Supplementary Material





Supplementary Figure S1. Related to Experimental Procedures. A crystal of AfuMep in the crystallization drop, and mounted in a cryoloop.

	2000		6.0	2000000000	
Fungalysin Thermolysin Vibriolysin Elastase Protealysin Aureolysin	40 TVDLNAFRLKS	LAKYVNATETVIE	APSSFAPFKP(QSYVEVATQHVKM VLNQQPTINNMVQ	SNSASLLSV
<i>Fungalysin</i> Fungalysin	$\begin{array}{ccc} \mathbf{TT} & \stackrel{\beta 3}{\longrightarrow} & \mathbf{TT} \\ & 90 \\ \\ \text{VDDHYVGDNGV} \end{array}$	β4 100 110 AHVHFRQTANGLD	β5 120 IDNADFNVNVC	TT $\beta 6$ 130 SKDGKVFSYGNSF	ر 140 YTGQIPSSA
Thermolysin Vibriolysin Elastase Protealysin Aureolysin	SPNQLIGLSVG	NELVVLKEFTSNN	GEVTRRYQQT	QQGIPVIGDTVSL	TFNNGMLKK
Fungalysin	α3 200 20 150	α4 <u>0000000000</u> 160 TALKCTTNTLOID	β7 170 170	$TT \xrightarrow{\beta 8} 180, 19$	0 CTUSDDKAK
Thermolysin Vibriolysin Elastase Protealysin Aureolysin	AHGAAVYNIDE	DLSDVSAKLTKKD	AILKGSKTGI	AKSVGLKKHNEQ	SRLAIWVDD
Fungalysin 2	β9 •• TT − 21	<u>β10</u> <u>ο</u> 22ο	β11 230	β12 2 4 0	β13 250 TT
Fungalysin Thermolysin Vibriolysin Elastase Protealysin Aureolysin	LVYFVKDDGTL QNKAHLVYEVS ARSVIPPYMLR	ALAWRVETDIDSN YVTYGKSPSRPYL RIIEHGSLPQRDC	WLLTYIDAKSC IIDANTGEVLI ALHTLNHV	GEEIHGVVDYVA <mark>E</mark> LSYDNLQHAN AAA	ADYQVYAWG ITGTST ATGPGGNLK EAGGPGG IGTGKGV
Fungalysin	η2 <u>β1</u> 260 1000	4 270 2 IKDDWDSVASEET	TT 80, 29	<u>β15</u> 90 300	TT T
Thermolysin Vibriolysin Elastase Protealysin Aureolysin	VGVGRGVLGDQ TGKYLYGTDFD NQKIGKYT	KNINTYSTYYL SLDVSQSGNTCSM YGSDYGPLIVNDR KTSTGG DININSIDGGFSL	QDNTR NNA CEMDDG EV EDLTH	GDGIFTYDAK NVRTINLN NVITVDMN IRDIYDAE QGKLSAYNFN	YRTTL.PG. GGTSG.S S.STDDSKT NSTQL.PG. DQTGQ.A
Fungalysin 3 Fungalysin	T 10 NNV D	TT 320	330 8880088	<u>0000000000</u> 340 VIDASI (01 PV)	x5 000000000 350
Thermolysin Vibriolysin Elastase Protealysin Aureolysin	.SLWA SAYS TPFR. .KQVRNEGQAS .TLIT	DADNQFFA FTCPE FAC N NEDENFVK	NTFKE]	. SYDAPAVDAHY INGAYSPLNDAHF /NGAYSPLNDAHF HDVAVDEAYD DDQRAGVDANY	YAGVTYDDYY FGNVIFNMY FGGVVFKLY YLGVTYDFF YAKQTYDYY
Fungalysin	٥٥ 36 0	тт 370	β16 380 [,] τη	β17 390 40	ρ β18
Fungalysin Thermolysin Vibriolysin Elastase Protealysin Aureolysin	YTLGFTEKAGN KNVHNRL NDWLGTA RDWFGTS WQAFKRN KNTFGRE	FEYNTNGQGGLGN SYDGNNAA .PLSFQ .PLTHK .SLDNQGLP .SYDNHGSPIVS	DYVILNAQDGS IRSSVHYS. .LQMRVHYS. .LYMKVHYG. .LTGSVHYG. .LTHVNHYGGC	SG.TINNANFATPP: .QGYNNAFWNG .SNYENAFWDG .RSVENAYWDG .KEYQNAFWNG .DNR <mark>NNA</mark> AWIG	DGQPGRMRM SEMVY SAMTF TAMLF QQMVF DKMIY



Supplementary Figure S2. Related to Figures 3, 5 and 6. AfuMep 31-634 aminoacid sequence from the crystal structure is aligned to that of bacterial M4 peptidases. AfuMep secondary structure elements are shown above the sequence alignment, helices as squiggles, strands as arrows, and labeled: α , α -helix; β , β -strand; η , 3_{10} helix; TT, β -turn; TTT, α -turn. Important aminoacid positions are highlighted by a color box or marked with a sign below, as follows. Grey, residues from loops that were not assigned in the crystal structure. Magenta, propeptide-catalytic domain boundary. Green, Ser/Pro-rich region. Yellow, cysteine that forms a disulfide bridge, the corresponding partner is

marked below with an oval sign (cyan/green). Red, white character, strictly identical and structurally equivalent residue. Blue frame, red character, similar and structurally equivalent residue. Triangles: magenta, calcium binding; black, Glu245-Ala246 cleavage point. Stars, zinc binding. Figure prepared with ESPript 1.6 [29].

Supplementary Table S1. Related to Figure 2. Prodomain-catalytic domain hydrogen bond interactions.

Prodomain-catalytic domain hydrogen bond interactions				
Catalytic domain	Prodomain	Donor-acceptor distance (Å)		
(residue ID/atom)	(residue ID/atom)			
Lys361 NZ	Val92 O	2.94		
Asn392 N δ 2	Glu245 Oɛ2	3.22		
Phe395 N	Ala244 O	2.78		
Phe395 O	Ala244 N	2.87		
Thr397 N	Tyr242 O	2.89		
Arg405 NH1	Asp218 Οδ2	2.89		
Arg405 NH2	Asp218 Οδ1	3.07		
Glu430 Oɛ1	Glu245 O	2.74		
Glu430 Oɛ2	Glu245 O	3.07		
His433 Nɛ2	Glu245 O	3.22		
Pro443 N	Asp89 Οδ2	3.28		
Ala444 N	Asp89 Οδ2	2.88		
Asn447 Nδ2	Tyr227 OH	2.90		
Asn450 O	Arg38 NH1	2.91		
Asn450 Οδ1	Asp241 O	2.99		
Asn450 N δ 2	Asp241 N	3.01		
Glu459 0ɛ1	Glu245 OXT ^a	2.96		
Glu459 Oɛ2	Glu245 OXT	3.22		
Asn517 O	Asn35 Nδ2	2.77		
His520 N _E 2	Glu245 OXT	2.85		
Lys565 NZ	Asp94 Οδ1	2.64		

Ala572 O	His99 Nδ1	3.28		
Leu573 O	Asn117 O δ 1	2.84		
Leu573 O	Asn119 N δ 2	3.02		
Gln582 Νε2	Ala43 O	2.80		
Asp585 Οδ2	Asn47 Nδ2	2.97		
Asp589 Οδ2	Tyr45OH	2.68		
Asp589 Οδ2	Ala48 N	2.92		
Tyr618 OH	Ser41 OG	3.27		
•••				

Notes

 $^{a}\text{Glu245}$ is the C-terminal residue of the propeptide, OXT refers the $\alpha\text{-}carboxylic$ acid oxygen atoms

 $^{\mathrm{b}}\textsc{Selected}$ interactions between O-N atoms, bond distance below 3.2 Å

Supplementary Table S2. Related to Figure 3. The Zn-binding site.

The Zn-binding site					
Protein residue ID	Atom and distance to Zn ²⁺ (Å)				
His429	Νε2	2.04			
His433	Νε2	1.99			
Glu459	Οε1	1.97			
Glu245	OXT ^a	1.96			
Notes					
^a Glu245 is the C-terminal residue of the					

propeptide, OXT indicates the α -carboxylic acid oxygen atom