



Supplemental Figure S1. *In vitro* cleavage of HSP65 by MMP-9 and MMP-25. HSP65 was co-incubated with the indicated amounts of MMPs. The digested samples were analyzed Western blotting with the HSP65 antibody. Where indicated, GM6001 (50 μ M) was added to the reactions to block MMP activity.

Supplemental Table S1. MMP proteolysis of HSP65 and a MALDI-TOF MS analysis of the digest fragments. The arrows indicate the scissile bonds.

MMP-2 fragments							
MAKTIAYDEE ¹⁰	ARRGLERGLN ²⁰	ALADAVK ↓ VTL ³⁰	GPKGRNVVLE ⁴⁰	KKWGAPITITN ⁵⁰	DGVSIAKEIE ⁶⁰	LEDPYEKIGA ⁷⁰	
EL ↓ VKEVAKKT ⁸⁰	DDVAGDGTTT ⁹⁰	ATVLA ↓ QALVR ¹⁰⁰	EGLRNVAAGA ¹¹⁰	NPLG ↓ LKRGIE ¹²⁰	KAVEKVTETL ¹³⁰	LKGAKEVETK ¹⁴⁰	
EQIAATAA ↓ IS ¹⁵⁰	AGDQSIGD ↓ LI ¹⁶⁰	AEAMDKVGNE ¹⁷⁰	GVITVEESNT ¹⁸⁰	FG ↓ LQ ↓ LELTE ↓ G ¹⁹⁰	MRFDKGYISG ²⁰⁰	Y ↓ FVTDPERQE ²¹⁰	
AVLEDPYILL ²²⁰ ↓	VSSKVST ↓ VKD ²³⁰	LLPLL ↓ EKVIG ²⁴⁰	AGKPLLI IAE ²⁵⁰	D ↓ VEGEALSTL ²⁶⁰	VVNKIRGTFK ²⁷⁰	SVAVKAPGFG ²⁸⁰	
DRRKAMLQDM ²⁹⁰	AILTGGQVIS ³⁰⁰	EEVGLTLENA ³¹⁰	DLSL ↓ LGKARK ³²⁰	VVTKDETTI ³³⁰	VEGAGDTDAI ³⁴⁰	AGRVAQ ↓ IRQE ³⁵⁰	
IENSDSDYDR ³⁶⁰	EKLQERLAK ↓ L ³⁷⁰	AGGV ↓ AVIKAG ³⁸⁰	AATEVELKER ³⁹⁰	KHRIEDAVRN ⁴⁰⁰ ↓	AKA ↓ AVEEGIV ⁴¹⁰	AGGGVTL ↓ LQA ⁴²⁰	
APTLDELKLE ⁴³⁰	GDEATGANIV ⁴⁴⁰	KVALEAPLK ↓ Q ⁴⁵⁰	IAFNGLPEG ⁴⁶⁰	VVAEK ↓ VRNLP ⁴⁷⁰	AGHGLNAQTG ⁴⁸⁰	VYED ↓ LLAAGV ⁴⁹⁰	
ADP ↓ VK ↓ VTRSA ⁵⁰⁰	LQNAASIAGL ⁵¹⁰	FLTTEAVVAD ⁵²⁰	KPEKEKASVP ⁵³⁰	GGGDMGGMDF ⁵⁴⁰			
Peptide sequences						Molecular mass, Da	
						Calculated	Measured
1	²³⁶ EKVIGAGKPLLI I AEDVEGEALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLQDMA I LTGGQV I SEEVGLTLENADLSLLGKARKVVVTKDETTIVEGAGDTDAIAGRVAQIRQEIENSDSDYDREKLQERLAKLAGGVAVIKAGAATEVELKERKHRIEDAVRNAKAAVEEGIVAGGGVTL LQAAPTLDELKLEGDEATGANIVKVALEAPLK ⁴⁴⁹					22458	22470
2	⁴⁰⁴ AVEEGIVAGGGVTL LQAAPTLDELKLEGDEATGANIVKVALEAPLKQ I AFNGLPEGVVAEKVRNLPAGHGLNAQTGVYEDLLAAGVADPVKVTRSA LQNAASIAGLFLTTEAVVADKPEKEKASVPGGGDMGGMDF ⁵⁴⁰					13753	13757
3	²⁰² VTDPERQEAVLEDPYILLVSSKVSTVKD L LPLLLEKVIGAGKPLLI I AEDVEGEALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLQDMA I LTGGQV I SEEVGLTLENADLSL ³¹⁴					12096	12089
4	³⁴⁷ IRQEIENSDSDYDREKLQERLAKLAGGVAVIKAGAATEVELKERKHRIEDAVRNAKAAVEEGIVAGGGVTL LQAAPTLDELKLEGDEATGANIVKVALEAPLK ⁴⁴⁹					10938	10945
5	³⁷⁰ LAGGVAVIKAGAATEVELKERKHRIEDAVRNAKAAVEEGIVAGGGVTL LQAAPTLDELKLEGDEATGANIVKVALEAPLKQ I AFNGLPEGVVAEK ⁴⁶⁵					9761	9753
6	⁹⁶ ATVLAQALVREGLRNVAAGANPLGLKRGIEKAVEKVTETLLKGAKEVETKEQIAATAA I SAGDQSIGDLIAEAMDKVGNEGVI TVEESNTFGLQ ¹⁸⁴					9228	9219
7	²⁸ VTLGPKGRNVVLEKKWGAPITITNDGVSIAKEIELEDPYEKIGAELVKEVAKKTDDVAGDGTTTATVLAQALVREGLRNVAAGANPLG ¹¹⁴					9035	9023
8	¹⁴⁹ ISAGDQSIGDLIAEAMDKVGNEGVI TVEESNTFGLQLELTEGMRFDKGYISGYFVTDPERQEAVLEDPYILLVSSKVST ²²⁷					8583	8573
9	⁴¹⁸ LQAAPTLDELKLEGDEATGANIVKVALEAPLKQ I AFNGLPEGVVAEKVRNLPAGHGLNAQTGVYEDLLAAGVADPVK ⁴⁹⁵ ¹¹⁵ LKRGIEKAVEKVTETLLKGAKEVETKEQIAATAA I SAGDQSIGDLIAEAMDKVGNEGVI TVEESNTFGLQLELTEG ¹⁹⁰					7983	7992
10	⁷³ VKEVAKKTDDVAGDGTTTATVLAQALVREGLRNVAAGANPLGLKRGIEKAVEKVTETLLKGAKEVETKEQIAATAA ¹⁴⁸ ³¹² LSLLGKARKVVVTKDETTIVEGAGDTDAIAGRVAQIRQEIENSDSDYDREKLQERLAKLAGGVAVIKAGA ³⁸¹					7810	7809
11	³⁴⁷ IRQEIENSDSDYDREKLQERLAKLAGGVAVIKAGAATEVELKERKHRIEDAVRN ⁴⁰⁰					6116	6117
12	⁴⁸⁵ LLAAGVADPVKVTRSA LQNAASIAGLFLTTEAVVADKPEKEKASVPGGGDMGGMDF ⁵⁴⁰					5570	5579
13	²⁰² VAVIKAGAATEVELKERKHRIEDAVRNAKAAVEEGIVAGGGVTL LQAAPTLDE ²⁵¹					5472	5468
14	⁴¹⁸ LQAAPTLDELKLEGDEATGANIVKVALEAPLKQ I AFNGLPEGVVAEK ⁴⁶⁵					4957	4959

15	⁴⁹⁴ VKVTR ⁵⁴⁰ SALQNAASIAGLFLTTEAVVADKPEKEKASVPGGGDMGGMDF	4762	4761
16	¹⁵⁹ LIAEAMDKVGN ²⁰¹ EGVITVEESNTFGLQLELTEGMRFDKGYISGY	4723	4723
17	³⁷⁴ VAVIKAGAATEVELKERKHRIE ⁴¹⁷ DAVRNAKAAVEEGIVAGGGVTL	4524	4525
18	¹⁸³ LQLELTEGMRFDKGYISGYFVTDPERQEAVLEDPYILL ²²⁰	4447	4438
19	⁷³ VKEVAKKTDDVAGDGT ¹¹⁴ TTATVLAQALVREGLRNVAAGANPLG	4176	4186

MMP-8 fragments

MAKTIAYDEE ¹⁰	ARRGLERGLN ²⁰	ALADA ↓ VK ↓ VTL ³⁰	GPKGRNVVLE ⁴⁰	KKWGAPTITN ⁵⁰	DGVSIAKEIE ⁶⁰	LEDPYEKIGA ⁷⁰
E ↓ L ↓ VKEVAKKT ⁸⁰	DDVAGDGTTT ⁹⁰	ATVLA ↓ QA ↓ LVR ¹⁰⁰	EGLRN ↓ VAA ↓ GA ¹¹⁰	NPLG ↓ LKRGIE ¹²⁰	KAVEK ↓ VTETL ¹³⁰	LKGAKEVETK ¹⁴⁰
EQIAATAA ↓ IS ¹⁵⁰	AGD ↓ QSIGD ↓ LI ¹⁶⁰	AE ↓ A ↓ MDKVGNE ¹⁷⁰	GVITVEESNT ¹⁸⁰	FGLQ ↓ LELTEG ¹⁹⁰ ↓	MRFDKGYISG ²⁰⁰	Y ↓ FVTDPER ↓ QE ²¹⁰
AVLEDPYIL ↓ L ²²⁰ ↓	VSSKVSTVKD ²³⁰	LLP ↓ LLEKVI ²⁴⁰	AGKP ↓ LLIIAE ²⁵⁰	D ↓ VEGEALST ↓ L ²⁶⁰	VVVK ↓ IRGTFK ²⁷⁰	SVAVKAPGFG ²⁸⁰
DRRKAMLQD ↓ M ²⁹⁰	AILTGGQVIS ³⁰⁰	EEVGLTLENA ³¹⁰	D ↓ LSLGKARK ³²⁰ ↓	VVVTKDETTI ³³⁰	VEGAGDTDAI ³⁴⁰	AGR ↓ VAQIRQE ³⁵⁰
IENSDDYDR ³⁶⁰	EKLQERLAKL ³⁷⁰	AGG ↓ VAV ↓ IKAG ³⁸⁰	AATEVELKER ³⁹⁰	KHRIEDAVRN ⁴⁰⁰ ↓	AKAAVEEGIV ⁴¹⁰	AGGGVTL ↓ LQA ⁴²⁰
APTLDELKLE ⁴³⁰	GDEATGANIV ⁴⁴⁰	KVALEAP ↓ LK ↓ Q ⁴⁵⁰	IAFNNGLEPG ⁴⁶⁰	VVAEK ↓ VRN ↓ LP ⁴⁷⁰	AGH ↓ GLNAQTG ⁴⁸⁰	VYED ↓ LLAAG ↓ V ⁴⁹⁰
ADPVKTRSA ⁵⁰⁰	LQNAASIAG ↓ L ⁵¹⁰ ↓	F ↓ LTTEAVVAD ⁵²⁰	KPEKEKASVP ⁵³⁰	GGGDMGG ↓ MDF ⁵⁴⁰		

Peptide sequences		Molecular mass, Da	
		Calculated	Measured
1	¹⁹¹ MRFDKGYISGYFVTDPERQEAVLEDPYILLVSSKVSTVKDLLP LLEKVI GAGKPLLI IAEDVEGEALSTLVVNKIRGTFKSVAVKAPGF GDRRKAMLQDMA ILTGGQVI SEEVGLTLENADLSLLGKARK ³²⁰	14067	14053
2	²⁶⁰ LVVNKIRGTFKSVAVKAPGFGDRRKAMLQDMA ILTGGQVI SEEVGLTLENADLSLLGKARKVVVTKDETTIVEGAGDTDAIAGRVAQIR QEIENSDDYDREKLQERLAKLAGG ³⁷³	12219	12229
3	¹⁵⁴ QSIGDLIAEAMDKVNEGVIITVEESNTFGLQLELTEGMRFKGYISGYFVTDPERQEAVLEDPYILLVSSKVSTVKDLLP LLEKVI GAG KPLLI IAEDVEGEALSTLVVNK ²⁶⁴	12018	12017
4	³⁷⁷ IKAGAATEVELKERKHRIEDAVRNAKAAVEEGIVAGGGVTL LQAAPTLDELKLEGDEATGANIVKVALEAPLKQIAFNNGLEPGVVAEK VRNLPAGH ⁴⁷³	10038	10040
5	⁴⁴⁸ LKQIAFNNGLEPGVVAEKVRNLPAGHGLNAQTGVYEDLLAAGVADPVKTRRSALQNAASIAGLFLTTEAVVADKPEKEKASVPGGGDMG GMD ⁵⁴⁰	9442	9440
6	⁹⁶ ATVLAQALVREGLRNVAAGANPLGLKRGIEKAVEKVTETLLKGAKEVETKEQIAATAAISAGDQSIGDLIAEAMDKVNEGVIITVEESNT FGLQ ¹⁸⁴	9228	9231
7	²⁸ VTLGPKGRNVVLEKKWGAPTITNDGVSIAKEIELEDPYEKI GAELVKEVAKKTDDVAGDGTTTATVLAQALVREGLRNVAAGANPLG ¹¹⁴	9035	9028
8	³²¹ VVVTKDETTIVEGAGDTDAIAGRVAQIRQEIENSDDYDREKLQERLAKLAGGVAVIKAGAATEVELKERKHRIEDAVRN ⁴⁰⁰	8713	8720
9	¹⁶³ AMDKVNEGVIITVEESNTFGLQLELTEGMRFKGYISGYFVTDPERQEAVLEDPYILLVSSKVSTVKDLLP ²³³	7878	7880
10	⁷³ VKEVAKKTDDVAGDGTTTATVLAQALVREGLRNVAAGANPLGLKRGIEKAVEKVTETLLKGAKEVETKEQIAATAA ¹⁴⁸	7810	7810
11	²²⁰ LVSSKVSTVKDLLP LLEKVI GAGKPLLI IAEDVEGEALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLQD ²⁸⁹		
12	²⁸ VTLGPKGRNVVLEKKWGAPTITNDGVSIAKEIELEDPYEKI GAELVKEVAKKTDDVAGDGTTTATVLAQA ⁹⁷	7427	7427
13	⁴⁰¹ AKAAVEEGIVAGGGVTL LQAAPTLDELKLEGDEATGANIVKVALEAPLKQIAFNNGLEPGVVAEKVRN ⁴⁶⁸	7347	7341
14	⁴⁴⁸ LKQIAFNNGLEPGVVAEKVRNLPAGHGLNAQTGVYEDLLAAGVADPVKTRRSALQNAASIAGL ⁵¹⁰	6848	6843
15	²⁵² VEGEALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLQDMA ILTGGQVI SEEVGLTLENAD ³¹¹	6378	6378
16	²⁰² FVTDPERQEAVLEDPYILLVSSKVSTVKDLLP LLEKVI GAGKPLLI IAEDVEGEALST ²⁵⁹	6328	6327
17	¹²⁶ VTETLLKGAKEVETKEQIAATAAISAGDQSIGDLIAEAMDKVNEGVIITVEESNTFGLQ ¹⁸⁴	6259	6250
18	⁴⁵⁰ QIAFNNGLEPGVVAEKVRNLPAGHGLNAQTGVYEDLLAAGVADPVKTRRSALQNAASIAG ⁵⁰⁹	6089	6093
19	¹⁰⁹ GANPLGLKRGIEKAVEKVTETLLKGAKEVETKEQIAATAAISAGDQSIGDLIAEA ¹⁶³	6024	6030
20	⁴⁸⁵ LLAAGVADPVKTRRSALQNAASIAGLFLTTEAVVADKPEKEKASVPGGGDMGGMD ⁵⁴⁰	5602	5598

21	²⁹⁰ MAILTGGQVISEEVGLTLENADLSLLGKARKVVVTKDETTIVEGAGDTDAIAGR ³⁴³	5570	5579
22	⁴⁸⁶ LAAGVADPVKVTRSALQNAASIAGLFLTTEAVVADKPEKEKASVPGGGDMGGMF ⁵⁴⁰	5524	5525
23	¹⁰⁶ VAAGANPLGLKRGIEKAVEKVTETLLKGAKEVETKEQIAATAAISAGDQSIGD ¹⁵⁸	5457	5459
24	¹⁶⁴ MDKVGNEGVIITVEESNTFGLQLELTEGMRFDKGYISGYFVTDPER ²⁰⁸	5346	5347
25	²⁶ VKVTLGPKGRNVVLEKKWGAPTITNDGVSIAKEIELEDPYEKIGAE ⁷¹	5070	5080
26	⁴¹⁸ LQAAPTLDLDELKLEGDEATGANIVKVALEAPLKQIAFNNGLEPGVVAEK ⁴⁶⁵	4991	4988
27	²⁴⁵ LLIIAEDVEGEALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLQD ²⁸⁹	4957	4947
28	⁴⁹⁰ VADPVKVTRSALQNAASIAGLFLTTEAVVADKPEKEKASVPGGGDMGG ⁵³⁷	4855	4857
29	²⁰² FVTDPERQEAVLEDPYILLVSSKVSTVKDLLPILLEKVIAGGK ²⁴⁴	4751	4746
30	⁴⁶⁶ VRNLPAGHGLNAQTGVYEDLLAAGVADPVKVTRSALQNAASIAGLF ⁵¹¹	4706	4710
31	²²¹ VSSKVSTVKDLLPILLEKVIAGGKPLIIAEDVEGEALSTLVVNK ²⁶⁴	4644	4642
32	³⁷⁴ VAVIKAGAATEVELKERKHRIEDAVRNAKAAVEEGIVAGGGVTL ⁴¹⁷	4585	4575
33	⁴⁶⁶ VRNLPAGHGLNAQTGVYEDLLAAGVADPVKVTRSALQNAASIAGL ⁵¹⁰	4524	4528
34	⁴⁶⁶ VRNLPAGHGLNAQTGVYEDLLAAGVADPVKVTRSALQNAASIAG ⁵⁰⁹	4497	4491
35	⁴⁴⁸ LKQIAFNNGLEPGVVAEKVRNLPAGHGLNAQTGVYEDLLAAG ⁴⁸⁹	4384	4395
36	¹⁸⁵ LELTEGMRFDKGYISGYFVTDPERQEAVLEDPYILL ²²⁰	4316	4310
37	²⁵² VEGEALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLQD ²⁸⁹	4206	4200

MMP-9 fragments

MAKTIAYDEE ¹⁰	ARRGLERGLN ²⁰	ALADAVK ↓ VTL ³⁰	GPKGRNVVLE ⁴⁰	KKWGAPTITN ⁵⁰	DGVSIACEIE ⁶⁰	LEDPYEKIGA ⁷⁰
EL ↓ VKEVAKKT ⁸⁰	DDVAGDGTTT ⁹⁰	ATVLA ↓ QALVR ¹⁰⁰	EGLRN ↓ VAA ↓ GA ¹¹⁰	NPLG ↓ LKRGIE ¹²⁰	KAVEKVTETL ¹³⁰	LKGAKEVETK ¹⁴⁰
EQIAATAAIS ¹⁵⁰	AGDQSIGD ↓ LI ¹⁶⁰	AEA ↓ MDKVGNE ¹⁷⁰	GVITVEESNT ¹⁸⁰	FGLQ ↓ LELTEG ¹⁹⁰ ↓	MRFDKGYISG ²⁰⁰	Y ↓ FVTDPER ↓ QE ²¹⁰
AVLEDPYILL ²²⁰ ↓	VSSKSVTVKD ²³⁰	LLPILLEKVI ²⁴⁰	AGKPLLI IAE ²⁵⁰	DVEGEALST ↓ L ²⁶⁰	VVNKIRGTFK ²⁷⁰	SVAVKAPGFG ²⁸⁰
DRRKAMLQD ↓ M ²⁹⁰	AILTGGQVIS ³⁰⁰	EEVGLTLENA ³¹⁰	D ↓ LSLLGKARK ³²⁰ ↓	VVVTKDETTI ³³⁰	VEGAGD TDAI ³⁴⁰	AGR ↓ VAQIRQE ³⁵⁰
IENSDSDYDR ³⁶⁰	EKLQERLAK ↓ L ³⁷⁰	AGG ↓ VAVIKAG ³⁸⁰	A ↓ ATEVELKER ³⁹⁰	KHRIEDAVRN ⁴⁰⁰	AKAAVEEGIV ⁴¹⁰	AGGGVTL ↓ LQA ⁴²⁰
APTLDE ↓ LK ↓ LE ⁴³⁰	GDEATGANIV ⁴⁴⁰	KVALEAP ↓ LK ↓ Q ⁴⁵⁰	IAFNGLPEP ⁴⁶⁰	VVAEK ↓ VRNLP ⁴⁷⁰	AGH ↓ GLNAQTG ⁴⁸⁰	VYEDLLAAG ↓ V ⁴⁹⁰
ADP ↓ VK ↓ VTRSA ⁵⁰⁰	LQNAASIAG ↓ L ⁵¹⁰ ↓	F ↓ LTTEAVVAD ⁵²⁰	KPEKEKASV ⁵³⁰	GGGDMGG ↓ MDF ⁵⁴⁰		

Peptide sequences		Molecular mass, Da	
		Calculated	Measured
1	²⁰² FVTDPERQEAVLEDPYILLVSSKSVTVKD LLPILLEKVI GAGKPLLI I AEDVEGEALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLQDMA I LTGGQVISEEVGLTLENADLSLLGKARKVVVTKDETTIVEGAGD TDAIAGRVAQIRQEIENSDSDYDREKLQERLAK ³⁶⁹	18162	18157
2	¹⁹¹ MRFDKGYISGYFVTDPERQEAVLEDPYILLVSSKSVTVKD LLPILLEKVI GAGKPLLI I AEDVEGEALSTLVVNKIRGTFKSVAVKAPGFG DRRKAMLQDMA I LTGGQVISEEVGLTLENADLSLLGKARK ³²⁰	14067	14056
3	³⁷⁰ LAGGVAVIKAGAAATEVELKERKHRIEDAVRNAKAAVEEGIVAGGGVTL LQAAPTLDELKLEGDEATGANIVKVALEAPLKQIAFNGLPEP GVVAEK ⁴⁶⁵	9761	9759
4	²²¹ VSSKSVTVKD LLPILLEKVI GAGKPLLI I AEDVEGEALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLQDMA I LTGGQVISEEVGLTLEN AD ³¹¹	9555	9562
5	⁴¹⁸ LQAAPTLDELKLEGDEATGANIVKVALEAPLKQIAFNGLPEPGVVAEKVRNLPAGHGLNAQTGVYEDLLAAGVADPVK VTRSA LQNAASI AGL ⁵¹⁰	9436	9435
6	⁹⁶ ATVLAQALVREGLRNVAAGANPLGLKRGIEKAVEKVTETLLKGAKEVETKEQIAATAAISAGDQSIGDLIAEAMDKVGNEGVITVEESNTF GLQ ¹⁸⁴	9228	9231
7	²⁸ VTLGPKGRNVVLEKKWGAPTITNDGVSIACEIELEDPYEKIGAE L VKEVAKKTDDVAGDGTTTATVLAQALVREGLRNVAAGANPLG ¹¹⁴	9035	9028
8	¹⁰⁶ VAAGANPLGLKRGIEKAVEKVTETLLKGAKEVETKEQIAATAAISAGDQSIGDLIAEAMDKVGNEGVITVEESNTFGLQLELTEG ¹⁹⁰	8733	8723
9	⁴¹⁸ LQAAPTLDELKLEGDEATGANIVKVALEAPLKQIAFNGLPEPGVVAEKVRNLPAGHGLNAQTGVYEDLLAAGVADPVK ⁴⁹⁵ ¹¹⁵ LKRGIEKAVEKVTETLLKGAKEVETKEQIAATAAISAGDQSIGDLIAEAMDKVGNEGVITVEESNTFGLQLELTEG ¹⁹⁰	7983	7976
10	³¹² LSLLGKARKVVVTKDETTIVEGAGD TDAIAGRVAQIRQEIENSDSDYDREKLQERLAKLAGGVAVIKAGA ³⁸¹	7405	7406
11	⁴²⁹ LEGDEATGANIVKVALEAPLKQIAFNGLPEPGVVAEKVRNLPAGHGLNAQTGVYEDLLAAGVADP ⁴⁹³	6576	6582
12	⁴⁷⁴ GLNAQTGVYEDLLAAGVADPVK VTRSA LQNAASIAGLFLTTEAVVADKPEKEKASVPGGGDMGG ⁵³⁷	6324	6320
13	²⁰² FVTDPERQEAVLEDPYILLVSSKSVTVKD LLPILLEKVI GAGKPLLI I AEDVEGEALST ²⁵⁹	6259	6249
14	⁴⁵⁰ QIAFNGLPEPGVVAEKVRNLPAGHGLNAQTGVYEDLLAAGVADPVK VTRSA LQNAASIAG ⁵⁰⁹	6024	6030
15	¹⁰⁹ GANPLGLKRGIEKAVEKVTETLLKGAKEVETKEQIAATAAISAGDQSIGDLIAEA ¹⁶³	5602	5595
16	²⁹⁰ MAILTGGQVISEEVGLTLENADLSLLGKARKVVVTKDETTIVEGAGD TDAIAGR ³⁴³	5524	5530
17	³⁷⁴ VAVIKAGAAATEVELKERKHRIEDAVRNAKAAVEEGIVAGGGVTL LQAAPTLDE ⁴²⁶	5462	5462
18	¹⁰⁶ VAAGANPLGLKRGIEKAVEKVTETLLKGAKEVETKEQIAATAAISAGDQSIGD ¹⁵⁸	5346	5350

19	¹⁶⁴ MDKVGNEGVI ²⁰⁸ TVEESNTFGLQLELTEGMREFDKGYISGYFVTDPER	5070	5077
20	⁴¹⁸ LQAAPTLDLKLKLEGDEATGANIVKVALEAPLKQIAFN ⁴⁶⁵ SGLEPGVVAEK	4957	4965
21	⁴⁹⁴ VKVTR ⁵⁴⁰ SALQNAAS IAGLFLTTEAVVADKPEKEKASVPGGGDMGGMDF	4762	4763
22	¹⁵⁹ LIAEAMDKVGNEGVI ²⁰¹ TVEESNTFGLQLELTEGMREFDKGYISGY	4723	4726
23	⁴⁶⁶ VRNLPAGHGLNAQTGVYEDLLAAGVADPVKVTR ⁵¹¹ SALQNAAS IAGLF	4644	4638
24	³⁷⁴ VAVIKAGAATEVELKERKHRIEDAVRNAKAAVEEGIVAGGGVTL ⁴¹⁷	4524	4528
25	⁴⁶⁶ VRNLPAGHGLNAQTGVYEDLLAAGVADPVKVTR ⁵¹⁰ SALQNAAS IAGL	4497	4500
26	⁴⁶⁶ VRNLPAGHGLNAQTGVYEDLLAAGVADPVKVTR ⁵⁰⁹ SALQNAAS IAG	4384	4396
27	⁴⁴⁸ LKQIAFN ⁴⁸⁹ SGLEPGVVAEKVRNLPAGHGLNAQTGVYEDLLAAG	4316	4321
28	⁷³ VKEVAKKTDDVAGDGT ¹¹⁴ TTATVLAQALVREGLRNVAAGANPLG	4176	4184
29	⁴⁵⁰ QIAFN ⁴⁸⁹ SGLEPGVVAEKVRNLPAGHGLNAQTGVYEDLLAAG	4075	4070

MMP-14 fragments

MAKTIAYDEE ¹⁰	ARRGLERGLN ²⁰	A ↓ LADAVKVTL ³⁰	GPKGRNVVLE ⁴⁰	KKWGAPTITN ⁵⁰	DGVSIAKEIE ⁶⁰	LEDPYE ↓ KIGA ⁷⁰
EL ↓ VKEVAKKT ⁸⁰	DDVAGDGT ⁹⁰	ATVLAQALVR ¹⁰⁰	EGLRN ↓ VAAGA ¹¹⁰	NPLG ↓ LKRGIE ¹²⁰	KAVEK ↓ VTETL ¹³⁰	LKGAKEVETK ¹⁴⁰
EQIAATAA ↓ IS ¹⁵⁰	AGDQSIGD ↓ LI ¹⁶⁰	AE ↓ AMDKVGNE ¹⁷⁰	GVITVEESNT ¹⁸⁰	FGLQLELTEG ¹⁹⁰ ↓	MRFDKGYISG ²⁰⁰	Y ↓ FVTDPERQE ²¹⁰
AVLEDPYILL ²²⁰	VSSKVST ↓ VKD ²³⁰ ↓	LLPLLEKVVIG ²⁴⁰	AGKPLLIIE ²⁵⁰	DVEGEALSTL ²⁶⁰	VVNKIRGTFK ²⁷⁰	SVAVKAPGFG ²⁸⁰
DRRKAM ↓ LQD ↓ M ²⁹⁰	AILTGGQVIS ³⁰⁰	EEVGLTLENA ³¹⁰	DLSELLGKARK ³²⁰	VVVTKDETTI ³³⁰	VEGAGDTDAI ³⁴⁰	AGRVAQIRQE ³⁵⁰
IENSDDYDR ³⁶⁰	EKLQERLAKL ³⁷⁰	AGGVAVIKAG ³⁸⁰	AATEVELKER ³⁹⁰	KHRIEDAVRN ⁴⁰⁰ ↓	AKA ↓ AVEEGIV ⁴¹⁰	AGGGVTL ↓ LQA ⁴²⁰
APTLDELKLE ⁴³⁰	GDEATGANIV ⁴⁴⁰	KVALEAP ↓ LKQ ⁴⁵⁰	IAFNNGLEPG ⁴⁶⁰	VVAEK ↓ VRNLP ⁴⁷⁰	AG ↓ HG ↓ LNAQTG ⁴⁸⁰	VYED ↓ L ↓ LAAG ↓ V ⁴⁹⁰
ADPVK ↓ VTRS ↓ A ⁵⁰⁰ ↓	LQNAASIALG ⁵¹⁰	FLTTEAVVAD ⁵²⁰	KPEKEKASVP ⁵³⁰	GGGDMGGMDF ⁵⁴⁰		

Peptide sequences		Molecular mass, Da	
		Calculated	Measured
1	²⁸⁷ LQDMAILTGGQVISEEVGLTLENADLSLLGKARKVVVTKDETTIVEGAGDTDAIAGRVAQIRQEIENSDDYDREKLQERLAKLAGGVAVIKAGAATEVELKERKHRIEDAVRN ⁴⁰⁰	12276	12283
2	²² LADAVKVTLGPKGRNVVLEKKWGAPTTITNDGVSIAKEIELEDPYEKIGAEKVKEVAKKTDDVAGDGT ¹²⁵ TATVLAQALVREGLRNVAAGANPLGLKRGIEKAVEK	10884	10877
3	⁶⁷ KIGELVKEVAKKTDDVAGDGT ¹⁶² TATVLAQALVREGLRNVAAGANPLGLKRGIEKAVEKVTETLLKGAKEVETKEQIAATAAISAGDQSIGD	9791	9791
4	¹⁰⁶ VAAGANPLGLKRGIEKAVEKVTETLLKGAKEVETKEQIAATAAISAGDQSIGDLIAEAMDKVNEGVIITVEESNTFGLQLELTEG ¹⁹⁰	8733	8731
5	¹⁴⁹ ISAGDQSIGDLIAEAMDKVNEGVIITVEESNTFGLQLELTEGMRFKGYISGYFVTDPERQEAVLEDPYILLVSSKVST ²²⁷	8583	8590
6	⁴¹⁸ LQAAPTLDELKLEGDEATGANIVKVALEAPLKQIAFNNGLEPGVVAEKVRNLPAGHGLNAQTGVYEDLLAAGVADPVK ⁴⁹⁵ ¹¹⁵ LKRGIEKAVEKVTETLLKGAKEVETKEQIAATAAISAGDQSIGDLIAEAMDKVNEGVIITVEESNTFGLQLELTEG ¹⁹⁰	7983	7978
7	⁴¹⁸ LQAAPTLDELKLEGDEATGANIVKVALEAPLKQIAFNNGLEPGVVAEKVRNLPAGHGLNAQTGVYEDLLAAG ⁴⁸⁹	7374	7375
8	⁴⁰⁴ AVEEGIVAGGGVTLQAAPTLDELKLEGDEATGANIVKVALEAPLKQIAFNNGLEPGVVAEKVRNLPAGHG ⁴⁷⁴	7111	7104
9	⁴⁴⁸ LKQIAFNNGLEPGVVAEKVRNLPAGHGLNAQTGVYEDLLAAGVADPVKVTRSALQNAASIALG ⁵¹⁰	6378	6373
10	²³¹ LLPLLEKVVIGAGKPLLIIEAEDVEGEALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLQD ²⁸⁹	6284	6279
11	⁴¹⁸ LQAAPTLDELKLEGDEATGANIVKVALEAPLKQIAFNNGLEPGVVAEKVRNLPAG ⁴⁷²	5664	5659
12	⁴⁸⁵ LLAAGVADPVKVTRSALQNAASIALGFLTTEAVVADKPEKEKASVPGGGDMGGMDF ⁵⁴⁰	5570	5579
13	⁴⁸⁶ LAAGVADPVKVTRSALQNAASIALGFLTTEAVVADKPEKEKASVPGGGDMGGMDF ⁵⁴⁰	5457	5450
14	¹⁵⁹ LIAEAMDKVNEGVIITVEESNTFGLQLELTEGMRFKGYISGY ²⁰¹	4723	4731
15	⁴⁹⁶ VTRSALQNAASIALGFLTTEAVVADKPEKEKASVPGGGDMGGMDF ⁵⁴⁰	4535	4531
16	⁴⁶⁶ VRNLPAGHGLNAQTGVYEDLLAAGVADPVKVTRSALQNAASIALG ⁵⁰⁹	4384	4390
17	⁴⁴⁸ LKQIAFNNGLEPGVVAEKVRNLPAGHGLNAQTGVYEDLLAAG ⁴⁸⁹	4316	4321
18	⁷³ VKEVAKKTDDVAGDGT ¹¹⁴ TATVLAQALVREGLRNVAAGANPLG	4176	4177
19	⁵⁰¹ LQNAASIALGFLTTEAVVADKPEKEKASVPGGGDMGGMDF ⁵⁴⁰	4021	4020
20	⁵¹⁰ FLTTEAVVADKPEKEKASVPGGGDMGGMDF ⁵⁴⁰	3196	3192

MMP-15 fragments

MAKTIAYDEE ¹⁰	ARRGLERGLN ²⁰	ALADA ↓ VK ↓ VTL ³⁰	GPKGRNVVLE ⁴⁰	KWGAPTITN ⁵⁰	DGVSIAKEIE ⁶⁰	LEDPYEKIGA ⁷⁰
ELVKEVAKKT ⁸⁰	DDVAGDGT ⁹⁰	ATVLA ↓ QA ↓ LVR ¹⁰⁰	EGLRNVAAGA ¹¹⁰	NPLG ↓ LKRGIE ¹²⁰	KAVEKVTETL ¹³⁰	LKGAKEVETK ¹⁴⁰
EQIAATAA ↓ IS ¹⁵⁰	AGD ↓ QSIGDLI ¹⁶⁰	AEAMDKVGNE ¹⁷⁰	GVITVEESNT ¹⁸⁰	FG ↓ LQLELTEG ¹⁹⁰	MRFDKGYISG ²⁰⁰	YFVTDPER ↓ QE ²¹⁰
AVLEDPYIL ↓ L ²²⁰	VSSKVSTVKD ²³⁰	LLP ²⁴⁰ LLEK ²⁴⁰ VIG ²⁴⁰	AGKP ↓ LLI ²⁵⁰ IAE ²⁵⁰	D ↓ VE ²⁶⁰ GEAL ²⁶⁰ ST ↓ L ²⁶⁰	VVN ²⁷⁰ KIR ²⁷⁰ GTFK ²⁷⁰	SVAVKAPGFG ²⁸⁰
DRRKAMLQD ↓ M ²⁹⁰	AILTGGQVIS ³⁰⁰	EEVGLTLENA ³¹⁰	DLSLLGKARK ³²⁰	VVVT ³³⁰ KDE ³³⁰ TTI ³³⁰	VEGAGD ³⁴⁰ TDAI ³⁴⁰	AGRVAQIRQE ³⁵⁰
IENS ³⁶⁰ SDSYDR ³⁶⁰	EKLQERLAK ↓ L ³⁷⁰	AGGVAV ↓ IKAG ³⁸⁰	AATEVELKER ³⁹⁰	KHRIE ⁴⁰⁰ DAVRN ⁴⁰⁰ ↓	AKA ↓ AVEEGIV ⁴¹⁰	AGGGV ⁴²⁰ TLLQA ⁴²⁰
AP ⁴³⁰ TLDE ↓ LKLE ⁴³⁰	GDEATGAN ↓ IV ⁴⁴⁰	KVALEAPLKQ ⁴⁵⁰	IAFN ⁴⁶⁰ SGL ⁴⁶⁰ EP ⁴⁶⁰ G ⁴⁶⁰	VVAEK ↓ VRNLP ⁴⁷⁰	AGH ↓ GLNA ↓ QTG ⁴⁸⁰	VYEDLLAAGV ⁴⁹⁰
ADP ↓ VKVTRSA ⁵⁰⁰	LQNAAS ↓ IAGL ⁵¹⁰	F ↓ LTTEAVVAD ⁵²⁰	KPEKEKASVP ⁵³⁰	GGGDMGGMDF ⁵⁴⁰		

Peptide sequences		Molecular mass, Da	
		Calculated	Measured
1	²⁶ VKVTILGPKGRNVVLEKKWGAPTITNDGVSIAKEIELEDPYEKIGAEELVKEVAKKTDDVAGDGT ¹⁴⁸ TTATVLAQALVREGLRNVAAGANPLGLKRGIEKAVEKVTETLLKGAKEVETKEQIAATAA ¹⁴⁸	12896	12889
2	⁴⁰¹ AKAAVEEGIVAGGGV ⁵¹¹ TLLQAAPTLD ⁵¹¹ ELKLEGDEATGANIVKVALEAPLKQIAFN ⁵¹¹ SGL ⁵¹¹ EPGVVAEKVRNLPAGHGLNAQTGVYEDLLAAGVADPVK ⁵¹¹ VTR ⁵¹¹ SALQNAAS ⁵¹¹ IAGL ⁵¹¹	11106	11107
3	³⁷⁰ L ⁴⁷⁷ AGGVAVIKAGAATEVELKERKHRIE ⁴⁷⁷ DAVRN ⁴⁷⁷ AKAAVEEGIVAGGGV ⁴⁷⁷ TLLQAAPTLD ⁴⁷⁷ ELKLEGDEATGANIVKVALEAPLKQIAFN ⁴⁷⁷ SGL ⁴⁷⁷ EPGVVAEKVRNLPAGHGLNA ⁴⁷⁷	10961	10970
4	¹⁵⁴ QSIGDLIAEAMDKVNEGVI ²⁵¹ TVEESNTFGLQLELTEGMRF ²⁵¹ DKGYISGYFVTDPERQEAVLEDPYILLVSSKVSTVKDLLP ²⁵¹ LLEK ²⁵¹ VIGAGKP	10678	10680
5	⁴⁰¹ AKAAVEEGIVAGGGV ⁵⁰⁶ TLLQAAPTLD ⁵⁰⁶ ELKLEGDEATGANIVKVALEAPLKQIAFN ⁵⁰⁶ SGL ⁵⁰⁶ EPGVVAEKVRNLPAGHGLNAQTGVYEDLLAAGVADPVK ⁵⁰⁶ VTR ⁵⁰⁶ SALQNAAS ⁵⁰⁶	10605	10604
6	³⁷⁷ IKAGAATEVELKERKHRIE ⁴⁷³ DAVRN ⁴⁷³ AKAAVEEGIVAGGGV ⁴⁷³ TLLQAAPTLD ⁴⁷³ ELKLEGDEATGANIVKVALEAPLKQIAFN ⁴⁷³ SGL ⁴⁷³ EPGVVAEKVRNLPAGH ⁴⁷³	10038	10032
7	³⁷⁷ IKAGAATEVELKERKHRIE ⁴⁶⁵ DAVRN ⁴⁶⁵ AKAAVEEGIVAGGGV ⁴⁶⁵ TLLQAAPTLD ⁴⁶⁵ ELKLEGDEATGANIVKVALEAPLKQIAFN ⁴⁶⁵ SGL ⁴⁶⁵ EPGVVAEK ⁴⁶⁵	9194	9194
8	²⁸ VTLGPKGRNVVLEKKWGAPTITNDGVSIAKEIELEDPYEKIGAEELVKEVAKKTDDVAGDGT ¹¹⁴ TTATVLAQALVREGLRNVAAGANPLG ¹¹⁴	9035	9033
9	²²⁰ LVSSKVSTVKDLLP ²⁸⁹ LLEK ²⁸⁹ VIGAGKPLLI ²⁸⁹ IAEDVEGEALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLQD ²⁸⁹	7427	7422
10	²⁸ VTLGPKGRNVVLEKKWGAPTITNDGVSIAKEIELEDPYEKIGAEELVKEVAKKTDDVAGDGT ⁹⁷ TTATVLAQA ⁹⁷	7347	7338
11	²⁸ VTLGPKGRNVVLEKKWGAPTITNDGVSIAKEIELEDPYEKIGAEELVKEVAKKTDDVAGDGT ⁹⁵ TTATVLA ⁹⁵	7147	7142
12	⁴³⁹ IVKVALEAPLKQIAFN ⁴⁹³ SGL ⁴⁹³ EPGVVAEKVRNLPAGHGLNAQTGVYEDLLAAGVADP ⁴⁹³	5619	5619
13	²⁰⁹ QEAVLEDPYILLVSSKVSTVKDLLP ²⁵⁹ LLEK ²⁵⁹ VIGAGKPLLI ²⁵⁹ IAEDVEGEALST ²⁵⁹	5415	5418
14	⁴²⁷ LKLEGDEATGANIVKVALEAPLKQIAFN ⁴⁷⁷ SGL ⁴⁷⁷ EPGVVAEKVRNLPAGHGLNA ⁴⁷⁷	5218	5213
15	²⁴⁵ LLI ²⁸⁹ IAEDVEGEALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLQD ²⁸⁹	4855	4850
16	⁴⁰⁴ AVEEGIVAGGGV ⁴⁵⁰ TLLQAAPTLD ⁴⁵⁰ ELKLEGDEATGANIVKVALEAPLKQ ⁴⁵⁰	4697	4697
17	¹⁸³ LQLELTEGMRF ²²⁰ DKGYISGYFVTDPERQEAVLEDPYILL ²²⁰	4447	4453
18	²⁵² VEGEALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLQD ²⁸⁹	4087	4083
19	⁴²⁷ LKLEGDEATGANIVKVALEAPLKQIAFN ⁴⁶⁵ SGL ⁴⁶⁵ EPGVVAEK ⁴⁶⁵	4018	4013

MMP-16 fragments

MAKTIAYDEE ¹⁰	ARRGLERGLN ²⁰	A ↓ LADAVKVTL ³⁰	GPKGRNVVLE ⁴⁰	KKWGAPTITN ⁵⁰	DGVSIAKEIE ⁶⁰	LEDPYEKIGA ⁷⁰
ELVKEVAKKT ⁸⁰	DDVAGDGT ⁹⁰	ATVLAQA ↓ LVR ¹⁰⁰	EGLRNVAAGA ¹¹⁰	NPLGLKRGIE ¹²⁰	KAVEK ↓ VTETL ¹³⁰	LKGAKEVETK ¹⁴⁰
EQIAATAAIS ¹⁵⁰	AGD ↓ QSIGDLI ¹⁶⁰	AEA ↓ MDKVGNE ¹⁷⁰	GVITVEESNT ¹⁸⁰	FGLQLELTEG ¹⁹⁰	MRFDKGYISG ²⁰⁰	YFVTDPER ↓ QE ²¹⁰
AVLEDPYILL ²²⁰	VSSKVST ↓ VKD ²³⁰ ↓	LLP LLEKVI G ²⁴⁰	AGKP ↓ LLIIAE ²⁵⁰	D ↓ VEGEALST ↓ L ²⁶⁰	VVNKIRGTFK ²⁷⁰	SVAVKAPGFG ²⁸⁰
DRRKAMLQD ↓ M ²⁹⁰	AILTGGQVIS ³⁰⁰	EEVGLTLENA ³¹⁰	DLS ↓ LLGKARK ³²⁰	VVVTKDETTI ³³⁰	VEGAGDTDAI ³⁴⁰	AGRVAQIRQE ³⁵⁰
IENS DSDYDR ³⁶⁰	EKLQERLAKL ³⁷⁰	AGGVAV ↓ IKAG ³⁸⁰	A ↓ ATEVELKER ³⁹⁰	KHRIEDAVRN ⁴⁰⁰ ↓	AKA ↓ AVEEGIV ⁴¹⁰	AGGGVTL LQA ⁴²⁰
APTLDE ↓ LK ↓ LE ⁴³⁰	GDEATGAN ↓ IV ⁴⁴⁰	KVALEAPLK ↓ Q ⁴⁵⁰ ↓	IAFN SGL EPG ⁴⁶⁰	VVAEK ↓ VRNLP ⁴⁷⁰	AGH ↓ GLNA ↓ QTG ⁴⁸⁰	VYED ↓ LLAAG ↓ V ⁴⁹⁰
ADP ↓ VKVTRSA ⁵⁰⁰	LQNAAS ↓ IAG ↓ L ⁵¹⁰ ↓	FLTTEAVVAD ⁵²⁰	KPEKEKASVP ⁵³⁰	GGGDMGG ↓ MDF ⁵⁴⁰		

Peptide sequences		Molecular mass, Da	
		Calculated	Measured
1	³¹⁴ LLGKARKVVVTKDETTIVEGAGDTDAIAGRVAQIRQEIENS DSDYDREKLQERLAKLAGGVAVIKAGAAATEVELKERKHRIEDAVRNAKA AVEEGIVAGGGVTL LQAAPT LDELKLEGDEATGANIVKVALEAPLK ⁴⁴⁹	14301	14302
2	⁹⁸ LVREGLRNVAAGANPLGLKRGIEKAVEKVTETLLKGAKEVETKEQIAATAAISAGDQSIGDLIAEAMDKVGN EGVITVEESNTFGLQLELT EGMRFDKGYISGYFVTDPERQEAVLEDPYILLVSSKVST ²²⁷	13905	13912
3	²² LADAVKVTLGPKGRNVVLEKKWGAPTITNDGVSIAKEIELEDPYEKIGAELVKEVAKKTDDVAGDGT TTTATVLAQALVREGLRNVAAGANP LGLKRGIEKAVEK ¹²⁵	10884	10880
4	⁴⁰⁴ AVEEGIVAGGGVTL LQAAPT LDELKLEGDEATGANIVKVALEAPLKQIAFN SGL EPGVVAEKVRNLPAGHGLNAQTGVYEDLLAAGVADPV KVTR SALQNAAS IAGL ⁵¹⁰	10689	10698
5	¹⁵⁴ QSIGDLIAEAMDKVGN EGVITVEESNTFGLQLELTEGMRFDKGYISGYFVTDPERQEAVLEDPYILLVSSKVSTVKDLLP LLEKVI GAGKP LLIIAE ²⁵¹	10678	10674
6	⁴⁰¹ AKAAVEEGIVAGGGVTL LQAAPT LDELKLEGDEATGANIVKVALEAPLKQIAFN SGL EPGVVAEKVRNLPAGHGLNAQTGVYEDLLAAGVA DPVKVTR SALQNAAS ⁵⁰⁶	10605	10596
7	⁴⁰⁴ AVEEGIVAGGGVTL LQAAPT LDELKLEGDEATGANIVKVALEAPLKQIAFN SGL EPGVVAEKVRNLPAGHGLNAQTGVYEDLLAAGVADPV KVTR SALQNAAS IAG ⁵⁰⁹	10576	10571
8	³⁷⁷ IKAGAAATEVELKERKHRIEDAVRNAKAAVEEGIVAGGGVTL LQAAPT LDELKLEGDEATGANIVKVALEAPLKQIAFN SGL EPGVVAEKVR NLPAGH ⁴⁷³	10038	10031
9	³⁷⁷ IKAGAAATEVELKERKHRIEDAVRNAKAAVEEGIVAGGGVTL LQAAPT LDELKLEGDEATGANIVKVALEAPLKQIAFN SGL EPGVVAEK ⁴⁶⁵	9194	9187
10	¹⁶⁴ MDKVGNEGVITVEESNTFGLQLELTEGMRFDKGYISGYFVTDPERQEAVLEDPYILLVSSKVSTVKD ²³⁰	7485	7477
11	⁴³⁹ IVKVALEAPLKQIAFN SGL EPGVVAEKVRNLPAGHGLNAQTGVYEDLLAAGVADP ⁴⁹³	5619	5617
12	⁴⁸⁵ LLAAGVADPVKVTR SALQNAAS IAGLFLTTEAVVADKPEKEKASVPGGDMGGMF ⁵⁴⁰	5570	5570
13	²⁰⁹ QEAVLEDPYILLVSSKVSTVKDLLP LLEKVI GAGKPLIIAE DVEGEALST ²⁵⁹	5415	5415
14	⁴²⁷ LKLEGDEATGANIVKVALEAPLKQIAFN SGL EPGVVAEKVRNLPAGHGLNA ⁴⁷⁷	5218	5213
15	³⁸² ATEVELKERKHRIEDAVRNAKAAVEEGIVAGGGVTL LQAAPT LDELK ⁴²⁸	4995	4999
16	²⁴⁵ LLIIAE DVEGEALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLQD ²⁸⁹	4855	4844
17	⁴⁹⁰ VADPVKVTR SALQNAAS IAGLFLTTEAVVADKPEKEKASVPGGDMGG ⁵³⁷	4751	4747
18	⁴⁰⁴ AVEEGIVAGGGVTL LQAAPT LDELKLEGDEATGANIVKVALEAPLKQ ⁴⁵⁰	4697	4693

19	⁴²⁷ LKLEGDEATGANIVKVALEAPLKQIAFNNGLEPGVVAEK ⁴⁶⁵	4018	4017
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MMP-17 fragments								
MAKTIAYDEE ¹⁰	ARRGLERGLN ²⁰	ALADAVKVTL ³⁰	GPKGRNVVLE ⁴⁰	KKWGAPTITN ⁵⁰	DGVSIAKEIE ⁶⁰	LEDPYEKIGA ⁷⁰		
E ↓ LVKEVAKKT ⁸⁰	DDVAGDGTTT ⁹⁰	ATVLAQALVR ¹⁰⁰	EGLRNVAAGA ¹¹⁰	NPLGLKRGIE ¹²⁰	KAVEKVTETL ¹³⁰	LKGAKEVETK ¹⁴⁰		
EQIAATAA ↓ IS ¹⁵⁰	AGDQSIGD ↓ LI ¹⁶⁰	AE ↓ A ↓ MDKVGNE ¹⁷⁰	GVITVEESNT ¹⁸⁰	FG ↓ LQLELTEG ¹⁹⁰ ↓	MRFDKGYISG ²⁰⁰ ↓	YFVTDPERQE ²¹⁰		
AVLEDPYI ↓ LL ²²⁰ ↓	VSSKVST ↓ VKD ²³⁰ ↓	LLP ↓ LLEKVI ²⁴⁰	AGKPLL ↓ IIAE ²⁵⁰	DVEGEALSTL ²⁶⁰	VVNKIRGTFK ²⁷⁰	SVAVKAPGFG ²⁸⁰		
DRRKAMLQD ↓ M ²⁹⁰	AILTGGQVIS ³⁰⁰	EEVGLTLENA ³¹⁰	DLS ↓ LLGKAR ³²⁰	VVVTKDETTI ³³⁰	VEGAGDTDAI ³⁴⁰	AGRVAQ ↓ IRQE ³⁵⁰		
IENSDDSDYDR ³⁶⁰	EKLQERLAK ↓ L ³⁷⁰	AGG ↓ VAVIKAG ³⁸⁰	A ↓ ATEVELKER ³⁹⁰	KHRIEDAVRN ⁴⁰⁰	AKAAVEEGIV ⁴¹⁰	AGGGVTL ↓ LQA ⁴²⁰		
APTLDELK ↓ LE ⁴³⁰	GDEATGAN ↓ IV ⁴⁴⁰	KVALEAP ↓ LK ↓ Q ⁴⁵⁰	IAFNNGLEPG ⁴⁶⁰	VVAEKVRNLP ⁴⁷⁰	AGHGLNA ↓ QTG ⁴⁸⁰	VYEDL ↓ LAAG ↓ V ⁴⁹⁰		
ADP ↓ VKVTRSA ⁵⁰⁰	LQNAASIAG ↓ L ⁵¹⁰	FLTTEAVVAD ⁵²⁰	KPEKEKASVP ⁵³⁰	GGGDMGGMDF ⁵⁴⁰				
Peptide sequences						Molecular mass, Da		
						Calculated	Measured	
1	²⁰¹ YFVTDPERQEAVLEDPYILLVSSKVS ²³⁰ TVKDLLP ²⁴⁶ LLEKVI ²⁶⁰ GAGKPLLI ²⁷⁷ IAEDVEGEALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLQDMA ³¹³ ILTGGQVISEEVGLTLENADLS ³¹³						12146	12152
2	¹⁶³ AMDKVGNEGVITVEESNTFGLQLELTEGMRFKGYISGYFVTDPERQEAVLEDPYILLVSSKVS ²³³ TVKDLLP ²⁴⁶ LLEKVI ²⁶⁰ GAGKPLL ²⁴⁶						9211	9214
3	²⁹⁰ MAILTGGQVISEEVGLTLENADLSLLGKARKVVVTKDETTIVEGAGDTDAIAGRVAQIRQEIENSDDSDYDREKLQERLAK ³⁶⁹						8638	8643
4	¹⁴⁹ ISAGDQSIGDLIAEAMDKVGNEGVITVEESNTFGLQLELTEGMRFKGYISGYFVTDPERQEAVLEDPYILLVSSKVS ²²⁷						8583	8584
5	¹⁶³ AMDKVGNEGVITVEESNTFGLQLELTEGMRFKGYISGYFVTDPERQEAVLEDPYILLVSSKVS ²³³ TVKDLLP ²³³						7878	7877
6	¹⁵⁹ IAEAMDKVGNEGVITVEESNTFGLQLELTEGMRFKGYISGYFVTDPERQEAVLEDPYILLVSSKVS ²²⁷						7640	7642
7	³⁷⁴ VAVIKAGAATEVELKERKHRIEDAVRNAKAAVEEGIVAGGGVTL ⁴²⁸ LQAAPTLDELKLEGDEATGANIVKVALEAP ⁴⁴⁷						7582	7581
8	⁴¹⁸ LQAAPTLDELKLEGDEATGANIVKVALEAPLKQIAFNNGLEPGVVAEKVRNLPAGHGLNAQTGVYEDLLAAG ⁴⁸⁹						7374	7383
9	¹⁶⁴ MDKVGNEGVITVEESNTFGLQLELTEGMRFKGYISGYFVTDPERQEAVLEDPYI ²¹⁸						6228	6234
10	⁴⁵⁰ QIAFNNGLEPGVVAEKVRNLPAGHGLNAQTGVYEDLLAAGVADPVKVTRSA ⁵⁰⁹ LQNAASIAG ⁵⁰⁹						6024	6026
11	²⁹⁰ MAILTGGQVISEEVGLTLENADLSLLGKARKVVVTKDETTIVEGAGDTDAIAGRVAQ ³⁴⁶						5822	5823
12	³⁷⁴ VAVIKAGAATEVELKERKHRIEDAVRNAKAAVEEGIVAGGGVTL ⁴²⁸ LQAAPTLDELK ⁴²⁸						5704	5698
13	⁴⁸⁶ LAAGVADPVKVTRSA ⁵⁴⁰ LQNAASIAGFLTTEAVVADKPEKEKASVPGGGDMGGMDF ⁵⁴⁰						5457	5452
14	⁴³⁹ IVKVALEAPLKQIAFNNGLEPGVVAEKVRNLPAGHGLNAQTGVYEDLLAAG ⁴⁸⁹						5237	5233
15	³⁸² ATEVELKERKHRIEDAVRNAKAAVEEGIVAGGGVTL ⁴²⁸ LQAAPTLDELK ⁴²⁸						4995	4993
16	⁴⁹⁴ VKVTRSA ⁵⁴⁰ LQNAASIAGFLTTEAVVADKPEKEKASVPGGGDMGGMDF ⁵⁴⁰						4762	4761
17	¹⁹¹ MRFDKGYISGYFVTDPERQEAVLEDPYILLVSSKVS ²³⁰ TVK ²³⁰						4594	4592
18	¹⁸³ LQLELTEGMRFKGYISGYFVTDPERQEAVLEDPYILL ²²⁰						4447	4455
19	⁴⁷⁸ QTGVYEDLLAAGVADPVKVTRSA ⁵⁰⁹ LQNAASIAG ⁵⁰⁹						3185	3185

MMP-24 fragments

MAKTIAYDEE ¹⁰	ARRGLERGLN ²⁰	ALADAVKVTI ³⁰	GPKGRNVVLE ⁴⁰	KKWGAPTITN ⁵⁰	DGVSIAKEIE ⁶⁰	LEDPYEKIGA ⁷⁰
ELVKEVAKKT ⁸⁰	DDVAGDGT ⁹⁰	ATVLAQALVR ¹⁰⁰	EGLRNVAAGA ¹¹⁰	NPLGLKRGIE ¹²⁰	KAVEKVTETI ¹³⁰	LKGAKEVETK ¹⁴⁰
EQIAATAA ↓ IS ¹⁵⁰	AGD ↓ QSIGDLI ¹⁶⁰	AEAMDKVGN ¹⁷⁰	GVITVEESNT ¹⁸⁰	FGLQ ↓ LELTEG ¹⁹⁰	MRFDKGYISG ²⁰⁰	Y ↓ FVTDPER ↓ QE ²¹⁰
AVLEDPYILL ²²⁰	VSSKVSTVKD ²³⁰	LLPILLEKVI ²⁴⁰	AGKPLIIIAE ²⁵⁰	DVEGEALST ↓ L ²⁶⁰	VVNKIRGTFK ²⁷⁰	SVAVKAPGFG ²⁸⁰
DRRKAMLQD ↓ M ²⁹⁰	AILTGGQVIS ³⁰⁰	EEVGLTLENA ³¹⁰	DLSSLGKARK ³²⁰	VVVTKDETTI ³³⁰	VEGAGDTDAI ³⁴⁰	AGRVAQIRQE ³⁵⁰
IENSDSDYDR ³⁶⁰	EKLQERLAKL ³⁷⁰	AGG ↓ VAVIKAG ³⁸⁰	A ↓ ATEVELKER ³⁹⁰	KHRIEDAVRN ⁴⁰⁰	AKA ↓ AVEEGIV ⁴¹⁰	AGGGVTLLQA ⁴²⁰
APTLDELK ↓ LE ⁴³⁰	GDEATGANIV ⁴⁴⁰	KVALEAPLKQ ⁴⁵⁰ ↓	IAFNNGLEPG ⁴⁶⁰	VVAEKVRNLP ⁴⁷⁰	AGHG ↓ LNAQTG ⁴⁸⁰	VYEDLLAAGV ⁴⁹⁰
ADPVKVTRSA ⁵⁰⁰ ↓	LQNAASIAGL ⁵¹⁰	FLTTEAVVAD ⁵²⁰	KPEKEKASVP ⁵³⁰	GGGDMGGMDF ⁵⁴⁰		

Peptide sequences		Molecular mass, Da	
		Calculated	Measured
1	¹⁴⁹ ISAGDQSIGDLIAEAMDKVGN ²⁵⁹ GVITVEESNTFGLQLELTEGMRFDKGYISGYFVTDPERQEAVLEDPYILLVSSKVSTVKDLLPILLEKVI GKPLIIIAEDVEGEALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLQD ²⁸⁹	15191	15189
2	¹⁸⁵ LELTEGMRFDKGYISGYFVTDPERQEAVLEDPYILLVSSKVSTVKDLLPILLEKVI GAGKPLIIIAEDVEGEALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLQD ²⁸⁹	11502	11505
3	³⁷⁴ VKAPGFGDRRKAMLQDMAILTGGQVISEEVGLTLENADLSLLGKARKVVVTKDETTIVEGAGDTDAIAGRVAQIRQEIENSDSDYDREKLQER LAKLAGGVAVIKAGAATEVELKERKHRIEDAVRNAKAAVEEGIVAGGGVTLLQAAPTLDELKLEGDEATGANIVKVALEAPLKQIAFNNGLEPGV VAEKVRNLPAGHG ⁴⁷⁴	10364	10373
4	²⁰⁹ QEAVLEDPYILLVSSKVSTVKDLLPILLEKVI GAGKPLIIIAEDVEGEALST ²⁵⁹	5415	5416
5	¹⁵⁴ QSIGDLIAEAMDKVGN ²⁵⁹ GVITVEESNTFGLQLELTEGMRFDKGYISGY ²⁰¹	5223	5224
6	³⁸² ATEVELKERKHRIEDAVRNAKAAVEEGIVAGGGVTLLQAAPTLDELK ⁴²⁸	4995	4998
7	⁴⁰⁴ AVEEGIVAGGGVTLLQAAPTLDELKLEGDEATGANIVKVALEAPLKQ ⁴⁵⁰	4697	4694
8	⁵⁰¹ LQNAASIAGLFLTTEAVVADKPEKEKASVPGGGDMGGMDF ⁵⁴⁰	4021	4021

MMP-25 fragments

MAKT ↓ IAYDEE ¹⁰	ARRGLERGLN ²⁰	ALADAVK ↓ VTL ³⁰	GPKGRNVVLE ⁴⁰	KKWGAPTITN ⁵⁰	DGVSIKE ↓ IE ⁶⁰	LEDPYEKIGA ⁷⁰
E ↓ L ↓ VKEVAKKT ⁸⁰	DDVAGDGT ⁹⁰	ATVLA ↓ QALVR ¹⁰⁰	EGLRNVA ↓ GA ¹¹⁰	NPLGLKRGIE ¹²⁰	KAVEK ↓ VTETL ¹³⁰	LKGAKEVETK ¹⁴⁰
EQIAATAA ↓ IS ¹⁵⁰	AGD ↓ QSIGD ↓ LI ¹⁶⁰	AEA ↓ MDKVGNE ¹⁷⁰	GVITVEESNT ¹⁸⁰	FGLQLELTEG ¹⁹⁰ ↓	MRFDKGYISG ²⁰⁰	Y ↓ FVTDPER ↓ QE ²¹⁰
AVLEDPYIL ↓ L ²²⁰	VSSKVVSTVKD ²³⁰	LLP ↓ LLEKVI ²⁴⁰	AGKPLL ↓ IIAE ²⁵⁰ ↓	VEGEALST ↓ L ²⁶⁰	VVNKIRGTFK ²⁷⁰	SVAVKAPGFG ²⁸⁰
DRRKAMLQD ↓ M ²⁹⁰	AILTGGQVIS ³⁰⁰	EEVGLT ↓ LENA ³¹⁰	DLSELLGKARK ³²⁰ ↓	VVVTKDETTI ³³⁰	VEGAGDTDAI ³⁴⁰	AGRVAQ ↓ IRQE ³⁵⁰
IENSDDSDYDR ³⁶⁰	EKLQERLAKL ³⁷⁰	AGG ↓ VAV ↓ IKAG ³⁸⁰	AATEVELKER ³⁹⁰	KHRIEDAVRN ⁴⁰⁰ ↓	AKA ↓ AVEEGIV ⁴¹⁰	AGGGVTL ↓ LQA ⁴²⁰
APTLDELKLE ⁴³⁰	GDEATGANIV ⁴⁴⁰	KVALEAP ↓ LKQ ⁴⁵⁰ ↓	IAFNGLPEP ⁴⁶⁰	VVAEK ↓ VRNLP ⁴⁷⁰	AG ↓ HGLNAQTG ⁴⁸⁰	VYED ↓ LLAAG ↓ V ⁴⁹⁰
ADPVKVTRSA ⁵⁰⁰	LQNAASIAG ↓ L ⁵¹⁰ ↓	FLTTEAVVAD ⁵²⁰	KPEKEKASVP ⁵³⁰	GGGDMGGMDF ⁵⁴⁰		

Peptide sequences		Molecular mass, Da	
		Calculated	Measured
1	³²¹ VVVTKDETTIVEGAGDTDAIAGRVAQIRQEIENSDDSDYDREKLQERLAKLAGGVAVIKAGAAATEVELKERKHRIEDAVRNAKAAVEEGIVAGGGVTL ⁴¹⁷	10235	10238
2	³⁷⁷ IKAGAAATEVELKERKHRIEDAVRNAKAAVEEGIVAGGGVTLQAAPTLDELKLEGDEATGANIVKVALEAPLKQIAFNGLPEPVGVAEK ⁴⁶⁵	9194	9188
3	³²¹ VVVTKDETTIVEGAGDTDAIAGRVAQIRQEIENSDDSDYDREKLQERLAKLAGGVAVIKAGAAATEVELKERKHRIEDAVRN ⁴⁰⁰	8713	8712
4	²⁴⁷ IIAEDVEGEALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLQDMAILTGGQVISEEVGLTLENADLSLLGKARK ³²⁰	7836	7835
5	⁴⁶⁶ VRNLPAGHGLNAQTGVYEDLLAAGVADPVKVTRSAALQNAASIALGLTTEAVVADKPEKEKASVPGGGDMGGMDF ⁵⁴⁰	7562	7565
6	²²⁰ LVSSKVVSTVKDLLPILLEKVIAGAGKPLLI AEDVEGEALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLQD ²⁸⁹	7427	7429
7	⁵ IAYDEEARRGLERGLNALADAVKVTLGPKGRNVVLEKKKWGAPTITNDGVSIKEIELEDPYEKIGAEL ⁷²	7388	7386
8	³⁰⁷ LENADLSLLGKARKVVVTKDETTIVEGAGDTDAIAGRVAQIRQEIENSDDSDYDREKLQERLAKLAGG ³⁷³	7238	7239
9	⁴⁰¹ AKAAVEEGIVAGGGVTLQAAPTLDELKLEGDEATGANIVKVALEAPLKQIAFNGLPEPVGVAEKVRNLPAG ⁴⁷²	7187	7188
10	²⁸ VTLGPKGRNVVLEKKKWGAPTITNDGVSIKEIELEDPYEKIGAELVKEVAKKTDDVAGDGT ⁹⁵	7147	7140
11	⁵⁹ IELEDPYEKIGAELVKEVAKKTDDVAGDGT ¹²⁵	7028	7021
12	⁴⁴⁸ LKQIAFNGLPEPVGVAEKVRNLPAGHGLNAQTGVYEDLLAAGVADPVKVTRSAALQNAASIALG ⁵¹⁰	6378	6374
13	³⁴⁷ IRQEIENSDDSDYDREKLQERLAKLAGGVAVIKAGAAATEVELKERKHRIEDAVRN ⁴⁰⁰	6116	6112
14	²³⁴ LLEKVIAGAGKPLLI AEDVEGEALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLQD ²⁸⁹	5960	5964
15	²⁵² VEGEALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLQDMAILTGGQVISEEVGLT ³⁰⁶	5786	5785
16	⁴¹⁸ LQAAPTLDELKLEGDEATGANIVKVALEAPLKQIAFNGLPEPVGVAEKVRNLPAG ⁴⁷²	5664	5660
17	⁴⁸⁵ LLAAGVADPVKVTRSAALQNAASIALGLTTEAVVADKPEKEKASVPGGGDMGGMDF ⁵⁴⁰	5570	5577
18	²⁰² VAVIKAGAAATEVELKERKHRIEDAVRNAKAAVEEGIVAGGGVTLQAAPTLDE ²⁵¹	5472	5470
19	²⁰⁹ QEAILEDYILLVSSKVVSTVKDLLPILLEKVIAGAGKPLLI AEDVEGEALST ²⁵⁹	5415	5415
20	¹⁵⁴ QSIGDLIAEAMDKVNEGVIITVEESNTFGLQLELTEGMRFDKGYISGY ²⁰¹	5223	5227
21	¹⁶⁴ MDKVGNEGVIITVEESNTFGLQLELTEGMRFDKGYISGYFVTDPER ²⁰⁸	5070	5062
22	¹⁹¹ MRFDKGYISGYFVTDPERQEAILEDYILLVSSKVVSTVKDLLP ²³³	4917	4910
23	¹⁵⁹ LIAEAMDKVNEGVIITVEESNTFGLQLELTEGMRFDKGYISGY ²⁰¹	4723	4728
24	⁴⁰⁴ AVEEGIVAGGGVTLQAAPTLDELKLEGDEATGANIVKVALEAPLKQ ⁴⁵⁰	4697	4690

25	³⁷⁴ VAVIKAGAATEVELKERKHRIEDAVRNAKAAVEEGIVAGGGVTL ⁴¹⁷	4524	4527
26	⁴⁶⁶ VRNLPAGHGLNAQTGVYEDLLAAGVADPVKVTRSAIQNAASIAG ⁵⁰⁹	4384	4394
27	⁴⁴⁸ LKQIAFNGLPGVVAEKVRNLPAGHGLNAQTGVYEDLLAAG ⁴⁸⁹	4316	4309
28	¹⁰⁹ GANPLGLKRGIEKAVEKVTETLLKGAKEVETKEQIAATAA ¹⁴⁸	4161	4166
29	²⁰⁹ QEAVLEDPYILLVSSKVSTVKDLLPLEKVIKAGKPLL ²⁴⁶	4087	4084

Supplemental Table S2. The P1' residue positions in the HSP65 cleavage peptides. PEX, hemopexin.

Residue	Gelatinases, MMPs		Simple PEX domain MMP	Membrane-associated MMPs				GPI-linked MMPs	
	-2	-9	-8	-14	-15	-16	-24	-17	-25
Ala	3	1	2	4	2	3	2	2	2
Val	9	11	11	7	5	6	1	5	8
Leu	8	12	17	11	9	10	5	12	9
Ile	2	0	3	1	4	4	2	4	6
Phe	1	2	2	1	0	1	1	0	2
Tyr	0	0	0	0	0	0	0	1	0
Met	0	4	4	2	1	3	1	3	3
Gln	2	3	4	0	4	4	2	2	3
Gly	1	2	2	0	1	1	0	0	1
Glu	1	0	0	0	0	0	0	0	0
Lys	0	0	0	1	0	0	0	0	0
His	0	0	0	1	1	1	0	0	1

Supplemental Table S3. The P1 residue positions in the HSP65 cleavage peptides. PEX, hemopexin.

Residue	Gelatinases, MMPs		Simple PEX domain MMP	Membrane-associated MMPs				GPI-linked MMPs	
	-2	-9	-8	-14	-15	-16	-24	-17	-25
Ala	3	4	5	4	6	6	3	4	5
Val	1	0	1	0	1	1	0	0	1
Leu	5	4	5	3	1	1	0	4	5
Ile	0	0	0	0	0	0	0	1	0
Phe	0	1	1	0	1	0	0	0	0
Tyr	1	1	1	1	0	0	1	0	1
Met	0	0	0	1	0	0	0	0	0
Gln	2	1	1	0	0	1	2	1	2
Gly	2	6	6	5	2	4	2	6	5
Glu	1	1	2	2	1	1	0	1	1
Asp	3	3	6	4	3	5	2	3	5
Asn	1	1	3	2	2	2	0	1	1
Lys	5	8	6	3	3	3	1	3	4
Arg	0	2	2	0	1	1	1	0	1
His	0	1	1	0	1	1	0	0	0
Ser	0	0	0	1	1	2	0	1	0
Thr	1	1	1	1	1	2	1	1	3
Pro	1	2	3	1	2	2	0	3	2

Supplemental Table S4. The P2 residue positions in the HSP65 cleavage peptides. PEX, hemopexin.

Residue	Gelatinases, MMPs		Simple PEX domain MMP	Membrane-associated MMPs				GPI-linked MMPs	
	-2	-9	-8	-14	-15	-16	-24	-17	-25
Ala	3	4	9	6	5	5	1	8	8
Val	2	2	1	1	1	0	0	0	1
Leu	6	5	7	1	3	3	2	6	4
Ile	0	0	1	0	1	0	0	0	1
Phe	1	0	0	0	1	0	0	1	0
Tyr	0	0	0	1	0	0	0	1	0
Gln	0	1	2	1	2	2	1	1	1
Gly	3	7	8	2	2	5	4	3	5
Glu	4	4	8	5	3	6	1	2	7
Asp	1	1	1	1	2	2	0	2	0
Asn	0	0	1	1	2	2	0	1	0
Lys	1	0	1	2	2	4	2	1	4
Arg	1	2	4	3	1	1	0	0	2
His	0	0	0	1	0	0	1	0	0
Ser	2	1	1	2	1	2	2	2	1
Thr	2	1	1	1	0	0	0	1	1

Supplemental Table S5. The P3 residue positions in the HSP65 cleavage peptides. PEX, hemopexin.

Residue	Gelatinases, MMPs		Simple PEX domain MMP	Membrane- associated MMPs				GPI-linked MMPs	
	-2	-9	-8	-14	-15	-16	-24	-17	-25
Ala	6	11	14	4	10	12	4	5	13
Val	5	3	8	5	3	5	0	4	7
Leu	3	5	4	3	5	6	3	4	4
Ile	2	3	4	2	0	1	0	5	2
Phe	0	0	0	0	0	0	0	0	0
Tyr	1	0	2	1	1	1	0	0	2
Met	0	1	1	0	0	1	0	0	0
Gly	2	11	4	1	3	2	2	1	1
Glu	0	11	1	2	0	1	1	3	1
Asp	0	0	0	0	0	1	0	1	0
Asn	0	1	1	0	0	0	0	0	0
Lys	0	0	0	1	0	0	0	0	0
Arg	0	0	0	1	0	0	1	0	0
Ser	1	1	1	1	0	0	1	0	1
Thr	2	1	2	3	2	0	1	3	2
Pro	4	4	2	4	2	2	1	3	3