Online Supplemental Material for
Ratts et al. http://www.jcb.org/cgi/doi/10.1083/jcb.200210028

Table SI. **Summary of information-dependent acquisition tandem MS sequence data from tryptic digests of human Hsp 90 (□ and □) and yeast TrR-1** .

Human Hsp 90 □ (30% coverage MS/MS only; 70% coverage MS 1 MS/MS)

AA	*m/z* (obs)	Mr(expt)	Mr(calc)	Delta	Sequence
47–60	520.94	1559.81	1559.82	20.01	ELISNSSDALDKIR
59–74	452.99	1807.94	1807.93	0.01	IRYESLTDPSKLDSGK
59–74	603.65	1807.93	1807.93	20.00	IRYESLTDPSKLDSGK
61–74	513.92	1538.74	1538.75	20.00	YESLTDPSKLDSGK
61–74	770.36	1538.71	1538.75	20.04	YESLTDPSKLDSGK
75–87	530.63	1588.87	1588.87	20.00	ELHINLIPNKQDR
88–100	675.36	1348.70	1348.73	20.03	TLTIVDTGIGMTK
183–201	576.06	2300.21	2300.20	0.00	GTKVILHLKEDQTEYLEER
186–201	504.51	2014.01	2014.04	20.03	VILHLKEDQTEYLEER
186–201	672.35	2014.02	2014.04	20.02	VILHLKEDQTEYLEER
186–201	1007.99	2013.96	2014.04	20.07	VILHLKEDQTEYLEER
284–292	576.28	1150.54	1150.55	20.01	YIDQEELNK
300–314	917.36	1832.70	1832.77	20.07	NPDDITNEEYGEFYK
315–327	509.92	1526.73	1526.74	20.01	SLTNDWEDHLAVK
315–327	764.35	1526.69	1526.74	20.05	SLTNDWEDHLAVK
328–338	674.82	1347.63	1347.66	20.03	HFSVEGQLEFR
339–345	408.26	814.50	814.51	20.00	ALLFVPR
346–355	422.22	1263.64	1263.64	0.00	RAPFDLFENR
347–355	554.77	1107.52	1107.53	20.01	APFDLFENR
387–400	505.26	1512.76	1512.78	20.02	GVVDSEDLPLNISR
387–400	757.36	1512.71	1512.78	20.07	GVVDSEDLPLNISR
437–443	474.73	947.44	947.44	0.00	FYEQFSK
465–478	783.83	1565.65	1565.69	20.04	YYTSASGDEMVSLK
465–483	754.66	2260.94	2260.96	20.02	YYTSASGDEMVSLKDYCTR
500–510	618.30	1234.58	1234.59	20.01	DQVANSAFVER
540–564	729.60	2914.37	2914.50	20.13	TLVSVTKEGLELPEDEEEKKKQEEK
547–564	729.68	2186.03	2186.06	20.03	EGLELPEDEEEKKKQEEK
574–581	495.29	988.56	988.56	0.00	IMKDILEK
632–647	479.50	1913.97	1914.03	20.06	KHLEINPDHSIIETLR

Human Hsp 90 □ (30% coverage MS/MS only; 65% coverage MS 1 MS/MS)

AA	*m/z* (obs)	Mr(expt)	Mr(calc)	Delta	Sequence
42–55	772.89	1543.77	1543.82	20.05	ELISNASDALDKIR
54–69	452.99	1807.94	1807.93	0.01	IRYESLTDPSKLDSGK
54–69	603.65	1807.93	1807.93	20.00	IRYESLTDPSKLDSGK
54–72	545.54	2178.14	2178.15	20.01	IRYESLTDPSKLDSGKELK
56–69	513.92	1538.74	1538.75	20.00	YESLTDPSKLDSGK
56–69	770.36	1538.71	1538.75	20.04	YESLTDPSKLDSGK
56–72	637.33	1908.95	1908.97	20.02	YESLTDPSKLDSGKELK
70–82	522.29	1563.85	1563.86	20.01	ELKIDIIPNPQER
83–95	675.36	1348.70	1348.73	20.03	TLTLVDTGIGMTK
96–107	622.34	1242.66	1241.70	0.96	ADLINNLGTIAK (N□ D)

178–196	576.06	2300.21	2300.20	0.00	GTKVILHLKEDQTEYLEER
181–196	504.51	2014.01	2014.04	20.03	VILHLKEDQTEYLEER
181–196	672.35	2014.02	2014.04	20.02	VILHLKEDQTEYLEER
181–196	1007.99	2013.96	2014.04	20.07	VILHLKEDQTEYLEER
276–284	576.28	1150.54	1150.55	20.01	YIDQEELNK
292–306	924.37	1846.73	1846.79	20.06	NPDDITQEEYGEFYK
307–319	509.58	1525.72	1526.74	21.01	SLTNDWEDHLAVK (D→ N)
307–319	509.92	1526.73	1526.74	20.01	SLTNDWEDHLAVK
307–319	764.35	1526.69	1526.74	20.05	SLTNDWEDHLAVK
320–330	674.82	1347.63	1347.66	20.03	HFSVEGQLEFR
331–337	415.27	828.52	828.52	20.00	ALLFIPR
338–348	455.58	1363.73	1363.72	0.00	RAPFDLFENKK
379–392	505.26	1512.76	1512.78	20.02	GVVDSEDLPLNISR
379–392	757.36	1512.71	1512.78	20.07	GVVDSEDLPLNISR
429–435	446.22	890.42	890.42	0.01	FYEAFSK
457–475	731.64	2191.89	2191.93	20.04	YHTSQSGDEMTSLSEYVSR
482–491	580.80	1159.58	1159.58	0.00	SIYYITGESK
492–502	625.30	1248.58	1248.61	20.03	EQVANSAFVER
566–573	495.29	988.56	988.56	0.00	LMKEILDK
624–639	478.26	1909.00	1910.04	21.04	KHLEINPDHPIVETLR (D→ N)
625–639	594.98	1781.92	1781.94	20.02	HLEINPDHPIVETLR
625–639	891.94	1781.87	1781.94	20.07	HLEINPDHPIVETLR

Yeast TrR-1 (57% coverage MS/MS only; 85% coverage MS 1 MS/MS)

AA	*m/z* (obs)	Mr(expt)	Mr(calc)	Delta	Sequence
1–24	627.60	2506.37	2506.35	0.02	MVHNKVTIIGSGPAAHTAAIYLAR Oxidation (M)
6–24	941.58	1881.14	1881.05	0.09	VTIIGSGPAAHTAAIYLAR
6–24	628.05	1881.12	1881.05	0.08	VTIIGSGPAAHTAAIYLAR
78–89	662.88	1323.75	1323.69	0.06	FGTEIITETVSK
90–98	510.82	1019.62	1019.57	0.05	VDLSSKPFK
99–124	921.80	2762.38	2762.36	0.01	LWTEFNEDAEPVTTDAIILATGASAK
125–137	564.30	1689.88	1689.79	0.08	RMHLPGEETYWQK Oxidation (M)
126–137	506.90	1517.68	1517.70	20.02	MHLPGEETYWQK
154–175	1153.13	2304.24	2304.14	0.10	NKPLAVIGGGDSACEEAQFLTK
199–217	726.10	2175.27	2175.18	0.10	AEKNEKIEILYNTVALEAK
205–217	738.96	1475.90	1475.82	0.08	IEILYNTVALEAK
205–221	612.00	1832.98	1832.99	20.01	IEILYNTVALEAKGDGK
205–221	917.54	1833.06	1832.99	0.07	IEILYNTVALEAKGDGK
233–244	651.36	1300.71	1300.65	0.06	KNEETDLPVSGL
233–255	622.85	2487.35	2487.26	0.09	KNEETDLPVSGLFYAIGHTPATK
245–255	402.57	1204.69	1204.62	0.07	FYAIGHTPATK
245–255	603.35	1204.69	1204.62	0.06	FYAIGHTPATK
271–293	756.40	2266.18	2266.11	0.06	TVPGSSLTSVPGFFAAGDVQDSK
296–313	890.01	1778.88	1778.93	20.05	QAITSAGSGCMAALDAEK

All peptide MS and MS/MS spectra were submitted to Mascot (*32*), and positive identifications were confirmed manually. Error tolerance was better than 50 ppm, except for three peptides, where either (N→ D) or (D→ N) conversion was observed.