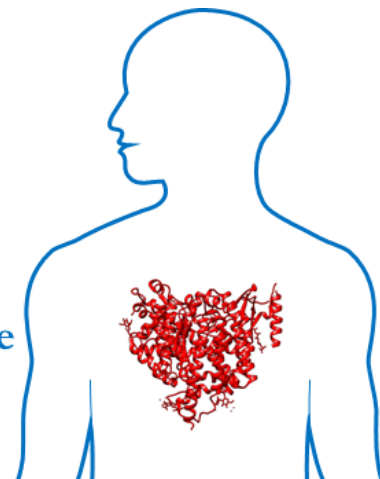




MRTBS 2024
I Międzynarodowa
Konferencja
Nowoczesne trendy badawcze w
naukach biomedycznych: holistyczne
ujęcie opieki zdrowotnej.
Opole, Polska, 17-19.04.2024



Metal ions – the eminence grise of antimicrobial peptides?

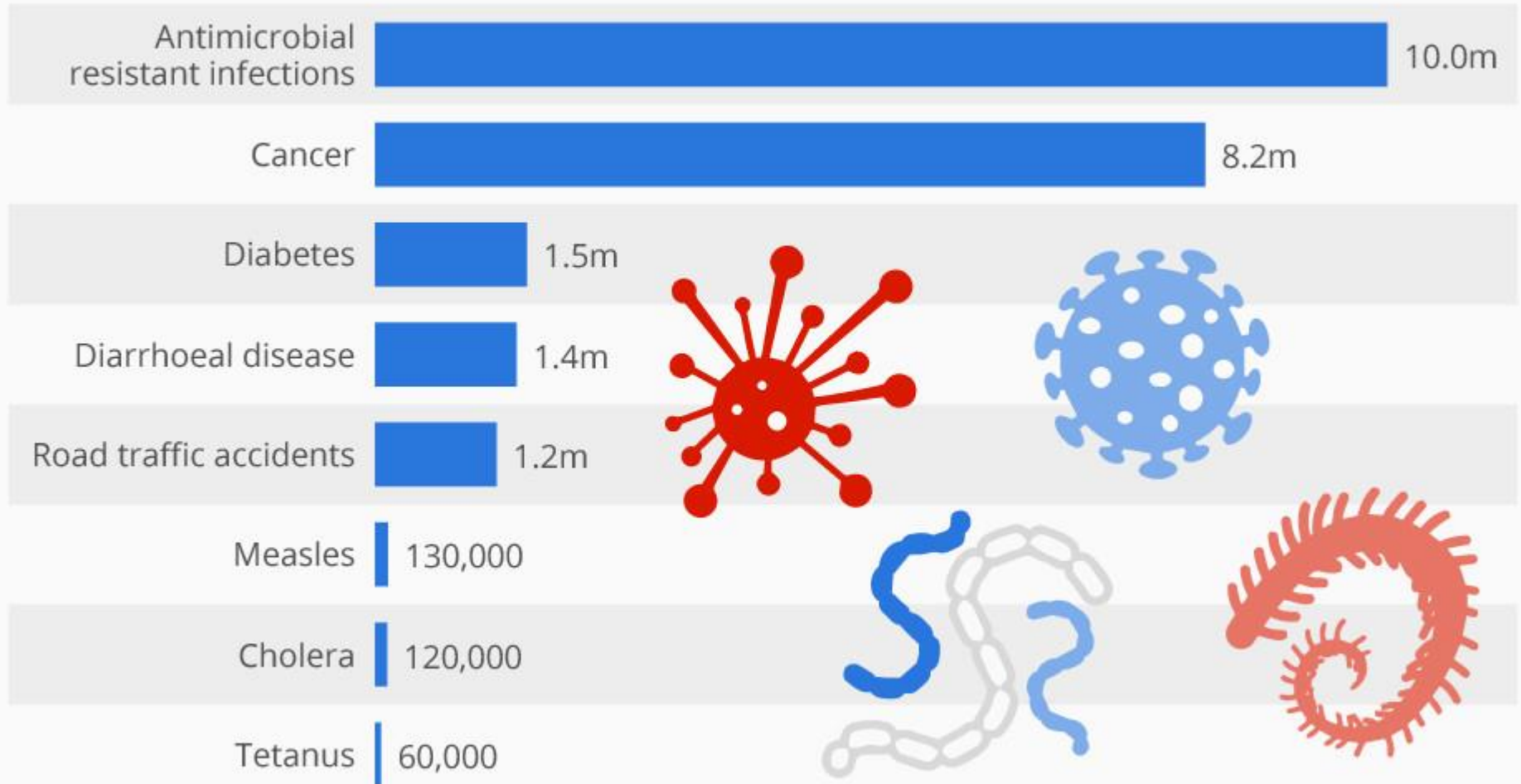
Magda Rowińska-Żyrek



Uniwersytet
Wrocławski

Deaths From Drug-Resistant Infections Set To Skyrocket

Deaths from antimicrobial resistant infections and other causes in 2050



@StatistaCharts

Source: Review on Antimicrobial Resistance

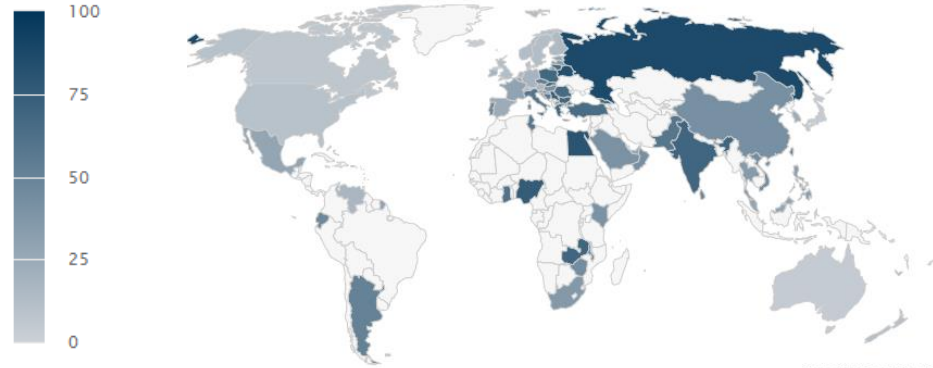
statista

K. pneumoniae

S. pneumoniae

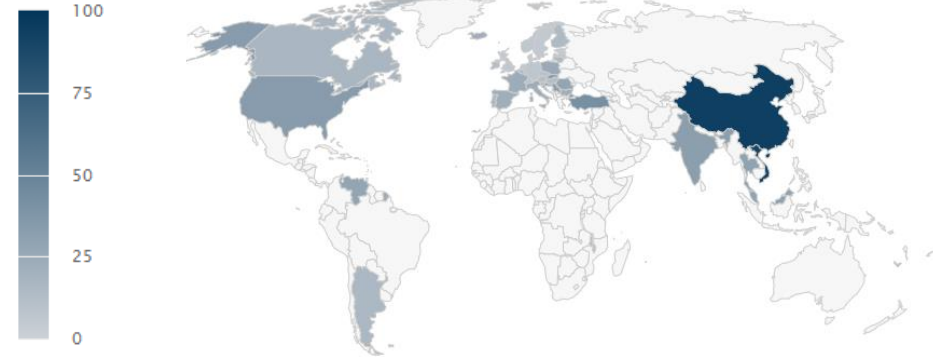
% Resistant (invasive isolates)

Resistance of *Klebsiella pneumoniae* to Fluoroquinolones



% Resistant (invasive isolates)

Resistance of *Streptococcus pneumoniae* to Macrolides



Fluoroquinolones

Macrolides

Antibiotic Resistance

Oxacillin (MRSA)

Amoxicillin-clavulanate

% Resistant (invasive isolates)

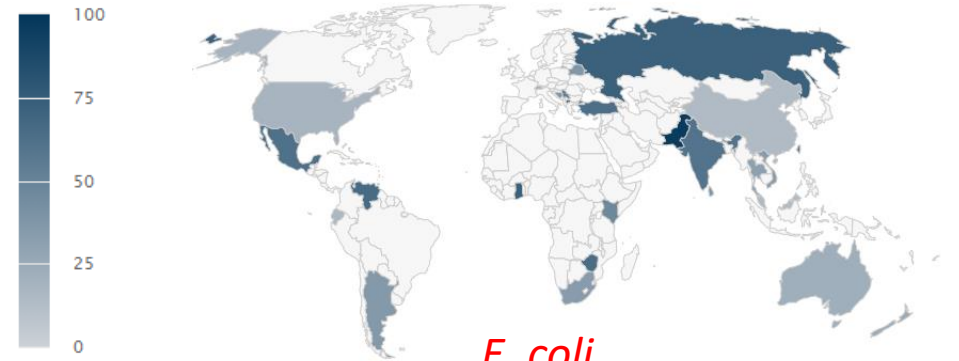
Resistance of *Staphylococcus aureus* to Oxacillin (MRSA)



S. aureus

% Resistant (invasive isolates)

Resistance of *Escherichia coli* to Amoxicillin-clavulanate



E. coli

AMPs (AntiMicrobial Peptides):

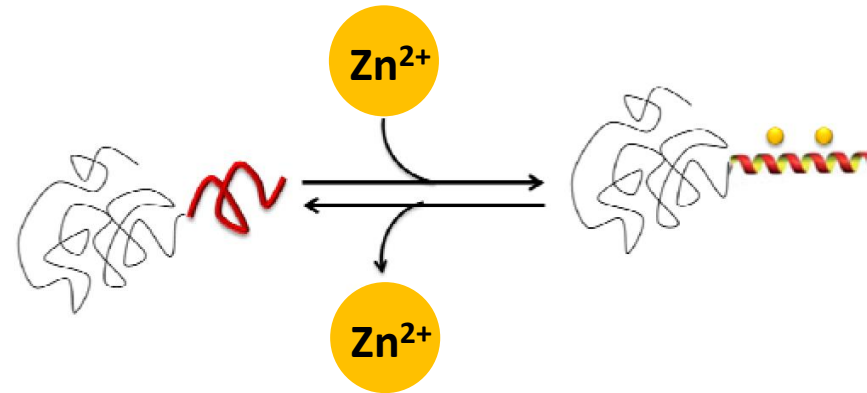
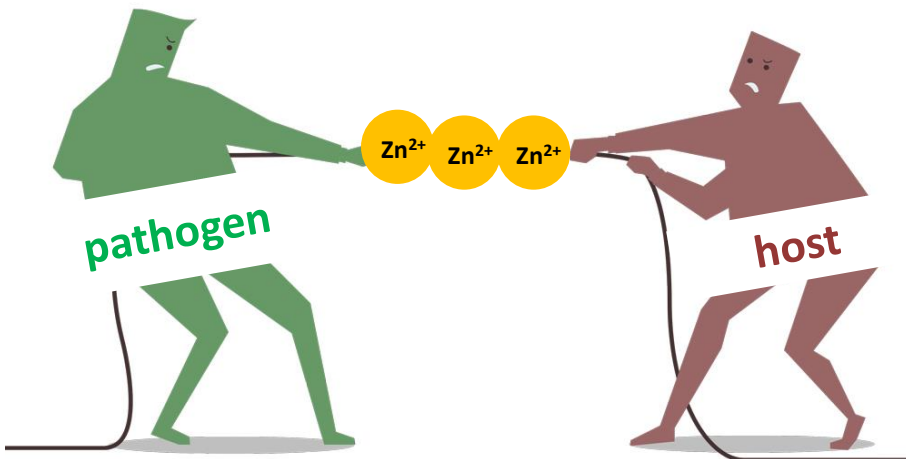
- Short, 7-100 amino acid peptides, active against bacteria, fungi, viruses and even cancer cells
- AMP mode of action: (i) disruption of lipid bilayers; (ii) inhibition of inner-cell processes; (iii) sequestering metal ions (taking part in 'nutritional immunity')

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Impact of metal ions on AMP activity:

- AMPs sequester metal ions, so that microbes cannot get enough of them for their survival and virulence
- AMPs need the metal to boost their antimicrobial efficiency, affecting the charge/structure of the peptide

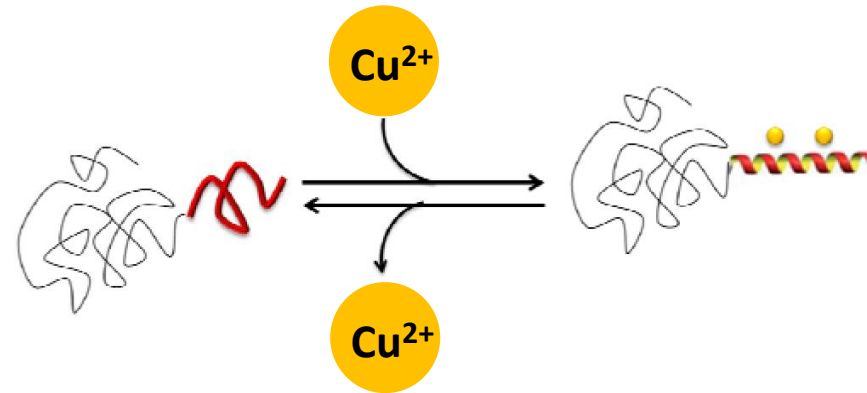
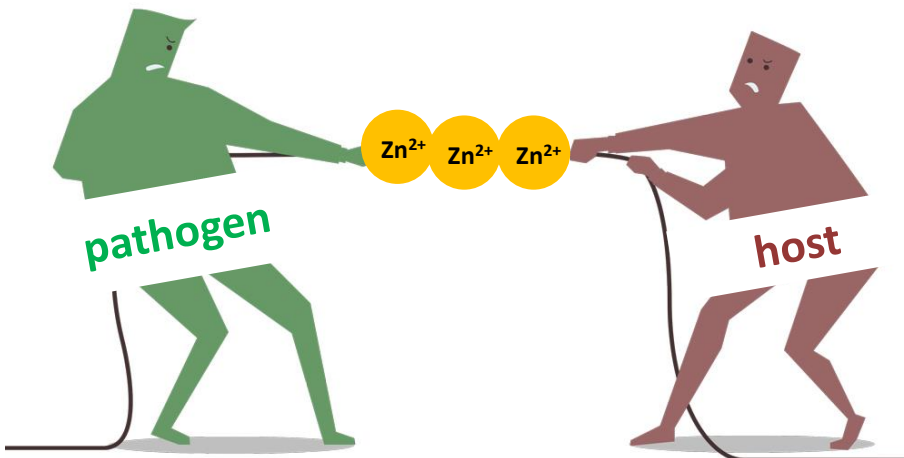


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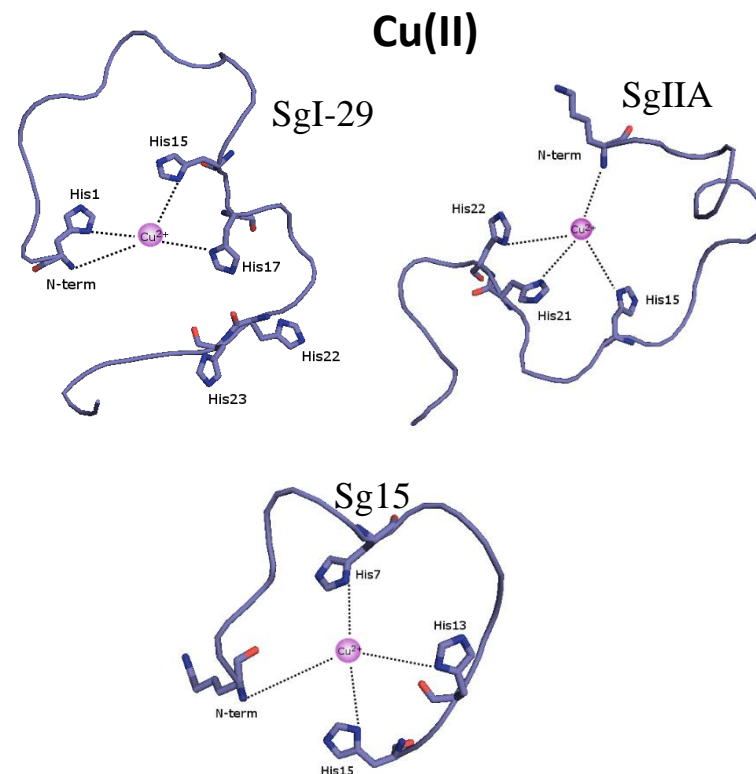
- AMPs sequester metal ions, so that microbes cannot get enough of them for their survival and virulence
- AMPs need the metal to boost their antimicrobial efficiency, affecting the charge/structure of the peptide



AMPs enhanced by Zn(II) and Cu(II):

Semenogelins

SgI	1	MKPNIIFVLSLLLLILEKQAAMVGQKGGSKGRLPSEFSQFPHGQKGQHYSGQKGGKQQTESK	60
SgII	1	MKSIIIFVLSLLLLILEKQAAMVGQKGGSKGQLPSGSSQFPHGQKGQHYFGQKDDQQTHTSK	60
SgI	61	GSFSIQTYHYVDANDHDQSRKQQYDLNALHKTTKSRHLGGSQLLNKQEGRDHDKSK	120
SgII	61	GSFSIQTYHYVDINDHDWTRKQQYDLNALHKATKSKQHLGGSQLLNKQEGRDHDKSK	120
SgI	121	GHFHRVVIHHKGGKAHRGTQNPSSQDQGNSSPSGKGISSQYSNTEERLWVHGLSKEQTSVSG	180
SgII	121	GHFHMIVVIHHKGGQAHHGTQNPSSQDQGNSSPSGKGLSSQCSNTEERLWVHGLSKEQASASG	180
SgI	181	AQKGRKQGGSSSYVLQTEELVANKQRETKNNSHQKNGHYQNVVVEEHSKQVQTSLCP	240
SgII	181	AQKGRKQGGSSSYVLQTEELVANKQRETKNNSHQKNGHYQNVVVEEHSKQVQTSLCP	240
SgI	241	AHQDKLQHGSKDIFSTQDELLVYNKNQHQTKNLNQDQQHGRKANKISYQSSSTEERLLHY	300
SgII	241	AHQDRLQHGPKDIFTTQDELLVYNKNQHQTKNLSQDQEHGRKAHKISYQSSRTEERQLLH	300
SgI	301	GENGVQKDVSSSIYS-----	316
SgII	301	GEKSVQKDVSKGISIQTEEKIHGKSQNQVTIHSQDQEHGKKNKISYQSSSTEERLLNC	360
SgI	316	-----	316
SgII	361	GEKGIQKGVSKGISIQTEEQIHGKSQNQVRIPSQAQEQYGHKKNKISYQSSSTEERLLNS	420
SgI	317	-----QTEEKAQKGSQKQITIPSQEQEHSQKANKISYQSSSTEERLLHY	360
SgII	421	GEKDVQKGVSKGISIQTEEKIHGKSQNQVRIPSQDQEHGKKNKMSYQSSSTEERLLNY	480
SgI	361	GENGVQKDVSSSIYSQTEKLVAGKSIQAPNPKQEPWHGENAKGESGQSTNREQDLLSH	420
SgII	481	GGKSTQKDVSSSISFQIEKLVGKSIQTPNPNQDQWSGQNAKGGKSGQSADSKQDLLSH	540
SgI	421	EQKGRHQHGSHGGLDIVIIIEQEDDSRHLAQLNNDRNPLFT	462
SgII	541	EQKGRYKQESSESHNIVITEHEVAQDDHLTQQYNEDRNPIST	582



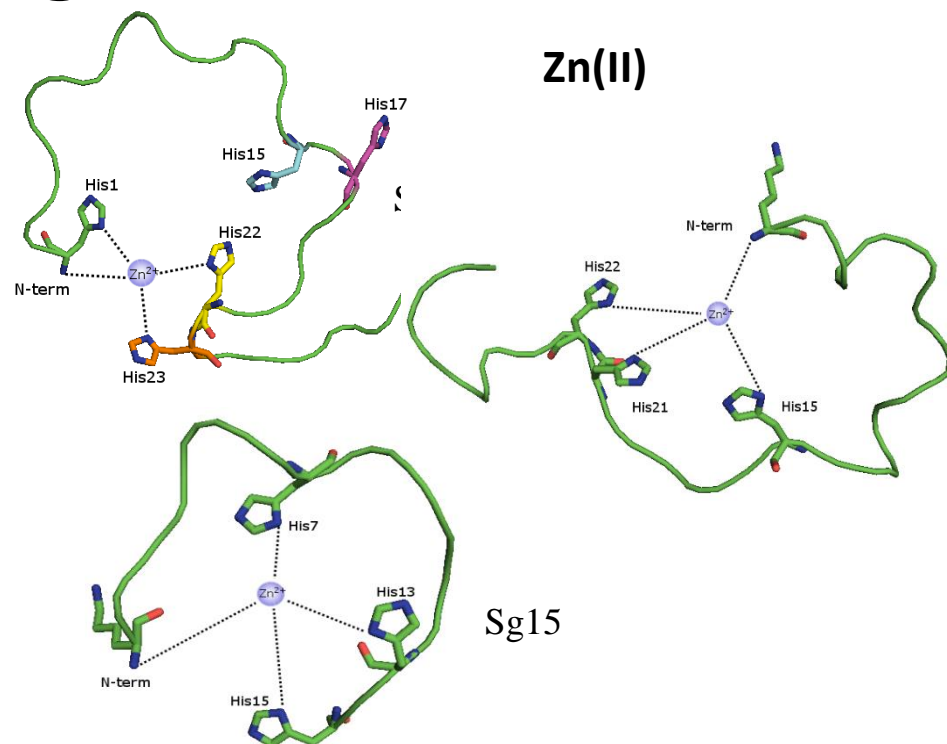
Antimicrobial fragments of semenogelins from the human semen (peptides: SgIIA, SgI-29 and their common 15-aa fragment, Sg-15) bind Zn(II) and Cu(II) ions via a $[NH_2, 3N_{im}]$ donor set at physiological pH

SgI-29	HNKQEGRDHDKSKGHFHRVVIHHKGGKAH
SgIIA	KQEGRDHDKSKGHFHMIVVIHHKGGQAHHG
Sg-15	KQEGRDHDKSKGHFH

AMPs enhanced by Zn(II) and Cu(II):

Semenogelins

Sgl	1	MKPNIIFVLSLLLLILEKQAAMVGMQKGGSKGRLPSEFSQFPHGQKGQHYSGQKQKQQTESK	60
SgII	1	MKSIIIFVLSLLLLILEKQAAMVGMQKGGSKGQLPSGSSQFPHGQKGQHYFGQKQDQQTHTKSK	60
Sgl	61	GSFSIQTYHYVDANDHDQSRKQQYDLNALHKTTSQRHLGGSQLLHNKQEGRDHDKSK	120
SgII	61	GSFSIQTYHYVDINDHDWTRKQQYDLNALHKATKSKQHLGGSQLLNYKQEGRDHDKSK	120
Sgl	121	GHFHRVVIIHHKGGKAHRGTQNPSQDQGNPSGKGISSQYSNTEERLWVHGLSKEQTSVSG	180
SgII	121	GHFHMIVIIHHKGGQAHHGTQNPSQDQGNPSGKGLSSQCSNTEERLWVHGLSKEQASASG	180
Sgl	181	AQKGRKQGGSSSYVLQTEELVANKQQRRETKNSHQKNGHYQNVVVEEHSKLVQTSLCP	240
SgII	181	AQKGRKQGGSSSYVLQTEELVNVKQQRRETKNSHQKNGHYQNVVVDVREEHSSKLQTSLHP	240
Sgl	241	AHQDKLQHGSKDIFSTQDELLVYNKNQHQTKNLNQDQQHGRKANKISYQSSSTEERRLHY	300
SgII	241	AHQDRLQHGPKDIFTTQDELLVYNKNQHQTKNLSQDQEHGRKAHKISYPSRSTEREQLLH	300
Sgl	301	GENGVQKDVSSSIYS-----	316
SgII	301	GEKSVQKDVSKGSISIQTEEKIHGKSQNQVTIHSQDQEHGHKENKISYQSSSTEERHLNC	360
Sgl	316	-----	316
SgII	361	GEKGIQKGVSKGSISIQTEEQIHGKSQNQVRIPSQAQEQYGHKENKISYQSSSTEERRLNS	420
Sgl	317	-----QTEEKAQKKSQKQITIPSQEQEHSQKANKISYQSSSTEERRLHY	360
SgII	421	GEKDVQKGVSKGSISIQTEEKIHGKSQNQVTIPSQDQEHGHKENKMSYQSSSTEERRLNY	480
Sgl	361	GENGVQKDVSSQRSIYSQTEKLVAGKSQIQAPNPKQEPWHGENAKGESGQSTNREQDLLSH	420
SgII	481	GGKSTQKDVSSSISFQIEKLVGKSSQIQTPNPNQDQWSGQNAKGSQGSADSKQDLLSH	540
Sgl	421	EQKGRHQHGSHGGLDIVIIIEQEDDSDRHLAQLNDRNPLFT	462
SgII	541	EQKGRYKQESSESHNIVITEHEVAQDDHLTQQYNEDRNP IST	582

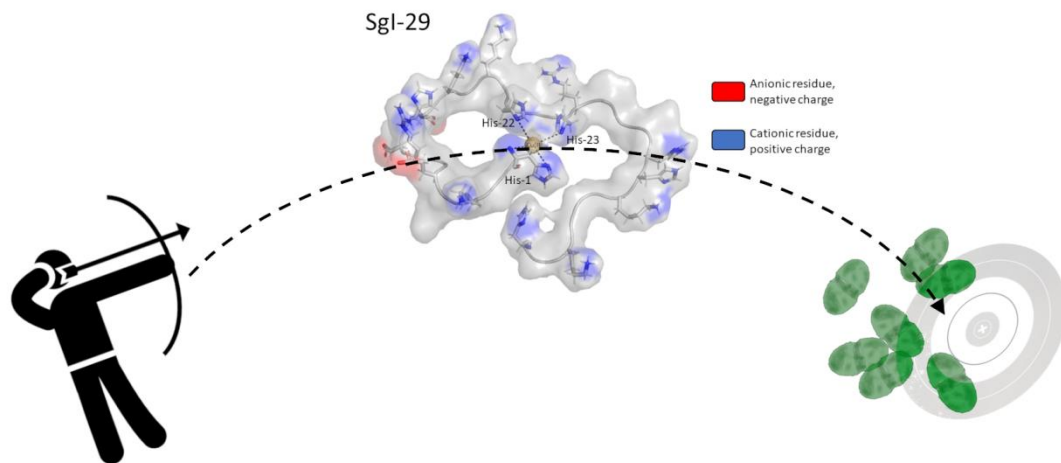


Antimicrobial fragments of semenogelins from the human semen (peptides: SgIIA, Sgl-29 and their common 15-aa fragment, Sg-15) bind Zn(II) and Cu(II) ions via a $[NH_2, 3N_{im}]$ donor set at physiological pH

Sgl-29	HNKQEGRDHDKSKGHFHRVVIHHKGGKAH
SgIIA	KQEGRDHDKSKGHFHMIVIIHHKGGQAHHG
Sg-15	KQEGRDHDKSKGHFH

AMPs enhanced by Zn(II) and Cu(II):

Semenogelins



<i>Enterococcus faecalis</i>	
MIC ($\mu\text{g/mL}$)	
Sg-15	n/s
Sg-15-Cu(II)	256
Sg-15-Zn(II)	n/s
SgI-29	256
SgI-29-Cu(II)	256
SgI-29-Zn(II)	256
SgIIA	n/s
SgIIA-Cu(II)	256
SgIIA-Zn(II)	256

Zn(II) and Cu(II) binding enhances semenogelins' antimicrobial activity, most probably due to **increase of the cationic character of the complexes**, that enable their interaction with negatively charged bacterial membranes.

In the case of the two native semenogelin fragment metal complexes, **the strong local positive charge in the metal-bound HH motif correlates well with their antimicrobial activity.**

SgI-29 **HNKQEGRDHDKSKGHFHRVVIHHKGGKAH**

SgIIA **KQEGRDHDKSKGHFMIVIHKGGQAHHG**

Sg-15 **KQEGRDHDKSKGHF**

PvHCt – an antimicrobial shrimp peptide

Peptide sequence:

FEDLPNFGHIQVKVFNHGEHIHH

Mass spectrometry:

Stoichiometry of the Zn(II) and Cu(II)-PvHCt complexes is 1:1

Potentiometric and spectroscopic studies:

Suggested modes of coordination (pH 7.4)

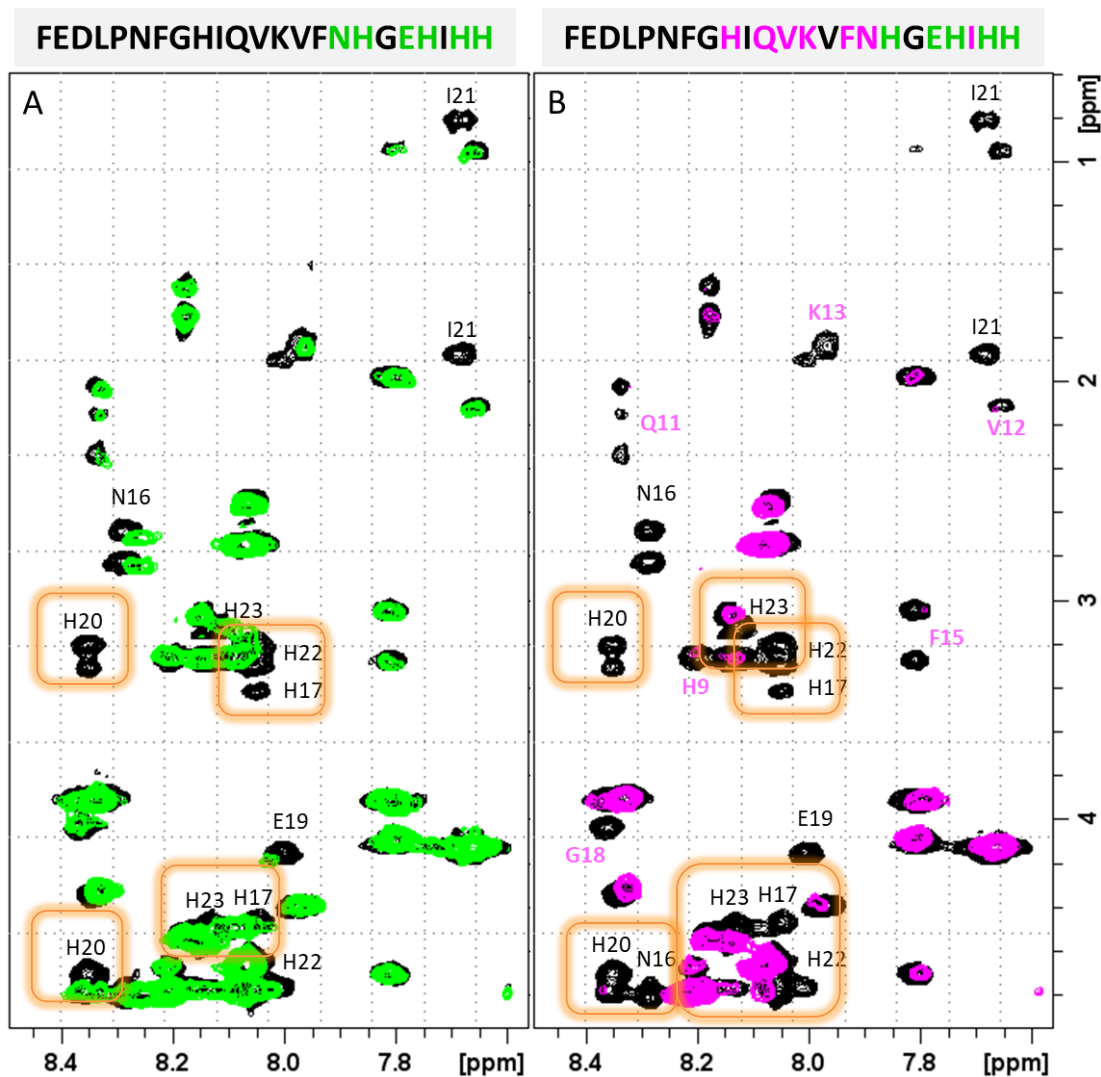
Zn(II) complexes: 3 N_{im} / 4 N_{im}

Cu(II) complexes: 2 N⁻, 1 N_{im}



Whiteleg shrimp
(*Litopenaeus vannamei*)

PvHCt: metal binding sites are indicated by NMR

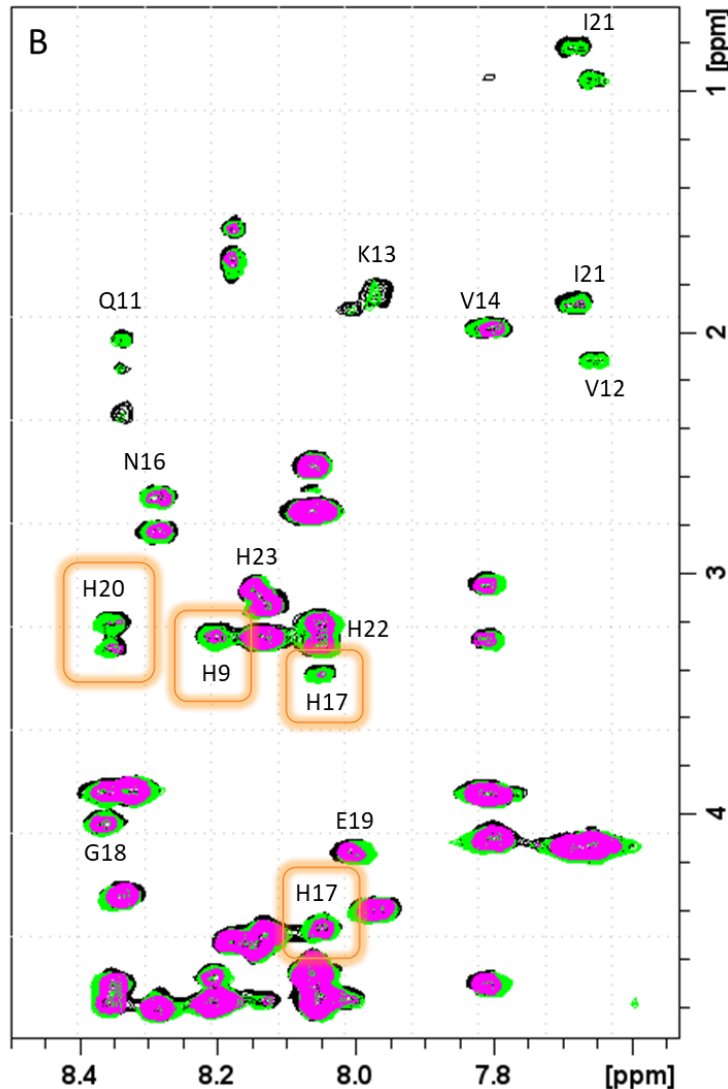


Zn(II) complexes:

- no metal addition
- 0.2 eq Zn(II)
- 0.6 eq Zn(II)

Changes for H17, H20, H22, H23 residues

PvHCt: metal binding sites are indicated by NMR



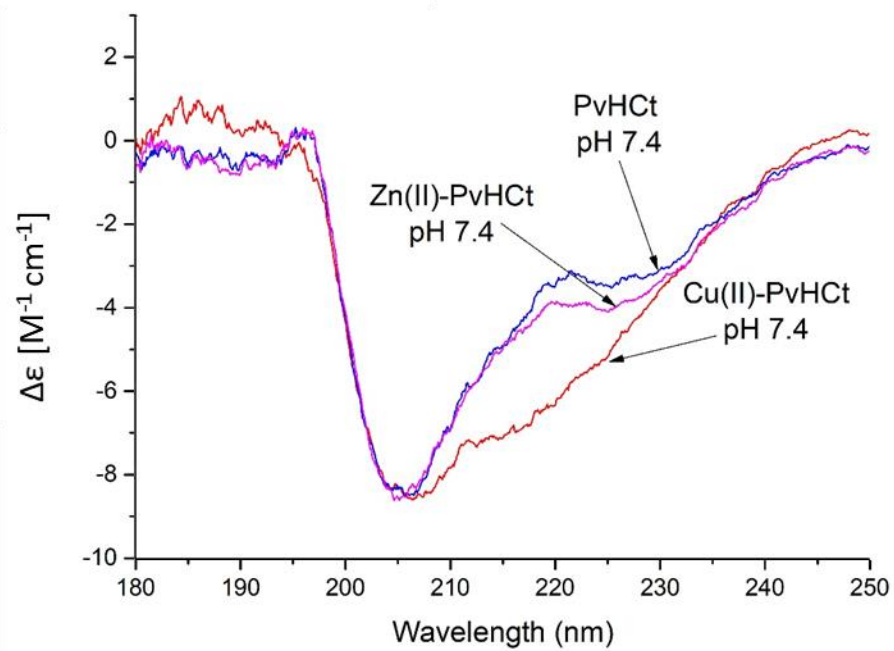
Cu(II) complexes:

- no metal addition
- 0.1 eq Cu(II)
- 0.2 eq Cu(II)

Changes for H9, H17, H20 residues

FEDLPNFGHIQVKVFNHGEIHH

PvHCt: Cu(II) induces a structural change



Whiteleg shrimp
(*Litopenaeus vannamei*)

PvHCt: Cu(II) triggers antimicrobial activity

	<i>Escherichia coli</i> ATCC 25922	MRSA ATCC 43300	<i>Enterococcus faecalis</i> ATCC 29212
	MIC ₅₀ [µg/mL]	MIC ₅₀ [µg/mL]	MIC ₅₀ [µg/mL]
PvHCt	n/s	n/s	n/s
Zn(II)-PvHCt	n/s	32	512
Cu(II)-PvHCt	16	16	16



Whiteleg shrimp
(*Litopenaeus vannamei*)

PvHCt: Cu(II) triggers antimicrobial activity

	<i>Escherichia coli</i> ATCC 25922	MRSA ATCC 43300	<i>Enterococcus faecalis</i> ATCC 29212
	MIC ₅₀ [µg/mL]	MIC ₅₀ [µg/mL]	MIC ₅₀ [µg/mL]
PvHCt	n/s	n/s	n/s
Zn(II)-PvHCt	n/s	32	512
Cu(II)-PvHCt	16	16	16



Whiteleg shrimp
(*Litopenaeus vannamei*)

- PvHCt shows antimicrobial activity only in presence of metal ions
- Cu(II) drastically increases the biological activity of PvHCt peptide

Clavanins

Clavanin A:

VFQFLGKIIHHVGNFV**H**GFShVF-COOH

Clavanin B:

VFQFLGRIIHHVGNFV**H**GFShVF-COOH

Clavanin C:

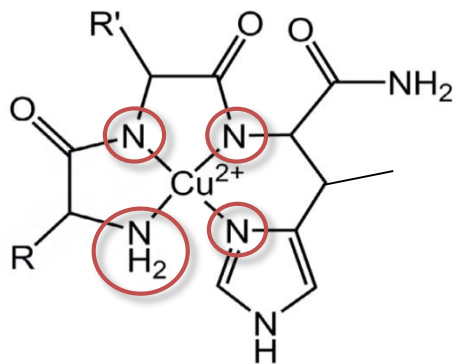
VFHLLGKIIHHVGNFV**Y**GFShVF-COOH

Clavanin D:

AFKLLGRIIHHVGNFV**Y**GFShVF-COOH

Clavanin E:

LFKLLGKIIHHVGNFV**H**GFShVF-COOH



Mass spectrometry:

Stoichiometry of the Zn(II) and Cu(II)-clavanin complexes is 1:1

Potentiometric titrations, NMR, UV-Vis and CD spectroscopy :

Suggested coordination modes

Zn(II) complexes (physiological pH): 3 N_{im}

Cu(II) complexes (physiological pH): 3 N_{im}, 1 N⁻

Cu(II) complexes (higher pH): 1 N_{im}, 3 N⁻

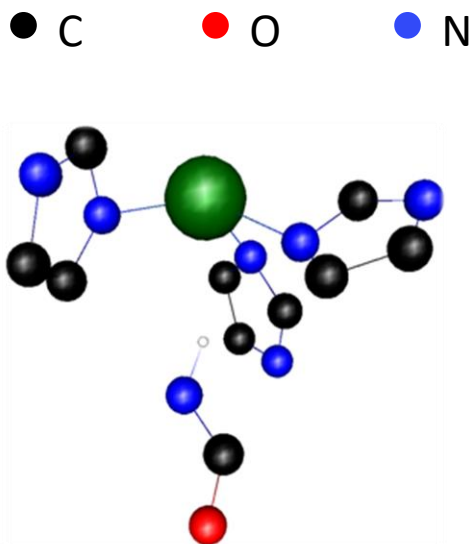
Cu(II) complexes of ClavC: NH₂, 2 N⁻, 1 N_{im}

Clavanins: antimicrobial efficiency at physiological pH

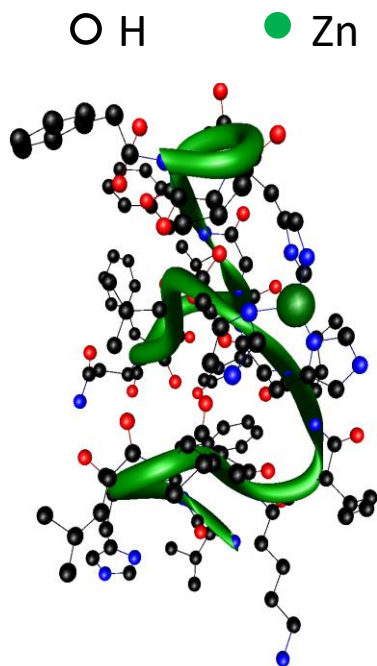
Strain	<i>Escherichia coli</i> (-) ATCC 25922	<i>Enterococcus faecalis</i> (+) ATCC 29212	<i>Staphylococcus aureus</i> (+) ATCC 43300	<i>Candida albicans</i> ATCC 10231
	MIC (µg/mL)	MIC (µg/mL)	MIC (µg/mL)	MIC (µg/mL)
Clavanin A	n/d	256	n/d	128
Cu(II)-Clavanin A	n/d	n/d	n/d	128
Zn(II)-Clavanin A	256	256	n/d	64
Clavanin B	256	256	n/d	64
Cu(II)-Clavanin B	256	8	n/d	64
Zn(II)-Clavanin B	n/d	8	n/d	128
Clavanin C	n/d	128	128	64
Cu(II)-Clavanin C	128	256	128	64
Zn(II)-Clavanin C	16	64	16	16
Clavanin D	64	128	128	16
Cu(II)-Clavanin D	256	128	128	32
Zn(II)-Clavanin D	256	128	128	64
Clavanin E	n/d	n/d	n/d	32
Cu(II)-Clavanin E	256	n/d	n/d	32
Zn(II)-Clavanin E	n/d	n/d	64	16

Fig 10) Clavanin C The highest activity of the fibriolecy clavanin family is observed, no metal-enhanced trend

Clavanins: DFT calculations, Zn(II), pH 7.4



Zn(II)-clavanin C
(structure of the
binding site)



Zn(II)-clavanin C

Clavanin A:
VFQFLGKIIHHVGNFV**H**GFSSHVF-COOH

Clavanin B:
VFQFLGR**II**HHVGNFV**H**GFSSHVF-COOH

Clavanin C:
VFHLLG**K**IIHHVGNFV**Y**GFSSHVF-COOH

Clavanin D:
AFKLLG**R**IIHHVGNFV**Y**GFSSHVF-COOH

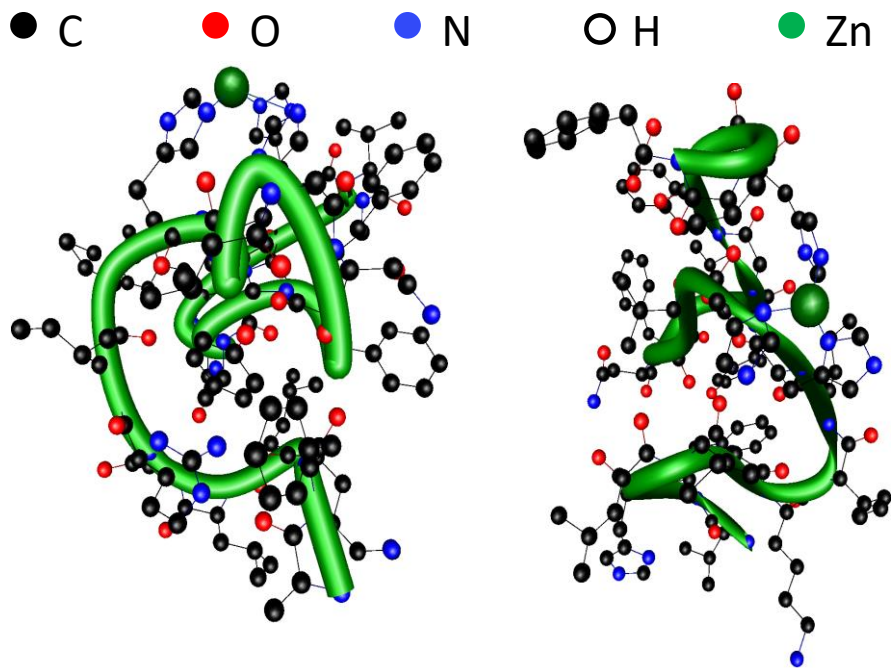
Clavanin E:
LFKLLG**K**IIHHVGNFV**H**GFSSHVF-COOH

Zn(II)-clavanin A, B, E: His10, His11 and His17 imidazoles

Zn(II)-clavanin C, D: His10, His11 and His21 imidazoles

The O=C-N-H fragment is directly below the Zn(II) ion and aims its hydrogen atom at the positively charged metal cation, pushing it out of its binding pocket = **the longest** (and most labile) **metal-ligand bonds** = easy metal dissociation

Clavanins: DFT calculations, Zn(II), pH 7.4



Zn(II)-clavanin D

Zn(II)-clavanin C

Pushing the metal out of its binding pocket was observed only for Zn(II)-ClavC. The different organization of the binding pocket is most likely due to the **pre-folding of the clavanin C peptide** before the addition of Zn(II) ions.

Clavanin A:
VFQFLGKIIHHVGNFVHGFSHFV-COOH

Clavanin B:
VFQFLGRIIHHVGNFVHGFSHFV-COOH

Clavanin C:
VFHLLGKIIHHVGNFVYGFSHVF-COOH

Clavanin D:
AFKLLGRIIHHVGNFVYGFSHVF-COOH

Clavanin E:
LFKLLGKIIHHVGNFVHGFSHFV-COOH

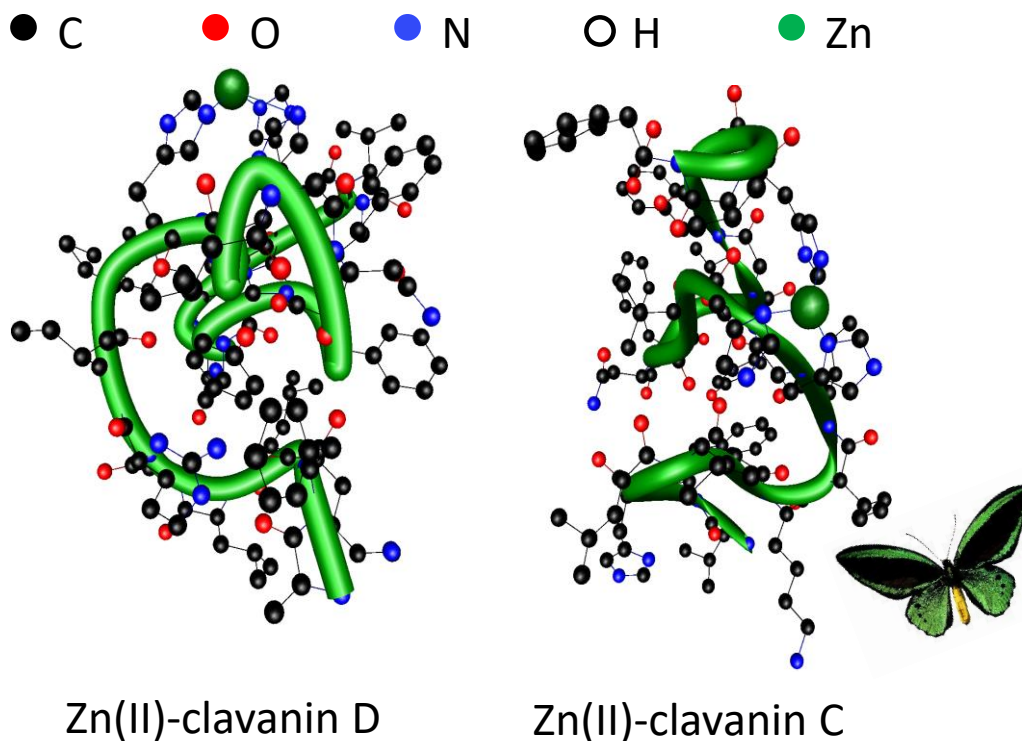
Zn(II)-clavanin A, B, E: His10, His11 and His17 imidazoles

Zn(II)-clavanin C, D: His10, His11 and His21 imidazoles

	ClavA	ClavB	ClavC	ClavD	ClavE
His10	2.106	2.107	2.170	2.164	2.192
His11	2.017	2.008	2.196	2.193	2.070
His17	2.038	2.016			2.054
His21			2.199	2.030	

Metal – ligand distances (in angstroms) for clavanin A, B, C, D, E and Zn(II) complexes

Clavanins: DFT calculations, Zn(II), pH 7.4



Clavanin A:
VFQFLGKIIHHVGNFVHGFSHFV-COOH

Clavanin B:
VFQFLGRIIHHVGNFVHGFSHFV-COOH

Clavanin C:
VFHLLGKIIHHVGNFVYGFSHVF-COOH

Clavanin D:
AFKLLGRIIHHVGNFVYGFSHVF-COOH

Clavanin E:
LFKLLGKIIHHVGNFVHGFSHFV-COOH

Zn(II)-clavanin A, B, E: His10, His11 and His17 imidazoles

Zn(II)-clavanin C, D: His10, His11 and His21 imidazoles

Pushing the metal out of its binding pocket was observed only for Zn(II)-ClavC. The different organization of the binding pocket is most likely due to the **pre-folding of the clavanin C peptide** before the addition of Zn(II) ions.

	ClavA	ClavB	ClavC	ClavD	ClavE
His10	2.106	2.107	2.170	2.164	2.192
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His21			2.199	2.030	

Metal – ligand distances (in angstroms) for clavanin A, B, C, D, E and Zn(II) complexes

Amylin and pramlintide

- Amylin (IAPP, *Islet Amyloid Polypeptide*) co-secreted with insulin from beta Langerhans cells of the pancreas
- Amyloid islets are present in 95% of type II diabetes patients
- In pramlintide, a non-fibrillating amylin analogue used in a T2D treatment, in which, as in the case of rat amylin, Ala25, Ser28 and Ser29 were substituted by proline residues, what resulted in the reduction of fibrilization

Biol. Chem., Vol. 393, pp. 641–646, July 2012 • Copyright © by Walter de Gruyter • Berlin • Boston. DOI 10.1515/hsz-2012-0107

Short Communication

Antimicrobial activity of human islet amyloid polypeptides: an insight into amyloid peptides' connection with antimicrobial peptides

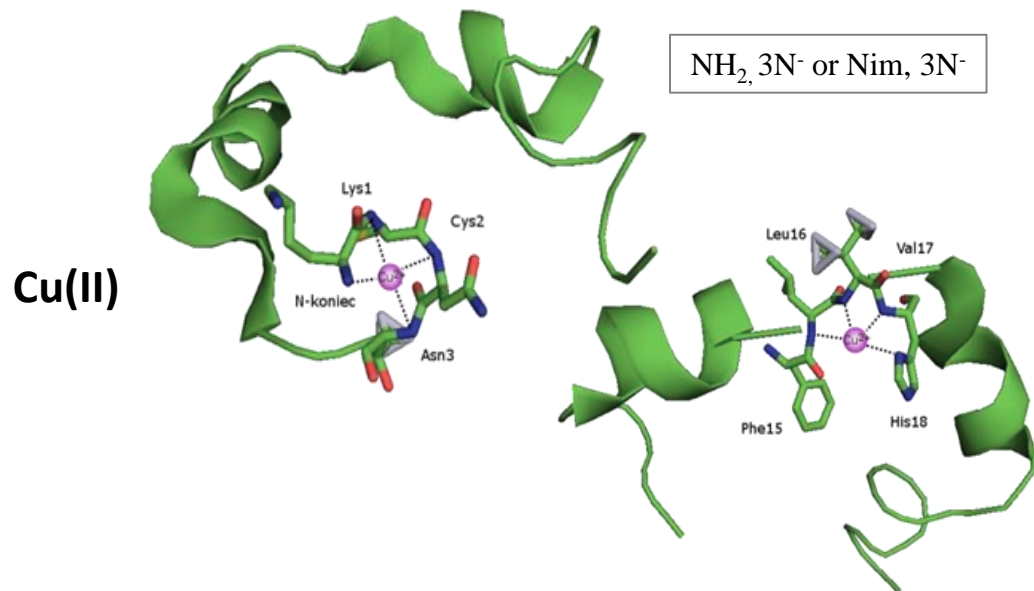
Effective against:

- *E. coli*
- *S. aureus*

Human amylin:	KCNTATCATQRLANFLVHSSN FGAIL SSTNVGSNTY-NH ₂
Rat amylin:	KCNTATCATQRLANFLVRSSN LG PVL P PTNVGSNTY-NH ₂
Pramlintide:	KCNTATCATQRLANFLVHSSN FG P IL P P PTNVGSNTY-NH ₂

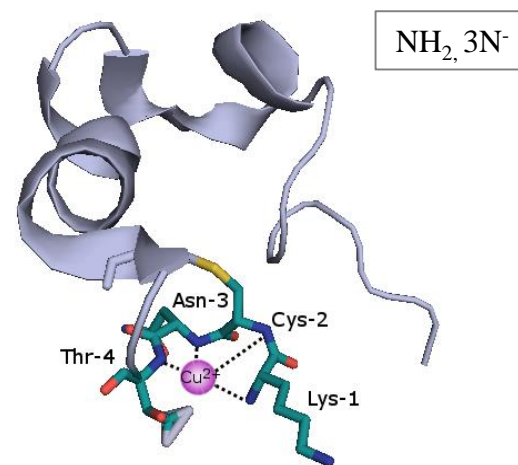
Pramlintide

KCNTATCATQRLANFLVHSSNNFGPILPPTNVGSNTY-NH₂



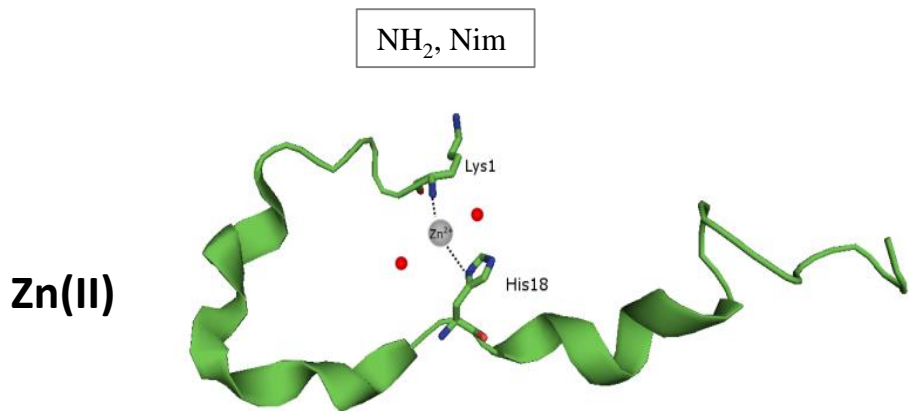
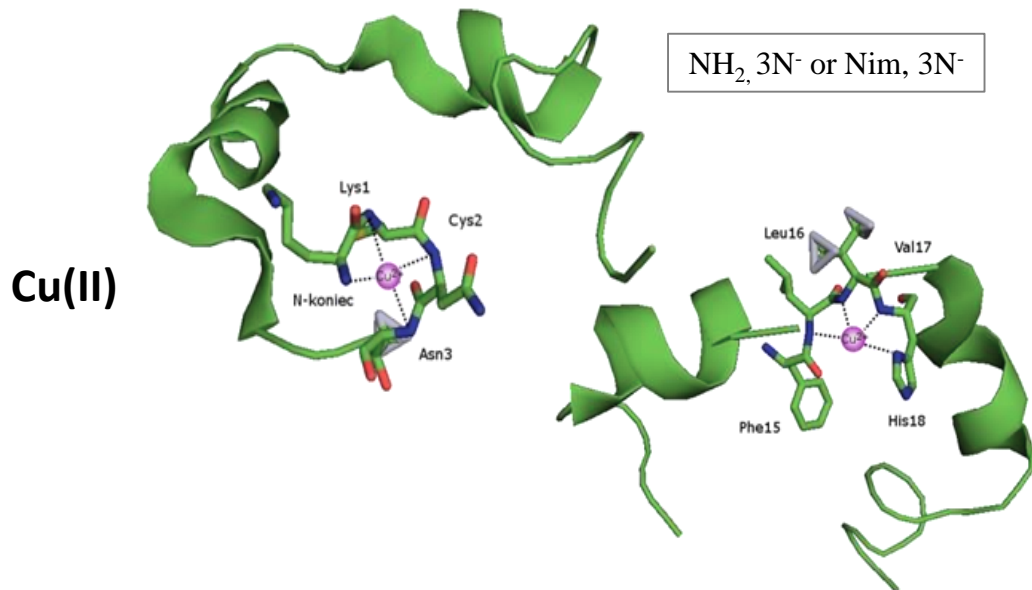
Rat amylin

KCNTATCATQRLANFLVRSSNNLGPVLPPTNVGSNTY-NH₂



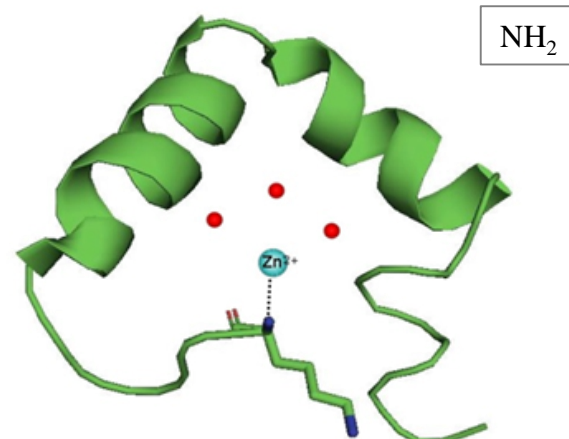
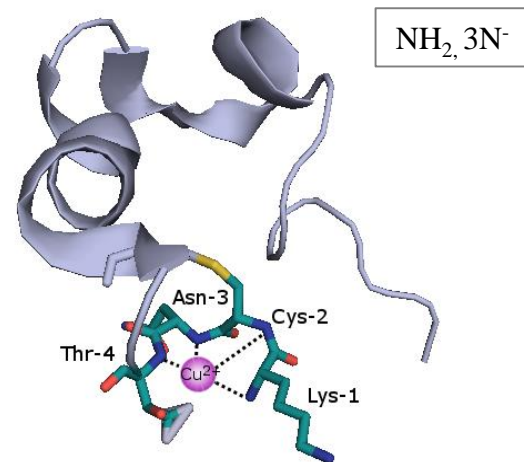
Pramlintide

KCNTATCATQRLANFLVHSSNNFGPILPPTNVGSNTY-NH₂



Rat amylin

KCNTATCATQRLANFLVRSSNNLGPVLPPTNVGSNTY-NH₂



Dudek Dorota, Alghrably Mawadda, Emwas Abdul-Hamid, Jarekko Łukasz, Jarekko Mariusz, Rowińska-Żyrek Magdalena, Copper(II) and amylin analogues: a complicated relationship, *Inorganic Chemistry*, 2020, 59, 2527-2535

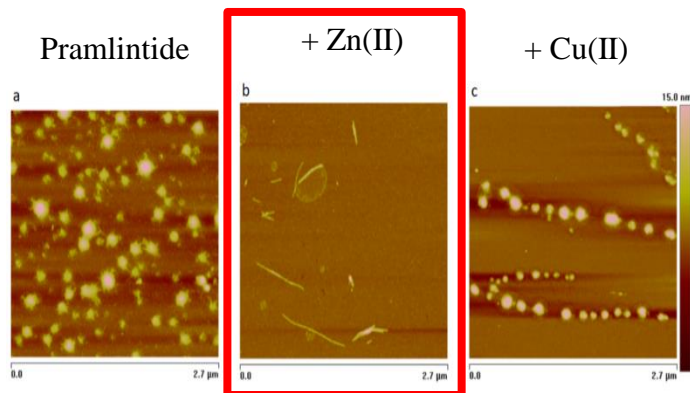
Dudek Dorota, Dzień Emilia, Mikołajczyk Aleksandra, Matera-Witkiewicz Agnieszka, Hajda Agata, Olesiak-Bańska Joanna, Rowińska-Żyrek Magdalena, Zn(II) binding to pramlintide results in a structural kink, fibril formation and antifungal activity, *Scientific Reports*, 2022, 12, 20543/1-20543/8

Antimicrobial activity

Strain	<i>Escherichia coli</i> ATCC 25922	<i>Staphylococcus aureus</i> ATCC 43300	<i>Candida albicans</i> ATCC 10231
	MIC (ug/mL)	MIC (ug/mL)	MIC (ug/mL)
rat amylin	n/d	n/d	n/d
Cu(II)-rat amylin	n/d	n/d	n/d
Zn(II)-rat amylin	n/d	n/d	n/d
pramlintide	n/d	n/d	n/d
Cu(II)-pramlintide	n/d	n/d	n/d
Zn(II)-pramlintide	n/d	n/d	256
Ac-pramlintide	n/d	n/d	n/d
Cu(II)-Ac-pramlintide	n/d	n/d	n/d
Zn(II)-Ac-pramlintide	n/d	n/d	n/d

Pramlintide forms amyloid fibrils in the presence of Zn(II)

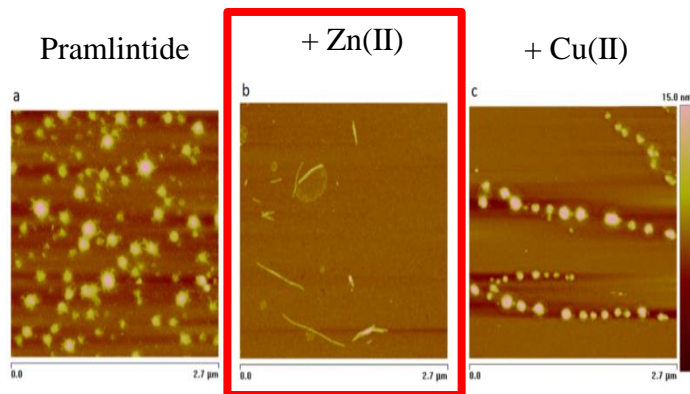
24h



Human amylin:	KCNTATCATQRLANFLVHSSNFGAILSSSTNVGSNTY-NH ₂
Rat amylin:	KCNTATCATQRLANFLVRSSNLLGPVLPPTNVGSNTY-NH ₂
Pramlintide:	KCNTATCATQRLANFLVHSSNFGPILPPTNVGSNTY-NH ₂

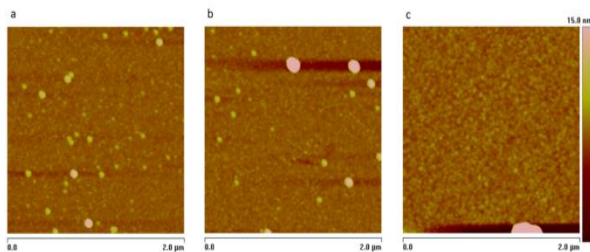
Pramlintide forms amyloid fibrils in the presence of Zn(II)

24h

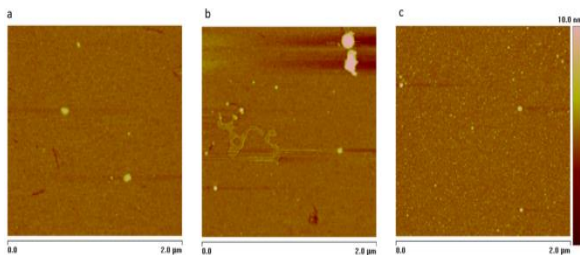


Human amylin:	KCNTATCATQRLANFLVHSSNFGAILSSTNVGSNTY-NH ₂
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Pramlintide:	KCNTATCATQRLANFLVHSSNFGPILPPTNVGSNTY-NH ₂

Ac -Pramlintide + Zn(II) + Cu(II)

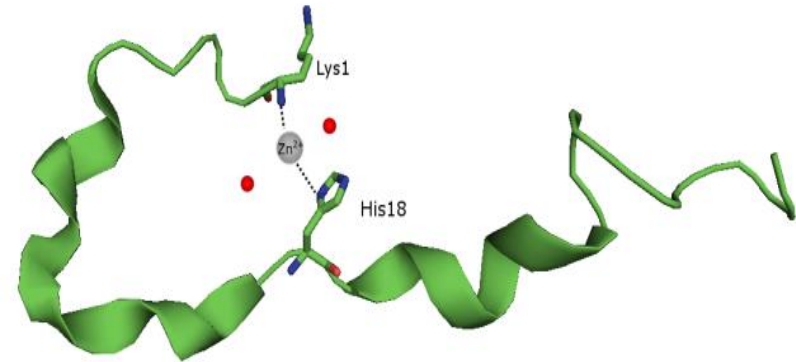
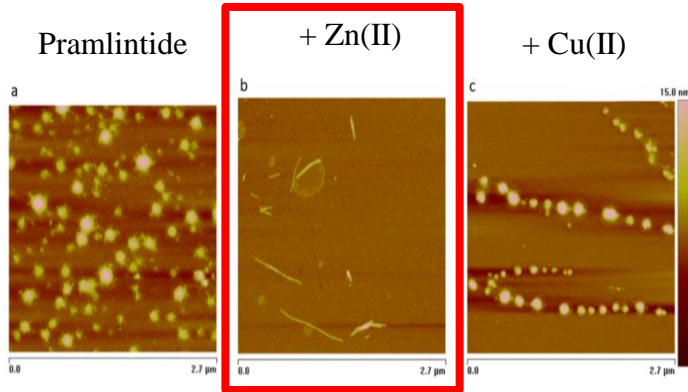


Rat amylin + Zn(II) + Cu(II)

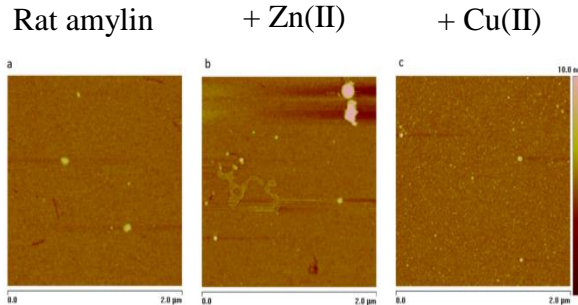
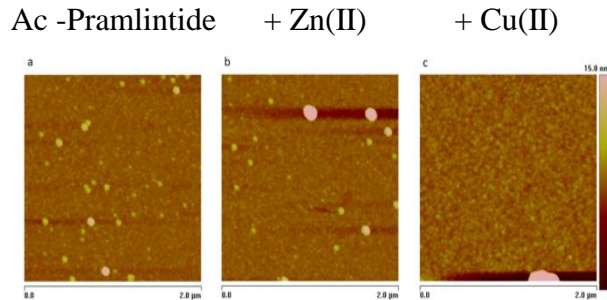


Conclusions: pramlintide

24h

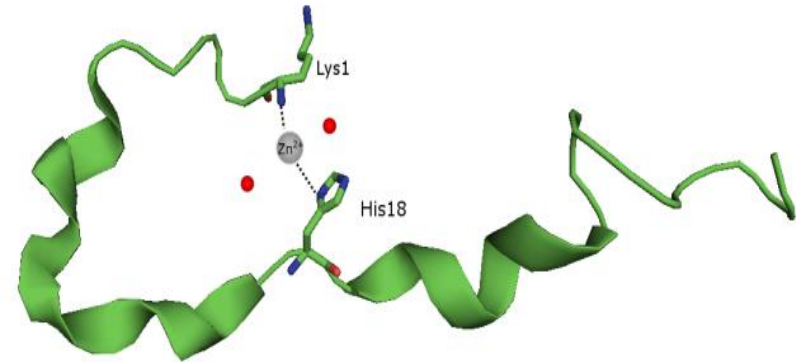
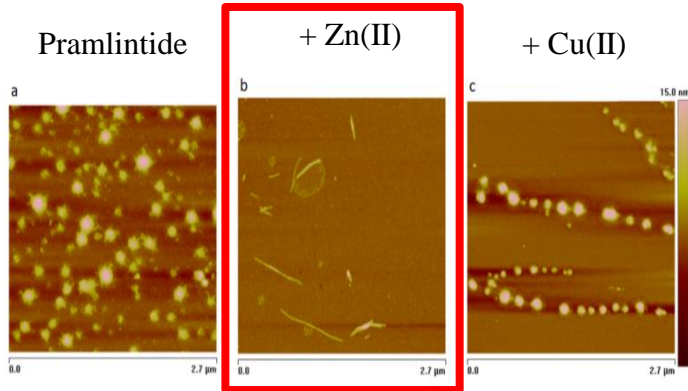


Zn(II) coordination to pramlintide induces a kink in the pramlintide structure, triggering fibril formation and most likely making the complex act like a needle that could disrupt *C. albicans* cell wall

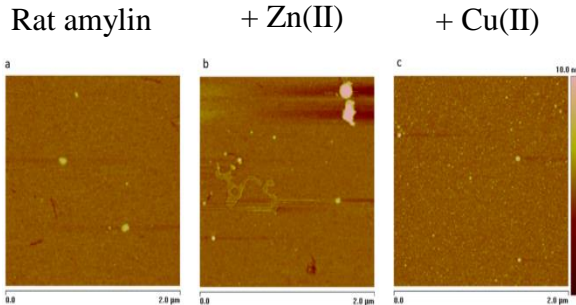
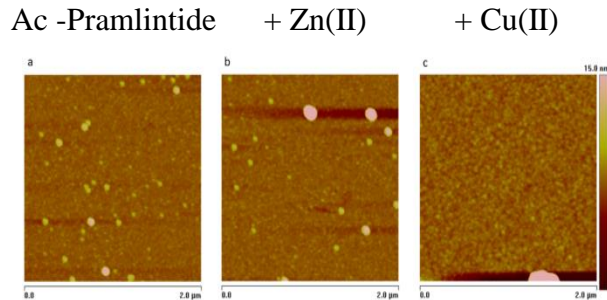


Conclusions: pramlintide

24h



Zn(II) coordination to pramlintide induces a kink in the pramlintide structure, triggering fibril formation and most likely making the complex act like a needle that could disrupt *C. albicans* cell wall



Shepherin forms amyloid fibrils in the presence of Zn(II)

Shepherin: **GYGGHGGHGGHGGHGGHGGHGGHGGGGHG**



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Shepherin: GYGGHGGHGGHGGHGGHGGHGGHGGHGGGGHG



Antimicrobial activity (MIC [$\mu\text{g}/\text{mL}$])

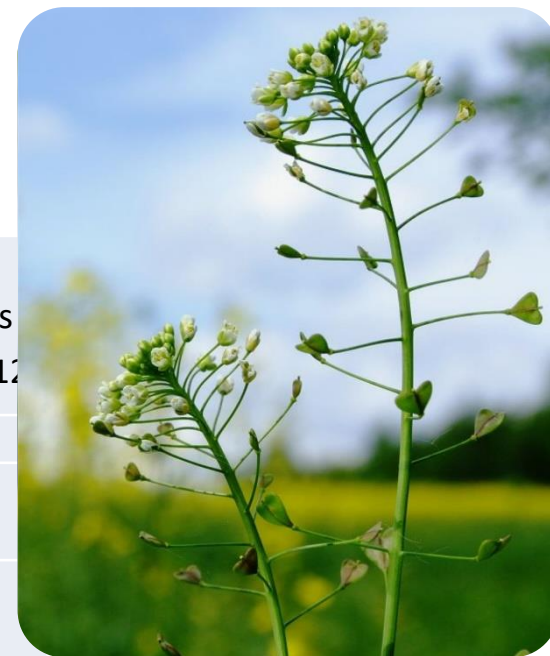
	C. albicans ATCC 10231	E. coli ATCC 25922	MRSA ATCC 43300	P. aeruginosa ATCC 27853	E. faecalis ATCC 29212	K. pneumoniae ATCC 700603	A. baumannii ATCC 19606
Shep I	n/d	n/d	n/d	n/d	n/d	n/d	n/d
Shep I – Cu(II)	n/d	n/d	n/d	n/d	n/d	n/d	n/d
Shep I – Zn(II)	16	n/d	n/d	n/d	n/d	n/d	n/d

Shepherin forms amyloid fibrils in the presence of Zn(II)

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Antimicrobial activity (MIC [$\mu\text{g}/\text{mL}$])

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Shep I	n/d	n/d	n/d	n/d	n/d
Shep I – Cu(II)	n/d	n/d	n/d	n/d	n/d
Shep I – Zn(II)	16	n/d	n/d	n/d	n/d

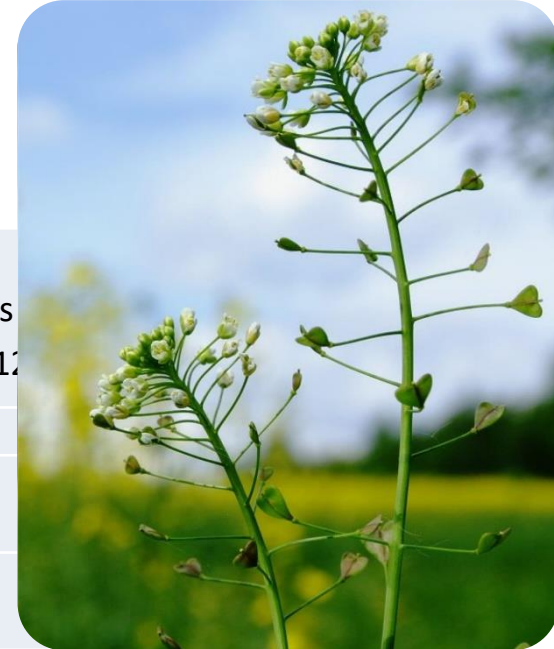


Shepherin forms amyloid fibrils in the presence of Zn(II)

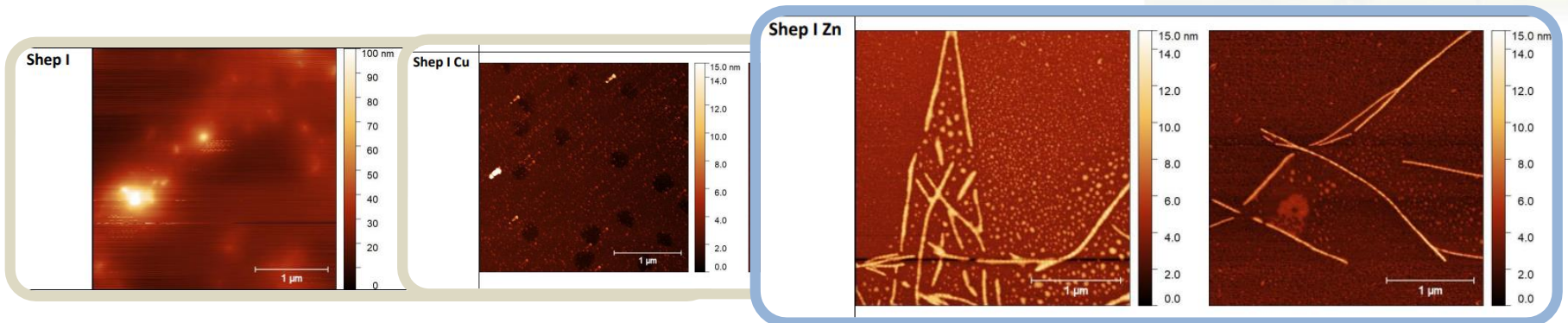
Shepherin: **GYGGHGGHGGHGGHGGHGGHGGHGGGGHG**

Antimicrobial activity (MIC [$\mu\text{g/mL}$])

	C. albicans ATCC 10231	E. coli ATCC 25922	MRSA ATCC 43300	P. aeruginosa ATCC 27853	E. faecalis ATCC 29212
Shep I	n/d	n/d	n/d	n/d	n/d
Shep I – Cu(II)	n/d	n/d	n/d	n/d	n/d
Shep I – Zn(II)	16	n/d	n/d	n/d	n/d



Ligand pH 7 \rightarrow addition of Zn(II) \rightarrow beta sheet structure \rightarrow **fibrils only in case of Zn(II)-shepherin complex**

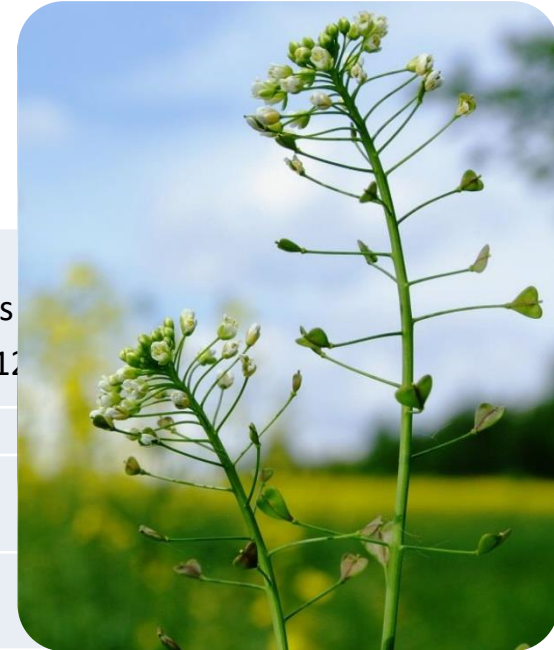


Shepherin forms amyloid fibrils in the presence of Zn(II)

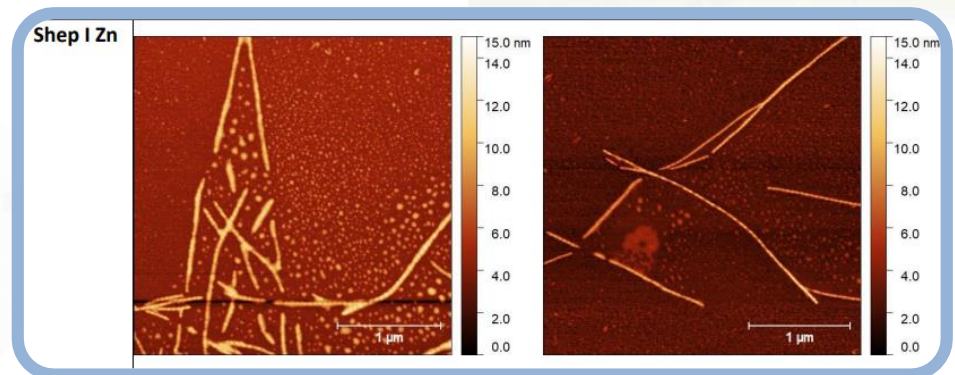
Shepherin: **GYGGHGGHGGHGGHGGHGGHGGHGGGGHG**

Antimicrobial activity (MIC [$\mu\text{g/mL}$])

	C. albicans ATCC 10231	E. coli ATCC 25922	MRSA ATCC 43300	P. aeruginosa ATCC 27853	E. faecalis ATCC 29212
Shep I	n/d	n/d	n/d	n/d	n/d
Shep I – Cu(II)	n/d	n/d	n/d	n/d	n/d
Shep I – Zn(II)	16	n/d	n/d	n/d	n/d



Ligand pH 7 \rightarrow addition of Zn(II) \rightarrow beta sheet structure \rightarrow **fibrils only in case of Zn(II)-shepherin complex**

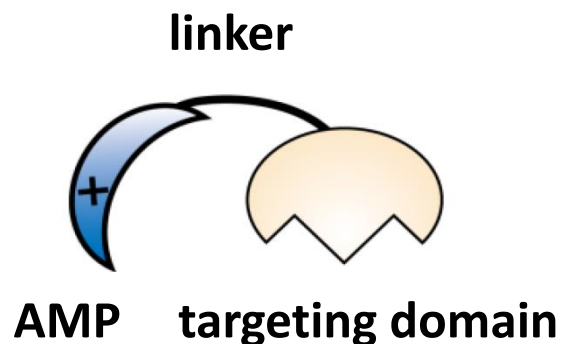


How to use this knowledge?

- In a rational design of novel AMP-metal complexes with **enhanced features which contribute to their antimicrobial efficiency**

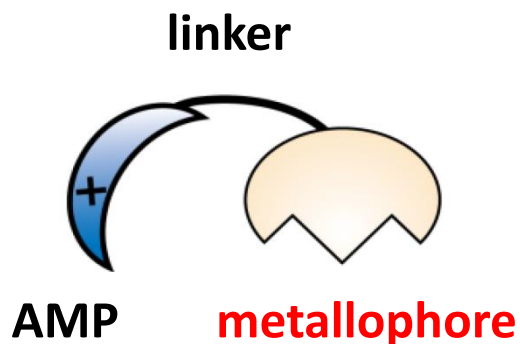
How to use this knowledge?

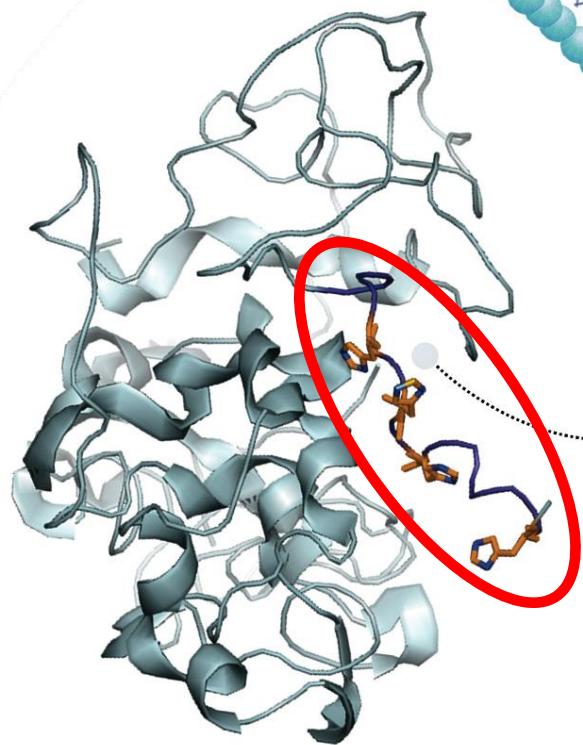
- In a rational design of novel AMP-metal complexes with **enhanced features which contribute to their antimicrobial efficiency**
- By attaching AMP complexes to commercially used drugs or appropriately designed **targeting domains**



How to use this knowledge?

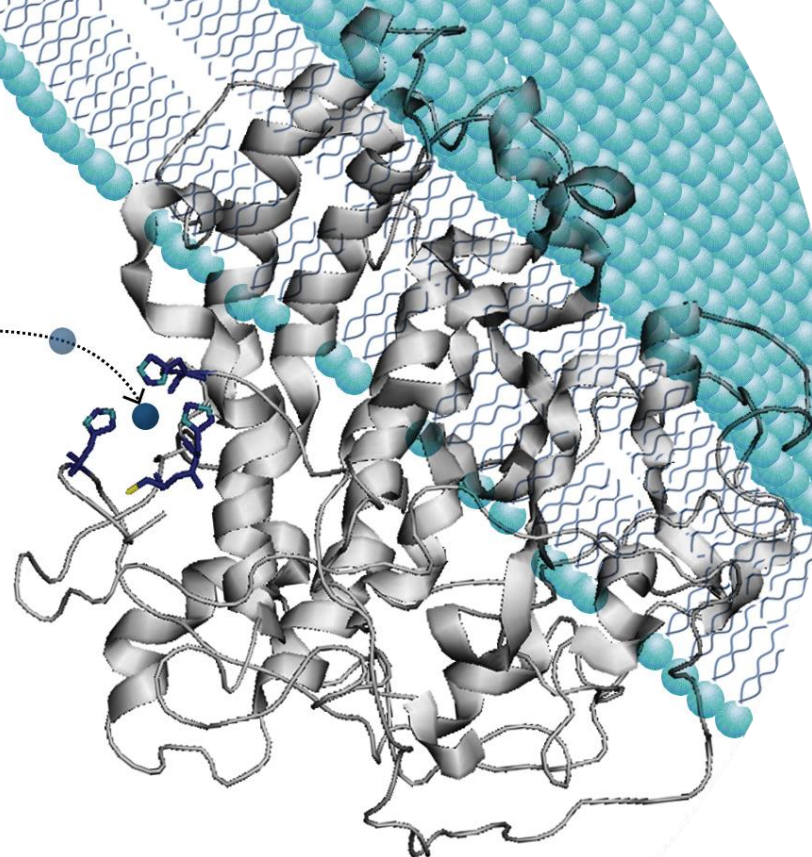
- In a rational design of novel AMP-metal complexes with **enhanced features which contribute to their antimicrobial efficiency**
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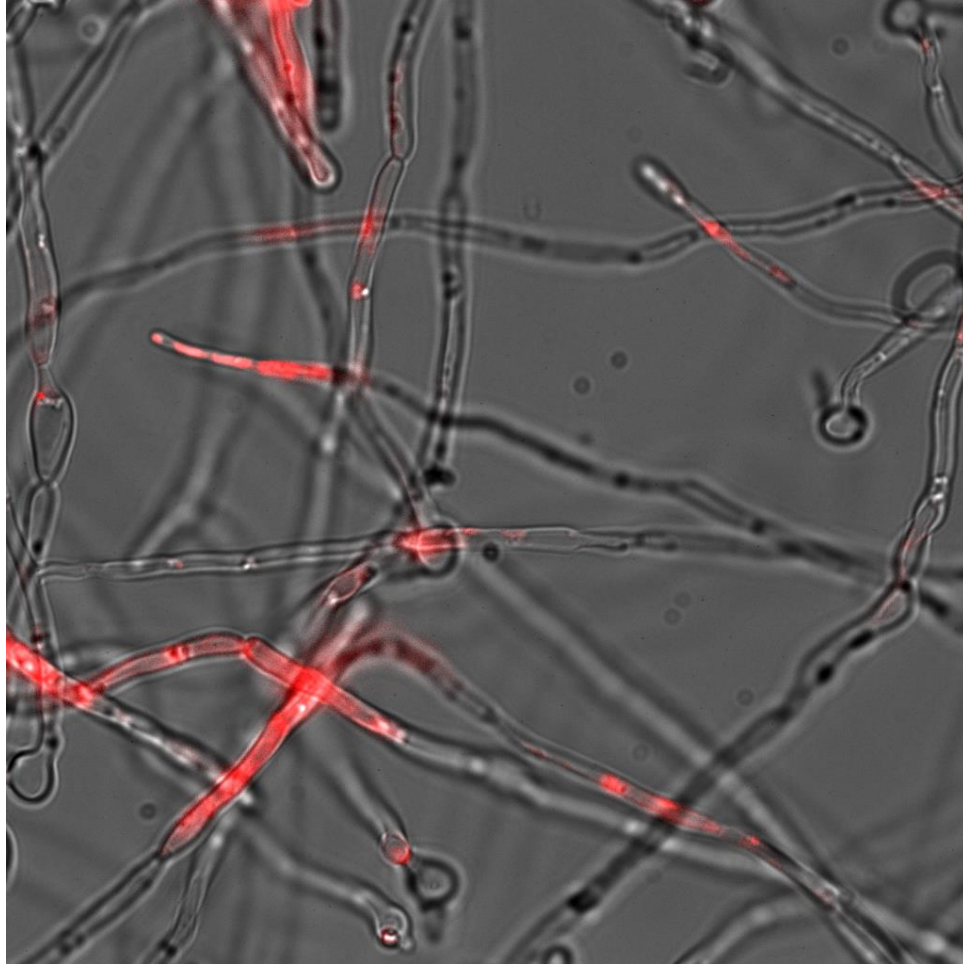
Pra1
(zincophore)

Zn^{2+}



Zrt1
(Zn(II) transporter)

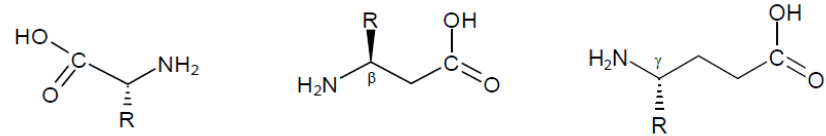
***C. albicans* selectively captures the fluorescently labelled C-terminal fragment of the Pra1 zincophore (AF647-SHQHTDSNPSATTDANSHCHTHADGEVHC)**



How to use this knowledge?

- In a rational design of novel AMP-metal complexes with **enhanced features which contribute to their antimicrobial efficiency**
- By attaching AMP complexes to commercially used drugs or appropriately designed **targeting domains**
- In a rational design of novel AMP-metal complexes with **enhanced proteolytic stability** (by using unnatural amino acids)

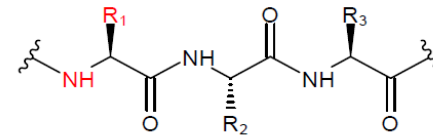
UNNATURAL AMINO ACIDS



D-Amino acids

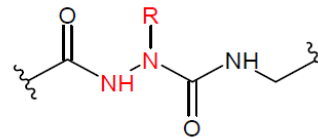
β-Amino acids

γ-Amino acids

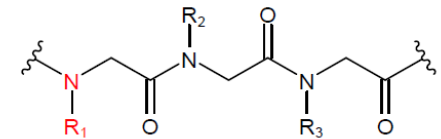


Peptides

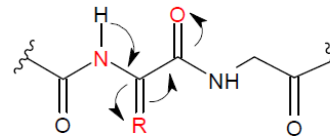
MODIFIED PEPTIDES



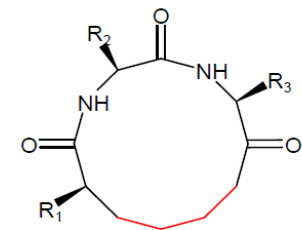
Azapeptides



Peptoids



Dehydropeptides



Cyclopeptides

How to enhance the stability of therapeutic AMPs? The „retro-inverso” strategy

VFHLLGKIIHHVGNFVYGFSHVF

clavanin C native sequence

vfhllgkiihhvgnfvvygfhshvf

D-amino acid based clavanin C sequence

fvhsfgyvfngvhhiikgllhfv

retro-inverso clavanin C

The N-terminal part of clavanin C is marked in red; the C-terminal one – in violet.
L-amino acids are in capitals, D-amino acids – in small letters





Adriana Miller



Dorota Dudek



Joanna Wątry



Emilia Dzień



Kinga Garstka



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AND LIFE SCIENCES



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Robert Wieczorek



Tomasz Janek



**Agnieszka
Matera-Witkiewicz**

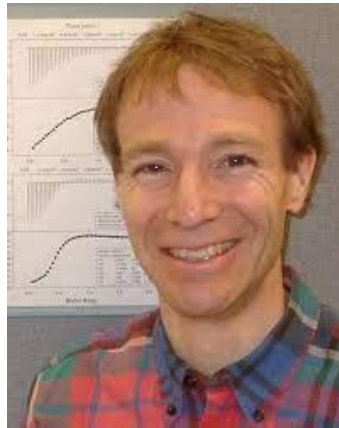


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Duncan Wilson
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Maurizio Remelli
University of Ferrara



Daniela Valensin
University of Siena



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