

Table S1. Peptides identified by MALDI-TOF analysis of EBA-175 tryptic digests

Peptide sequence ^a	residue numbers	calculated m/z ^b	observed m/z	\pm ppm
FNELDKKK	41–48	1021.568	1021.574	5.3
IFTFIENK	59–66	1011.551	1011.538	–13.7
LDILNNSKFNK	67–7	1305.717	1305.710	–5.4
NTSSNNEVLSNCR	147–159	1494.661	1494.685	16.4
SNYVCIPDRR	176–185	1279.622	1279.649	21.7
TYTKETMK (Met ox)	198–205	1017.493	1017.521	28.3
FCNDLK	231–236	796.366	796.347	–24.0
IQEVFK	264–269	763.435	763.422	–17.6
GAHGEISEHK	270–279	1064.512	1064.546	31.8
IKNFR	280–284	677.410	677.446	53.6
KKWWNEFR	285–292	1193.622	1193.626	3.2
LWEAMLSEHK	295–304	1243.614	1243.662	38.2
EWHGELLER	326–335	1315.643	1325.683	30.1
YRDWIIR	366–372	1021.558	1021.541	–16.7
SKFEWHTLSK	373–382	1262.653	1262.693	31.7
ENAENYLIK	392–400	1093.553	1093.542	–10.4
HTTTLVK	429–435	799.468	799.438	–37.7
SVLNGNDNTIK	436–446	1174.607	1174.588	–15.9
DVCVPPR	486–492	842.419	842.449	34.9
RQELCLGNIDR	493–503	1373.696	1373.724	20.6
EHILAIAYESR	514–525	1414.769	1414.846	54.5
TFADIR	546–551	722.384	722.401	23.8
DIIGTDYWNLSNR	552–566	1738.804	1738.854	28.9
INTNSNYVHR	572–581	1217.603	1217.628	20.5
NKQNDKLFK	582–590	1162.633	1162.634	0.4
LFRDEWWK	588–595	1179.595	1179.608	11.1
TVCKEDDIENIPQFFR	613–628	2010.959	2011.033	36.4
WFSEWGDDYQCQDK	629–641	1735.670	1735.731	35.1
TKMIETLKVECK	642–653	1479.791	1479.864	49.4
EKPCEDDNCKRK	654–664	1450.605	1450.639	23.1
MYSEFK (Met ox)	698–703	820.355	820.363	9.6
SIKPEVYLK	704–712	1076.636	1076.608	–25.3
DVPISIIR	747–754	912.552	912.539	–14.2
NNEQTSQEAVPEESTEIAHR	755–774	2269.033	2269.027	–2.6
GEDQTLGK	834–841	847.416	847.459	50.5
SDAIPNIGEPETGISTTEESRHEEGHMK	842–869	3034.399	3034.442	14.1
KRDDDSLK	932–940	1063.538	1063.532	–5.7
ISVSPENSRPETDAKDTSNLLK	941–962	2401.221	2401.320	41.4
ISNNEYKVNER	1088–1098	1365.676	1365.713	26.9
TVGDLGTTTHVQNEISVPVTGEIDEKLR	1174–1200	2907.506	2907.568	21.2
IHKAEER	1207–1214	1011.522	1011.511	–11.6
LSHTDIHKINPEDR	1215–1228	1674.856	1674.902	27.1
INPEDRNSNTLHLK	1223–1236	1650.856	1650.890	20.1
DIRNEENER	1237–1245	1174.545	1174.563	15.3
HLTNQNINISQER	1246–1258	1566.799	1566.833	21.8
HLTNQNINISQERDLQK	1246–1262	2051.063	2051.04	–11.5
HGFHTMNNLHGDGVSER	1263–1279	1907.857	1907.828	–15.0
HGFHTMNNLHGDGVSER (Met ox)	1263–1279	1923.852	1923.917	34.0
SQINHSHHGK	1280–1290	1286.610	1286.642	24.3
SQINHSHHGKQDR	1280–1293	1685.797	1685.851	32.3
GGNSGNVLNMR	1294–1304	1134.532	1134.560	24.4
SNNNNFNNIPSR	1305–1316	1390.646	1390.682	25.5
YNLYDK	1317–1322	815.394	815.401	9.2
LDLDLYENRNDSTTK	1324–1338	1796.867	1796.920	29.6
EFDDPSYTCFR	1406–1416	1436.579	1436.609	21.0
EFDDPSYTCFRK	1406–1417	1564.674	1564.701	17.3

^aNote that the predicted TMD of EBA-175 extends from Tyr1425-Ser1442.

^bAll calculated m/z values for cysteine-containing peptides are for the carbamidomethylated form.

Table S2. Oligonucleotide primers used in this study.

Name	Sequence (5'-3')	Restriction sites			
		Bold	Bold and italics	underlined	italics
PPeba-A	CCGGAATTCGACGACAGCACCACC AAGGAGCTGATCAAG			EcoRI	
PPeba-B	GCTACGCGGCCGCTAATGATGGTG ATGGTGGTGCATGCTGCTGAAGGCT TCCTTCCGGAA	NotI			
HAROMtagF	<i>GCTNAGCCCTAGGCTTAAGGCATA</i> CCCTTACGATGTTCTGAC	AvrII		AflIII	EspI
HAROMtagR	<i>CTCGAGGGCGCCTTAATGAGCGTA</i> ATCTGGAACGTCG		XhoI		
PfROM1F	CCTAGGTCGTTATTTCTATTATAACA GTTGATTG	AvrII			
PfROM1R	<u>CTTAAGACATGTACGAGGTATTGTA</u> AATAAAACGAC			AflIII	
PfROM4upF	AGATCTGACAATTATATATATATAT ATATATGAAC				BglIII
PfROM4upR	CTCGAGTGTTAAATGTAATAGTGA ATAAATAATTTTAAC	XhoI			
pSecHAfor	GGTACCCTTACGATGTTCTGACTA TGCG				
pSecHArev	AGAGTCGACATATGGAATTCAGCGT AATCTGG			EcoRI	
EBA-175-S ₃₂₀₈ pHH1-Pbdt-AS EBAactivefor1	GAGAGGGAAGATGAGAGAACG CATGCATGTGCATGCAC GCAGCATGCCCTACTACTACGGAG CCGGCGTGCTG				
EBAactiverrev1	CAGCACGCCGGCTCCGTAGTAGTA GGGCATGCTGC				
EBAmut12for	GACAGCGAGGAGTACTACGACTGC ACCAAGCGGGAGTTTCG				
EBAmut12rev	CGAACTCCCGCTTGGTGCAGTCGTA GTACTCCTCGCTGTC				
EBAmut13for	GATTACGCTGAATTCGACGACAGC ACCACC				
EBAmut13rev	GGTGGTGCTGTGTCGAATTCAGCG TAATC				
EBATMmutfor1	GCATGCCCTACTACGCCTTCTTCGG CGTGCTGTTCA				
EBATMmutrev1	TGAACAGCACGCCGAAGAAGGCGT AGTAGGGCATGC				
EBATMmutfor2	GGTGATCCTGTTCTTCAGCCAGGCC AAGTA				
EBATMmutrev2	TACTTGGCCTGGCTGAAGAACAGG ATCACC				
ROM4mutfor	TGCGGCGTGACAATTGGCGCCGCA GGGAGTCTGTATGGG				
ROM4mutrev	CCCATACAGACTCCCTGCGGCGCC AATTGTCACGCCGCA				
EBA175GA1/FF-S	ATGCCATATTATGCATTTTTTGGTGT GTTATTTATTATATTGG				
EBA175GA1/FF- AS	CCAATATAATAAATAACACACCAA AAAATGCATAATATGGCAT				
EBA175GA2/FF-S	GGTGTGTTATTTATTATATTGGTTAT TTTATTTTTTTTACAAGCC				
EBA175 GA2/FF- AS	GGCTTGTGAAAAAATAAAAATAAC CAATATAATAAATAACACACC				
EBA175-S ₃₄₄₃	TGAGGATCCAGGAAATGATACATCT GAAATGTGCGC			BamHI	
EBA175-AS	AGTCTCGAGTCATATCTTAAATTTA ATATCATT			XhoI	
HH1-S	GCTCAGAGATTGCATGCAAGC				
HH1-AS	CATGCATGTGCATGCAC				
175 ₃₂₅₉ -S	GGGAAGATGAGAGAACG				
175-AS _{stop})	TCATATCTTAAATTTAATATC				