef100_Q	5	6	6.30%	907	1E+05	6	Hect domain and RLD 4

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q5	5	6	6.00%	947	1E+05	7	Isoform 6 of Q5GLZ8
UniRef100_Q5	5	6	5.80%	979	1E+05	7	Isoform 3 of Q5GLZ8
UniRef100_Q5	5	6	5.40%	1049	1E+05	6	Isoform 2 of Q5GLZ8
UniRef100_Q5	2	2	5.40%	774	85900	7	G protein-coupled receptor kinase interactor 1 variant
UniRef100_Q9	2	2	5.50%	761	84341	7	ARF GTPase-activating protein GIT1
UniRef100_P1	4	11	5.40%	742	81554	5	CD44 antigen precursor
UniRef100_UI	4	11	8.10%	493	53411	5	CD44 antigen isoform 3 precursor
UniRef100_UI	4	11	5.70%	699	76612	5	CD44 antigen isoform 2 precursor
UniRef100_UI	4	11	5.40%	742	81538	5	CD44 antigen isoform 1 precursor
UniRef100_Q9	4	11	5.90%	676	73929	5	CD44 molecule
UniRef100_Q9	4	11	8.50%	470	50728	5	CD44 molecule
UniRef100_Q9	4	11	5.60%	719	78854	5	CD44 molecule
UniRef100_Q9	4	11	11.80%	338	36733	5	CD44 molecule
UniRef100_P1	4	11	5.90%	674	74404	5	Isoform 8 of P16070
UniRef100_P1	4	11	5.60%	713	78461	5	Isoform 7 of P16070
UniRef100_P1	4	11	5.70%	699	76692	5	Isoform 6 of P16070
UniRef100_P1	4	11	5.40%	734	80806	5	Isoform 5 of P16070
UniRef100_P1	4	11	5.70%	699	76628	5	Isoform 4 of P16070
UniRef100_P1	4	11	5.60%	711	77999	5	Isoform 3 of P16070
UniRef100_P1	4	11	5.80%	691	75945	5	Isoform 17 of P16070
UniRef100_P1	4	11	6.00%	668	73138	5	Isoform 16 of P16070
UniRef100_P1	4	11	10.10%	396	43157	5	Isoform 14 of P16070
UniRef100_P1	4	11	9.40%	425	46249	5	Isoform 13 of P16070
UniRef100_P1	4	11	9.30%	429	46565	6	Isoform 11 of P16070
UniRef100_P1	4	11	8.10%	493	53399	5	Isoform 10 of P16070
UniRef100_P0	3	4	5.40%	626	68955	7	Platelet glycoprotein Ib alpha chain precursor (Glycoprotein Ibalpha) (GP-Ib alpha) (GPIbA) (GPIb-alpha) (Antigen CD42b-alpha) (CD42b antigen) [Contains: Glycocalicin]
UniRef100_UI	3	4	5.40%	627	68967	7	Platelet glycoprotein Ib alpha chain precursor (Glycoprotein Ibalpha) (GP-Ib alpha) (GPIbA) (GPIb-alpha) (Antigen CD42b-alpha) (CD42b antigen) [Contains: Glycocalicin].
UniRef100_P4	2	2	5.40%	572	64150	6	NADP-dependent malic enzyme
UniRef100_Q9	3	5	5.40%	572	61640	8	Far upstream element-binding protein 3
UniRef100_Q4	2	2	5.40%	553	60606	9	Cytokine-like nuclear factor n-pac
UniRef100_UI	2	2	5.60%	536	58637	9	cytokine-like nuclear factor n-pac
UniRef100_UI	2	2	5.40%	553	60556	9	cytokine-like nuclear factor n-pac
UniRef100_Q9	2	2	5.50%	547	59828	9	Cytokine-like nuclear factor n-pac
UniRef100_Q9	2	2	5.70%	523	57215	9	Similar to RIKEN cDNA 3930401K13 gene
UniRef100_Q6	2	2	5.40%	553	60547	9	Cytokine-like nuclear factor n-pac-like protein
UniRef100_Q6	2	2	6.20%	484	52550	9	N-PAC protein
UniRef100_Q5	2	2	5.40%	553	60548	9	Cytokine-like nuclear factor n-pac

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P1	2	2	5.40%	480	54466	7	Lysosomal protective protein precursor (EC 3.4.16.5) (Cathepsin A) (Carboxypeptidase C) (Protective protein for beta-galactosidase) [Contains: Lysosomal protective protein 32 kDa chain; Lysosomal protective protein 20 kDa chain]
UniRef100_Q5	2	2	5.20%	497	56120	7	Carrier family 6 , member 8 variant
UniRef100_Q5	2	2	5.40%	404	46816	7	Sorting nexin 5 variant
UniRef100_Q9	2	2	5.40%	404	46817	7	Sorting nexin-5
UniRef100_Q6	2	2	5.30%	412	47438	8	SNX5 protein
UniRef100_Q5	2	2	8.20%	269	31030	7	Sorting nexin 5
UniRef100_Q5	2	2	9.60%	228	26305	6	Sorting nexin 5
UniRef100_O7	2	2	5.40%	350	39641	5	Protein XRP2
UniRef100_UI	2	2	5.40%	350	39642	5	XRP2 protein
UniRef100_P0	2	2	5.40%	224	25039	6	C-reactive protein precursor [Contains: C-reactive protein(1-205)]
UniRef100_Q9	2	3	5.30%	628	68723	6	Set1/Ash2 histone methyltransferase complex subunit ASH2
UniRef100_UI	2	3	5.30%	628	68683	6	ash2-like
UniRef100_Q9	2	3	6.20%	534	60208	7	Isoform 3 of Q9UBL3
UniRef100_P0	2	3	5.30%	532	57825	8	Intercellular adhesion molecule 1 precursor
UniRef100_UI	2	3	5.30%	532	57826	8	intercellular adhesion molecule 1 precursor
UniRef100_Q5	2	3	5.30%	532	57882	8	Intercellular adhesion molecule 1
UniRef100_Q5	2	3	5.30%	528	57502	8	Intercellular adhesion molecule 1
UniRef100_Q5	2	2	5.30%	469	52787	6	OTTHUMP00000028646
UniRef100_Q8	2	2	5.30%	469	52753	6	Hypothetical protein FLJ20699
UniRef100_P2	3	7	5.30%	488	52739	6	Annexin A7
UniRef100_Q5	3	7	5.30%	488	52739	6	Annexin A7
UniRef100_Q5	3	7	5.60%	466	50316	7	Annexin A7
UniRef100_Q5	3	7	5.60%	466	50228	7	Annexin VII isoform 1 variant
UniRef100_Q5	5	8	5.20%	1110	1E+05	7	Tripartite motif-containing 33
UniRef100_Q9	5	8	5.20%	1110	1E+05	7	Isoform Beta of Q9UPN9
UniRef100_P0	4	4	5.20%	1048	1E+05	6	Integrin alpha-V precursor (Vitronectin receptor subunit alpha) (CD51 antigen) [Contains: Integrin alpha-V heavy chain; Integrin alpha-V light chain]
UniRef100_UI	4	4	5.20%	1048	1E+05	6	integrin alpha-V precursor
UniRef100_P0	4	4	5.30%	1012	1E+05	6	Isoform 2 of P06756
UniRef100_Q0	2	2	5.20%	498	56946	8	Tripartite motif-containing 22
UniRef100_UI	2	2	5.90%	439	49848	7	Tripartite motif-containing protein 22 (RING finger protein 94) (50 kDa-stimulated trans-acting factor) (Staf-50).
UniRef100_UI	2	2	5.20%	496	56398	8	Tripartite motif-containing protein 22 (RING finger protein 94) (50 kDa-stimulated trans-acting factor) (Staf-50).
UniRef100_Q8	2	2	5.30%	494	56429	8	Isoform 2 of Q8IYM9
UniRef100_Q8	2	2	5.20%	498	56947	8	Tripartite motif-containing protein 22
UniRef100_Q4	2	2	9.50%	273	30870	9	Tripartite binding motif 22
UniRef100_Q0	2	6	5.20%	484	53542	#	Splicing factor arginine/serine-rich 11
UniRef100_Q8	2	6	5.20%	483	53414	#	Splicing factor, arginine/serine-rich 11

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	2	6	7.80%	321	34277	#	SFRS11 protein
UniRef100_Q	2	6	10.10%	247	24976	7	SFRS11 protein
UniRef100_Q	2	6	6.30%	394	42957	#	SFRS11 protein
UniRef100_Q	2	6	6.40%	389	42316	#	Splicing factor, arginine/serine-rich 11
UniRef100_Q	2	6	10.20%	246	24847	6	Hypothetical protein
UniRef100_A	6	7	5.10%	1438	2E+05	5	CLIP1 protein
UniRef100_Q	6	7	5.10%	1438	2E+05	5	CLIP1 protein
UniRef100_P	6	7	5.20%	1392	2E+05	5	Isoform Short of P30622
UniRef100_P	6	7	5.10%	1427	2E+05	5	CAP-Gly domain-containing linker protein 1
UniRef100_Q	4	4	5.10%	973	1E+05	6	Vacuolar protein sorting-associated protein 18 homolog
UniRef100_Q	3	4	5.10%	885	1E+05	9	Exosome component 10
UniRef100_Q	3	4	5.20%	860	98089	8	Exosome component 10
UniRef100_Q	3	4	10.40%	431	49222	6	Exosome component 10 isoform 2 variant
UniRef100_P	3	4	5.10%	512	58574	7	Tyrosine-protein kinase Lyn
UniRef100_U	3	4	5.20%	504	57241	7	Tyrosine-protein kinase HCK (EC 2.7.10.2) (p59-HCK/p60-HCK) (Hemopoietic cell kinase).
UniRef100_U	3	4	4.90%	526	59582	7	Tyrosine-protein kinase HCK (EC 2.7.10.2) (p59-HCK/p60-HCK) (Hemopoietic cell kinase).
UniRef100_Q	3	4	4.50%	582	65809	9	LYN protein
UniRef100_P	3	4	4.90%	526	59600	7	Tyrosine-protein kinase HCK
UniRef100_Q	2	3	5.10%	313	36566	8	Ras-related GTP-binding protein A
UniRef100_Q	10	19	5.00%	2828	3E+05	8	Matrix-remodelling-associated protein 5 precursor
UniRef100_U	10	19	5.00%	2828	3E+05	8	Matrix-remodelling-associated protein 5 precursor (Adhesion protein with leucine-rich repeats and immunoglobulin domains related to perlecan) (Adlican).
UniRef100_U	10	19	5.00%	2828	3E+05	8	adlican
UniRef100_O	3	8	5.00%	884	1E+05	9	ERPROT 213-21
UniRef100_U	3	8	4.80%	916	1E+05	9	calcium homeostasis endoplasmic reticulum protein
UniRef100_Q	3	8	5.00%	884	99992	9	Calcium homeostasis endoplasmic reticulum protein
UniRef100_Q	3	8	4.80%	916	1E+05	9	Calcium homeostasis endoplasmic reticulum protein
UniRef100_Q	2	2	5.00%	535	59845	5	Nuclear receptor-binding protein
UniRef100_Q	2	4	5.00%	479	54558	6	Something about silencing protein 10
UniRef100_P	2	6	5.00%	421	44969	8	Regulator of chromosome condensation
UniRef100_U	2	6	4.80%	438	46753	8	regulator of chromosome condensation 1 isoform b
UniRef100_Q	2	6	4.60%	452	48146	8	Regulator of chromosome condensation 1
UniRef100_Q	6	6	4.90%	1498	2E+05	5	Golgin subfamily A member 3
UniRef100_Q	6	6	5.00%	1458	2E+05	5	Isoform 3 of Q08378
UniRef100_Q	6	6	5.30%	1390	2E+05	5	Isoform 2 of Q08378
UniRef100_Q	5	5	4.90%	1439	2E+05	6	Receptor-type tyrosine-protein phosphatase kappa precursor
UniRef100_U	5	5	9.60%	741	83178	8	Receptor-type tyrosine-protein phosphatase kappa precursor (EC 3.1.3.48) (Protein-tyrosine phosphatase kappa) (R-PTP-kappa).
UniRef100_U	5	5	4.90%	1457	2E+05	6	Receptor-type tyrosine-protein phosphatase kappa precursor (EC 3.1.3.48) (Protein-tyrosine phosphatase kappa) (R-PTP-kappa).
UniRef100_Q	5	5	4.90%	1440	2E+05	6	Mutant receptor type protein tyrosine phosphatase K

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	5	5	4.90%	1440	2E+05	6	Hypothetical protein DKFZp686C2268
UniRef100_Q	5	5	4.90%	1458	2E+05	6	Protein tyrosine phosphatase, receptor type, K
UniRef100_Q	5	5	4.90%	1440	2E+05	6	Protein tyrosine phosphatase, receptor type, K
UniRef100_Q	5	5	4.90%	1439	2E+05	6	Protein tyrosine phosphatase, receptor type, K
UniRef100_Q	5	5	9.60%	742	83074	8	Protein tyrosine phosphatase, receptor type, K variant
UniRef100_Q	4	5	4.90%	1244	1E+05	7	Hypothetical protein DKFZp762L185
UniRef100_O	4	5	4.90%	1153	1E+05	9	AP-3 complex subunit delta-1
UniRef100_UI	4	5	5.60%	1023	1E+05	8	AP-3 complex subunit delta-1 (Adapter-related protein complex 3 subunit delta-1) (Delta-adaptin 3) (AP-3 complex subunit delta) (Delta-adaptin).
UniRef100_UI	4	5	4.90%	1155	1E+05	9	AP-3 complex subunit delta-1 (Adapter-related protein complex 3 subunit delta-1) (Delta-adaptin 3) (AP-3 complex subunit delta) (Delta-adaptin).
UniRef100_O	4	5	4.70%	1215	1E+05	8	Isoform 5 of O14617
UniRef100_O	4	5	5.60%	1021	1E+05	8	Isoform 4 of O14617
UniRef100_Q	4	5	4.90%	981	1E+05	6	Rab3 GTPase-activating protein catalytic subunit
UniRef100_O	3	10	4.90%	968	1E+05	6	Catenin delta-1 (p120 catenin) (p120(ctn)) (Cadherin-associated Src substrate) (CAS) (p120(cas))
UniRef100_UI	3	10	5.00%	939	1E+05	7	Catenin delta-1 (p120 catenin) (p120(ctn)) (Cadherin-associated Src substrate) (CAS) (p120(cas)).
UniRef100_UI	3	10	5.00%	947	1E+05	6	Catenin delta-1 (p120 catenin) (p120(ctn)) (Cadherin-associated Src substrate) (CAS) (p120(cas)).
UniRef100_UI	3	10	7.60%	618	68834	7	PREDICTED: similar to catenin (cadherin-associated protein), delta 1
UniRef100_UI	3	10	5.00%	941	1E+05	6	catenin (cadherin-associated protein), delta 1
UniRef100_Q	3	10	5.70%	830	92388	7	CTNND1 protein
UniRef100_Q	3	10	7.70%	610	68003	8	Catenin (Cadherin-associated protein), delta 1
UniRef100_Q	3	10	5.00%	933	1E+05	7	CTNND1 protein
UniRef100_Q	3	10	5.00%	938	1E+05	7	Hypothetical protein DKFZp781O2021
UniRef100_O	3	10	5.10%	913	1E+05	7	Isoform 1 of O60716
UniRef100_O	3	10	5.10%	919	1E+05	7	Isoform 1C of O60716
UniRef100_O	3	10	5.00%	942	1E+05	6	Isoform 1B of O60716
UniRef100_O	3	10	5.00%	933	1E+05	7	Isoform 1A of O60716
UniRef100_O	3	10	5.00%	948	1E+05	6	Isoform 1BC of O60716
UniRef100_O	3	10	8.00%	590	65756	8	Isoform 4 of O60716
UniRef100_O	3	10	7.90%	596	66577	8	Isoform 4C of O60716
UniRef100_O	3	10	7.60%	619	68949	7	Isoform 4B of O60716
UniRef100_O	3	10	5.00%	939	1E+05	7	Isoform 1AC of O60716
UniRef100_O	3	10	7.70%	610	68031	8	Isoform 4A of O60716
UniRef100_O	3	10	7.60%	616	68852	8	Isoform 4AC of O60716
UniRef100_O	3	10	7.40%	639	71225	7	Isoform 4AB of O60716
UniRef100_O	3	10	5.80%	812	90399	7	Isoform 3 of O60716
UniRef100_O	3	10	5.70%	818	91220	7	Isoform 3C of O60716
UniRef100_O	3	10	5.60%	841	93593	6	Isoform 3B of O60716

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_O	3	10	5.60%	832	92675	7	Isoform 3A of O60716
UniRef100_O	3	10	4.90%	962	1E+05	6	Isoform 1AB of O60716
UniRef100_O	3	10	5.60%	838	93496	7	Isoform 3AC of O60716
UniRef100_O	3	10	5.50%	861	95868	6	Isoform 3AB of O60716
UniRef100_O	3	10	5.50%	859	95773	7	Isoform 2 of O60716
UniRef100_O	3	10	5.40%	865	96594	7	Isoform 2C of O60716
UniRef100_O	3	10	5.30%	888	98967	7	Isoform 2B of O60716
UniRef100_O	3	10	5.30%	879	98049	8	Isoform 2A of O60716
UniRef100_O	3	10	5.30%	885	98870	7	Isoform 2AC of O60716
UniRef100_O	3	10	5.20%	908	1E+05	7	Isoform 2AB of O60716
UniRef100_Q	2	5	4.90%	740	83554	8	Protein deltex 3-like protein
UniRef100_Q	3	3	4.90%	757	83536	6	Kin of IRRE-like protein 1 precursor
UniRef100_Q	3	7	4.90%	691	79491	6	TBC1 domain family member 15
UniRef100_Q	3	7	5.00%	674	77395	5	Isoform 2 of Q8TC07
UniRef100_Q	2	6	4.90%	647	70724	#	WW domain-containing adapter protein with coiled-coil
UniRef100_U	2	6	4.90%	648	70819	9	WW domain-containing adapter protein with coiled-coil.
UniRef100_P	2	6	4.90%	593	63545	7	Granulins precursor (Proepithelin) (PEPI) [Contains: Acrogranin; Paragranulin; Granulin-1 (Granulin G); Granulin-2 (Granulin F); Granulin-3 (Granulin B); Granulin-4 (Granulin A); Granulin-5 (Granulin C); Granulin-6 (Granulin D); Granulin-7 (Granulin E)]
UniRef100_U	2	6	6.60%	440	47177	7	Granulins precursor (Proepithelin) (PEPI) [Contains: Acrogranin; Paragranulin; Granulin-1 (Granulin G); Granulin-2 (Granulin F); Granulin-3 (Granulin B); Granulin-4 (Granulin A); Granulin-5 (Granulin C); Granulin-6 (Granulin D); Granulin-7 (Granulin E)].
UniRef100_Q	2	6	6.60%	438	46991	7	Granulin
UniRef100_Q	2	6	4.90%	593	63545	7	Granulin variant
UniRef100_O	2	3	4.90%	514	57194	9	Pleiotropic regulator 1
UniRef100_O	2	3	5.00%	505	56290	9	Isoform 2 of O43660
UniRef100_O	2	8	4.90%	528	55596	6	Podocalyxin-like protein 1 precursor
UniRef100_U	2	8	4.90%	526	55347	6	Podocalyxin-like protein 1 precursor.
UniRef100_U	2	8	4.70%	558	58635	6	podocalyxin-like precursor isoform 1
UniRef100_Q	2	8	5.00%	518	54577	6	CDNA FLJ31254 fis, clone KIDNE2005526, highly similar to Homo sapiens podocalyxin-like protein mRNA
UniRef100_Q	2	8	4.90%	526	55400	6	Podocalyxin-like variant
UniRef100_Q	2	8	4.90%	526	55386	6	Podocalyxin-like
UniRef100_Q	3	4	4.80%	1204	1E+05	6	Integrator complex subunit 2
UniRef100_U	3	4	4.80%	1208	1E+05	6	Integrator complex subunit 2 (Int2).
UniRef100_Q	5	8	4.80%	1151	1E+05	5	Exportin-4
UniRef100_P	3	3	4.80%	794	90647	6	Signal transducer and activator of transcription 5A
UniRef100_Q	3	3	4.80%	791	90350	6	Signal transducer and activator of transcription 5A
UniRef100_Q	3	3	5.00%	765	87535	7	Signal transducer and activator of transcription 5A variant
UniRef100_Q	3	3	5.00%	764	86949	6	Signal transducer and activator of transcription 5A variant delta5

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P	3	3	4.80%	752	83268	7	Complement C2 precursor (EC 3.4.21.43) (C3/C5 convertase) [Contains: Complement C2b fragment; Complement C2a fragment]
UniRef100_U	3	3	7.10%	509	57388	7	Complement C2
UniRef100_U	3	3	7.30%	496	54882	7	Complement C2 precursor (EC 3.4.21.43) (C3/C5 convertase) [Contains: Complement C2b fragment; Complement C2a fragment].
UniRef100_Q	3	3	6.20%	577	63458	7	C2 protein
UniRef100_Q	3	3	9.90%	363	40524	6	Hypothetical protein DKFZp779M0311
UniRef100_Q	3	3	6.90%	525	58789	8	Complement component 2
UniRef100_Q	3	3	4.80%	752	83284	7	Complement component 2 variant
UniRef100_Q	3	3	4.80%	752	83337	8	Complement component 2 variant
UniRef100_Q	3	3	7.60%	473	52567	8	Complement component 2
UniRef100_O	3	4	4.80%	703	77960	6	Autophagy-related protein 7
UniRef100_O	3	4	5.00%	676	75002	6	Isoform 2 of O95352
UniRef100_Q	2	3	4.80%	671	70460	5	Complement component 1, q subcomponent, receptor 1 variant
UniRef100_Q	2	3	4.90%	652	68560	5	Complement component C1q receptor precursor (Complement component 1 q subcomponent receptor 1) (C1qR) (C1qRp) (C1qR(p))
UniRef100_Q	2	3	4.90%	652	68522	5	C1q receptor protein precursor
UniRef100_Q	2	2	4.80%	606	63877	9	Ribonucleoprotein PTB-binding 1
UniRef100_U	2	2	3.80%	756	79579	9	RAVER1
UniRef100_U	2	2	4.80%	605	63600	8	Ribonucleoprotein PTB-binding 1 (Protein raver-1).
UniRef100_Q	2	2	3.90%	739	77860	9	Isoform 2 of Q8IY67
UniRef100_Q	2	2	4.80%	524	59242	5	Leucine-rich repeat-containing protein 1
UniRef100_P	2	2	4.80%	416	44773	9	Lysosome-associated membrane glycoprotein 1 precursor
UniRef100_U	2	2	4.80%	415	44591	9	Lysosome-associated membrane glycoprotein 1 precursor (LAMP-1) (CD107a antigen).
UniRef100_Q	2	2	5.60%	355	38358	8	Lysosomal-associated membrane glycoprotein-1
UniRef100_Q	2	2	6.50%	308	33376	8	LAMP1 protein
UniRef100_Q	2	2	4.80%	417	44882	9	Lysosomal-associated membrane protein 1
UniRef100_P	6	14	4.70%	1816	2E+05	7	Afadin
UniRef100_U	6	14	5.20%	1665	2E+05	7	Afadin (Protein AF-6).
UniRef100_U	6	14	4.70%	1824	2E+05	7	Afadin (Protein AF-6).
UniRef100_U	6	14	5.20%	1651	2E+05	7	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 isoform 2
UniRef100_U	6	14	4.70%	1816	2E+05	7	Afadin (Protein AF-6).
UniRef100_Q	6	14	5.30%	1612	2E+05	7	Myeloid/lymphoid or mixed-lineage leukemia (Trithorax homolog, Drosophila); translocated to, 4
UniRef100_Q	6	14	5.20%	1665	2E+05	7	Myeloid/lymphoid or mixed-lineage leukemia (Trithorax homolog, Drosophila); translocated to, 4
UniRef100_Q	6	14	5.20%	1639	2E+05	7	Afadin variant
UniRef100_P	6	14	4.70%	1824	2E+05	7	Isoform 4 of P55196
UniRef100_P	6	14	4.90%	1743	2E+05	7	Isoform 3 of P55196
UniRef100_P	6	14	5.30%	1611	2E+05	7	Isoform 1 of P55196
UniRef100_Q	2	2	4.70%	665	74678	7	Myotubularin-related protein 1
UniRef100_Q	2	2	5.50%	568	63330	8	Isoform 1A of Q13613

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	2	2	4.70%	555	62736	5	Glypican-6 precursor
UniRef100_Q	2	3	4.70%	549	61957	9	Nucleostemin
UniRef100_UI	2	3	4.80%	537	60540	9	guanine nucleotide binding protein-like 3 isoform 2
UniRef100_UI	2	3	4.70%	549	61993	9	guanine nucleotide binding protein-like 3 isoform 1
UniRef100_Q	2	3	4.70%	549	61997	9	Guanine nucleotide-binding protein-like 3
UniRef100_P	2	6	4.70%	529	57945	5	4F2 cell-surface antigen heavy chain
UniRef100_UI	2	6	4.00%	631	68101	5	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 isoform b
UniRef100_UI	2	6	3.80%	661	71123	5	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 isoform a
UniRef100_UI	2	6	4.20%	599	64873	5	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 isoform d
UniRef100_UI	2	6	4.00%	630	67994	5	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 isoform c
UniRef100_O	2	2	4.70%	533	56896	9	Ubiquitin domain-containing protein UBFD1
UniRef100_UI	2	2	8.10%	309	33382	6	ubiquitin-binding protein homolog
UniRef100_A	2	2	4.70%	508	55394	7	Signal-regulatory protein alpha
UniRef100_UI	2	2	4.80%	504	54967	7	signal-regulatory protein alpha precursor
UniRef100_P	2	2	6.00%	402	44165	7	Isoform 3 of P78324
UniRef100_P	2	2	4.70%	507	55240	7	Isoform 2 of P78324
UniRef100_P	2	2	4.80%	503	54813	7	Tyrosine-protein phosphatase non-receptor type substrate 1 precursor
UniRef100_A	2	5	4.70%	408	45918	#	Novel protein
UniRef100_P	2	5	4.40%	430	48565	#	RNA-binding protein 34
UniRef100_Q	8	20	4.60%	2760	3E+05	6	Neurobeachin-like protein 2
UniRef100_P	5	10	4.60%	1054	1E+05	8	Probable global transcription activator SNF2L1
UniRef100_UI	5	10	4.90%	1005	1E+05	8	Probable global transcription activator SNF2L1 (EC 3.6.1.-) (Nucleosome remodeling factor subunit SNF2L) (ATP-dependent helicase SMARCA1) (SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 1).
UniRef100_Q	5	10	4.90%	1005	1E+05	8	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1
UniRef100_P	5	10	4.70%	1042	1E+05	8	Isoform 2 of P28370
UniRef100_Q	3	4	4.60%	1052	1E+05	7	Focal adhesion kinase 1
UniRef100_Q	3	4	4.80%	1006	1E+05	7	PTK2 protein
UniRef100_O	4	18	4.60%	1029	1E+05	9	U2-associated protein SR140
UniRef100_UI	4	18	4.60%	1029	1E+05	9	U2-associated SR140 protein
UniRef100_O	4	18	7.60%	620	72524	8	Isoform 3 of O15042
UniRef100_O	4	18	4.60%	1028	1E+05	9	Isoform 2 of O15042
UniRef100_P	3	4	4.60%	870	98064	8	Dynamin-2
UniRef100_UI	3	4	4.60%	866	97663	7	Dynamin-2 (EC 3.6.5.5).
UniRef100_UI	3	4	4.60%	870	98021	7	Dynamin-2 (EC 3.6.5.5).
UniRef100_P	3	4	4.60%	866	97652	8	Isoform 2 of P50570

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_P5	3	3	4.60%	787	89866	6	Signal transducer and activator of transcription 5B
UniRef100_Q8	3	3	9.20%	390	44947	7	STAT5B protein
UniRef100_Q5	3	3	4.60%	788	89966	6	Signal transducer and activator of transcription 5B variant
UniRef100_Q5	3	3	4.60%	782	88879	9	Eukaryotic translation initiation factor 2C, 1
UniRef100_Q9	3	3	4.20%	857	97214	9	Eukaryotic translation initiation factor 2C 1
UniRef100_Q9	2	3	4.60%	755	85077	7	Anaphase-promoting complex subunit 5
UniRef100_P5	2	2	4.60%	743	82167	7	Alpha-N-acetylglucosaminidase precursor (EC 3.2.1.50) (N-acetyl-alpha- glucosaminidase) (NAG) [Contains: Alpha-N-acetylglucosaminidase 82 kDa form; Alpha-N-acetylglucosaminidase 77 kDa form]
UniRef100_UI	2	2	8.10%	419	47120	8	Alpha-N-acetylglucosaminidase precursor (EC 3.2.1.50) (N-acetyl-alpha- glucosaminidase) (NAG) [Contains: Alpha-N-acetylglucosaminidase 82 kDa form; Alpha-N-acetylglucosaminidase 77 kDa form].
UniRef100_UI	2	2	4.60%	743	82266	7	alpha-N-acetylglucosaminidase precursor
UniRef100_Q5	2	2	7.60%	449	50312	7	Huntingtin interacting protein-1-related
UniRef100_Q	2	2	5.30%	639	72028	6	Alpha-N-acetylglucosaminidase
UniRef100_P4	2	2	4.60%	635	72066	8	Tyrosine-protein kinase SYK
UniRef100_Q5	2	2	4.70%	612	69510	8	Spleen tyrosine kinase
UniRef100_P0	2	11	4.60%	543	61517	5	Neurofilament light polypeptide
UniRef100_UI	2	11	4.60%	542	61430	5	Neurofilament triplet L protein (68 kDa neurofilament protein) (Neurofilament light polypeptide) (NF-L).
UniRef100_Q	2	3	4.60%	501	55828	5	Periodic tryptophan protein 1 homolog
UniRef100_Q9	2	3	4.60%	501	55879	5	PWP1 homolog
UniRef100_Q5	2	3	4.60%	501	55729	5	Nuclear phosphoprotein similar to S. cerevisiae PWP1 variant
UniRef100_A2	3	4	4.50%	1323	1E+05	7	KIAA1219
UniRef100_Q8	3	4	4.00%	1490	2E+05	7	Isoform 3 of Q86X10
UniRef100_Q8	3	4	4.60%	1273	1E+05	7	Isoform 2 of Q86X10
UniRef100_Q8	3	4	3.90%	1494	2E+05	7	Protein KIAA1219
UniRef100_Q5	3	4	4.00%	1491	2E+05	7	KIAA1219
UniRef100_A0	4	4	4.50%	1414	1E+05	9	Hypothetical protein
UniRef100_UI	4	4	4.40%	1451	1E+05	9	Treacher Collins-Franceschetti syndrome 1 isoform b
UniRef100_UI	4	4	4.50%	1412	1E+05	9	Treacher Collins-Franceschetti syndrome 1 isoform b
UniRef100_UI	4	4	4.40%	1450	1E+05	9	Treacher Collins-Franceschetti syndrome 1 isoform a
UniRef100_UI	4	4	4.50%	1411	1E+05	9	Treacher Collins-Franceschetti syndrome 1 isoform b
UniRef100_Q	4	4	4.20%	1524	2E+05	9	Isoform 4 of Q13428
UniRef100_Q	4	4	4.30%	1489	2E+05	9	Isoform 3 of Q13428
UniRef100_Q	4	4	4.50%	1412	1E+05	9	Isoform 2 of Q13428
UniRef100_Q	4	4	4.30%	1488	2E+05	9	Treacle protein
UniRef100_A2	3	3	4.50%	712	82325	8	Origin recognition complex, subunit 3-like
UniRef100_Q9	3	3	4.50%	711	82254	8	Origin recognition complex subunit 3
UniRef100_Q8	3	3	4.70%	676	78276	8	Similar to Origin recognition complex subunit 3
UniRef100_Q5	3	3	4.50%	711	82332	8	Origin recognition complex, subunit 3 isoform 2 variant

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	2	2	4.50%	445	51353	5	PACSIN2 protein
UniRef100_U	2	2	4.10%	486	55905	5	protein kinase C and casein kinase substrate in neurons 2
UniRef100_Q	2	2	4.10%	486	55739	5	Protein kinase C and casein kinase substrate in neurons protein 2
UniRef100_Q	2	2	4.50%	425	48446	5	SERPINB12 protein
UniRef100_Q	2	2	4.70%	405	46276	6	Serpin B12
UniRef100_Q	6	8	4.40%	2012	2E+05	6	Nuclear pore complex protein Nup205
UniRef100_U	6	8	4.40%	2012	2E+05	6	Nuclear pore complex protein Nup205 (Nucleoporin Nup205) (205 kDa nucleoporin).
UniRef100_Q	7	7	4.40%	1843	2E+05	7	Proteasome activator complex subunit 4
UniRef100_Q	4	15	4.40%	1244	1E+05	5	FK506-binding protein 15
UniRef100_U	4	15	4.10%	1342	1E+05	6	PREDICTED: similar to Golgin subfamily A member 6 (Golgin linked to PML) (Golgin-like protein)
UniRef100_Q	4	15	4.50%	1234	1E+05	5	KIAA0674 protein
UniRef100_Q	6	13	4.40%	1150	1E+05	6	Cell division cycle and apoptosis regulator protein 1
UniRef100_Q	5	7	4.40%	1172	1E+05	7	Laminin subunit beta-3 precursor
UniRef100_O	3	3	4.40%	956	1E+05	6	Matrilin-2 precursor
UniRef100_U	3	3	4.60%	915	1E+05	6	Matrilin-2 precursor.
UniRef100_U	3	3	4.40%	956	1E+05	6	Matrilin-2 precursor.
UniRef100_U	3	3	4.50%	937	1E+05	6	matrilin 2 isoform b precursor
UniRef100_U	3	3	4.40%	956	1E+05	6	matrilin 2 isoform a precursor
UniRef100_Q	3	3	7.80%	537	60235	6	CDNA FLJ14869 fis, clone PLACE1002474, moderately similar to Mus musculus matrilin-2 mRNA
UniRef100_O	3	3	4.60%	915	1E+05	6	Isoform 3 of O00339
UniRef100_O	3	3	4.50%	937	1E+05	6	Isoform 2 of O00339
UniRef100_Q	2	3	4.40%	664	75216	5	SPARC-like protein 1 precursor
UniRef100_U	2	3	4.40%	664	75208	5	SPARC-like protein 1 precursor (High endothelial venule protein) (Hevin) (MAST 9).
UniRef100_U	2	3	4.40%	664	75248	5	SPARC-like 1
UniRef100_Q	2	3	4.40%	664	75230	5	SPARC-like 1
UniRef100_P	2	2	4.40%	594	67569	7	Syntaxin-binding protein 1
UniRef100_Q	2	2	4.30%	603	68736	7	Syntaxin binding protein 1
UniRef100_Q	2	2	4.40%	567	64682	#	Hypothetical protein KIAA1805
UniRef100_U	2	2	4.40%	567	64708	#	Zinc finger protein 512.
UniRef100_Q	2	2	4.40%	567	64613	#	Zinc finger protein 512
UniRef100_Q	2	3	4.40%	389	43396	#	Chromobox protein homolog 8
UniRef100_Q	3	3	4.40%	318	36805	7	Ubiquitin-like domain-containing CTD phosphatase 1
UniRef100_U	3	3	4.40%	318	36733	7	ubiquitin-like domain containing CTD phosphatase 1
UniRef100_O	2	3	4.40%	339	36467	#	F25451_2
UniRef100_Q	2	3	3.30%	451	47393	#	MGC10433 protein
UniRef100_Q	2	3	3.10%	480	50414	#	Hypothetical protein MGC10433
UniRef100_Q	2	3	3.30%	450	47322	#	MGC10433 protein
UniRef100_Q	12	14	4.30%	3657	4E+05	7	Serine/threonine-protein kinase SMG1

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_UI	12	14	4.30%	3665	4E+05	7	Serine/threonine-protein kinase SMG1 (EC 2.7.11.1) (SMG-1) (hSMG-1) (Lambda/iota protein kinase C-interacting protein) (Lambda-interacting protein) (61E3.4).
UniRef100_UI	12	14	4.30%	3661	4E+05	7	PI-3-kinase-related kinase SMG-1
UniRef100_Q9	12	14	5.20%	3031	3E+05	6	Isoform 3 of Q96Q15
UniRef100_Q9	12	14	4.50%	3521	4E+05	6	Isoform 2 of Q96Q15
UniRef100_A2	7	10	4.30%	2148	2E+05	5	Tenascin XB
UniRef100_O7	5	8	4.30%	1294	1E+05	9	CLIP-associating protein 2
UniRef100_UI	5	8	4.30%	1293	1E+05	9	CLIP-associating protein 2 (Cytoplasmic linker-associated protein 2) (hOrbit2).
UniRef100_UI	5	8	3.70%	1506	2E+05	8	CLIP-associating protein 2
UniRef100_UI	5	8	6.40%	856	94222	8	CLIP-associating protein 2 (Cytoplasmic linker-associated protein 2) (hOrbit2).
UniRef100_Q9	5	8	6.40%	857	94378	8	Hypothetical protein
UniRef100_Q6	5	8	7.80%	709	79002	6	Hypothetical protein DKFZp686D11262
UniRef100_Q0	2	4	4.30%	676	77477	8	Protein kinase C delta type
UniRef100_Q8	2	4	4.30%	676	77505	8	Protein kinase C, delta
UniRef100_Q9	2	2	4.30%	605	66607	9	Methyl-CpG-binding domain protein 1
UniRef100_Q9	2	2	4.70%	549	60001	9	Isoform 7 of Q9UIS9
UniRef100_Q9	2	2	4.70%	550	60848	9	Isoform 6 of Q9UIS9
UniRef100_Q9	2	2	4.70%	556	61265	9	Isoform 5 of Q9UIS9
UniRef100_Q9	2	2	4.70%	549	60001	9	Isoform 3 of Q9UIS9
UniRef100_Q9	2	2	4.40%	586	64677	9	Isoform 2 of Q9UIS9
UniRef100_Q9	2	4	4.30%	541	61175	7	EH domain-containing protein 4
UniRef100_Q5	2	2	4.30%	324	36430	9	PHD finger protein 6
UniRef100_Q8	2	2	3.80%	365	41290	9	PHD finger protein 6
UniRef100_Q5	2	2	4.50%	312	35329	9	PHD finger protein 6
UniRef100_Q9	7	8	4.20%	2649	3E+05	8	Peroxisomal proliferator-activated receptor A-interacting complex 285 kDa protein
UniRef100_UI	7	8	4.20%	2649	3E+05	8	PPAR-alpha interacting complex protein 285 isoform 1
UniRef100_UI	7	8	5.30%	2080	2E+05	8	Peroxisomal proliferator-activated receptor A-interacting complex 285 kDa protein (EC 3.6.1.-) (ATP-dependent helicase PRIC285) (PPAR-alpha- interacting complex protein 285) (PPAR-gamma DBD-interacting protein 1) (PDIP1).
UniRef100_UI	7	8	4.20%	2649	3E+05	8	Peroxisomal proliferator-activated receptor A-interacting complex 285 kDa protein (EC 3.6.1.-) (ATP-dependent helicase PRIC285) (PPAR-alpha- interacting complex protein 285) (PPAR-gamma DBD-interacting protein 1) (PDIP1).
UniRef100_UI	7	8	5.30%	2080	2E+05	8	PPAR-alpha interacting complex protein 285 isoform 2
UniRef100_Q9	7	8	5.30%	2114	2E+05	8	Isoform 3 of Q9BYK8
UniRef100_Q9	7	8	5.30%	2080	2E+05	8	Isoform 2 of Q9BYK8
UniRef100_Q7	9	16	4.20%	1995	2E+05	6	Myosin-14
UniRef100_UI	9	16	4.10%	2003	2E+05	6	myosin, heavy chain 14 isoform 1
UniRef100_UI	9	16	4.20%	1995	2E+05	6	myosin, heavy chain 14 isoform 2
UniRef100_Q7	9	16	4.10%	2028	2E+05	6	Isoform 2 of Q7Z406
UniRef100_P2	3	3	4.20%	1445	2E+05	7	Receptor-type tyrosine-protein phosphatase gamma precursor

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_U	3	3	4.20%	1445	2E+05	6	Receptor-type tyrosine-protein phosphatase gamma precursor (EC 3.1.3.48) (Protein-tyrosine phosphatase gamma) (R-PTP-gamma).
UniRef100_U	3	3	4.20%	1445	2E+05	7	protein tyrosine phosphatase, receptor type, G precursor
UniRef100_P	3	3	4.30%	1416	2E+05	6	Isoform 2 of P23470
UniRef100_Q	2	2	4.20%	915	1E+05	7	LRAP protein
UniRef100_Q	2	2	4.00%	960	1E+05	7	Aminopeptidase
UniRef100_Q	2	2	4.00%	960	1E+05	7	Leukocyte-derived arginine aminopeptidase long form variant
UniRef100_Q	2	2	4.20%	800	92548	9	Nucleolar complex protein 3 homolog
UniRef100_U	2	2	4.20%	800	92624	9	Nucleolar complex protein 3 homolog (NOC3 protein homolog) (NOC3-like protein) (Nucleolar complex-associated protein 3-like protein) (Factor for adipocyte differentiation 24).
UniRef100_Q	2	2	4.20%	808	92044	6	Anaphase promoting complex subunit 4
UniRef100_U	2	2	4.20%	808	92116	6	anaphase-promoting complex subunit 4
UniRef100_Q	3	5	4.20%	734	83065	5	LAS1-like protein
UniRef100_Q	3	5	10.70%	291	33108	5	Isoform 4 of Q9Y4W2
UniRef100_Q	3	5	4.30%	717	81243	5	Isoform 2 of Q9Y4W2
UniRef100_O	3	7	4.20%	692	76108	5	A-kinase anchor protein 8
UniRef100_Q	3	7	8.10%	358	39938	5	Hypothetical protein DKFZp586B1222
UniRef100_Q	3	7	4.20%	692	76166	5	AKAP8 protein
UniRef100_Q	2	2	4.20%	673	75509	7	Armadillo repeat-containing protein 8
UniRef100_U	2	2	4.30%	658	73863	7	armadillo repeat containing 8 isoform 1
UniRef100_Q	2	2	6.50%	431	48631	7	Isoform 5 of Q8IUR7
UniRef100_Q	2	2	4.40%	631	70796	7	Isoform 3 of Q8IUR7
UniRef100_Q	2	2	4.20%	659	73994	7	Isoform 2 of Q8IUR7
UniRef100_Q	2	2	4.20%	661	72124	6	WD repeat protein 26
UniRef100_U	2	2	5.40%	514	58604	6	WD repeat domain 26
UniRef100_Q	2	2	4.30%	645	70460	6	Isoform 2 of Q9H7D7
UniRef100_P	2	2	4.20%	625	70109	8	Coagulation factor XI precursor (EC 3.4.21.27) (Plasma thromboplastin antecedent) (PTA) (FXI) [Contains: Coagulation factor XIa heavy chain; Coagulation factor XIa light chain]
UniRef100_U	2	2	4.50%	573	64053	8	Coagulation factor XI precursor (EC 3.4.21.27) (Plasma thromboplastin antecedent) (PTA) (FXI) [Contains: Coagulation factor XIa heavy chain; Coagulation factor XIa light chain].
UniRef100_P	2	2	4.60%	571	63840	8	Isoform 2 of P03951
UniRef100_Q	2	2	4.20%	518	57471	5	Uncharacterized protein C15orf44
UniRef100_Q	2	2	4.20%	518	57341	5	Hypothetical protein DKFZp564O1664
UniRef100_Q	2	2	4.20%	518	57519	5	CDNA FLJ14569 fis, clone NT2RM4000514
UniRef100_Q	2	11	4.20%	499	55391	5	Alpha-internexin
UniRef100_Q	6	7	4.10%	1724	2E+05	6	Poly (ADP-ribose) polymerase family, member 4
UniRef100_Q	6	7	4.10%	1724	2E+05	6	Poly [ADP-ribose] polymerase 4 (EC 2.4.2.30) (PARP-4) (Vault poly(ADP- ribose) polymerase)
UniRef100_O	4	7	4.10%	1391	2E+05	9	DNA-directed RNA polymerase III largest subunit
UniRef100_Q	4	7	4.10%	1390	2E+05	9	DNA-directed RNA polymerase
UniRef100_O	4	5	4.10%	1105	1E+05	5	Ran-binding protein 6
UniRef100_O	3	8	4.10%	1098	1E+05	9	Transcription elongation regulator 1

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_U	3	8	4.10%	1098	1E+05	9	transcription elongation regulator 1 isoform 1
UniRef100_Q	3	8	4.20%	1081	1E+05	9	Transcription elongation regulator 1 variant
UniRef100_Q	3	3	4.10%	974	1E+05	7	Exocyst complex component 4
UniRef100_Q	3	3	4.10%	974	1E+05	7	Exocyst complex component 4
UniRef100_P	2	5	4.10%	956	1E+05	5	Thrombospondin-3 precursor
UniRef100_Q	2	5	4.10%	956	1E+05	5	Thrombospondin 3 variant
UniRef100_Q	2	5	4.10%	956	1E+05	5	Thrombospondin 3,
UniRef100_Q	2	2	4.10%	677	76211	7	WD repeat protein 48
UniRef100_Q	3	3	4.10%	654	72661	7	Tumor necrosis factor, alpha-induced protein 2
UniRef100_Q	3	3	4.10%	665	72133	6	ATPase WRNIP1
UniRef100_Q	3	3	4.20%	640	69459	6	Isoform 2 of Q96S55
UniRef100_Q	3	4	4.10%	587	65266	7	FAD1 flavin adenine dinucleotide synthetase homolog
UniRef100_O	3	4	4.00%	1302	1E+05	7	Ubiquitin conjugation factor E4 B
UniRef100_U	3	4	4.40%	1175	1E+05	6	Ubiquitin conjugation factor E4 B (Ubiquitin fusion degradation protein 2) (Homozygously deleted in neuroblastoma 1).
UniRef100_O	3	4	4.90%	1061	1E+05	6	Isoform 3 of O95155
UniRef100_O	3	4	4.40%	1173	1E+05	6	Isoform 2 of O95155
UniRef100_O	4	9	4.00%	1246	1E+05	6	Putative RNA helicase Ski2w
UniRef100_Q	4	9	4.00%	1245	1E+05	6	DJ34F7.7 (Superkiller viralicidic activity 2 (S. cerevisiae homolog)- like (SKI2W))
UniRef100_Q	4	9	4.00%	1246	1E+05	6	Superkiller viralicidic activity 2-like
UniRef100_Q	4	9	4.00%	1246	1E+05	6	Superkiller viralicidic activity 2-like
UniRef100_Q	4	9	4.00%	1246	1E+05	6	Superkiller viralicidic activity 2-like
UniRef100_Q	3	3	4.00%	1102	1E+05	7	Activity-dependent neuroprotector
UniRef100_Q	3	3	4.00%	1102	1E+05	7	Activity-dependent neuroprotector
UniRef100_Q	3	3	4.00%	1084	1E+05	6	L-fucose kinase
UniRef100_Q	3	3	3.90%	1090	1E+05	6	Isoform 2 of Q8N0W3
UniRef100_Q	4	4	4.00%	932	97396	9	RNA-binding protein 12
UniRef100_O	2	4	4.00%	747	82578	9	Sulfhydryl oxidase 1 precursor
UniRef100_Q	2	4	3.80%	793	86396	9	Bone-derived growth factor
UniRef100_O	2	4	5.00%	604	66861	9	Isoform 2 of O00391
UniRef100_Q	2	2	4.00%	632	71175	7	Fragile X mental retardation 1 protein
UniRef100_U	2	2	4.20%	592	66786	7	Fragile X mental retardation 1 protein (Protein FMR-1) (FMRP).
UniRef100_U	2	2	4.30%	582	65822	8	Fragile X mental retardation 1 protein (Protein FMR-1) (FMRP).
UniRef100_Q	2	2	8.40%	297	34115	6	FMR1 protein
UniRef100_Q	2	2	4.30%	586	66246	9	FMR1 protein
UniRef100_Q	2	2	4.70%	527	59154	9	Fragile X mental retardation 1 variant
UniRef100_Q	2	2	4.10%	615	69179	7	Isoform 7 of Q06787
UniRef100_Q	2	2	4.20%	590	66460	8	Isoform 5 of Q06787
UniRef100_Q	2	2	4.10%	607	68455	9	Isoform 4 of Q06787
UniRef100_Q	2	2	4.10%	603	68030	8	Isoform 3 of Q06787
UniRef100_Q	2	2	4.00%	620	70025	8	Isoform 2 of Q06787

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	2	2	4.20%	594	66971	7	Isoform 1 of Q06787
UniRef100_O	8	12	3.90%	2982	3E+05	6	Zinc finger ZZ-type with EF-hand domain protein 1
UniRef100_U	8	12	3.90%	2961	3E+05	6	zinc finger, ZZ type with EF hand domain 1
UniRef100_Q	4	7	3.90%	1755	2E+05	6	Isoform 4 of Q8IWV8
UniRef100_P	4	5	3.90%	1066	1E+05	7	Integrin alpha-3 precursor (Galactoprotein B3) (GAPB3) (VLA-3 alpha chain) (FRP-2) (CD49c antigen) [Contains: Integrin alpha-3 heavy chain; Integrin alpha-3 light chain]
UniRef100_U	4	5	3.90%	1066	1E+05	7	integrin alpha 3 isoform b, precursor
UniRef100_P	4	5	4.00%	1051	1E+05	7	Isoform Alpha
UniRef100_P	3	3	3.90%	1047	1E+05	7	Ras GTPase-activating protein 1
UniRef100_U	3	3	3.90%	1047	1E+05	7	Ras GTPase-activating protein 1 (GTPase-activating protein) (GAP) (Ras p21 protein activator) (p120GAP) (RasGAP).
UniRef100_P	3	3	4.70%	870	1E+05	8	Isoform 2 of P20936
UniRef100_Q	3	4	3.90%	948	1E+05	7	ARHGEF1 protein
UniRef100_U	3	4	3.90%	947	1E+05	7	Rho guanine nucleotide exchange factor 1 (p115-RhoGEF) (p115RhoGEF) (115 kDa guanine nucleotide exchange factor) (Sub1.5).
UniRef100_Q	3	4	4.20%	879	98768	6	Isoform 2 of Q92888
UniRef100_Q	3	4	4.10%	912	1E+05	6	Rho guanine nucleotide exchange factor 1
UniRef100_O	2	3	3.90%	690	75701	8	Sodium-dependent phosphate transport protein 2B (Sodium/phosphate cotransporter 2B) (Na(+)/Pi cotransporter 2B) (Sodium-phosphate transport protein 2B) (Na(+)-dependent phosphate cotransporter 2B)
UniRef100_U	2	3	3.90%	690	75759	8	Sodium-dependent phosphate transport protein 2B (Sodium/phosphate cotransporter 2B) (Na(+)/Pi cotransporter 2B) (Sodium-phosphate transport protein 2B) (Na(+)-dependent phosphate cotransporter 2B) (NaPi-2b) (Solute carrier family 34 member 2) (NaPi3b).
UniRef100_O	2	3	3.90%	689	75599	8	Isoform 2 of O95436
UniRef100_Q	2	2	3.90%	583	66243	5	USP28 protein
UniRef100_Q	2	2	2.10%	1077	1E+05	5	Ubiquitin carboxyl-terminal hydrolase 28
UniRef100_Q	2	2	3.90%	544	58344	8	CUGBP1 variant protein
UniRef100_Q	2	2	4.30%	483	51617	9	Isoform 3 of Q92879
UniRef100_Q	2	2	4.40%	482	51546	9	Isoform 2 of Q92879
UniRef100_Q	2	2	4.30%	486	52063	9	CUG triplet repeat RNA-binding protein 1
UniRef100_P	4	7	3.80%	1466	1E+05	7	Collagen alpha-1(III) chain precursor
UniRef100_U	4	7	4.80%	1163	1E+05	6	Collagen alpha-1(III) chain precursor.
UniRef100_U	4	7	3.80%	1466	1E+05	7	collagen, type III, alpha 1 preproprotein
UniRef100_Q	3	3	3.80%	734	81668	7	Probable carboxypeptidase X1 precursor
UniRef100_Q	2	2	3.80%	605	66180	5	CDNA FLJ44925 fis, clone BRAMY3014613, highly similar to Homo sapiens SH3-domain binding protein 1
UniRef100_Q	3	19	3.80%	600	64895	8	Keratin type II cuticular Hb4
UniRef100_U	3	19	3.80%	600	64842	8	keratin, hair, basic, 4
UniRef100_Q	3	5	3.70%	1227	1E+05	7	Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16
UniRef100_Q	2	2	3.70%	929	1E+05	9	Testis-expressed sequence 10 protein
UniRef100_U	2	2	3.70%	929	1E+05	9	testis expressed sequence 10

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	2	5	3.70%	381	41945	6	Potassium channel modulatory factor 1
UniRef100_U	2	5	3.10%	451	49300	6	PREDICTED: similar to potassium channel modulatory factor 1
UniRef100_U	2	5	3.60%	386	42636	6	potassium channel modulatory factor 1
UniRef100_Q	2	5	3.70%	381	41973	6	Potassium channel modulatory factor
UniRef100_Q	2	5	3.70%	381	41873	6	CDNA FLJ13341 fis, clone OVARC1001943, highly similar to Mus musculus DEBT-91 mRNA
UniRef100_Q	8	8	3.60%	2644	3E+05	7	Serine/threonine-protein kinase ATR
UniRef100_U	8	8	3.70%	2612	3E+05	8	PREDICTED: similar to Serine/threonine-protein kinase ATR (Ataxia telangiectasia and Rad3-related protein) (FRAP-related protein 1)
UniRef100_U	8	8	3.70%	2582	3E+05	8	Serine/threonine-protein kinase ATR (EC 2.7.11.1) (Ataxia telangiectasia and Rad3-related protein) (FRAP-related protein 1).
UniRef100_U	8	8	3.60%	2646	3E+05	8	Serine/threonine-protein kinase ATR (EC 2.7.11.1) (Ataxia telangiectasia and Rad3-related protein) (FRAP-related protein 1).
UniRef100_U	8	8	3.60%	2644	3E+05	8	ataxia telangiectasia and Rad3 related protein
UniRef100_Q	8	8	3.70%	2580	3E+05	7	Isoform 2 of Q13535
UniRef100_Q	5	6	3.60%	1785	2E+05	6	Brefeldin A-inhibited guanine nucleotide-exchange protein 2
UniRef100_U	5	6	3.60%	1785	2E+05	7	ADP-ribosylation factor guanine nucleotide-exchange factor 2
UniRef100_Q	3	3	3.60%	870	97153	8	SEMA4D variant protein
UniRef100_U	3	3	3.60%	862	96208	8	semaphorin 4D
UniRef100_Q	3	3	3.60%	862	96150	8	Semaphorin-4D precursor
UniRef100_Q	2	2	3.60%	727	83550	7	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 precursor
UniRef100_Q	2	4	3.60%	665	75564	6	Protein-arginine deiminase type-2
UniRef100_Q	2	2	3.60%	619	70182	9	Nuclear RNA export factor 1
UniRef100_Q	3	3	3.50%	861	97113	6	Probable E3 ubiquitin-protein ligase HECTD3
UniRef100_Q	2	2	3.50%	771	87978	8	U3 small nucleolar RNA-associated protein 14 homolog A
UniRef100_Q	2	2	3.50%	707	79641	7	KIAA0859 protein variant
UniRef100_Q	2	2	4.10%	613	68689	7	Isoform 3 of Q8N6R0
UniRef100_Q	2	2	4.60%	543	61128	6	Isoform 4 of Q8N6R0
UniRef100_Q	2	2	3.60%	699	78768	7	Uncharacterized protein KIAA0859
UniRef100_Q	2	27	3.50%	656	68478	9	RNA-binding protein EWS
UniRef100_U	2	27	3.80%	600	62508	9	RNA-binding protein EWS (EWS oncogene) (Ewing sarcoma breakpoint region 1 protein).
UniRef100_U	2	27	3.90%	583	61287	9	Ewing sarcoma breakpoint region 1 isoform EWS-b
UniRef100_Q	2	27	3.50%	661	68966	9	CDNA FLJ31747 fis, clone NT2RI2007377, highly similar to RNA-BINDING PROTEIN EWS
UniRef100_Q	2	27	3.80%	600	62478	9	CDNA FLJ32119 fis, clone PEBLM1000034, highly similar to RNA-BINDING PROTEIN EWS
UniRef100_Q	2	27	3.50%	655	68391	9	Ewing sarcoma breakpoint region 1
UniRef100_Q	2	27	3.90%	583	61217	9	Isoform EWS
UniRef100_Q	5	9	3.40%	1778	2E+05	6	Uncharacterized protein C14orf125
UniRef100_Q	5	9	3.80%	1590	2E+05	6	KIAA1316 protein
UniRef100_P	4	4	3.40%	1729	2E+05	6	Nuclear pore complex protein Nup98-Nup96 precursor [Contains: Nuclear pore complex protein Nup98 (Nucleoporin Nup98) (98 kDa nucleoporin); Nuclear pore complex protein Nup96 (Nucleoporin Nup96) (96 kDa nucleoporin)]

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_UI	4	4	3.40%	1729	2E+05	6	Nuclear pore complex protein Nup98-Nup96 precursor [Contains: Nuclear pore complex protein Nup98 (Nucleoporin Nup98) (98 kDa nucleoporin); Nuclear pore complex protein Nup96 (Nucleoporin Nup96) (96 kDa nucleoporin)].
UniRef100_UI	4	4	3.40%	1726	2E+05	7	nucleoporin 98kD isoform 4
UniRef100_P	4	4	3.20%	1800	2E+05	6	Isoform 5 of P52948
UniRef100_P	4	4	3.50%	1638	2E+05	6	Isoform 2 of P52948
UniRef100_Q	2	4	3.40%	833	95368	5	SMEK homolog 1
UniRef100_UI	2	4	3.00%	920	1E+05	5	SMEK homolog 1.
UniRef100_Q	2	4	5.20%	540	62020	5	Isoform 5 of Q6IN85
UniRef100_Q	2	4	4.70%	594	67812	5	Isoform 4 of Q6IN85
UniRef100_Q	2	4	4.00%	696	79637	5	Isoform 3 of Q6IN85
UniRef100_Q	2	4	3.40%	820	93896	5	Isoform 2 of Q6IN85
UniRef100_UI	6	12	3.30%	1674	2E+05	5	Tenascin-X
UniRef100_Q	3	5	3.30%	1478	2E+05	5	FYVE and coiled-coil domain-containing protein 1
UniRef100_UI	3	5	3.30%	1478	2E+05	5	FYVE and coiled-coil domain-containing protein 1 (Zinc finger FYVE domain-containing protein 7).
UniRef100_UI	3	5	3.30%	1478	2E+05	5	FYVE and coiled-coil domain containing 1
UniRef100_Q	4	11	3.30%	1341	2E+05	6	Apoptotic chromatin condensation inducer in the nucleus
UniRef100_UI	4	11	3.30%	1341	2E+05	6	Apoptotic chromatin condensation inducer in the nucleus (Acinus).
UniRef100_Q	2	2	3.30%	892	97264	#	Zinc finger protein KIAA1196
UniRef100_Q	2	2	3.30%	855	94770	7	Suppressor of tumorigenicity protein 14
UniRef100_O	2	2	3.30%	631	71690	5	Double-strand-break repair protein rad21 homolog
UniRef100_Q	2	2	3.30%	539	62166	5	Tripartite motif-containing protein 26
UniRef100_UI	2	2	8.80%	204	22982	8	PREDICTED: similar to Tripartite motif protein 26 (Zinc finger protein 173) (Acid finger protein) (AFP) (RING finger protein 95)
UniRef100_Q	8	9	3.20%	3277	4E+05	7	Laminin alpha 3 splice variant b2
UniRef100_UI	8	9	3.10%	3335	4E+05	7	Laminin subunit alpha-3 precursor (Epiligrin 170 kDa subunit) (E170) (Nicein subunit alpha).
UniRef100_Q	8	9	3.10%	3333	4E+05	7	Laminin alpha 3b chain
UniRef100_Q	8	9	3.10%	3333	4E+05	7	Laminin alpha 3 splice variant b1
UniRef100_O	4	13	3.20%	1268	1E+05	7	Protein transport protein Sec24B
UniRef100_UI	4	13	3.20%	1268	1E+05	7	SEC24 (S. cerevisiae) homolog B isoform a
UniRef100_UI	4	13	3.20%	1266	1E+05	7	Protein transport protein Sec24B (SEC24-related protein B).
UniRef100_Q	4	13	3.30%	1233	1E+05	7	SEC24 related gene family, member B
UniRef100_Q	2	2	3.20%	954	1E+05	7	Zinc finger protein 618
UniRef100_Q	2	2	3.60%	871	96756	7	ZNF618 protein
UniRef100_P	2	2	3.20%	896	98656	5	Epidermal growth factor receptor substrate 15
UniRef100_Q	2	2	3.80%	762	83673	5	EPS15 protein
UniRef100_Q	2	2	3.80%	762	83655	5	Epidermal growth factor receptor pathway substrate 15
UniRef100_Q	2	2	3.20%	811	91354	6	Hephaestin
UniRef100_Q	2	2	2.20%	1157	1E+05	6	Isoform 2 of Q9BQS7
UniRef100_Q	2	2	2.20%	1158	1E+05	6	Hephaestin precursor

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	2	2	3.20%	708	79818	6	RUN and FYVE domain-containing protein 1
UniRef100_UI	2	2	3.30%	706	79619	6	RUN and FYVE domain-containing protein 1 (FYVE-finger protein EIP1) (Zinc finger FYVE domain-containing protein 12) (La-binding protein 1) (Rab4-interacting protein).
UniRef100_Q	2	2	3.20%	530	59612	5	Synembryn-A
UniRef100_UI	2	2	3.20%	537	60372	5	resistance to inhibitors of cholinesterase 8 homolog A
UniRef100_Q	2	2	3.20%	536	60275	5	Isoform 3 of Q9NPQ8
UniRef100_Q	2	2	3.20%	524	58846	7	Isoform 2 of Q9NPQ8
UniRef100_Q	5	7	3.10%	1944	2E+05	6	Anaphase-promoting complex subunit 1
UniRef100_Q	3	9	3.10%	1431	2E+05	5	Remodeling and spacing factor 1
UniRef100_UI	3	9	3.20%	1400	2E+05	5	Remodeling and spacing factor 1 (Rsf-1) (Hepatitis B virus X- associated protein) (HBV pX-associated protein 8) (p325 subunit of RSF chromatin remodelling complex).
UniRef100_UI	3	9	3.10%	1441	2E+05	5	remodeling and spacing factor 1
UniRef100_Q	3	9	3.20%	1400	2E+05	5	Isoform 2 of Q96T23
UniRef100_P2	3	6	3.10%	1241	1E+05	7	Plasma membrane calcium-transporting ATPase 4
UniRef100_Q	3	6	3.20%	1205	1E+05	7	Cation-transporting ATPase
UniRef100_Q	3	6	3.20%	1205	1E+05	7	Cation-transporting ATPase
UniRef100_Q	3	6	3.30%	1170	1E+05	8	Cation-transporting ATPase
UniRef100_Q	3	6	3.20%	1205	1E+05	6	Cation-transporting ATPase
UniRef100_P2	3	6	3.20%	1229	1E+05	6	Isoform ZD of P23634
UniRef100_P2	3	6	3.30%	1193	1E+05	6	Isoform ZB of P23634
UniRef100_P2	3	6	3.50%	1122	1E+05	7	Isoform ZK of P23634
UniRef100_P2	3	6	3.40%	1134	1E+05	8	Isoform XK of P23634
UniRef100_P2	3	6	3.40%	1158	1E+05	7	Isoform ZA of P23634
UniRef100_Q	2	6	3.10%	1087	1E+05	7	Ubiquitin-associated protein 2-like
UniRef100_Q	2	6	3.20%	1068	1E+05	7	Isoform 3 of Q14157
UniRef100_Q	2	6	3.50%	983	1E+05	7	Isoform 2 of Q14157
UniRef100_Q	2	2	3.10%	721	80366	5	Translation initiation factor eIF-2B subunit epsilon
UniRef100_UI	2	2	3.10%	721	80380	5	eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kDa
UniRef100_Q	2	2	3.10%	684	75127	7	Sec1 family domain-containing protein 2
UniRef100_UI	2	2	3.30%	641	70176	7	Sec1 family domain-containing protein 2 (Syntaxin-binding protein 1- like 1).
UniRef100_UI	2	2	3.10%	684	75112	7	Sec1 family domain-containing protein 2 (Syntaxin-binding protein 1- like 1).
UniRef100_Q	2	2	3.30%	639	69992	7	Isoform 2 of Q8WU76
UniRef100_P	2	2	3.10%	637	72766	6	Glutamate--cysteine ligase catalytic subunit
UniRef100_P1	2	2	3.10%	519	55440	7	Steroid hormone receptor ERR1
UniRef100_UI	2	2	3.40%	475	50612	6	Steroid hormone receptor ERR1 (Estrogen-related receptor, alpha) (ERR- alpha) (Estrogen receptor-like 1).
UniRef100_Q	2	2	5.00%	320	35027	8	ESRRA protein
UniRef100_Q	2	2	5.40%	299	32629	8	Similar to estrogen-related receptor alpha
UniRef100_Q	2	2	3.80%	423	45510	6	ESRRA protein
UniRef100_Q	8	11	3.00%	3395	4E+05	6	Ubiquitin carboxyl-terminal hydrolase 34

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_U	8	11	3.00%	3394	4E+05	6	Ubiquitin carboxyl-terminal hydrolase 34 (EC 3.1.2.15) (Ubiquitin thioesterase 34) (Ubiquitin-specific-processing protease 34) (Deubiquitinating enzyme 34).
UniRef100_U	8	11	2.90%	3546	4E+05	6	ubiquitin specific protease 34
UniRef100_Q	8	11	3.10%	3312	4E+05	6	Isoform 2 of Q70CQ2
UniRef100_Q	5	5	3.00%	2032	2E+05	8	Cytoskeleton associated protein 5
UniRef100_U	5	5	3.00%	1972	2E+05	8	colonic and hepatic tumor over-expressed protein isoform b
UniRef100_Q	5	5	3.00%	2032	2E+05	8	Cytoskeleton-associated protein 5
UniRef100_Q	3	3	3.00%	1144	1E+05	8	Alpha-mannosidase 2
UniRef100_U	3	3	3.00%	1144	1E+05	8	mannosidase, alpha, class 2A, member 1
UniRef100_P	2	4	3.00%	919	1E+05	6	DNA ligase 1
UniRef100_Q	2	4	3.40%	832	91953	6	DNA ligase I variant
UniRef100_Q	2	4	3.50%	801	88516	6	LIG1 protein
UniRef100_Q	10	11	2.90%	4829	5E+05	6	Baculoviral IAP repeat-containing protein 6
UniRef100_U	10	11	2.90%	4829	5E+05	6	Baculoviral IAP repeat-containing protein 6 (Ubiquitin-conjugating BIR domain enzyme apollon).
UniRef100_U	10	11	2.90%	4829	5E+05	6	baculoviral IAP repeat-containing 6
UniRef100_U	10	11	2.90%	4829	5E+05	6	Baculoviral IAP repeat-containing protein 6 (Ubiquitin-conjugating BIR domain enzyme apollon).
UniRef100_P	3	3	2.90%	1462	2E+05	6	DNA polymerase alpha catalytic subunit
UniRef100_U	3	3	2.90%	1468	2E+05	6	DNA polymerase alpha catalytic subunit (EC 2.7.7.7).
UniRef100_Q	3	4	2.90%	1461	2E+05	7	Neogenin precursor
UniRef100_U	3	4	3.10%	1408	2E+05	6	Neogenin precursor.
UniRef100_U	3	4	2.90%	1461	2E+05	7	neogenin homolog 1
UniRef100_Q	3	4	3.10%	1408	2E+05	6	Isoform 2 of Q92859
UniRef100_Q	2	4	2.90%	963	1E+05	6	Squamous cell carcinoma antigen recognized by T-cells 3
UniRef100_Q	2	2	2.90%	963	1E+05	6	Integrator complex subunit 4
UniRef100_Q	2	2	2.90%	952	1E+05	8	POLR1B protein
UniRef100_U	2	2	6.10%	458	51544	6	DNA-directed RNA polymerase I 135 kDa polypeptide (EC 2.7.7.6) (RNA polymerase I subunit 2) (RPA135).
UniRef100_Q	2	2	2.60%	1079	1E+05	8	Isoform 2 of Q9H9Y6
UniRef100_Q	2	2	2.50%	1135	1E+05	8	DNA-directed RNA polymerase I 135 kDa polypeptide
UniRef100_Q	2	2	6.10%	459	51619	6	CDNA: FLJ21921 fis, clone HEP04058
UniRef100_Q	2	2	4.80%	582	65486	7	POLR1B protein
UniRef100_Q	2	2	5.00%	560	63176	7	POLR1B protein
UniRef100_Q	2	2	4.70%	594	66804	7	POLR1B protein
UniRef100_A	2	3	2.90%	921	1E+05	9	Protein FAM62B
UniRef100_A	2	3	3.00%	893	98902	9	KIAA1228 protein
UniRef100_A	2	3	8.20%	328	35846	#	Isoform 5 of A0FGR8
UniRef100_Q	2	5	2.90%	615	70703	9	Lamin-B receptor
UniRef100_Q	4	5	2.80%	1865	2E+05	8	Dedicator of cytokinesis protein 1
UniRef100_Q	4	5	2.80%	1865	2E+05	8	Dedicator of cytokinesis 1
UniRef100_Q	4	12	2.80%	1720	2E+05	8	Poly [ADP-ribose] polymerase 14
UniRef100_Q	2	4	2.80%	1636	2E+05	7	Tyrosine-protein phosphatase non-receptor type 23

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	3	3	2.80%	1586	2E+05	7	KIAA1414 protein
UniRef100_Q	3	3	2.80%	1436	2E+05	6	Nucleoporin 160kDa
UniRef100_U	3	3	3.00%	1316	1E+05	6	Nuclear pore complex protein Nup160 (Nucleoporin Nup160) (160 kDa nucleoporin).
UniRef100_U	3	3	2.80%	1436	2E+05	6	nucleoporin 160kDa
UniRef100_Q	3	3	3.00%	1316	1E+05	6	Nuclear pore complex protein Nup160
UniRef100_Q	3	4	2.80%	1461	2E+05	7	Uncharacterized protein KIAA0460
UniRef100_Q	3	4	2.90%	1435	2E+05	7	Isoform 3 of Q5VT52
UniRef100_O	3	4	2.80%	1288	1E+05	7	5-oxoprolinase
UniRef100_U	3	4	2.80%	1287	1E+05	7	5-oxoprolinase (EC 3.5.2.9) (5-oxo-L-prolinase) (Pyroglutamase) (5- OPase).
UniRef100_O	2	2	2.80%	1068	1E+05	7	Huntingtin-interacting protein 1-related protein
UniRef100_U	2	2	2.90%	1048	1E+05	6	PREDICTED: similar to Huntingtin-interacting protein 1-related protein (Hip1-related) (Hip 12)
UniRef100_U	2	2	2.80%	1068	1E+05	7	Huntingtin-interacting protein 1-related protein (Hip1-related) (Hip 12).
UniRef100_Q	2	3	2.80%	1007	1E+05	9	RNA-binding protein 26
UniRef100_Q	2	3	23.30%	120	13644	5	Isoform 6 of Q5T8P6
UniRef100_Q	2	3	2.90%	980	1E+05	9	Isoform 3 of Q5T8P6
UniRef100_Q	2	3	2.80%	983	1E+05	9	Isoform 2 of Q5T8P6
UniRef100_P	9	15	2.70%	4289	5E+05	5	Tenascin-X precursor
UniRef100_U	9	15	2.70%	4289	5E+05	5	tenascin XB isoform 1
UniRef100_Q	9	15	2.70%	4288	5E+05	5	DJ34F7.1.1 (Tenascin XB (Isoform 1))
UniRef100_Q	4	9	2.70%	1748	2E+05	7	Tight junction protein ZO-1
UniRef100_U	4	9	2.80%	1676	2E+05	7	Tight junction protein ZO-1 (Zonula occludens 1 protein) (Zona occludens 1 protein) (Tight junction protein 1).
UniRef100_U	4	9	2.70%	1736	2E+05	7	Tight junction protein ZO-1 (Zonula occludens 1 protein) (Zona occludens 1 protein) (Tight junction protein 1).
UniRef100_Q	4	9	2.80%	1692	2E+05	7	Hypothetical protein DKFZp686A1195
UniRef100_Q	4	9	2.80%	1668	2E+05	7	Isoform Short of Q07157
UniRef100_Q	3	7	2.70%	1729	2E+05	5	182 kDa tankyrase 1-binding protein
UniRef100_U	3	7	2.70%	1729	2E+05	5	tankyrase 1-binding protein 1
UniRef100_Q	3	6	2.70%	1401	2E+05	7	Condensin complex subunit 1
UniRef100_U	3	6	2.70%	1401	2E+05	7	Condensin complex subunit 1 (Non-SMC condensin I complex subunit D2) (Chromosome condensation-related SMC-associated protein 1) (Chromosome-associated protein D2) (hCAP-D2) (XCAP-D2 homolog).
UniRef100_O	2	2	2.70%	1321	1E+05	5	C-jun-amino-terminal kinase-interacting protein 4
UniRef100_U	2	2	2.80%	1309	1E+05	5	C-jun-amino-terminal kinase-interacting protein 4 (JNK-interacting protein 4) (JIP-4) (JNK-associated leucine-zipper protein) (JLP) (Sperm-associated antigen 9) (Mitogen-activated protein kinase 8- interacting protein 4) (Human lung cancer protein 6) (HLC
UniRef100_U	2	2	2.70%	1313	1E+05	5	C-jun-amino-terminal kinase-interacting protein 4 (JNK-interacting protein 4) (JIP-4) (JNK-associated leucine-zipper protein) (JLP) (Sperm-associated antigen 9) (Mitogen-activated protein kinase 8- interacting protein 4) (Human lung cancer protein 6) (HLC

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_U	2	2	4.90%	736	79452	5	C-jun-amino-terminal kinase-interacting protein 4 (JNK-interacting protein 4) (JIP-4) (JNK-associated leucine-zipper protein) (JLP) (Sperm-associated antigen 9) (Mitogen-activated protein kinase 8- interacting protein 4) (Human lung cancer protein 6) (HLC
UniRef100_O	2	2	4.10%	877	95835	5	Isoform 6 of O60271
UniRef100_O	2	2	3.90%	931	1E+05	5	Isoform 5 of O60271
UniRef100_O	2	2	2.80%	1307	1E+05	5	Isoform 4 of O60271
UniRef100_O	2	2	3.80%	945	1E+05	5	Isoform 3 of O60271
UniRef100_O	2	2	2.70%	1311	1E+05	5	Isoform 2 of O60271
UniRef100_P	2	3	2.70%	1127	1E+05	7	Nck-associated protein 1-like
UniRef100_Q	2	3	3.50%	865	97846	7	NCKAP1L protein
UniRef100_Q	2	3	3.60%	837	94703	7	NCKAP1L protein
UniRef100_Q	2	3	4.20%	712	80465	7	NCKAP1L protein
UniRef100_Q	2	3	2.70%	1127	1E+05	7	NCK-associated protein 1-like
UniRef100_Q	2	4	2.70%	1146	1E+05	8	Nucleolar protein 6
UniRef100_Q	2	4	2.70%	1143	1E+05	8	Isoform 4 of Q9H6R4
UniRef100_U	2	2	2.70%	1034	1E+05	8	modulator of estrogen induced transcription isoform a
UniRef100_Q	2	2	2.70%	1046	1E+05	7	CAP-Gly domain-containing linker protein 2
UniRef100_U	2	2	2.70%	1046	1E+05	7	CAP-GLY domain containing linker protein 2 isoform 1
UniRef100_U	2	2	2.80%	1011	1E+05	7	CAP-GLY domain containing linker protein 2 isoform 2
UniRef100_Q	4	7	2.60%	2391	2E+05	8	Ifapsoriasin
UniRef100_U	4	7	3.50%	1797	2E+05	8	PREDICTED: similar to filaggrin 2
UniRef100_Q	2	2	2.60%	1015	1E+05	6	Non-SMC condensin I complex, subunit G
UniRef100_Q	2	2	2.60%	1015	1E+05	6	Condensin complex subunit 3
UniRef100_P	2	7	2.60%	780	85182	8	6-phosphofructokinase, muscle type
UniRef100_Q	2	7	2.70%	747	81543	8	PFKM protein
UniRef100_Q	2	7	2.40%	851	93220	8	CDNA FLJ44241 fis, clone THYMU3008436, highly similar to 6- phosphofructokinase, muscle type
UniRef100_Q	2	5	2.60%	680	77948	#	BCLAF1 protein
UniRef100_U	2	5	2.10%	869	1E+05	#	PREDICTED: similar to Bcl-2-associated transcription factor 1 (Btf)
UniRef100_U	2	5	2.10%	869	1E+05	#	Bcl-2-associated transcription factor 1 (Btf).
UniRef100_Q	2	5	2.40%	747	85937	#	Isoform 4 of Q9NYF8
UniRef100_Q	2	5	2.10%	869	1E+05	#	Isoform 3 of Q9NYF8
UniRef100_Q	2	5	2.00%	918	1E+05	#	Isoform 2 of Q9NYF8
UniRef100_Q	2	5	2.00%	920	1E+05	#	Bcl-2-associated transcription factor 1
UniRef100_Q	4	5	2.50%	1855	2E+05	6	GBF1 protein
UniRef100_Q	4	5	2.50%	1859	2E+05	6	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1
UniRef100_Q	4	5	2.50%	1855	2E+05	6	GBF1 protein
UniRef100_P	3	8	2.50%	1712	2E+05	9	Collagen alpha-2(IV) chain precursor [Contains: Canstatin]
UniRef100_U	3	8	2.50%	1706	2E+05	9	Collagen alpha-2(IV) chain precursor.
UniRef100_U	3	8	2.50%	1712	2E+05	9	Collagen alpha-2(IV) chain precursor.
UniRef100_U	3	8	2.50%	1706	2E+05	9	Collagen alpha-2(IV) chain precursor.

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_A	2	2	2.50%	1265	1E+05	6	5-methyltetrahydrofolate-homocysteine methyltransferase
UniRef100_U	2	2	2.40%	1267	1E+05	6	Methionine synthase (EC 2.1.1.13) (5-methyltetrahydrofolate-- homocysteine methyltransferase) (Methionine synthase, vitamin-B12 dependent) (MS).
UniRef100_U	2	2	2.50%	1265	1E+05	6	5-methyltetrahydrofolate-homocysteine methyltransferase
UniRef100_Q	2	2	2.50%	1265	1E+05	6	Methionine synthase
UniRef100_P	2	3	2.50%	1093	1E+05	5	TATA element modulatory factor
UniRef100_U	2	3	2.50%	1091	1E+05	5	TATA element modulatory factor (TMF).
UniRef100_Q	2	3	2.50%	1096	1E+05	5	TATA element modulatory factor 1 variant
UniRef100_O	2	3	2.50%	1041	1E+05	7	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16
UniRef100_U	2	3	2.50%	1041	1E+05	7	DEAH (Asp-Glu-Ala-His) box polypeptide 16
UniRef100_Q	2	3	2.50%	1041	1E+05	7	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 16
UniRef100_O	2	2	2.50%	968	1E+05	7	Serine/threonine-protein kinase 10
UniRef100_U	2	2	2.50%	974	1E+05	7	Serine/threonine-protein kinase 10 (EC 2.7.11.1) (Lymphocyte-oriented kinase).
UniRef100_Q	2	2	2.50%	968	1E+05	7	Serine/threonine kinase 10
UniRef100_Q	7	7	2.40%	3753	4E+05	7	Vacuolar protein sorting-associated protein 13C
UniRef100_U	7	7	2.50%	3585	4E+05	6	vacuolar protein sorting 13C protein isoform 1B
UniRef100_Q	7	7	2.50%	3584	4E+05	6	Isoform 4 of Q709C8
UniRef100_Q	7	7	2.50%	3710	4E+05	7	Isoform 3 of Q709C8
UniRef100_Q	7	7	2.50%	3627	4E+05	7	Isoform 2 of Q709C8
UniRef100_Q	2	3	2.40%	1267	1E+05	6	Histone-lysine N-methyltransferase, H3 lysine-9 specific 5
UniRef100_U	2	3	2.60%	1153	1E+05	6	Histone-lysine N-methyltransferase, H3 lysine-9 specific 5 (EC 2.1.1.43) (Histone H3-K9 methyltransferase 5) (H3-K9-HMTase 5) (Euchromatic histone-lysine N-methyltransferase 1) (Eu-HMTase1) (G9a- like protein 1) (GLP1).
UniRef100_U	2	3	3.70%	803	88240	6	Histone-lysine N-methyltransferase, H3 lysine-9 specific 5 (EC 2.1.1.43) (Histone H3-K9 methyltransferase 5) (H3-K9-HMTase 5) (Euchromatic histone-lysine N-methyltransferase 1) (Eu-HMTase1) (G9a- like protein 1) (GLP1).
UniRef100_Q	2	3	2.60%	1153	1E+05	6	Isoform 3 of Q9H9B1
UniRef100_Q	2	2	2.40%	962	1E+05	8	Integrator complex subunit 7
UniRef100_U	2	2	2.40%	963	1E+05	8	Integrator complex subunit 7 (Int7).
UniRef100_Q	2	2	2.40%	942	1E+05	8	Isoform 3 of Q9NVH2
UniRef100_Q	2	2	2.40%	948	1E+05	8	Isoform 2 of Q9NVH2
UniRef100_Q	2	2	2.40%	824	93533	5	Protein bicaudal D homolog 2
UniRef100_Q	2	2	2.30%	855	96806	5	Isoform 2 of Q8TD16
UniRef100_P	2	2	2.40%	795	92707	6	PITSLRE serine/threonine-protein kinase CDC2L1
UniRef100_U	2	2	3.20%	593	67740	5	PREDICTED: similar to cell division cycle 2-like 1 (PITSLRE proteins) isoform 1
UniRef100_U	2	2	2.50%	750	86357	5	cell division cycle 2-like 1 (PITSLRE proteins) isoform 3
UniRef100_U	2	2	2.40%	785	90626	5	cell division cycle 2-like 1 (PITSLRE proteins) isoform 3
UniRef100_U	2	2	2.40%	797	91867	5	cell division cycle 2-like 1 (PITSLRE proteins) isoform 3
UniRef100_U	2	2	2.50%	770	90045	5	PITSLRE serine/threonine-protein kinase CDC2L2 (EC 2.7.11.22) (Galactosyltransferase-associated protein kinase p58/GTA) (Cell division cycle 2-like protein kinase 2) (CDK11).

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_UI	2	2	2.40%	783	91362	5	PITSLRE serine/threonine-protein kinase CDC2L2 (EC 2.7.11.22) (Galactosyltransferase-associated protein kinase p58/GTA) (Cell division cycle 2-like protein kinase 2) (CDK11).
UniRef100_UI	2	2	2.40%	780	91018	5	PITSLRE serine/threonine-protein kinase CDC2L2 (EC 2.7.11.22) (Galactosyltransferase-associated protein kinase p58/GTA) (Cell division cycle 2-like protein kinase 2) (CDK11).
UniRef100_UI	2	2	2.40%	777	90663	6	cell division cycle 2-like 2 isoform 1
UniRef100_UI	2	2	2.50%	775	90394	5	cell division cycle 2-like 2 isoform 9
UniRef100_UI	2	2	2.50%	771	90047	5	cell division cycle 2-like 1 (PITSLRE proteins) isoform 9
UniRef100_UI	2	2	2.40%	780	91009	5	cell division cycle 2-like 1 (PITSLRE proteins) isoform 8
UniRef100_UI	2	2	2.40%	776	90698	5	cell division cycle 2-like 2 isoform 3
UniRef100_UI	2	2	2.50%	767	89688	5	cell division cycle 2-like 2 isoform 4
UniRef100_UI	2	2	2.40%	777	90661	6	cell division cycle 2-like 2 isoform 1
UniRef100_UI	2	2	2.40%	780	91063	5	cell division cycle 2-like 2 isoform 5
UniRef100_UI	2	2	2.60%	737	85906	5	cell division cycle 2-like 1 (PITSLRE proteins) isoform 4
UniRef100_Q	2	2	2.50%	767	89658	5	Isoform SV3 of Q9UQ88
UniRef100_Q	2	2	2.40%	776	90668	5	Isoform SV2 of Q9UQ88
UniRef100_Q	2	2	2.40%	777	90631	6	Isoform SV1 of Q9UQ88
UniRef100_Q	2	2	4.30%	439	49624	6	Isoform 4 of Q9UQ88
UniRef100_Q	2	2	2.40%	780	90974	5	PITSLRE serine/threonine-protein kinase CDC2L2
UniRef100_Q	2	2	4.10%	464	52406	5	CDC2L2 protein
UniRef100_Q	2	2	4.00%	475	53688	5	CDC2L1 protein
UniRef100_Q	2	2	2.50%	746	86824	5	Cell division cycle 2-like 2
UniRef100_Q	2	2	2.40%	779	91007	5	Cell division cycle 2-like 2
UniRef100_Q	2	2	4.00%	475	53757	5	CDC2L2 protein
UniRef100_Q	2	2	4.80%	397	45229	9	Cell division cycle 2-like 2
UniRef100_P	2	2	2.50%	748	87138	5	Isoform SV10 of P21127
UniRef100_P	2	2	2.50%	772	90256	5	Isoform 8 of P21127
UniRef100_P	2	2	2.60%	738	86063	5	Isoform SV5 of P21127
UniRef100_P	2	2	4.10%	461	51925	5	Isoform 3 of P21127
UniRef100_P	2	2	2.40%	781	91219	5	Isoform 2 of P21127
UniRef100_P	2	2	2.40%	782	91332	6	Isoform SV1 of P21127
UniRef100_P	2	2	4.30%	439	49555	6	Isoform 7 of P21127
UniRef100_P	2	2	3.40%	565	63937	5	Isoform SV11 of P21127
UniRef100_Q	11	14	2.30%	5596	6E+05	6	Midasin
UniRef100_Q	4	4	2.30%	2472	3E+05	6	Telomere-associated protein RIF1
UniRef100_UI	4	4	2.30%	2448	3E+05	5	Telomere-associated protein RIF1 (Rap1-interacting factor 1 homolog).
UniRef100_UI	4	4	2.30%	2474	3E+05	6	Telomere-associated protein RIF1 (Rap1-interacting factor 1 homolog).
UniRef100_Q	4	4	2.30%	2446	3E+05	5	Isoform 2 of Q5UIP0
UniRef100_P	2	4	2.30%	907	1E+05	7	Eukaryotic translation initiation factor 4 gamma 2
UniRef100_UI	2	4	8.30%	253	29152	8	Eukaryotic translation initiation factor 4 gamma 2 (eIF-4-gamma 2) (eIF-4G 2) (eIF4G 2) (p97) (Death-associated protein 5) (DAP-5).

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_U	2	4	2.30%	907	1E+05	7	Eukaryotic translation initiation factor 4 gamma 2 (eIF-4-gamma 2) (eIF-4G 2) (eIF4G 2) (p97) (Death-associated protein 5) (DAP-5).
UniRef100_Q	2	4	2.20%	940	1E+05	7	Eukaryotic translation initiation factor 4 gamma, 2 variant
UniRef100_Q	2	4	2.30%	907	1E+05	7	Eukaryotic translation initiation factor 4 gamma, 2
UniRef100_Q	2	4	11.10%	189	22027	9	Hypothetical protein Nbla00315
UniRef100_Q	2	4	3.00%	701	79614	7	Aging-associated protein 1
UniRef100_Q	2	4	2.40%	869	98150	7	Eukaryotic translation initiation factor 4 gamma, 2
UniRef100_Q	2	4	2.30%	907	1E+05	7	Eukaryotic translation initiation factor 4 gamma, 2
UniRef100_P	2	3	2.30%	879	1E+05	8	Nuclear autoantigen Sp-100
UniRef100_U	2	3	2.30%	885	1E+05	7	nuclear antigen Sp100 isoform 1
UniRef100_Q	2	3	2.40%	843	96549	8	Hypothetical protein SP100
UniRef100_P	2	3	4.20%	472	53113	5	Isoform SpAlt
UniRef100_P	2	3	2.30%	886	1E+05	8	Isoform Sp100
UniRef100_P	2	3	2.90%	688	78144	8	Isoform Sp100
UniRef100_P	2	3	4.20%	480	53768	5	Isoform Sp100
UniRef100_P	2	3	2.30%	817	89787	6	Protein-glutamine gamma-glutamyltransferase K (EC 2.3.2.13) (Transglutaminase K) (TGase K) (TGK) (TG(K))
UniRef100_P	2	5	2.30%	621	69692	6	Fragile X mental retardation syndrome-related protein 1
UniRef100_U	2	5	2.30%	621	69721	6	fragile X mental retardation-related protein 1 isoform a
UniRef100_U	2	5	2.60%	539	60792	6	fragile X mental retardation-related protein 1 isoform b
UniRef100_Q	2	5	2.50%	568	63947	6	Fragile X mental retardation syndrome-related protein 1
UniRef100_P	2	5	2.60%	536	59919	7	Isoform 3 of P51114
UniRef100_P	2	5	2.60%	539	60763	7	Isoform 2 of P51114
UniRef100_P	4	8	2.20%	2549	3E+05	7	FKBP12-rapamycin complex-associated protein
UniRef100_U	4	8	2.20%	2551	3E+05	7	FKBP12-rapamycin complex-associated protein (FK506-binding protein 12- rapamycin complex-associated protein 1) (Rapamycin target protein) (RAPT1) (Mammalian target of rapamycin) (mTOR).
UniRef100_Q	4	8	2.10%	2583	3E+05	8	FRAP1 variant protein
UniRef100_Q	4	7	2.20%	2230	3E+05	5	Golgin subfamily A member 4
UniRef100_U	4	7	2.20%	2184	3E+05	5	Golgin subfamily A member 4 (Trans-Golgi p230) (256 kDa golgin) (Golgin-245) (Protein 72.1).
UniRef100_Q	4	7	3.70%	1310	2E+05	6	Golgi autoantigen, golgin subfamily a, 4 variant
UniRef100_Q	4	7	2.20%	2228	3E+05	5	Isoform 4 of Q13439
UniRef100_Q	4	7	2.20%	2223	3E+05	5	Isoform 3 of Q13439
UniRef100_Q	4	7	2.20%	2185	3E+05	5	Isoform 2 of Q13439
UniRef100_O	3	3	2.20%	1429	2E+05	7	Attractin precursor
UniRef100_U	3	3	2.30%	1362	2E+05	7	Attractin precursor (Mahogany homolog) (DPPT-L).
UniRef100_O	3	3	2.70%	1198	1E+05	7	Isoform 3 of O75882
UniRef100_O	3	3	2.50%	1272	1E+05	7	Isoform 2 of O75882
UniRef100_O	2	3	2.20%	1248	1E+05	6	Apoptotic protease-activating factor 1
UniRef100_O	2	3	2.30%	1205	1E+05	6	Isoform 4 of O14727
UniRef100_O	2	3	2.30%	1194	1E+05	6	Isoform 3 of O14727

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_O	2	3	2.30%	1237	1E+05	6	Isoform 2 of O14727
UniRef100_P	2	2	2.20%	1152	1E+05	7	Integrin alpha-M precursor
UniRef100_Q	2	2	2.20%	1152	1E+05	7	Integrin, alpha M
UniRef100_Q	2	2	2.20%	1152	1E+05	7	Integrin, alpha M
UniRef100_A	2	3	2.20%	1016	1E+05	7	Transcriptional intermediary factor 1
UniRef100_O	2	3	2.10%	1050	1E+05	7	Transcription intermediary factor 1-alpha
UniRef100_Q	3	3	2.10%	2769	3E+05	7	Teneurin-4
UniRef100_U	3	3	2.10%	2825	3E+05	6	Teneurin-4 (Ten-4) (Tenascin-M4) (Ten-m4) (Protein Odd Oz/ten-m homolog 4).
UniRef100_A	2	2	2.10%	2033	2E+05	7	Envoplakin
UniRef100_U	2	2	2.10%	2033	2E+05	7	Envoplakin (210 kDa paraneoplastic pemphigus antigen) (p210) (210 kDa cornified envelope precursor protein).
UniRef100_Q	2	2	2.10%	2033	2E+05	7	Envoplakin
UniRef100_Q	3	3	2.10%	1835	2E+05	7	Zipzap protein
UniRef100_Q	3	3	2.10%	1835	2E+05	7	AT-rich interactive domain-containing protein 2
UniRef100_Q	2	2	2.10%	1630	2E+05	5	Protein LAP4
UniRef100_U	2	2	2.10%	1654	2E+05	5	Protein LAP4 (Protein scribble homolog) (hScrib).
UniRef100_U	2	2	2.10%	1655	2E+05	5	Protein LAP4 (Protein scribble homolog) (hScrib).
UniRef100_U	2	2	2.10%	1630	2E+05	5	Protein LAP4 (Protein scribble homolog) (hScrib).
UniRef100_Q	2	2	2.10%	1654	2E+05	5	Isoform 4 of Q14160
UniRef100_Q	2	2	2.10%	1655	2E+05	5	Isoform 3 of Q14160
UniRef100_Q	2	2	2.10%	1447	2E+05	9	Hypothetical protein
UniRef100_U	2	2	2.10%	1449	2E+05	9	androgen-induced prostate proliferative shutoff associated protein
UniRef100_Q	2	2	2.20%	1391	2E+05	9	Androgen-induced prostate proliferative shutoff associated protein
UniRef100_Q	2	2	2.00%	1483	2E+05	9	Androgen-induced proliferation inhibitor
UniRef100_Q	2	2	2.10%	1220	1E+05	8	ATP-dependent RNA helicase DHX8
UniRef100_Q	2	2	2.10%	1220	1E+05	8	DEAH (Asp-Glu-Ala-His) box polypeptide 8
UniRef100_Q	2	2	2.10%	1220	1E+05	8	DEAH (Asp-Glu-Ala-His) box polypeptide 8
UniRef100_Q	2	2	2.10%	1125	1E+05	6	Exportin-6
UniRef100_O	2	2	2.10%	1030	1E+05	5	Protein phosphatase 1 regulatory subunit 12A
UniRef100_U	2	2	2.30%	972	1E+05	5	Protein phosphatase 1 regulatory subunit 12A (Myosin phosphatase- targeting subunit 1) (Myosin phosphatase target subunit 1) (Protein phosphatase myosin-binding subunit).
UniRef100_U	2	2	2.30%	969	1E+05	5	Protein phosphatase 1 regulatory subunit 12A (Myosin phosphatase- targeting subunit 1) (Myosin phosphatase target subunit 1) (Protein phosphatase myosin-binding subunit).
UniRef100_U	2	2	2.10%	1028	1E+05	5	Protein phosphatase 1 regulatory subunit 12A (Myosin phosphatase- targeting subunit 1) (Myosin phosphatase target subunit 1) (Protein phosphatase myosin-binding subunit).
UniRef100_U	2	2	2.20%	993	1E+05	5	Protein phosphatase 1 regulatory subunit 12A (Myosin phosphatase- targeting subunit 1) (Myosin phosphatase target subunit 1) (Protein phosphatase myosin-binding subunit).
UniRef100_Q	2	2	3.00%	730	80101	6	PPP1R12A protein
UniRef100_Q	2	2	2.10%	1030	1E+05	5	PPP1R12A protein
UniRef100_O	2	2	2.30%	971	1E+05	5	Isoform 4 of O14974
UniRef100_O	2	2	2.30%	974	1E+05	5	Isoform 3 of O14974

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_O	2	2	2.20%	995	1E+05	5	Isoform 2 of O14974
UniRef100_Q	2	2	2.10%	890	1E+05	7	Oxysterol-binding protein
UniRef100_UI	2	2	2.20%	847	96956	8	oxysterol-binding protein-like protein 8 isoform b
UniRef100_Q	2	2	2.20%	874	99714	7	Isoform 2 of Q9BZF1
UniRef100_Q	2	2	2.10%	889	1E+05	7	Oxysterol-binding protein-related protein 8
UniRef100_Q	2	2	2.20%	847	96924	8	Oxysterol-binding protein
UniRef100_Q	2	2	2.60%	728	82554	7	OSBPL8 protein
UniRef100_Q	2	9	2.10%	624	71650	#	Isoform 2 of Q8WXA9
UniRef100_Q	4	4	2.00%	3174	4E+05	6	Vacuolar protein sorting-associated protein 13A
UniRef100_UI	4	4	2.10%	3071	3E+05	6	Vacuolar protein sorting-associated protein 13A (Chorein) (Chorea- acanthocytosis protein).
UniRef100_UI	4	4	2.00%	3137	4E+05	6	Vacuolar protein sorting-associated protein 13A (Chorein) (Chorea- acanthocytosis protein).
UniRef100_UI	4	4	2.10%	3097	4E+05	6	Vacuolar protein sorting-associated protein 13A (Chorein) (Chorea- acanthocytosis protein).
UniRef100_UI	4	4	2.00%	3176	4E+05	6	Vacuolar protein sorting-associated protein 13A (Chorein) (Chorea- acanthocytosis protein).
UniRef100_Q	4	4	2.10%	3069	3E+05	6	Isoform 4 of Q96RL7
UniRef100_Q	4	4	2.00%	3135	4E+05	6	Isoform 3 of Q96RL7
UniRef100_Q	4	4	2.10%	3095	4E+05	6	Isoform 2 of Q96RL7
UniRef100_Q	3	3	2.00%	1801	2E+05	7	Protein KIAA1797
UniRef100_UI	3	3	2.00%	1803	2E+05	7	KIAA1797 (KIAA1797), mRNA
UniRef100_Q	3	3	2.80%	1281	1E+05	7	KIAA1797 protein
UniRef100_Q	3	3	2.00%	1801	2E+05	7	Hypothetical protein
UniRef100_Q	2	2	2.00%	1069	1E+05	6	Elongation factor Tu GTP-binding domain-containing protein 1
UniRef100_UI	2	2	2.00%	1069	1E+05	6	elongation factor Tu GTP binding domain containing 1 isoform 2
UniRef100_UI	2	2	1.90%	1120	1E+05	6	elongation factor Tu GTP binding domain containing 1 isoform 1
UniRef100_Q	2	2	2.50%	857	96078	6	CDNA FLJ13119 fis, clone NT2RP3002671, weakly similar to ELONGATION FACTOR 2
UniRef100_Q	2	7	2.00%	891	1E+05	8	Schlafen family member 5
UniRef100_Q	2	2	2.00%	706	80152	9	Choline transporter-like protein 2
UniRef100_UI	2	2	2.00%	706	80208	8	Choline transporter-like protein 2 (Solute carrier family 44 member 2).
UniRef100_UI	2	2	2.00%	706	80124	9	Choline transporter-like protein 2 (Solute carrier family 44 member 2).
UniRef100_UI	2	2	2.00%	706	80136	9	CTL2 protein
UniRef100_Q	2	2	2.00%	706	80189	8	Isoform 2 of Q8IWA5
UniRef100_Q	2	3	2.00%	559	62056	9	Protein ENL
UniRef100_A	5	7	1.90%	3830	4E+05	8	Transformation/transcription domain-associated protein
UniRef100_Q	5	7	1.90%	3859	4E+05	8	Transformation/transcription domain-associated protein
UniRef100_Q	5	7	2.00%	3587	4E+05	8	Transformation/transcription domain-associated protein variant
UniRef100_P	5	8	1.90%	3224	4E+05	6	E3 SUMO-protein ligase RanBP2
UniRef100_UI	5	8	1.90%	3224	4E+05	6	RAN binding protein 2
UniRef100_O	4	4	1.90%	3013	3E+05	6	Protein furry homolog-like
UniRef100_Q	2	2	1.90%	1761	2E+05	7	JmjC domain-containing histone demethylation protein 2B
UniRef100_UI	2	2	1.90%	1761	2E+05	7	JmjC domain-containing histone demethylation protein 2B (EC 1.14.11.-) (Jumonji domain-containing protein 1B) (Nuclear protein 5qNCA).
UniRef100_A	2	4	1.90%	1395	2E+05	5	Latent transforming growth factor beta binding protein 1

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_U	2	4	1.90%	1396	2E+05	5	Latent-transforming growth factor beta-binding protein, isoform 1L precursor (LTBP-1) (Transforming growth factor beta-1-binding protein 1) (TGF-beta1-BP-1).
UniRef100_U	2	4	1.50%	1722	2E+05	6	Latent-transforming growth factor beta-binding protein, isoform 1L precursor (LTBP-1) (Transforming growth factor beta-1-binding protein 1) (TGF-beta1-BP-1).
UniRef100_U	2	4	1.60%	1596	2E+05	6	Latent-transforming growth factor beta-binding protein, isoform 1L precursor (LTBP-1) (Transforming growth factor beta-1-binding protein 1) (TGF-beta1-BP-1).
UniRef100_U	2	4	1.50%	1723	2E+05	6	Latent-transforming growth factor beta-binding protein, isoform 1L precursor (LTBP-1) (Transforming growth factor beta-1-binding protein 1) (TGF-beta1-BP-1).
UniRef100_U	2	4	1.50%	1722	2E+05	6	latent transforming growth factor beta binding protein 1 isoform LTBP-1L
UniRef100_U	2	4	1.90%	1396	2E+05	5	latent transforming growth factor beta binding protein 1 isoform LTBP-1S
UniRef100_Q	2	4	1.90%	1348	1E+05	5	Latent transforming growth factor beta binding protein 1 isoform LTBP- 1S variant
UniRef100_Q	2	4	3.70%	697	76777	4	Hypothetical protein LTBP1
UniRef100_Q	2	4	1.60%	1595	2E+05	6	Latent-transforming growth factor beta-binding protein, isoform 1L precursor
UniRef100_P	2	4	1.90%	1394	2E+05	5	Latent-transforming growth factor beta-binding protein, isoform 1S precursor
UniRef100_Q	11	17	1.80%	8407	1E+06	6	Spectrin-like protein of the nuclear envelope and Golgi
UniRef100_U	11	17	1.80%	8797	1E+06	6	Nesprin-1 (Nuclear envelope spectrin repeat protein 1) (Synaptic nuclear envelope protein 1) (Syne-1) (Myocyte nuclear envelope protein 1) (Myne-1) (Enaptin).
UniRef100_U	11	17	1.80%	8749	1E+06	6	Nesprin-1 (Nuclear envelope spectrin repeat protein 1) (Synaptic nuclear envelope protein 1) (Syne-1) (Myocyte nuclear envelope protein 1) (Myne-1) (Enaptin).
UniRef100_U	11	17	1.80%	8797	1E+06	6	Nesprin-1 (Nuclear envelope spectrin repeat protein 1) (Synaptic nuclear envelope protein 1) (Syne-1) (Myocyte nuclear envelope protein 1) (Myne-1) (Enaptin).
UniRef100_U	11	17	1.80%	8749	1E+06	6	nesprin 1 isoform longer
UniRef100_U	11	17	1.80%	8797	1E+06	6	nesprin 1 longest
UniRef100_Q	11	17	1.80%	8797	1E+06	6	Nesprin-1
UniRef100_Q	4	6	1.80%	2804	3E+05	8	Transcriptional regulator
UniRef100_Q	4	6	1.90%	2697	3E+05	8	Isoform 2 of Q6KC79
UniRef100_Q	4	6	1.80%	2804	3E+05	8	Nipped-B-like protein
UniRef100_A	4	7	1.80%	2089	2E+05	6	Mediator of DNA damage checkpoint 1
UniRef100_U	4	7	2.00%	1825	2E+05	6	UPI0000D6113B UniRef100 entry
UniRef100_U	4	7	1.80%	2089	2E+05	6	UPI00004A3B34 UniRef100 entry
UniRef100_Q	4	7	1.80%	2089	2E+05	6	Mediator of DNA damage checkpoint 1
UniRef100_Q	4	7	1.80%	2089	2E+05	6	Mediator of DNA damage checkpoint protein 1
UniRef100_Q	4	7	1.80%	2089	2E+05	6	KIAA0170 protein
UniRef100_O	2	2	1.80%	1722	2E+05	7	Lymphocyte antigen 75 precursor
UniRef100_U	2	2	1.80%	1722	2E+05	7	Lymphocyte antigen 75 precursor (DEC-205) (gp200-MR6) (CD205 antigen).
UniRef100_O	2	2	1.70%	1817	2E+05	6	Isoform 3 of O60449
UniRef100_O	2	2	1.70%	1873	2E+05	6	Isoform 2 of O60449
UniRef100_A	3	5	1.80%	1652	2E+05	7	PB1 protein
UniRef100_Q	3	5	2.90%	1047	1E+05	7	CDNA FLJ31979 fis, clone NT2RP7008441, highly similar to Polybromo 1 protein
UniRef100_Q	3	5	1.90%	1582	2E+05	7	Isoform 5 of Q86U86
UniRef100_Q	3	5	1.90%	1582	2E+05	7	Isoform 4 of Q86U86

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	3	5	1.80%	1634	2E+05	7	Isoform 2 of Q86U86
UniRef100_Q	3	5	1.80%	1689	2E+05	7	Protein polybromo-1
UniRef100_Q	3	5	2.10%	1454	2E+05	7	PB1 protein
UniRef100_Q	3	5	1.90%	1540	2E+05	7	PB1 protein
UniRef100_A	3	5	1.90%	1615	2E+05	7	PB1 protein
UniRef100_A	3	5	1.90%	1597	2E+05	7	PB1 protein
UniRef100_Q	2	3	1.80%	1583	2E+05	5	Ran-binding protein 2-like 4
UniRef100_U	2	3	1.70%	1684	2E+05	5	Ran-binding protein 2-like 4 (RanBP2L4).
UniRef100_Q	2	3	1.80%	1583	2E+05	5	GRIP and coiled-coil domain-containing protein 2
UniRef100_Q	4	5	1.70%	2944	3E+05	6	Collagen alpha-1(VII) chain precursor
UniRef100_Q	4	5	1.80%	2912	3E+05	6	Isoform 2 of Q02388
UniRef100_P	2	8	1.70%	2090	2E+05	7	Nuclear pore complex protein Nup214
UniRef100_U	2	8	1.70%	2096	2E+05	8	Nuclear pore complex protein Nup214 (Nucleoporin Nup214) (214 kDa nucleoporin) (CAN protein).
UniRef100_U	2	8	1.70%	2090	2E+05	8	Nuclear pore complex protein Nup214 (Nucleoporin Nup214) (214 kDa nucleoporin) (CAN protein).
UniRef100_Q	2	8	1.70%	2090	2E+05	8	Nucleoporin 214kDa
UniRef100_Q	2	8	1.70%	2091	2E+05	8	KIAA0023 splice variant 1
UniRef100_Q	2	8	2.10%	1684	2E+05	9	Nucleoporin 214kDa
UniRef100_Q	2	8	1.70%	2080	2E+05	7	NUP214 protein
UniRef100_Q	2	8	1.70%	2093	2E+05	8	KIAA0023 protein
UniRef100_Q	2	2	1.70%	1506	2E+05	5	VPRBP protein
UniRef100_U	2	2	1.60%	1521	2E+05	5	VPRBP protein.
UniRef100_Q	2	2	1.60%	1521	2E+05	5	HIV-1 Vpr-binding protein
UniRef100_Q	2	2	1.70%	1375	2E+05	5	Ubiquitin carboxyl-terminal hydrolase 47
UniRef100_U	2	2	1.80%	1362	2E+05	5	Ubiquitin carboxyl-terminal hydrolase 47 (EC 3.1.2.15) (Ubiquitin thioesterase 47) (Ubiquitin-specific-processing protease 47) (Deubiquitinating enzyme 47).
UniRef100_Q	2	2	1.90%	1287	1E+05	5	Isoform 2 of Q96K76
UniRef100_Q	2	2	1.70%	1374	2E+05	8	Cofactor required for Sp1 transcriptional activation, subunit 3, 130kDa
UniRef100_U	2	2	1.70%	1381	2E+05	8	CRSP complex subunit 3 (Cofactor required for Sp1 transcriptional activation subunit 3) (Transcriptional coactivator CRSP130) (Vitamin D3 receptor-interacting protein complex 130 kDa component) (DRIP130) (Activator-recruited cofactor 130 kDa component) (A
UniRef100_U	2	2	1.70%	1375	2E+05	8	CRSP complex subunit 3 (Cofactor required for Sp1 transcriptional activation subunit 3) (Transcriptional coactivator CRSP130) (Vitamin D3 receptor-interacting protein complex 130 kDa component) (DRIP130) (Activator-recruited cofactor 130 kDa component) (A
UniRef100_Q	2	2	1.70%	1368	2E+05	7	CRSP complex subunit 3
UniRef100_Q	2	2	1.70%	1359	2E+05	7	CRSP3 protein
UniRef100_Q	2	2	1.70%	1365	2E+05	7	Cofactor required for Sp1 transcriptional activation, subunit 3, 130kDa
UniRef100_Q	2	2	1.70%	1364	2E+05	7	Cofactor required for Sp1 transcriptional activation, subunit 3, 130kDa
UniRef100_Q	2	9	1.70%	1273	1E+05	7	Paired amphipathic helix protein Sin3a
UniRef100_Q	2	6	1.70%	782	88487	5	Cleavage and polyadenylation specificity factor subunit 2

Supplemental Table 2B: Protein Groups Identified in the Ovarian Tumor Secretome

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_Q	2	2	1.60%	1765	2E+05	6	Ran-binding protein 2-like 2
UniRef100_U	2	2	1.70%	1655	2E+05	7	PREDICTED: similar to RAN binding protein 2 isoform 3
UniRef100_U	2	2	1.60%	1734	2E+05	6	PREDICTED: similar to RAN binding protein 2 isoform 5
UniRef100_U	2	2	1.60%	1756	2E+05	7	PREDICTED: similar to RAN binding protein 2 isoform 4
UniRef100_Q	2	3	1.50%	2193	3E+05	7	OTTHUMP00000016904
UniRef100_U	2	3	1.50%	2192	3E+05	7	Activating signal cointegrator 1 complex subunit 3 (EC 3.6.1.-) (ASC-1 complex subunit p200) (Trip4 complex subunit p200) (Helicase, ATP binding 1).
UniRef100_U	2	3	1.50%	2202	3E+05	7	activating signal cointegrator 1 complex subunit 3 isoform a
UniRef100_Q	2	3	1.50%	2193	3E+05	7	Isoform 2 of Q8N3C0
UniRef100_Q	2	3	1.50%	2202	3E+05	7	Activating signal cointegrator 1 complex subunit 3
UniRef100_Q	2	2	1.50%	1992	2E+05	9	Probable E3 ubiquitin-protein ligase TRIP12
UniRef100_U	2	2	1.50%	1991	2E+05	9	Thyroid receptor-interacting protein 12 (TRIP12).
UniRef100_Q	2	2	1.70%	1722	2E+05	7	TRIP12 protein
UniRef100_Q	2	2	1.40%	2040	2E+05	9	TRIP12 protein
UniRef100_Q	2	6	1.50%	1365	2E+05	8	Structural maintenance of chromosomes flexible hinge domain-containing protein 1
UniRef100_U	2	6	1.50%	1365	2E+05	8	CDNA FLJ44350 fis, clone TRACH3006228.
UniRef100_Q	2	9	1.50%	1096	1E+05	9	La-related protein 1
UniRef100_U	2	9	1.50%	1095	1E+05	9	La-related protein 1 (La ribonucleoprotein domain family member 1).
UniRef100_Q	2	9	1.60%	1019	1E+05	9	Isoform 3 of Q6PKG0
UniRef100_Q	2	9	1.50%	1096	1E+05	9	Isoform 2 of Q6PKG0
UniRef100_Q	2	8	1.40%	2701	3E+05	9	Hypothetical protein
UniRef100_U	2	8	1.30%	2817	3E+05	9	HBxAg transactivated protein 2
UniRef100_U	2	8	1.40%	2703	3E+05	9	HBxAg transactivated protein 2
UniRef100_Q	2	2	1.40%	1749	2E+05	6	E3 ubiquitin-protein ligase UBR1
UniRef100_Q	5	5	1.30%	4377	5E+05	7	Ankyrin-3
UniRef100_U	5	5	1.30%	4377	5E+05	7	ankyrin 3 isoform 1
UniRef100_Q	5	5	3.00%	1861	2E+05	7	Hypothetical protein DKFZp686P17114
UniRef100_Q	2	2	1.30%	1873	2E+05	6	Protein C20orf74
UniRef100_U	2	2	1.30%	1873	2E+05	6	hypothetical protein LOC57186
UniRef100_Q	2	2	1.30%	1508	2E+05	7	Gem-associated protein 5
UniRef100_U	2	2	1.30%	1508	2E+05	7	Gem-associated protein 5 (Gemin5).
UniRef100_Q	3	6	1.20%	2752	3E+05	#	Serine/arginine repetitive matrix protein 2
UniRef100_U	3	6	1.40%	2293	3E+05	#	Serine/arginine repetitive matrix protein 2 (Serine/arginine-rich splicing factor-related nuclear matrix protein of 300 kDa) (Ser/Arg- related nuclear matrix protein) (SR-related nuclear matrix protein of 300 kDa) (Splicing coactivator subunit SRm300) (30
UniRef100_Q	3	6	1.40%	2334	3E+05	#	Isoform 2 of Q9UQ35
UniRef100_Q	2	5	1.20%	2061	2E+05	6	Myoferlin
UniRef100_U	2	5	1.50%	1577	2E+05	6	Myoferlin (Fer-1-like protein 3).
UniRef100_U	2	5	1.20%	2060	2E+05	6	Myoferlin (Fer-1-like protein 3).
UniRef100_U	2	5	1.20%	2047	2E+05	6	Myoferlin (Fer-1-like protein 3).
UniRef100_U	2	5	1.20%	2048	2E+05	6	Myoferlin (Fer-1-like protein 3).

Protein Acc.	Sequence Count	Spectrum Count	Sequence Coverage	Length	MolWt	pI	Descriptive Name
UniRef100_U	2	5	1.20%	2061	2E+05	6	Myoferlin (Fer-1-like protein 3).
UniRef100_Q	2	5	1.20%	2048	2E+05	6	Isoform 6 of Q9NZM1
UniRef100_Q	2	5	1.50%	1577	2E+05	6	Isoform 5 of Q9NZM1
UniRef100_Q	2	5	1.20%	2050	2E+05	6	Isoform 3 of Q9NZM1
UniRef100_Q	2	5	1.20%	2019	2E+05	6	Isoform 2 of Q9NZM1
UniRef100_Q	3	3	1.20%	1698	2E+05	6	Cullin-7
UniRef100_U	3	3	1.20%	1698	2E+05	6	cullin 7
UniRef100_Q	21	29	1.10%	22152	2E+06	6	Mucin-16
UniRef100_A	2	3	1.10%	1318	1E+05	8	Collagen type IV alpha 1
UniRef100_U	2	3	0.80%	1670	2E+05	8	Collagen alpha-1(IV) chain precursor.
UniRef100_U	2	3	0.80%	1688	2E+05	8	alpha 5 type IV collagen isoform 3, precursor
UniRef100_U	2	3	0.80%	1669	2E+05	8	alpha 1 type IV collagen preproprotein
UniRef100_Q	2	3	1.70%	847	82980	9	COL4A1 protein variant
UniRef100_P	2	3	0.80%	1685	2E+05	8	Collagen alpha-5(IV) chain precursor
UniRef100_P	2	3	0.80%	1669	2E+05	8	Collagen alpha-1(IV) chain precursor
UniRef100_Q	4	6	1.00%	2002	2E+05	6	Beta spectrin IV
UniRef100_U	4	6	1.60%	1309	1E+05	6	Spectrin beta chain, brain 3 (Spectrin, non-erythroid beta chain 3) (Beta-IV spectrin).
UniRef100_Q	4	6	1.00%	2154	2E+05	6	Isoform 4 of Q9H254
UniRef100_Q	4	6	1.60%	1309	1E+05	6	Isoform 2 of Q9H254
UniRef100_Q	4	6	0.80%	2564	3E+05	6	Spectrin beta chain, brain 3
UniRef100_Q	4	6	0.80%	2564	3E+05	6	Non-erythrocytic beta-spectrin 4
UniRef100_P	2	2	0.90%	3210	4E+05	5	Centromere protein F
UniRef100_Q	2	2	0.90%	3114	4E+05	5	Centromere protein F, 350/400ka
UniRef100_P	3	7	0.80%	4548	5E+05	6	Apolipoprotein(a) precursor (EC 3.4.21.-) (Apo(a)) (Lp(a))
UniRef100_Q	3	7	1.90%	2040	2E+05	6	Lipoprotein, Lp
UniRef100_Q	3	7	1.90%	2040	2E+05	6	Lipoprotein, Lp
UniRef100_Q	2	2	0.60%	3924	4E+05	5	Ankyrin-2
UniRef100_U	2	2	0.60%	3924	4E+05	5	Ankyrin-2 (Brain ankyrin) (Ankyrin-B) (Ankyrin, nonerythroid).
UniRef100_U	2	2	1.30%	1872	2E+05	6	Ankyrin-2 (Brain ankyrin) (Ankyrin-B) (Ankyrin, nonerythroid).
UniRef100_U	2	2	1.30%	1872	2E+05	6	ankyrin 2 isoform 2
UniRef100_U	2	2	0.60%	3957	4E+05	5	ankyrin 2 isoform 1
UniRef100_Q	2	2	1.30%	1863	2E+05	6	Hypothetical protein DKFZp686H0688
UniRef100_Q	2	2	1.30%	1839	2E+05	6	Isoform 3 of Q01484
UniRef100_Q	2	2	1.30%	1872	2E+05	6	Isoform 2 of Q01484
UniRef100_Q	2	2	0.40%	4243	5E+05	6	Fibrocystin L
UniRef100_U	2	2	0.40%	4243	5E+05	6	fibrocystin L
UniRef100_U	2	2	0.40%	4247	5E+05	6	fibrocystin L
UniRef100_Q	2	2	0.30%	4599	5E+05	5	Low-density lipoprotein receptor-related protein 1B precursor
UniRef100_U	2	2	0.30%	4601	5E+05	5	Low-density lipoprotein receptor-related protein 1B precursor (Low- density lipoprotein receptor-related protein-deleted in tumor) (LRP- DIT).