Table S2. The result of LC-MS/MS for each band of gel.

Band 1: Mucin-6 OS=Homo sapiens GN=MUC6 PE=1 SV=3
Accession: MUC6_HUMAN **Score:** 66.19
Database: SwissProt **MW [kDa]:** 256.90
Seq. Coverage [%]: 3.50 % **pI:** 7.48
No. of Peptides: 7
Modification(s): Carbamidomethyl

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2893	2	640.8352	-0.16	2	24.0	17.1	0	77-87	K.DAFPTFSVQLR.R	
350	3	619.7979	-1.21	2	13.2	26.8	0	183-193	K.VTNEFVSEEGK.F	
97	5	581.2793	0.83	2	12.0	21.6	0	280-289	R.QCSMVGQPVR.R	Carbamidomethyl: 2
2041	5	631.0016	-0.85	3	20.2	36.2	0	442-459	K.SGVSHSETSLVAVVYLSR.Q	
1366	1	858.9291	564.91	2	17.0	15.8	0	463-478	K.IVISQDEVVTNNGEAK.W	
457	1	702.8388	-1.76	2	13.6	17.8	0	605-616	R.CHATVNPAPFYK.R	Carbamidomethyl: 1
2864	2	493.7827	1.15	2	23.8	27.9	0	647-654	R.GVLLWGWR.S	

Band 2: Angiotensin-converting enzyme OS=Homo sapiens GN=ACE PE=1 SV=1
Accession: ACE_HUMAN **Score:** 102.04
Database: SwissProt **MW [kDa]:** 149.60
Seq. Coverage [%]: 7.90 % **pI:** 5.94
No. of Peptides: 9
Modification(s): Oxidation

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1728	2	490.2844	0.44	2	19.1	20.7	0	797-804	R.AILQFYPK.Y	
1350	1	676.8146	-0.73	2	17.4	17.8	0	815-826	R.LNGYVDAGDSWR.S	
1872	5	849.3856	-2.81	2	19.8	26.6	0	827-840	R.SMYETPSLEQDLER.L	
1627	4	857.3825	-3.45	2	18.6	26.7	0	827-840	R.SMYETPSLEQDLER.L	Oxidation: 2
1568	3	392.2409	2.94	2	18.4	33.4	0	1001-1007	K.DLPVALR.E	
2746	2	770.3965	-0.95	3	24.0	25.0	0	1008-1030	R.EGANPGFHEAIGDVLALSVSTPK .H	
4332	4	877.9617	-5.85	2	31.0	25.2	0	1060-1073	K.IAFIPFSYLVDQWR.W	
2233	5	762.8451	-2.37	2	21.5	35.5	0	1084-1094	K.ENYNQEWWSLR.L	
2926	4	766.9065	-0.63	2	24.9	28.9	0	1243-1256	R.VSFLGLDLDAQQAR.V	

Band 3: Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5
Accession: HS90A_HUMAN **Score:** 496.11
Database: SwissProt **MW [kDa]:** 84.60
Seq. Coverage [%]: 29.80 % **pI:** 4.79
No. of Peptides: 19
Modification(s): Carbamidomethyl

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Unique	Modification
794	3	646.3214	-1.59	2	15.2	42.1	0	47-58	R.ELISNSSDALDK.I	U	
315	1	654.8425	-1.30	2	13.3	18.0	1	59-69	K.IRYESLTDPSK.L		
1406	3	397.5684	1.28	3	17.8	26.2	0	75-84	K.ELHINLIPNK.Q	U	
2046	3	675.3706	-0.38	2	20.8	25.8	0	88-100	R.TLTIVDTGIGMTK.A		
1957	7	621.8558	-0.76	2	20.4	51.7	0	101-112	K.ADLINNLGTIAK.S		
520	5	656.2876	-1.52	2	14.2	32.3	0	192-201	K.EDQTEYLEER.R		
2710	1	889.9748	-2.91	2	24.0	17.0	0	210-224	K.HSQFIGYPITLFVEK.E	U	
220	2	576.2823	-0.48	2	12.9	28.7	0	284-292	K.YIDQEELNK.T		
1748	5	917.3893	-5.45	2	19.3	36.6	0	300-314	R.NPDDITNEEYGEFYK.S	U	
1528	3	764.3749	-0.85	2	18.3	18.2	0	315-327	K.SLTNDWEDHLAVK.H		
1327	4	450.2268	1.03	3	17.4	34.3	0	328-338	K.HFSVEGQLEFR.A		
1796	3	408.2609	0.98	2	19.6	49.6	0	339-345	R.ALLFVPR.R	U	
2241	4	554.7741	-1.06	2	21.6	27.6	0	347-355	R.APFDLFENR.K	U	
2178	9	757.3949	-2.01	2	21.3	58.7	0	387-400	R.GVVDSEDLPLNISR.E		
505	1	474.7270	0.55	2	14.1	18.9	0	437-443	K.FYEQFSK.N	U	
574	4	365.7273	2.16	2	14.4	46.1	0	459-464	K.LSELLR.Y		
712	10	618.3032	-1.96	2	14.9	41.2	0	500-510	K.DQVANSAFVER.L	U	
3081	2	859.7609	-1.82	3	25.9	23.9	0	514-534	K.HGLEVIYMIEPIDEYCVQQLK.E	U	Carbamidomethyl: 16
1236	4	708.8209	-2.27	2	17.1	27.9	0	547-558	K.EGLELPEDEEEK.K		

Band 3: Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4

Accession: HS90B_HUMAN **Score:** 330.61

Database: SwissProt **MW [kDa]:** 83.20

Seq. Coverage [%]: 23.90 % **pI:** 4.82

No. of Peptides: 15

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Unique	Modification
315	1	654.8425	-1.30	2	13.3	18.0	1	54-64	K.IRYESLTDPSK.L		
1521	3	597.8270	-0.83	2	18.3	17.2	0	73-82	K.IDIIPNPQER.T	U	
2046	3	675.3706	-0.38	2	20.8	25.8	0	83-95	R.TLTLVDTGIGMTK.A	U	
1957	7	621.8558	-0.76	2	20.4	51.7	0	96-107	K.ADLINNLGTIAK.S		
520	5	656.2876	-1.52	2	14.2	32.3	0	187-196	K.EDQTEYLEER.R		
220	2	576.2823	-0.48	2	12.9	28.7	0	276-284	K.YIDQEELNK.T		
1795	1	924.3992	-3.21	2	19.5	26.4	0	292-306	R.NPDDITQEEYGEFYK.S	U	
1528	3	764.3749	-0.85	2	18.3	18.2	0	307-319	K.SLTNDWEDHLAVK.H		
1327	4	450.2268	1.03	3	17.4	34.3	0	320-330	K.HFSVEGQLEFR.A		
2064	2	415.2653	-7.34	2	20.9	37.7	0	331-337	R.ALLFIPR.R	U	
2178	9	757.3949	-2.01	2	21.3	58.7	0	379-392	R.GVVDSEDLPLNISR.E		
574	4	365.7273	2.16	2	14.4	46.1	0	451-456	R.LSELLR.Y		
1380	1	726.3172	-3.78	3	17.7	25.6	0	457-475	R.YHTSQSGDEMTSLSEYVSR.M	U	
477	1	625.3117	-0.80	2	14.0	17.8	0	492-502	K.EQVANSAFVER.V	U	
1236	4	708.8209	-2.27	2	17.1	27.9	0	539-550	K.EGLELPEDEEEK.K		

Band 4: Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1

Accession: HSP72_HUMAN **Score:** 530.88

Database: SwissProt **MW [kDa]:** 70.00

Seq. Coverage [%]: 26.80 % **pI:** 5.44

No. of Peptides: 15

Modification(s): Carbamidomethyl, Oxidation

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Unique	Modification
2471	1	759.7131	-3.72	3	22.4	23.5	0	5-26	R.GPAIGIDLGTTYSCVGVFQHGK.V	U	Carbamidomethyl:14
279	6	614.8165	-1.87	2	13.0	39.2	0	27-37	K.VEIIANDQGNR.T		
1386	2	744.3524	-2.51	2	17.6	51.3	0	38-50	R.TTPSYVAFTDTER.L		
1332	3	840.4055	-1.24	2	17.3	42.0	0	58-72	K.NQVAMNPTNTIFDAK.R	U	Oxidation:5
1803	7	832.4048	-5.09	2	19.5	51.4	0	58-72	K.NQVAMNPTNTIFDAK.R	U	
758	1	655.3438	-1.30	2	15.0	18.0	1	128-139	K.MKEIAEAYLGGK.V	U	
937	3	525.7770	0.15	2	15.7	31.4	0	130-139	K.EIAEAYLGGK.V	U	
1659	6	635.3256	-2.06	3	18.7	47.4	0	140-156	K.VHSAVITVPAYFNDSQR.Q	U	
2244	7	615.3456	-0.78	2	21.4	44.1	0	161-172	K.DAGTITGLNVLR.I	U	
2303	5	830.4481	-3.74	2	21.7	33.8	0	173-188	R.IINEPTAAAIAYGLDK.K		
268	1	564.5796	-0.84	3	13.0	22.5	0	224-239	K.STAGDTHLGGEDFDNR.M	U	
1831	1	494.2563	0.11	3	19.6	17.0	1	303-314	R.ARFEELNADLFR.G	U	
2351	5	627.3108	-1.38	2	21.9	55.0	0	305-314	R.FEELNADLFR.G	U	
1850	11	728.9080	-2.12	2	19.6	47.7	0	332-345	K.GQIQEIVLVGGSTR.I	U	
1331	8	658.3292	-1.27	2	17.3	28.4	0	543-553	K.NALESYTYNIK.Q	U	

Band 4: Heat shock 70 kDa protein 1-like OS=Homo sapiens GN=HSPA1L PE=1 SV=2

Accession: HS71L_HUMAN **Score:** 178.47

Database: SwissProt **MW [kDa]:** 70.30

Seq. Coverage [%]: 15.60 % **pI:** 5.67

No. of Peptides: 9

Modification(s): Carbamidomethyl, Oxidation

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Unique	Modification
279	6	614.8165	-1.87	2	13.0	39.2	0	28-38	K.VEIIANDQGNR.T		
1386	2	744.3524	-2.51	2	17.6	51.3	0	39-51	R.TTPSYVAFTDTER.L		
1343	7	838.9021	-5.49	2	17.4	39.5	0	59-73	K.NQVAMNPQNTVFDAK.R	U	
2705	11	599.3506	-0.96	2	23.4	29.7	0	162-173	K.DAGVIAGLNVLR.I	U	
2303	5	830.4481	-3.74	2	21.7	33.8	0	174-189	R.IINEPTAAAIAYGLDK.G		
2476	1	650.3038	-2.66	2	22.4	15.6	0	304-313	R.FEELCADLFR.G	U	Carbamidomethyl: 5
743	2	633.8604	-2.30	2	14.9	15.7	0	333-344	K.IHDIVLVGGSTR.I	U	
1235	1	652.3043	1.94	2	16.9	15.8	0	542-552	K.NALESYAFNMK.S	U	Oxidation:10
1810	4	644.3052	-0.46	2	19.5	16.2	0	542-552	K.NALESYAFNMK.S	U	

Band 4: Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5

Accession: HSP71_HUMAN **Score:** 120.86

Database: SwissProt **MW [kDa]:** 70.00

Seq. Coverage [%]: 9.70 % **pI:** 5.36

No. of Peptides: 6

Modification(s): Oxidation

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Unique	Modification
279	6	614.8165	-1.87	2	13.0	39.2	0	26-36	K.VEIIANDQGNR.T		
1386	2	744.3524	-2.51	2	17.6	51.3	0	37-49	R.TTPSYVAFTDTER.L		
1611	5	829.9253	-3.78	2	18.5	27.7	0	57-71	K.NQVALNPQNTVFDAK.R	U	
2705	11	599.3506	-0.96	2	23.4	29.7	0	160-171	K.DAGVIAGLNVLR.I	U	
1235	1	652.3043	1.94	2	16.9	15.8	0	540-550	K.NALESYAFNMK.S	U	Oxidation:10
1810	4	644.3052	-0.46	2	19.5	16.2	0	540-550	K.NALESYAFNMK.S	U	

Band 5: Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1

Accession: TBB4B_HUMAN **Score:** 182.70

Database: SwissProt **MW [kDa]:** 49.80

Seq. Coverage [%]: 37.80 % **pI:** 4.65

No. of Peptides: 15

Modification(s): Carbamidomethyl, Oxidation

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
776	5	664.8251	-3.91	2	14.8	27.9	0	47-58	R.INVYYNEATGGK.Y	
2420	7	801.4118	-2.45	2	22.0	40.8	0	63-77	R.AVLVDLEPGTMDSVR.S	
2980	2	653.6637	-2.71	3	24.6	44.0	0	104-121	K.GHYTEGAELVDSVLDVVR.K	
1946	4	660.3546	-0.64	2	19.7	32.8	0	163-174	R.IMNTFSVVPSPK.V	
1485	5	565.8007	-1.01	2	17.8	30.7	0	242-251	R.FPGQLNADLR.K	
2356	4	572.3206	-0.41	2	21.6	33.5	0	253-262	K.LAVNMVPFPR.L	
2832	1	540.9497	-0.66	3	23.9	16.7	0	263-276	R.LHFFMPGFAPLTSR.G	
2225	1	854.4309	-4.44	2	21.1	17.2	0	283-297	R.ALTVPELTQQMFDAK.N	Oxidation: 11
2946	6	846.4330	-5.12	2	24.4	26.0	0	283-297	R.ALTVPELTQQMFDAK.N	
1030	1	723.8465	-2.50	2	15.8	27.0	0	325-336	K.EVDEQMLNVQNK.N	
2717	6	848.9180	-2.51	2	23.3	25.3	0	337-350	K.NSSYFVEWIPNNVK.T	
396	18	514.7632	-0.17	2	13.3	39.7	0	351-359	K.TAVCDIPPR.G	Carbamidomethyl: 4
3303	2	929.4698	-4.89	2	26.2	16.4	0	363-379	K.MSATFIGNSTAIQELFK.R	
3114	1	937.4692	-2.82	2	25.2	24.9	0	363-379	K.MSATFIGNSTAIQELFK.R	Oxidation: 1
2161	1	615.3026	-0.26	2	20.7	31.2	0	381-390	R.ISEQFTAMFR.R	