

XXVIII Symposium on Bioinformatics and Computer-Aided Drug Discovery  
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# AMYLOIDOGENIC PEPTIDES: NEW CLASS OF ANTIMICROBIAL PEPTIDES WITH THE NOVEL MECHANISM OF ACTIVITY

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**Institute of Protein Research**

# The beginning of the golden age of antibiotics

## **The Nobel Prize in Physiology or Medicine 1945**

"for the discovery of penicillin and its curative effect in various infectious diseases"



Photo from the Nobel Foundation archive.

**Sir Alexander  
Fleming**

Prize share: 1/3



Photo from the Nobel Foundation archive.

**Ernst Boris Chain**

Prize share: 1/3



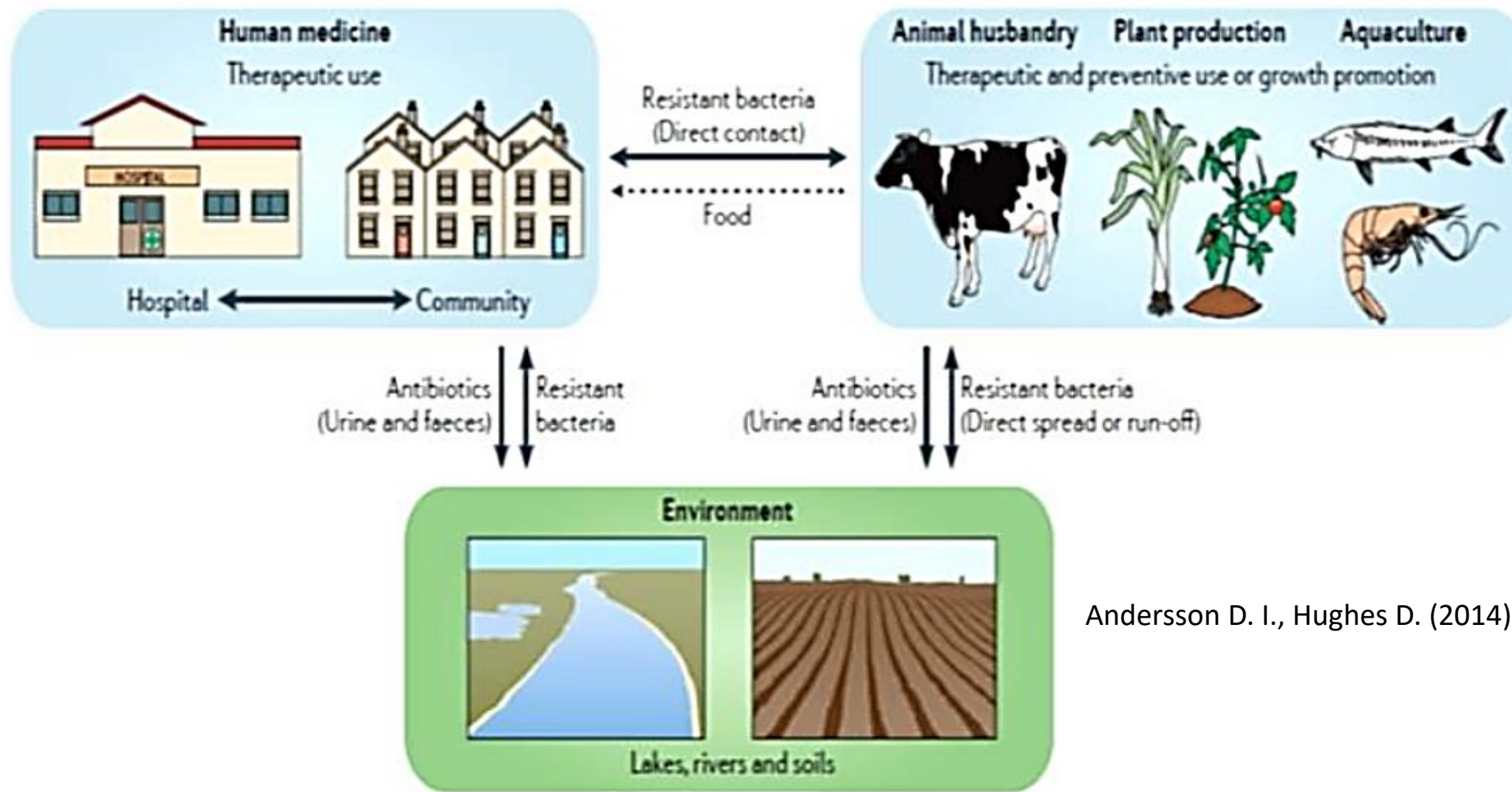
Photo from the Nobel Foundation archive.

**Sir Howard Walter  
Florey**

Prize share: 1/3

[nobelprize.org/prizes/medicine/1945/summary/](https://nobelprize.org/prizes/medicine/1945/summary/) I would like to remind you that thanks to these scientists, the discovery of antibiotics has become an important event in the development of science and medicine, and not only in these areas.

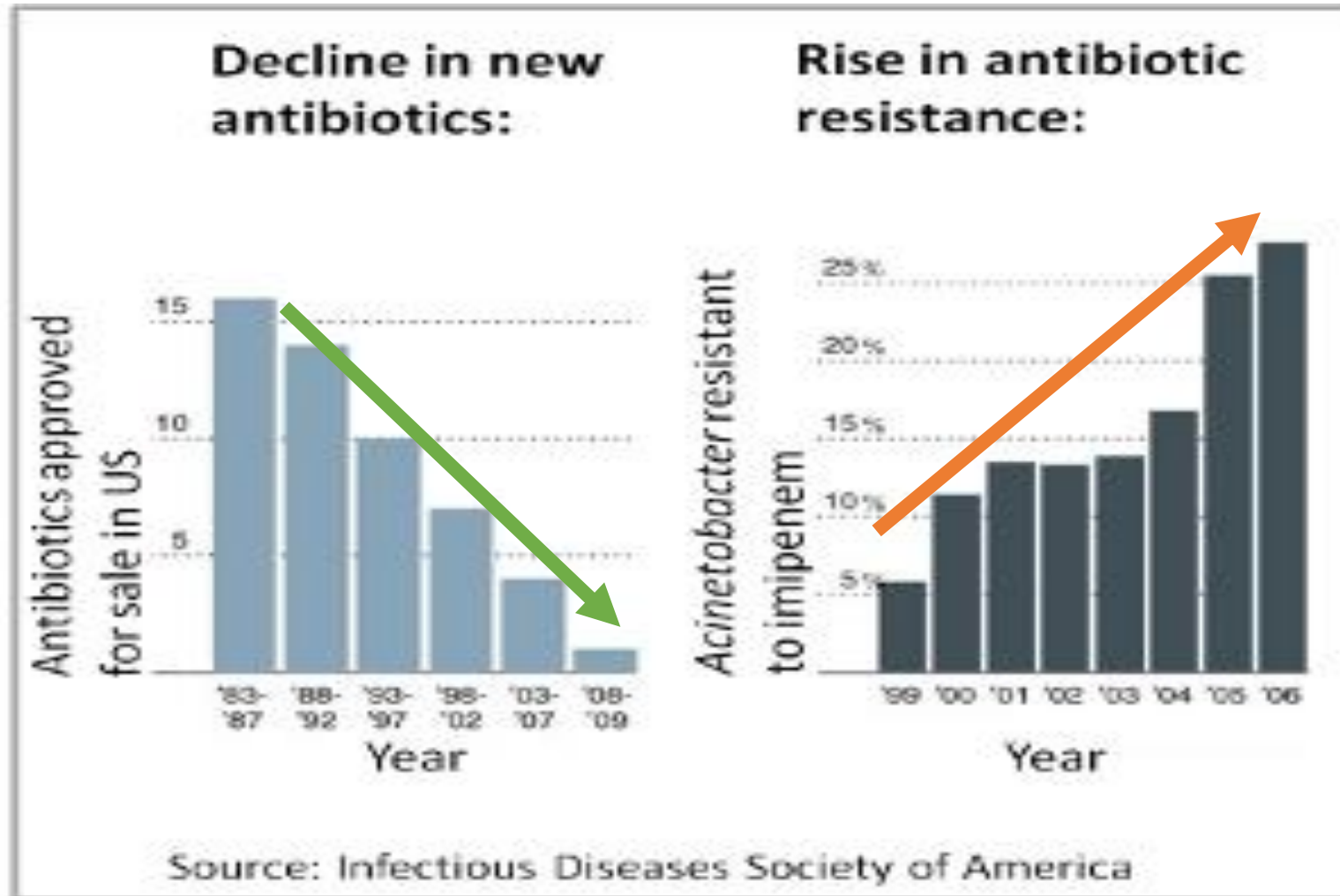
# Widespread use of antibiotics



Andersson D. I., Hughes D. (2014). 10.1038/nrmicro3270

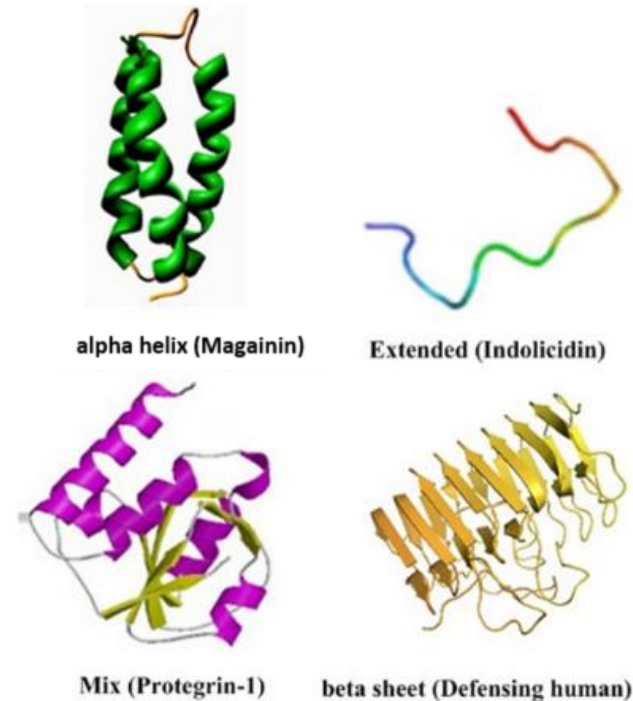
The widespread use of antibiotics in medicine, animal husbandry, aquaculture, plant growing forced the microworld to adapt, which led not only to antibiotic resistance, but also the spread of this phenomenon among various taxa of microorganisms.

# The problem of antibiotic resistance



# Antimicrobial peptides

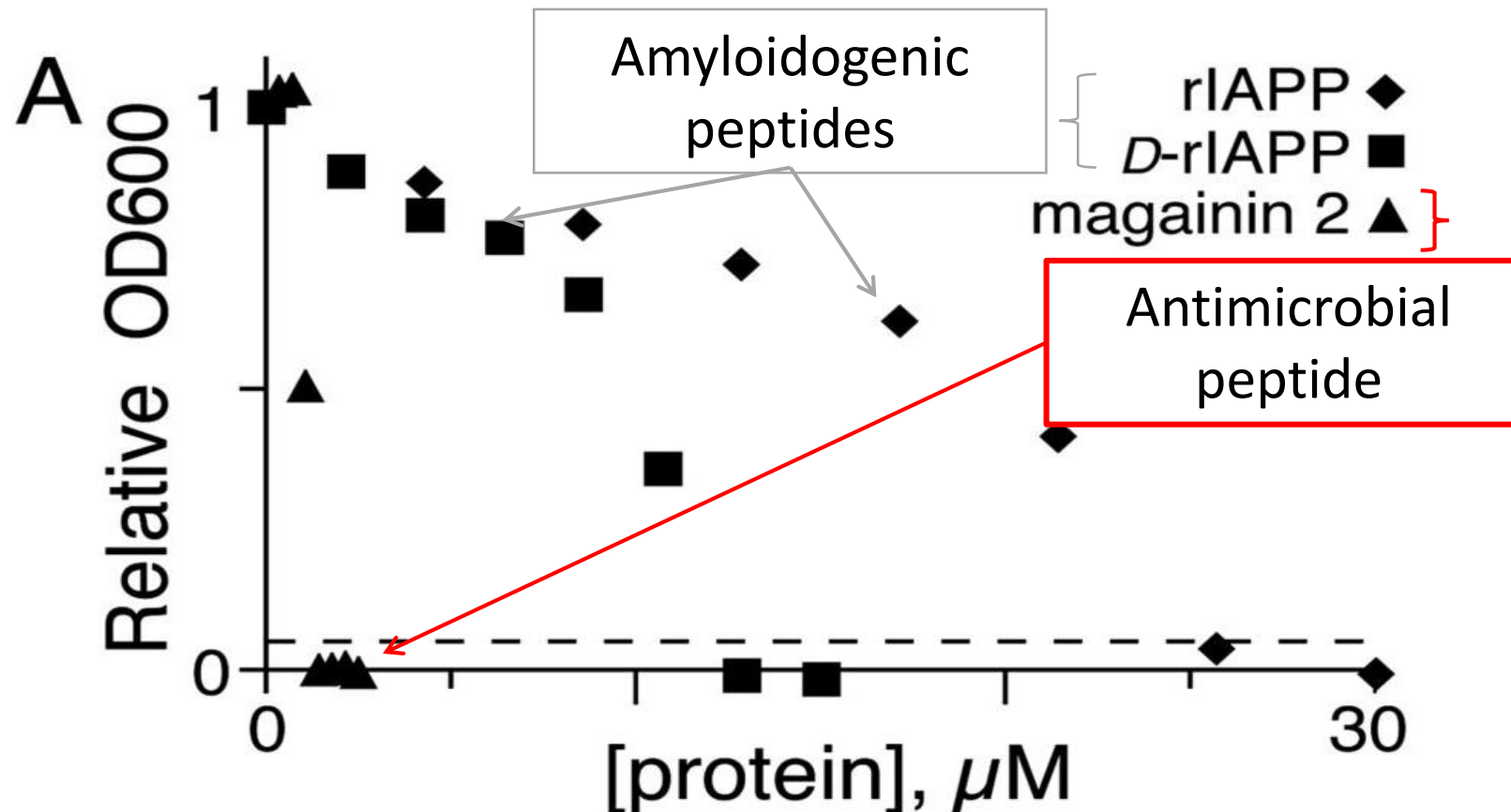
Biological action:  
Antimicrobial  
Immunomodulatory  
Antibiofilm Anticancer  
Antiviral



Structural classes of antimicrobial peptides

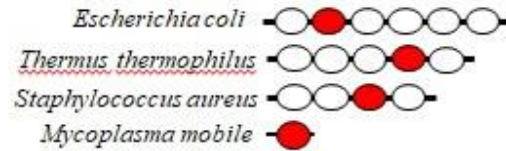
# The ability of amyloidogenic peptides to exhibit antimicrobial activity

Dependence of the optical density of the cell culture of *Paracoccus denitrificans* on the concentration of peptides

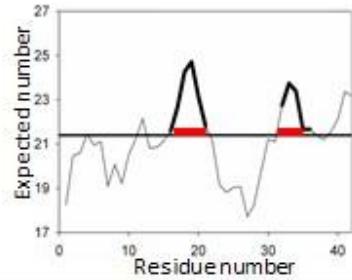


# Creation of new antibacterial peptides based on targeted protein aggregation

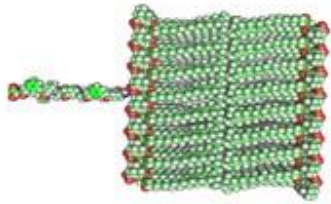
## Theoretical methods



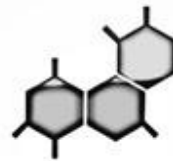
Search for unique domains in the bacterial proteins



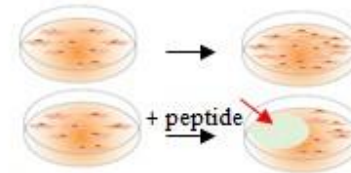
Bioinformatics search for amyloidogenic regions



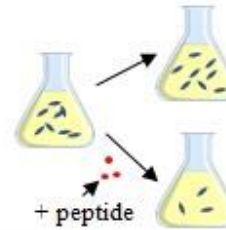
Molecular dynamics modeling of the penetration of peptides through the lipid layer



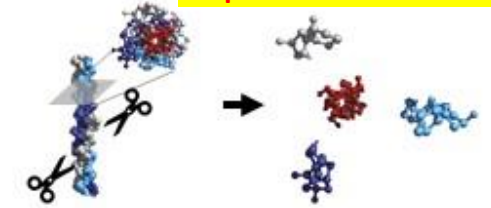
Design and synthesis of the amyloidogenic/antibacterial peptides



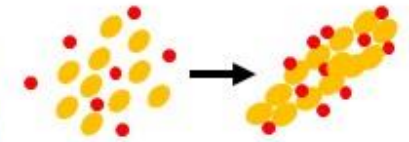
Toxicity testing of peptide against fibroblasts



Determine the antimicrobial activities of peptide



Identification of protein regions in the backbone of amyloid fibrils by mass spectrometry analysis



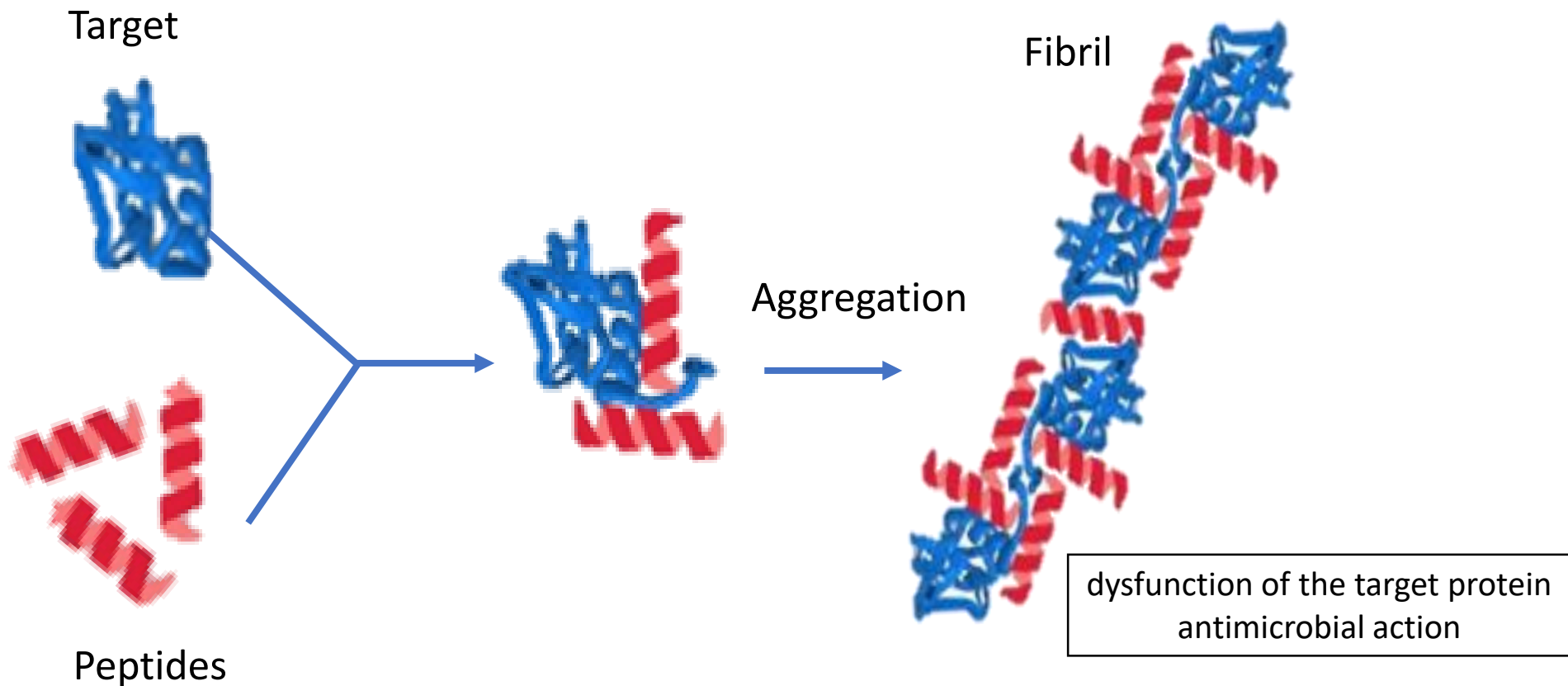
Co-aggregation of amyloidogenic peptide and protein-target



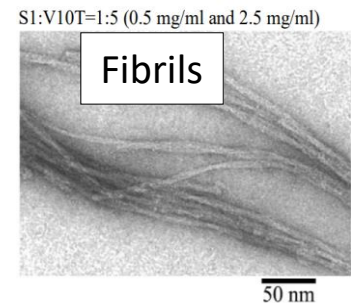
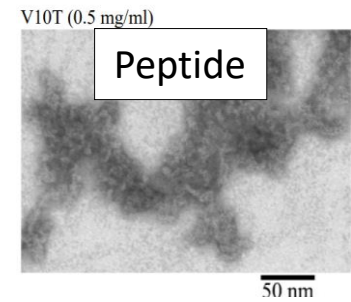
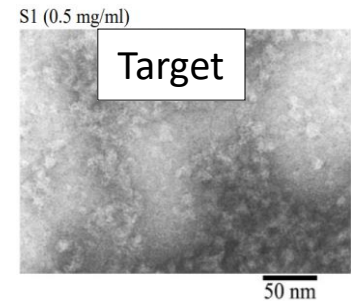
Studies of the process of fibril formation by AMPs

## Experimental methods

# A model of directed co-aggregation of an amyloidogenic peptide based on the S1 ribosomal protein and the protein itself



## Experimental data

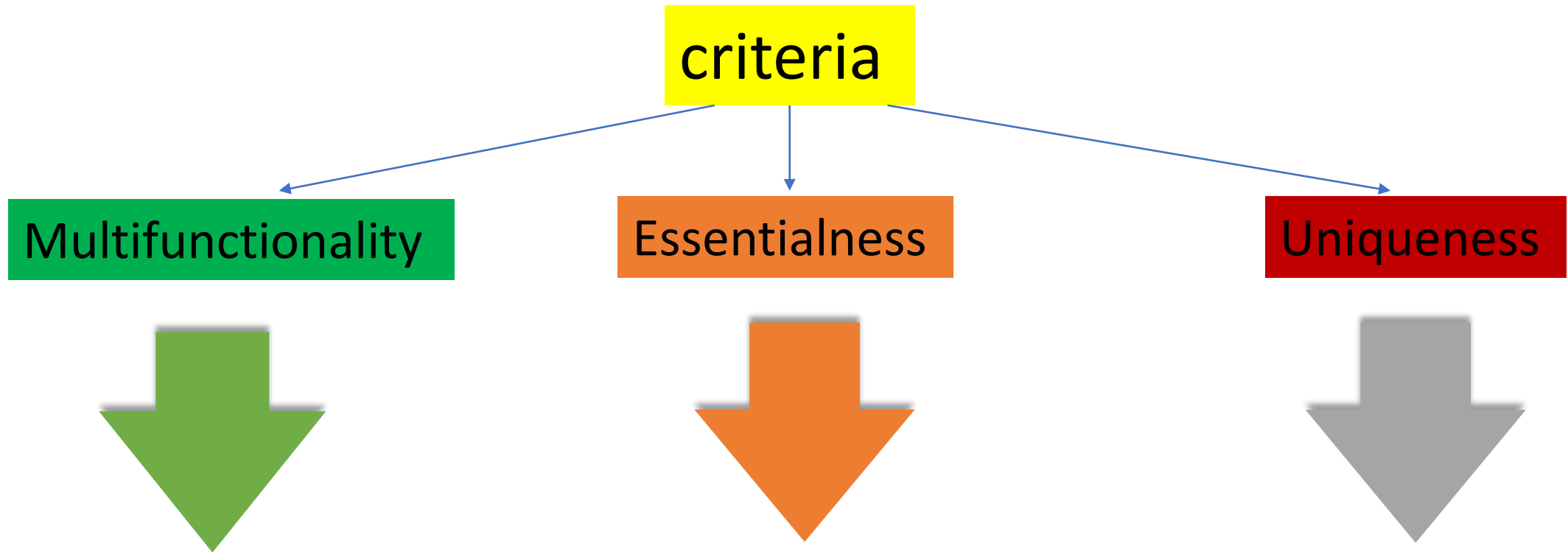


## Antimicrobial and Amyloidogenic Activity of Peptides Synthesized on the Basis of the Ribosomal S1 Protein from *Thermus Thermophilus*

by [Stanislav R. Kurpe](#)<sup>1</sup>, [Sergei Yu. Grishin](#)<sup>1</sup>, [Alexey K. Surin](#)<sup>1,2,3</sup>, [Olga M. Selivanova](#)<sup>1</sup>,  
[Roman S. Fadeev](#)<sup>4</sup>, [Ulyana F. Dzhus](#)<sup>1</sup>, [Elena Yu. Gorbunova](#)<sup>2</sup>, [Leila G. Mustaeva](#)<sup>2</sup>,  
[Vyacheslav N. Azev](#)<sup>2</sup> and [Oxana V. Galzitskaya](#)<sup>1,4,\*</sup>



# Choosing the target protein



## Ribosomal S1 protein

Participates in translation  
Initiation and regulation

S1 knockout leads  
to cell death

Only present in the  
bacterial cell

# Number of structural S1 domains in bacteria changes strictly within a limited range from one to six

A

**Source:** *Mycoplasma hominis*  
**Source phylum:** Tenericutes  
**UniProt ID:** D1J8E8  
**Length:** 111 a.a.

**Source:** *Listeria aquatica*  
**Source phylum:** Firmicutes  
**UniProt ID:** W7BIQ4  
**Length:** 170 a.a.

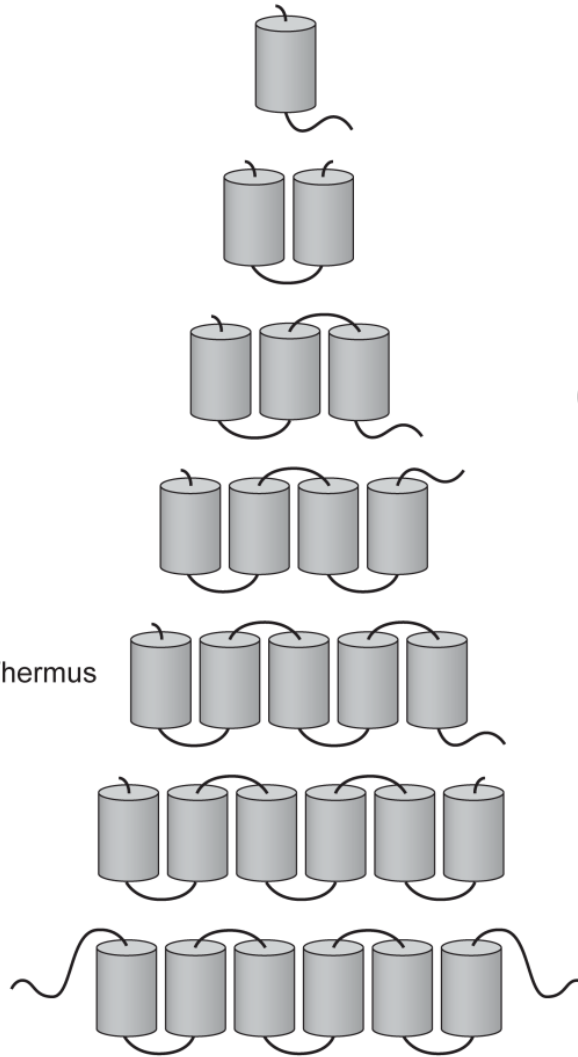
**Source:** *Microcystis aeruginosa*  
**Source phylum:** Cyanobacteria  
**UniProt ID:** L7E4P2  
**Length:** 330 a.a.

**Source:** *Bifidobacterium bifidum*  
**Source phylum:** Actinobacteria  
**UniProt ID:** E4V933  
**Length:** 490 a.a.

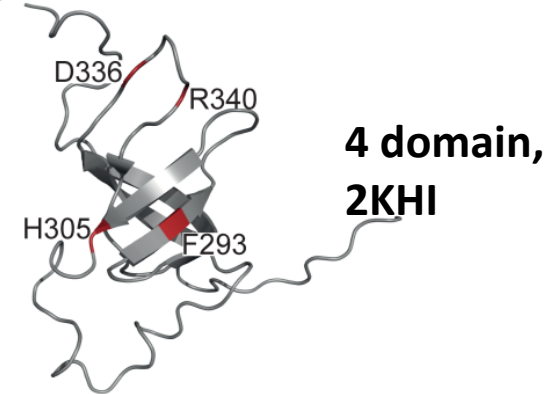
**Source:** *Thermus thermophilus*  
**Source phylum:** Deinococcus-Thermus  
**UniProt ID:** Q83YV9  
**Length:** 536 a.a.

**Source:** *Escherichia coli*  
**Source phylum:** Proteobacteria  
**UniProt ID:** P0AG67  
**Length:** 557 a.a.

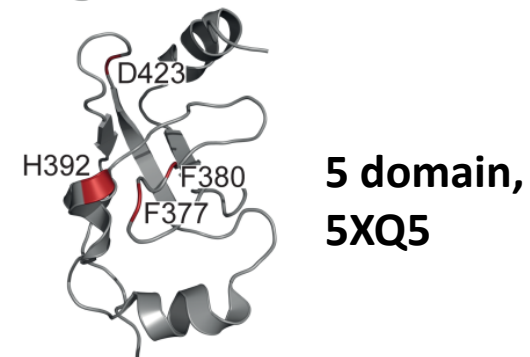
**Source:** *Salinibacter ruber*  
**Source phylum:** Bacteroidetes  
**UniProt ID:** D5HA65  
**Length:** 876 a.a.



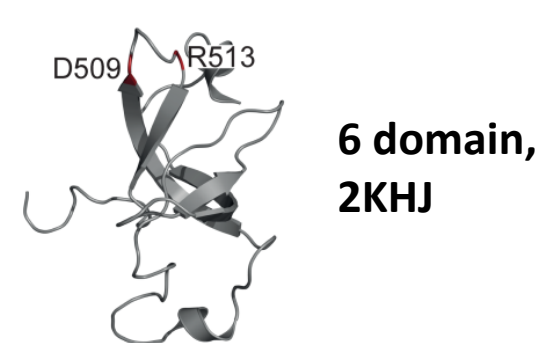
B



C



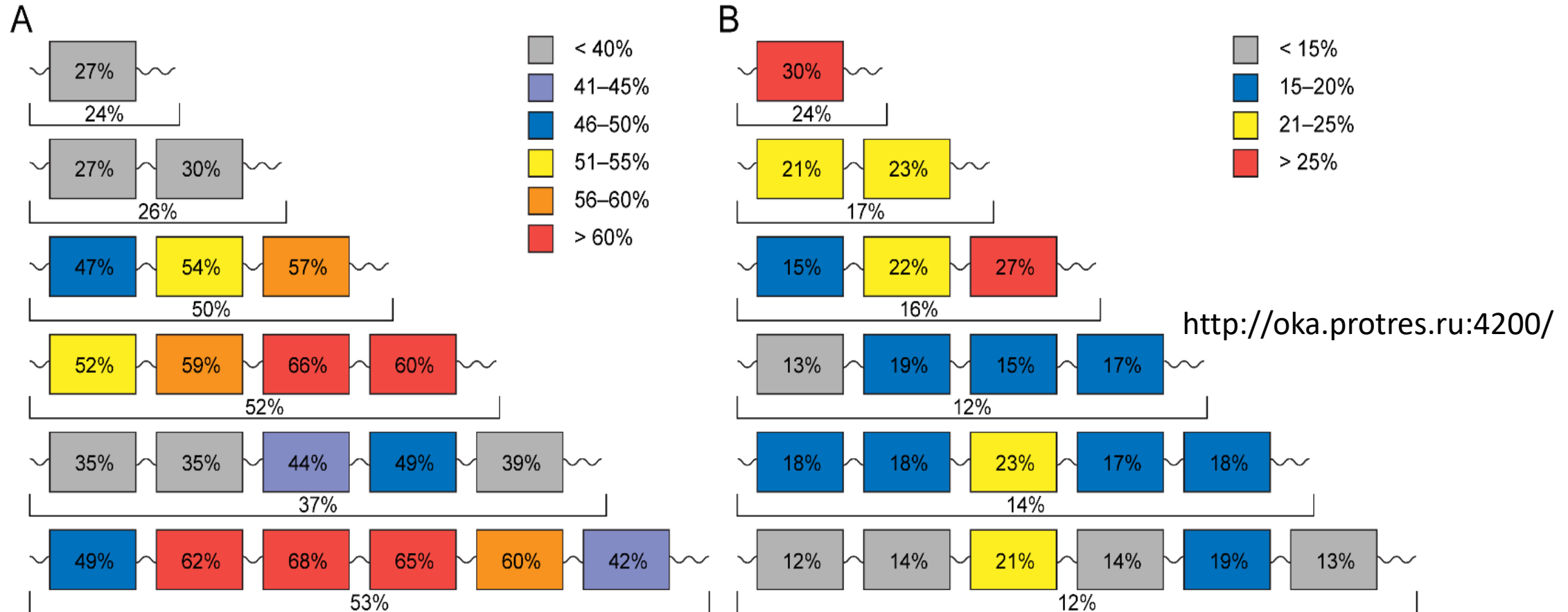
D



(A) Number of structural S1 domains in different bacteria (according to the SMART database). (B), (C), (D) NMR structures of the fourth (2KHI), fifth (5XQ5) and sixth (2KHJ) S1 domains from E.coli.

# Analysis of amyloidogenicity of the 1453 sequences of S1 proteins and its domains

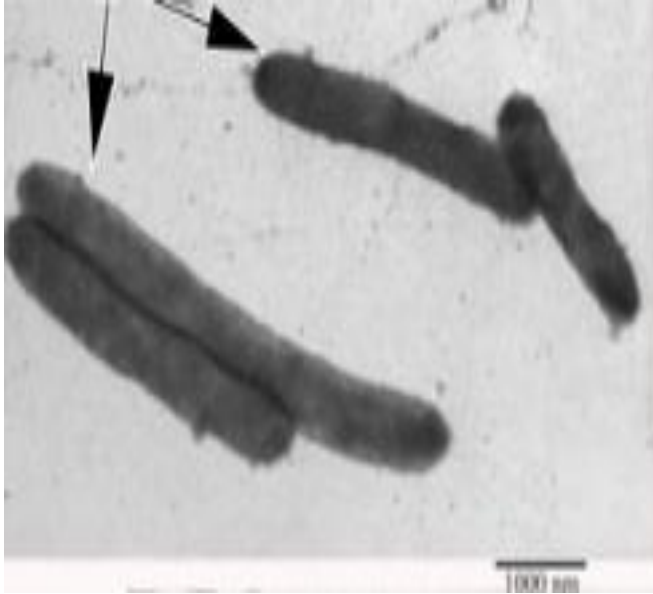
Average percentage of identity (A) and amyloidogenic regions (B) predicted by the FoldAmyloid program



Sequence and evolutionary analysis of bacterial ribosomal S1 proteins. *Proteins*. doi:10.1002/prot.26084

<http://bioinfo.protres.ru/fold-amyloid/> Bioinformatics. 2010 Feb 1;26(3):326-32.

# *Thermus thermophilus* as a model organism for molecular biotechnology research



EM image of cells *T. thermophilus*

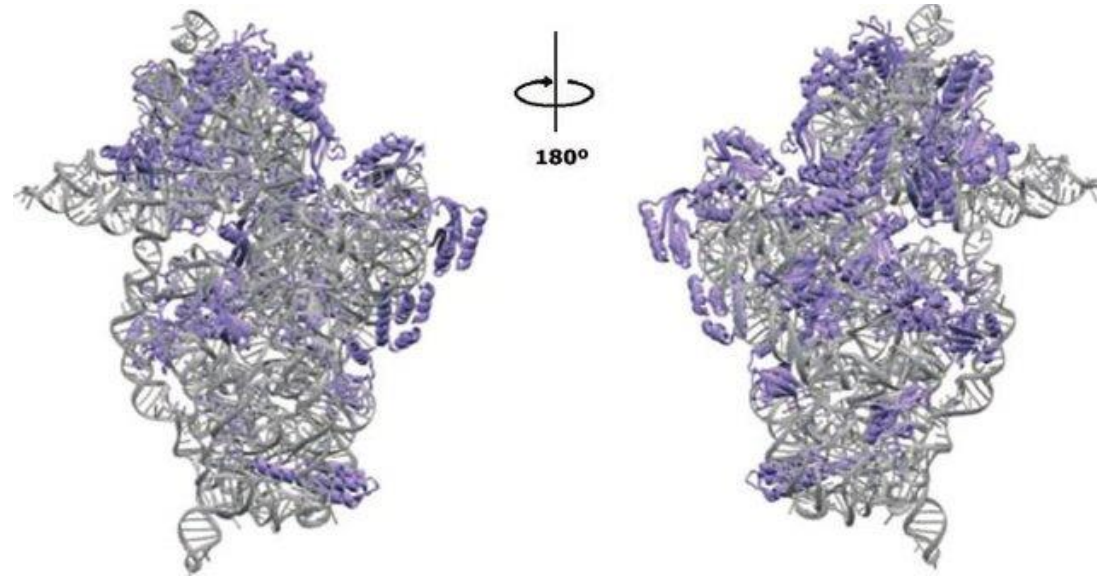


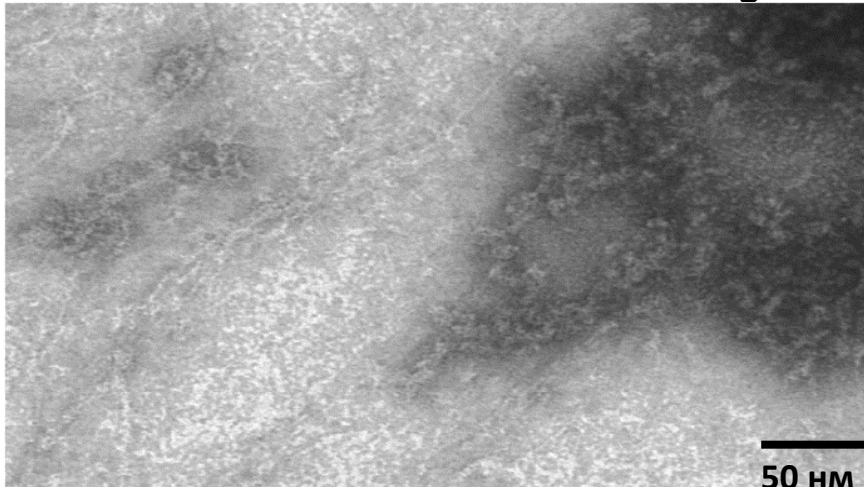
Figure 50S ribosome subunit  
*T. thermophilus*

(<https://www.researchgate.net/publication/41058475>,  
2009)

*T. thermophilus*, *E. coli* are model organisms

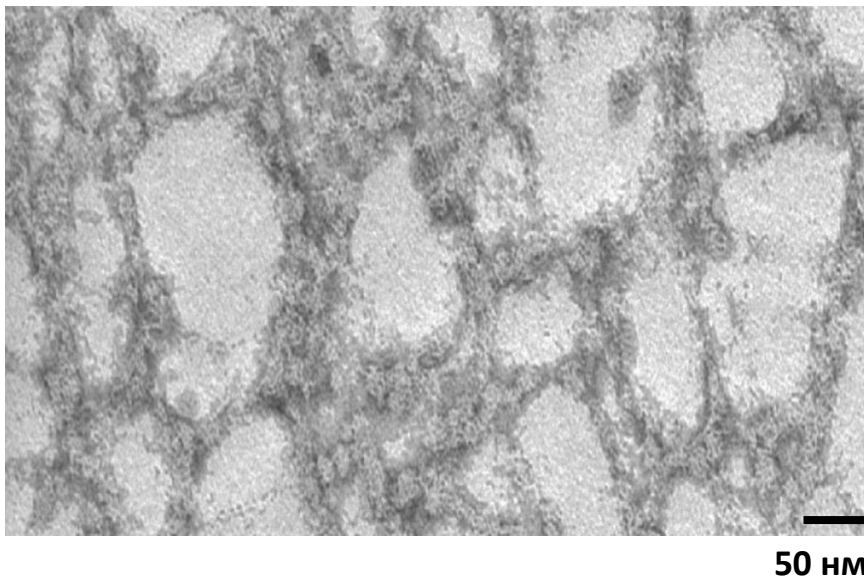
*Pseudomonas aeruginosa*, *Staphylococcus aureus* are pathogenic organisms

# Aggregation of S1 ribosomal proteins, problems with crystallization



EM images of S1 protein aggregates from *T. thermophilus* (bS1)

Grishin et al. Biochemistry (Mosc). 2020 Mar;85(3):344-354.



EM images of S1 protein aggregates from *P. aeruginosa* (bPaS1)

Grishin et al., Int J Mol Sci. 2021 Jul 7;22(14):7291.

Purpose: Development of amyloidogenic and antibacterial peptides based on the S1 protein from *T. thermophilus*, *E. coli*, *P. aeruginosa*, *S. aureus*

## Tasks:

1. Search for amyloidogenic regions of the S1 protein.
2. Synthesize peptides based on the identified amyloidogenic sites.
3. Check the amyloidogenic and antibacterial properties of the obtained peptides.
4. Determine the minimum inhibitory concentration (MIC).
5. Determine the response of the cell proteome to treatment with AMP.
6. Determine the toxicity of peptides for eukaryotic cells.

## S1 from *E. coli*

1 MTES**FAQLFE**ESLKTIE TRPGS**IVRGVVVAID**KD**VVLVDAG**LKSESAIPAEQFKNAQGEL 60

61 EIQVGDEVDVALDAVEDGFGETLLSREKAKR**HEAWIT**LEKAYEEA**ETVVG**VINGKVK**GGF** 120

121 **TVELNGIRAF**L**P****GSLVD**VRPVRDTLHLEGKELE**FKVIK**LDQKRNNVVVSRRAVIESENSA 180

181 ERDQLEENLQEGMEVKGIVKNLTDY**GAFVDLGGVDGLLHITDMAWKR**VKHPSEIVNV**VGDE** 240

241 **ITVKVLKF**DRERTRVSLGLKQLGEDPWV**AIAKR**YPEG**TKLTGRVTNL****TDYGC**FVEIE**EGV** 300

301 **EGLVHVSE**MDWTNKNIHPS**SKVVNVGDVVEV****MVLD**IDEERRRISLGLKQCKNNPWQQFAET 360

361 HNK**GDRVEG**KIKS**ITDFGIFIGLDG**IDGL**VHLSDISWNV**AGEEAVREYKKGD**EIAAVVL** 420

421 **QVD**AERERISLGVKQLAEDPF**NNWVA**LNKKGAI**VNGKVTAVDAK**GATVELADGVEGYLRA 480

481 SEASRDRVEDATLVLNVGDDVEAKFTGVDRKNRAISLSVR**AKDEADEKDAIATVNKQEDA** 540

541 NFSNNAMAEAFKAAKGE

Amyloidogenic regions

**FoldAmyloid**

Waltz

**AGGRESAN**

**PASTA 2.0**

1 S1 motif: 1) **IVRGVVVAID** (23-32)

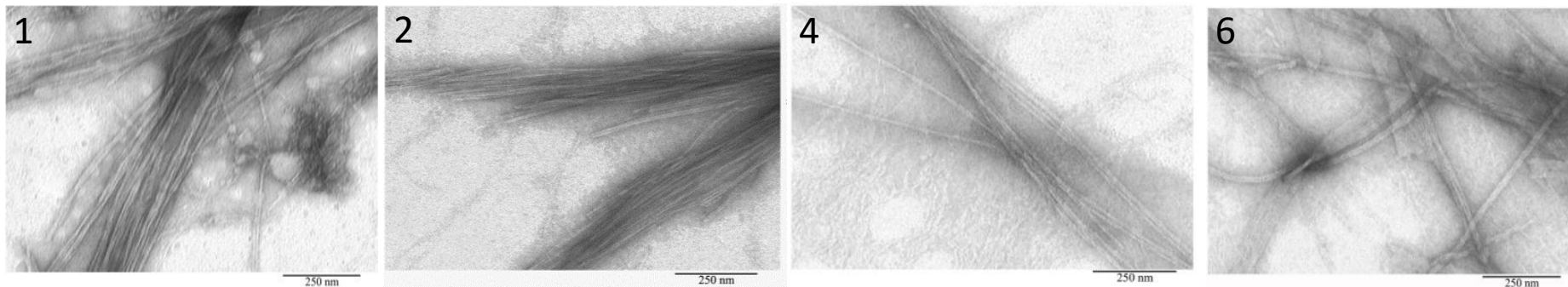
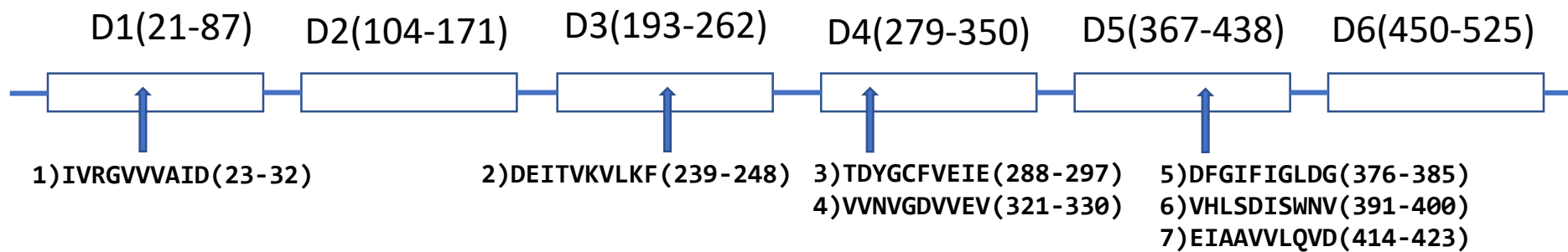
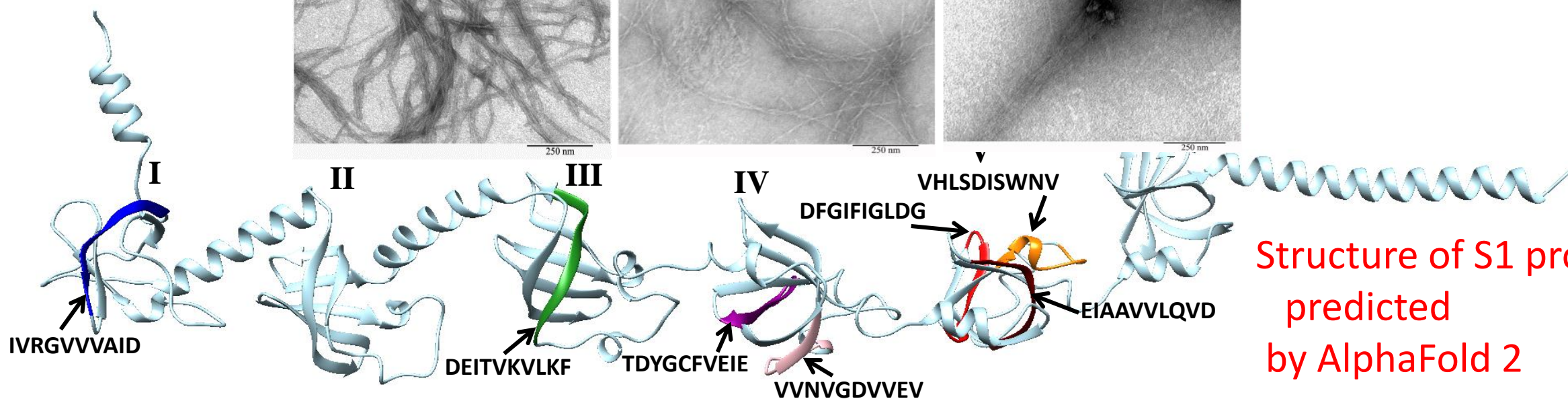
2 S1 motif

3 домен: 2) **DEITVKVLKF** (239-248)

4 домен: 3) **TDYGC**FVEIE (288-297) и 4) **VNVGDVVEV** (321-330)

5 домен: 5) **DFGIFIGLDG** (376-385), 6) **VHLSDISWNV** (391-400) и 7) **EIAAVVLQVD** (414-423)

6 домен

**A****S1 from *E. coli*****B *E. coli***

Structure of S1 protein  
predicted  
by AlphaFold 2



# S1 from *T. thermophilus*

1 MEDKATQTPEQTFSMEEAALQETEARLEKRVRP**GOILTGKVVLVGSEGVAVDIGAKTEGI I** 60  
61 **PFNQ**LTTKPLSEELRNLLSPGDEVK**VQVLR**VDPETG**QILLS**SRKKIEAQEKWDRIQELYE 120  
121 KGEPTVTVTIKERVKGGV**VAELDGIQG**FMPASQLDLRRVFNLDEFVGG**QVLAKIIEFHRRK** 180  
181 GRVILSRRAVLEEEQKKAREAFKLSLEPG**QVVEGTVVEVTDFGVFNLG**PVDGLVHRSE**I** 240  
241 **TWGR**FNHPREVIQKGQVKARVLSVDPEKERVN**LSIKALI**PDPWTTVAEKYPV**GTRVRGK** 300  
301 **VVGLTQFGAFVEVE**PGLE**GLIHISEL**SWTKRPKHPSEVVKEGDEVE**AVVLR**LDPEERRLS 360  
361 LGLKQTQPDWQQLTEKYPP**GTVLKGV**TV**VTDFGVFVEI**EP**GGIEGLVHV**SELDHKRVEN 420  
421 PAALFKKGD**EMEVVVLNID**PVEQRVSL**SRKR**LLPPPLPQEEERP**RRARS**GKERARRKGAP 480  
481 RREDRREYEG**AVAEYNLYDA**SSVPTTTATVKLG**DLYGDLLA**SLGLEEEAEKSRG

Amyloidogenic regions:

**FoldAmyloid**

Waltz

**AGGRESCAN**

**PASTA 2.0**

1 domain

2 domain

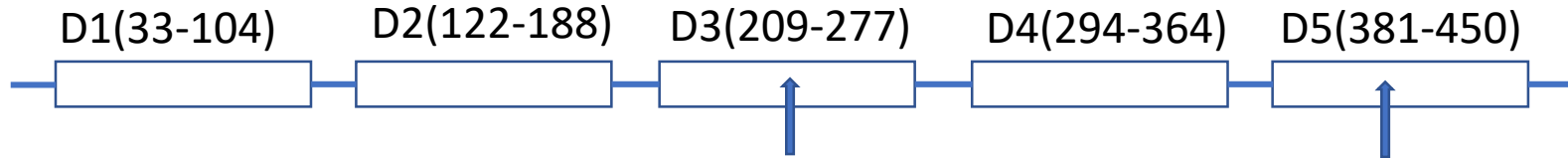
3 domain: 1) VVEGTVVEVT (211-220) и 2) DFGVFNLG (221-229)

4 domain

5 domain: 3) VTDFGVFVEI (391-400) и 4) EMEVVVLNID (430-439)

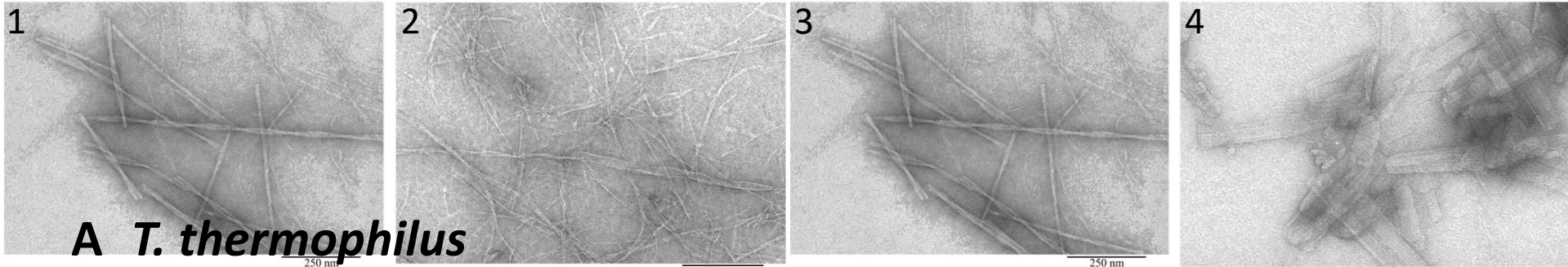
B

# S1 from *T. thermophilus*

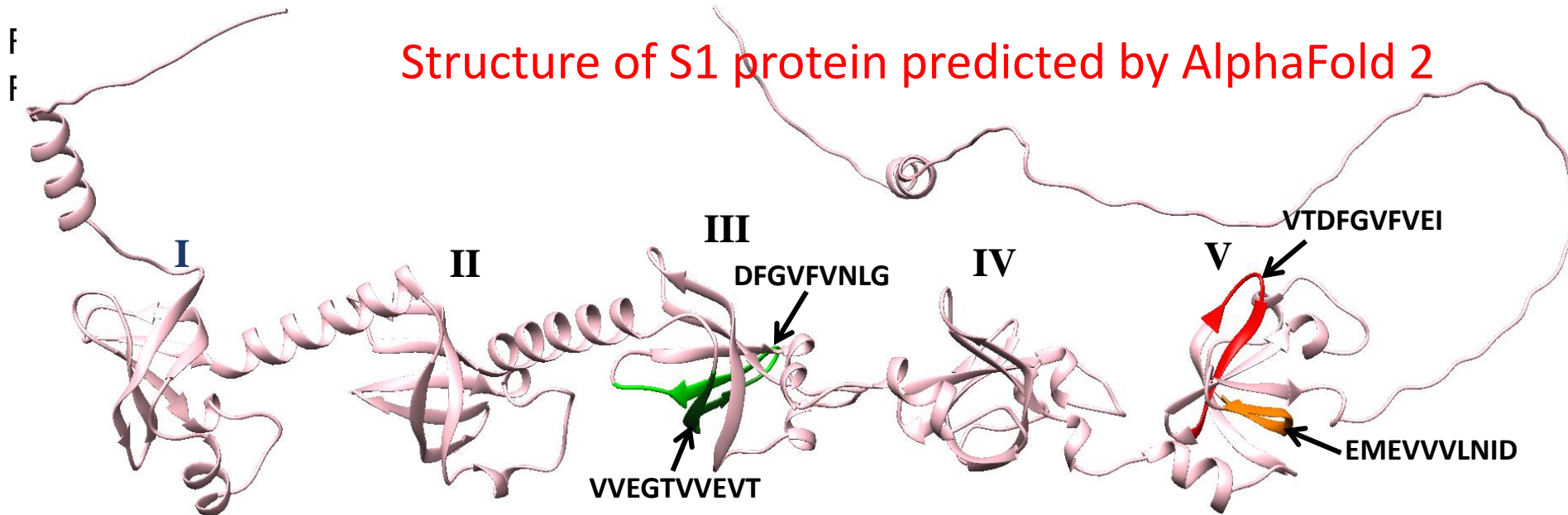


1) VVEGTVVEVT (211-220)  
2) DFGVFNLG (221-229)

3) VTDFGVFVEI (391-400)  
4) EMEVVVLNID (430-439)

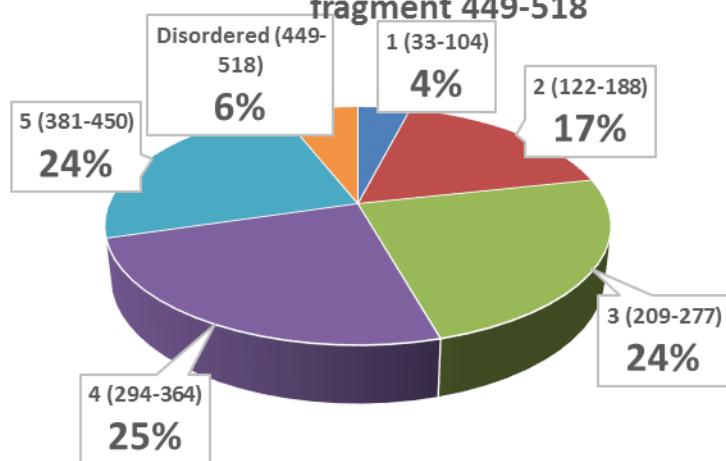


Structure of S1 protein predicted by AlphaFold 2

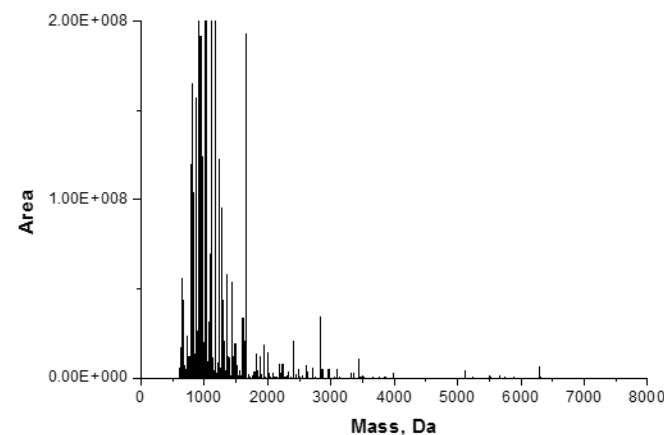


# Results of HPLC-MS analysis products of the hydrolysis of S1 protein from *Thermus Thermophilus*

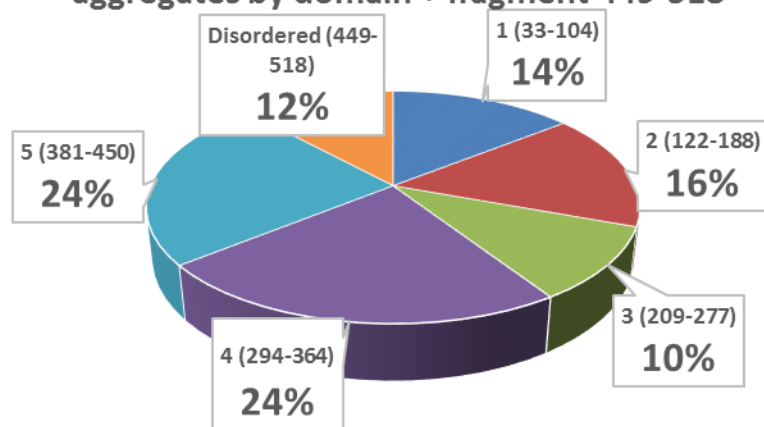
The proportion of the number of peptides of the S1 protein (non aggregated) by domain + fragment 449-518



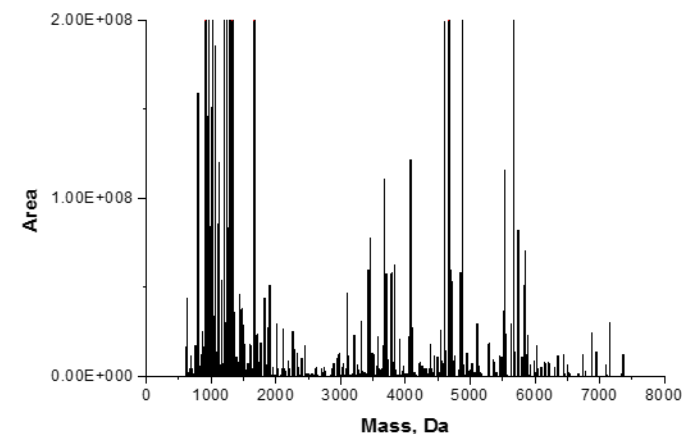
The Peptide Mapping for products of the hydrolysis of S1 protein (non aggregated)



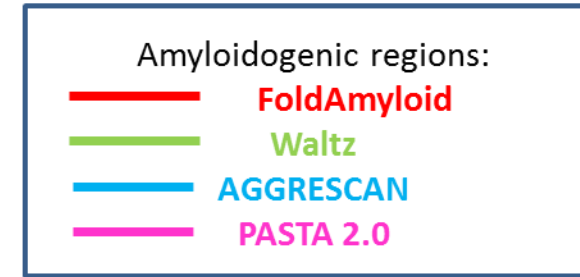
The proportion of the number of peptides of S1 aggregates by domain + fragment 449-518



The Peptide Mapping for products of the hydrolysis of S1 aggregates



# Peptides from products of limited proteolysis of associates S1 Thermus:



F.SMEAALQETEAR.L 14-25

R.VRPGQ**ILTGKVVLVGSEGVA**VDIGAKTEGI**IPF**.N 30-62

F.**NQ**LTTKPLSEELRNLLSPGDEVK**VQVLR**VPETG**QILLS**SRKKIEAQEKWDR.I 63-114

R.RVPNLDEFVGG**QVLAKIIEFHR**RKGRVILSR.R 157-187

R.VKGGV**VAELDGIQG**FMPASQL.D 133-153

K.SLEPGQ**VVEGTVVEVTDFGVFN**LG**PVDGLVHRSEITWGR**FNHPREVIQKGQK.V 205-257 **211-220, 221-229**

K.SLEPGQ**VVEGTVVEVTDFGVFN**LG**PVDGLVHRSEITWGR**FNHPR.E 205-249

R.**VRGKVVGLTQFGAFVEVE**PGLE**GLIHISEL**SWTKRPHKHPSEVVKEGDEVEAVVL.R 297-350

R.**VRGKVVGLTQFGAFVEVE**PGLE**GLIHISEL**SW.T 297-328

K.**ALI**PDPWTTVAEKYPVGT**RVRGKVVGLTQFGAFVEVE**PGLE**GLIHISEL**SW.T 278-328

K.**ALI**PDPWTTVAEKYPVGT**RVRGKVVGLTQFGAFVEVE**PGLE**GLIHISEL**SWTKRPHKHPSEVVK.E 278-340

F.KKGDEM**EVVVLNID**PVEQRVLSRKRLPPPLPQEEERPR.R 426-465

K.RVENPAALFKKGDEM**EVVVLNID**PVEQRVLSRKRLPPPLPQEEERPR.R 417-465 **430-439**

K.QTQPDPWQQLTEKYPPGT**VLKGVVTDFGVFEIE**PGIEGLVHVSELDHK.R 365-416 **391-400**

Y.**DASSVPTTTATVK**.L 500-512

R.REDRREYEYGA**VAEYNLYDA**SSVPTTTATVKLG**DLYGDLLA**SLGLEEEAEEK.S 482-533

R.KGAPRREDRREYEYGA**VAEYNLYDA**SSVPTTTATVKLG**DLYGDLLA**SLGLEEEAEEK.S 477-533

# Search results for amyloidogenic sites bPaS1

— Results of HPLC-MS analysis of bPaS1 aggregates

— Results of HPLC-MS analysis of "unaggregated" bPaS1

1 MSESFAELFE ESLKSLDMQP **GAIITGIVVD** IDGDWVTVHA GLKSEGVIPV EQFYNEQGEL  
 61 TIKVGDEVHV ALDAVEDGFG **ETKLSREKAK** **RAESWIVLEA** AFAADEVVKG VINGKVKGGF  
 121 TVDVNGIRAF LPGSLVDVRP VRDTTHLEGG **ELEFKVIKLD** QKRNNVVVSR RSVLEAENSA  
 181 EREALLESIQ EGQQVKGIVK NLT DYGAFVD LGGVDGLLHI **TDMAWKRIKH** PSEIVNVGDE  
 241 IDVKVLKFR ERNRVSLGLK QLGEDPWVAI KARYPEGTRV MARVTNLTDY GCFAELEEGV  
 301 EGLVHVSEMD WTNKNIHPSK VVQVGDEVEV **QVL DIDEERR** RISLGIKQCK SNPWEDFSSQ  
 361 FNKGDRISGT **IKSITDFGIF** IGLDGGIDGL VHLSDISWNE VGEEAVRRFK KGDELETVIL  
 421 SVDPERERIS LGIKQLEDDP FSNYASLHEK GSIVRGTVKE VDAKGAVISL GDDIEGILKA  
 481 SEISRDRVED ARNVLKEGEE VEAKIISIDR KSRVISLSVK SKDVDDEKDA MKELRKQEVE  
 541 SAGPTTIGDL IRAQMENQG

FoldAmyloid

Aggrescan

Waltz

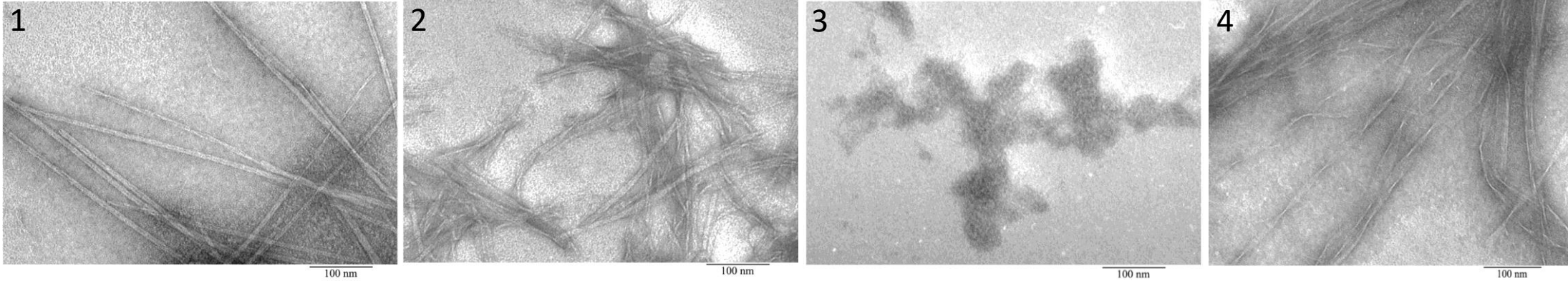
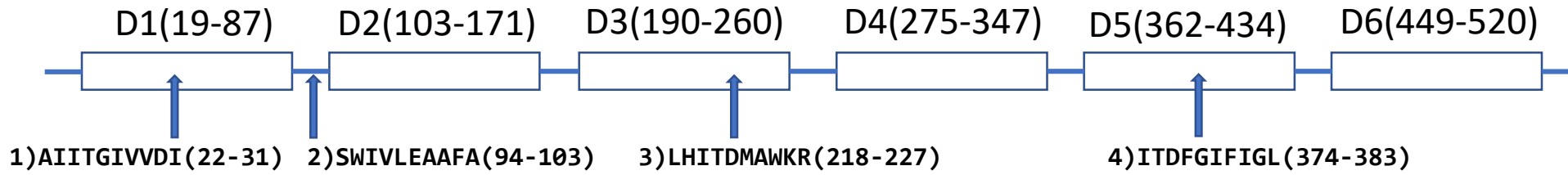
Pasta 2.0

Domain organization scheme bPaS1 :



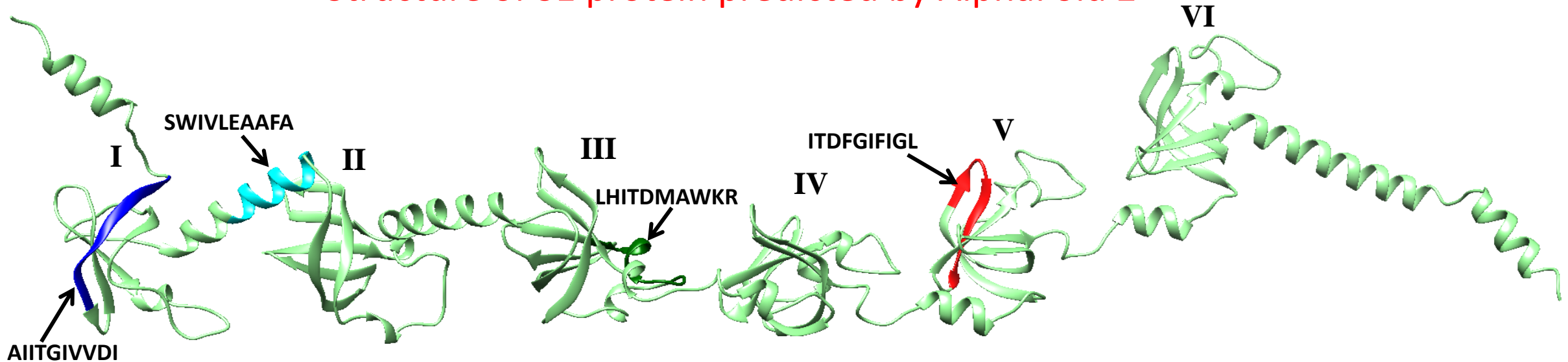
C

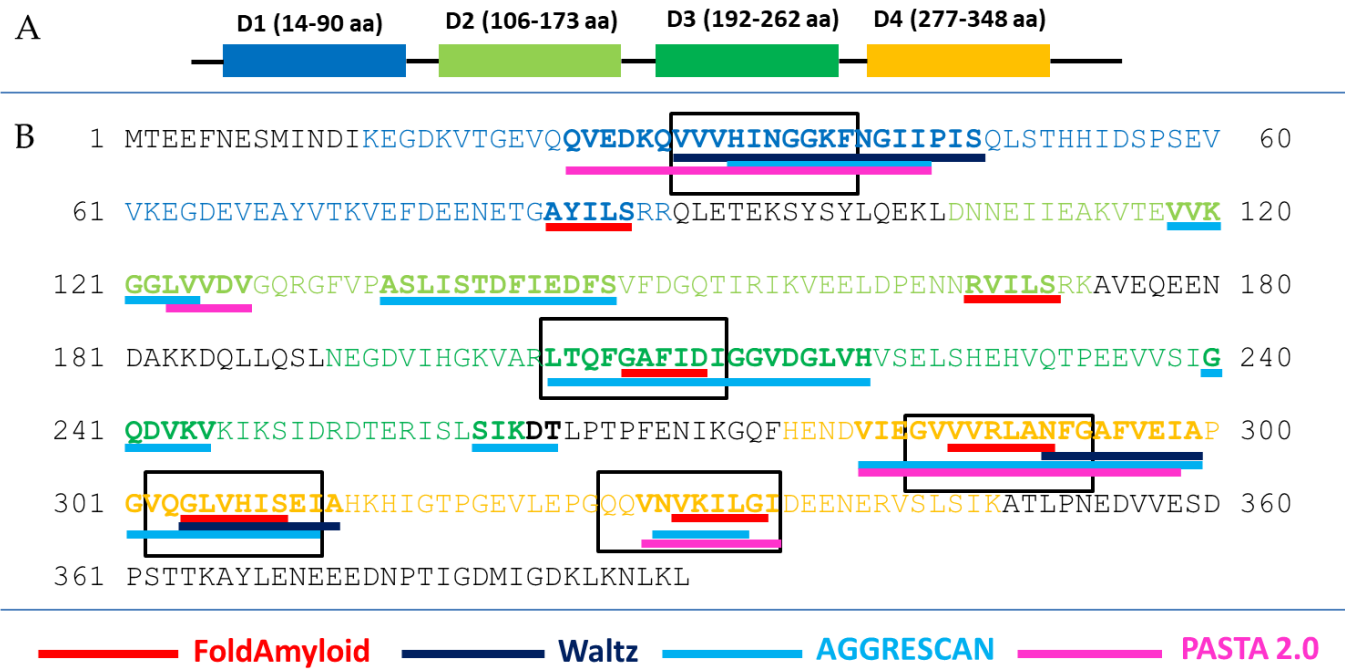
# S1 from *P. aeruginosa*



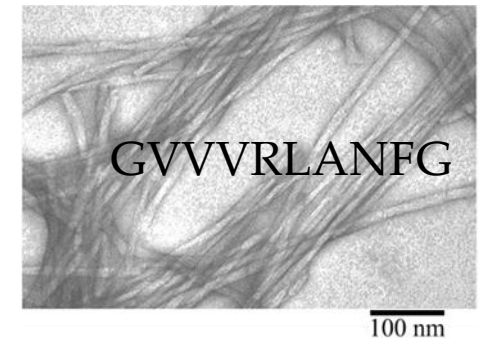
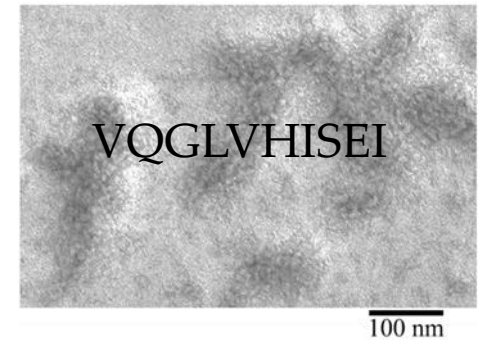
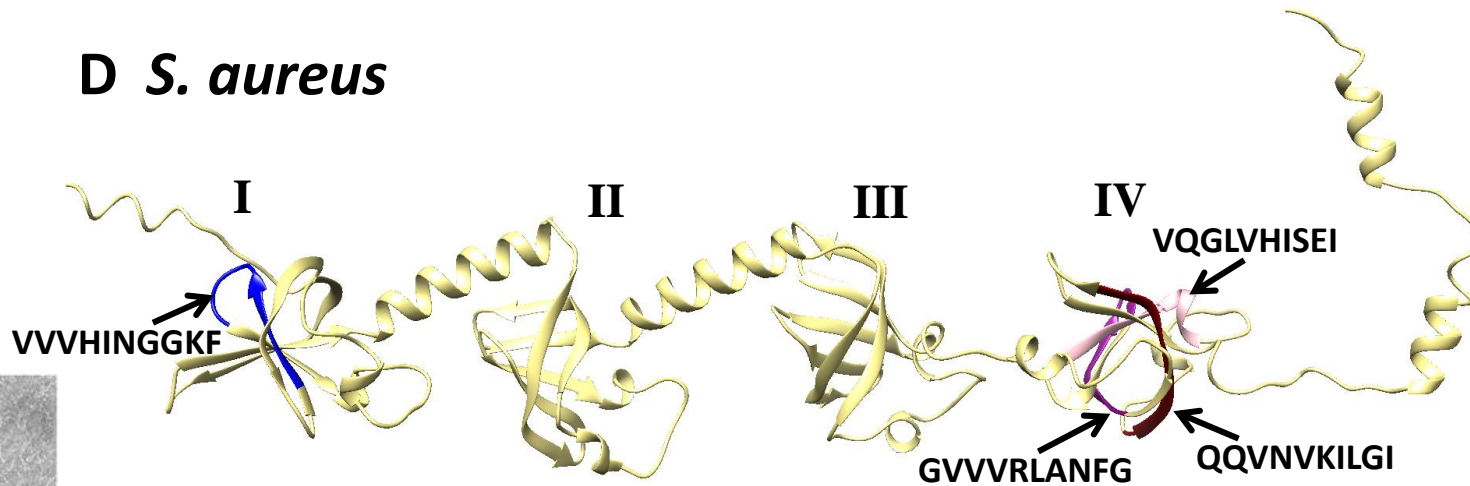
C *P. aeruginosa*

Structure of S1 protein predicted by AlphaFold 2





**D *S. aureus***



Structure of S1 protein predicted by AlphaFold 2

# Development and design of peptides based on the ribosomal S1 protein *T. thermophilus*

Peptide	Sequence	Prediction of antimicrobial activity (CAMPR3)		
		Support vector machine (SVM)	Random Tree Method (RF)	Discriminant Analysis (DA)
D9G	DFGVFVNLG	0.00	0.41	0.03
E10D	EMEVVVLNID	0.10	0.45	0.01
<u>V10I</u>	VTDFGVFVEI	<b>0.80</b>	0.44	0.03
V10T	VVEGTVVEVT	0.08	0.50	0.00



# Development and design of peptides based on the ribosomal S1 protein *T. thermophilus*

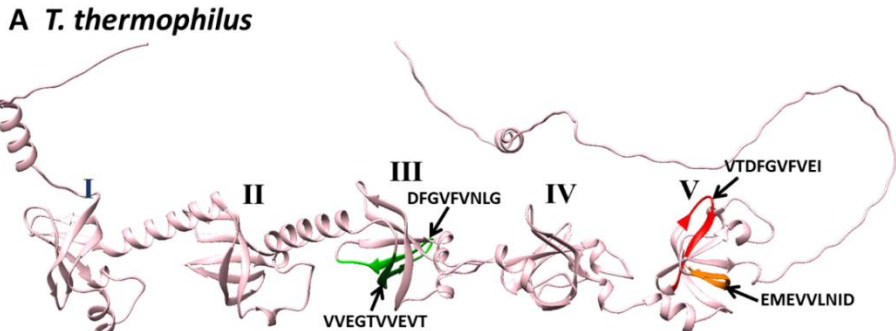
Peptide	Sequence	Prediction of antimicrobial activity (CAMPR3)		
		Support vector machine (SVM)	Random Tree Method (RF)	Discriminant Analysis (DA)
<u>R23I</u>	<b>RKKRRQRRR</b> GGAGVTDFGVFVEI	0.03	<b>0.51</b>	<b>0.99</b>
<u>R23T</u>	<b>RKKRRQRRR</b> GGAGVVEGTVVEVT	0.01	0.47	<b>0.59</b>

Fragment of the HIV-1 TAT pepti

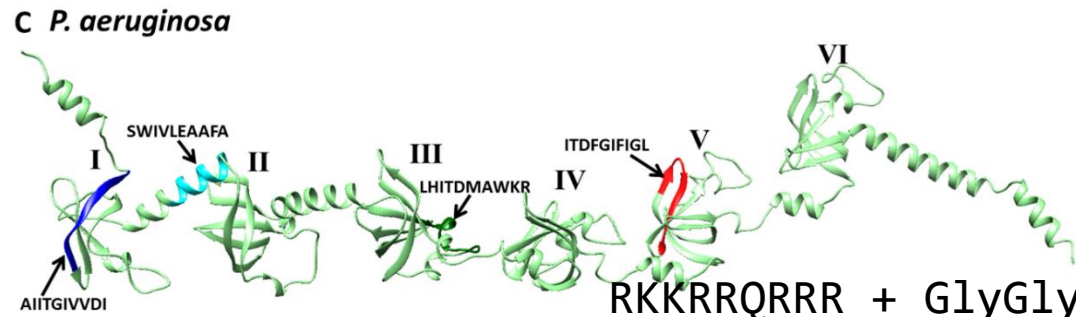
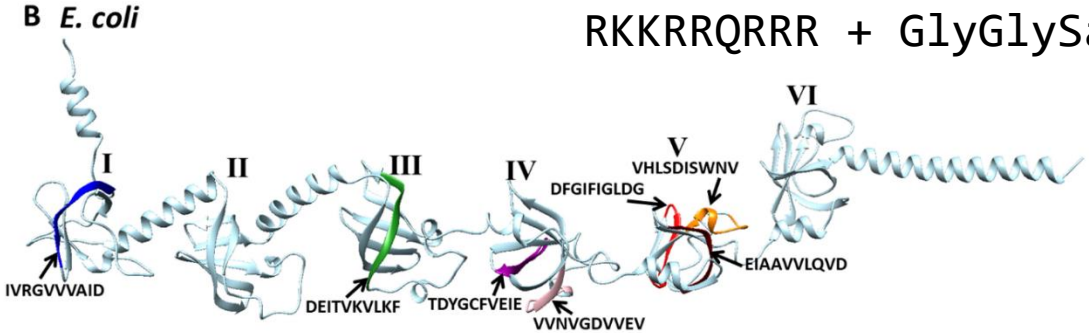
1. Increases antimicrobial activity
2. Promotes penetration into the eukaryotic cell
3. Does not interfere with the formation of aggregates of proteins and fibrils

**Structures of S1 proteins predicted by AlphaFold 2**

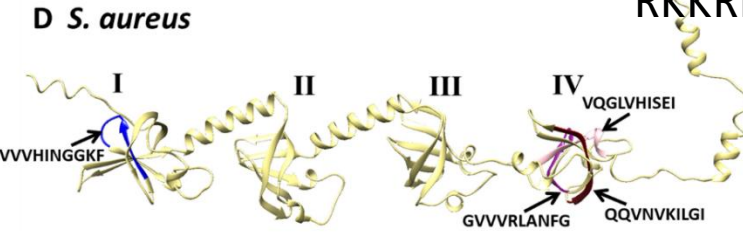
**Construction of hybrid peptides**



RKKRRQRRR + GlyGlySarGly + VVEGTVVEVT      R23T  
 RKKRRQRRR + GlyGlySarGly + VTDFGVFVEI      R23I



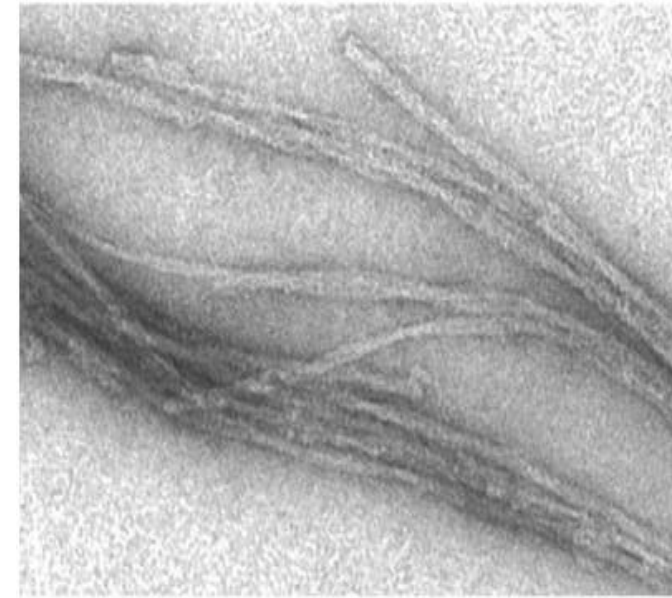
RKKRRQRRR + GlyGlySarGly + LHITDMAWKR      R23R  
 RKKRRQRRR + GlyGlySarGly + ITDFGIFIGL      R23L



RKKRRQRRRGGSarGVVWHI-Asi-GGKF      R23F  
 RKKRRQRRRGGSarGLTQFGAFIDI      R23DI  
 RKKRRQRRRGGSarGVQGLVHISEI      R23EI

# Co-aggregation of amyloidogenic peptides and ribosomal S1 protein

S1:R23T=1:5 (0.5 mg/ml and 2.5 mg/ml)



50 nm

S1:V10T=1:5 (0.5 mg/ml and 2.5 mg/ml)



50 nm

S1:R23I=1:5  
(0.5 mg/ml  
and 2.5  
mg/ml) from  
*T.*  
*thermophilus*



50 nm

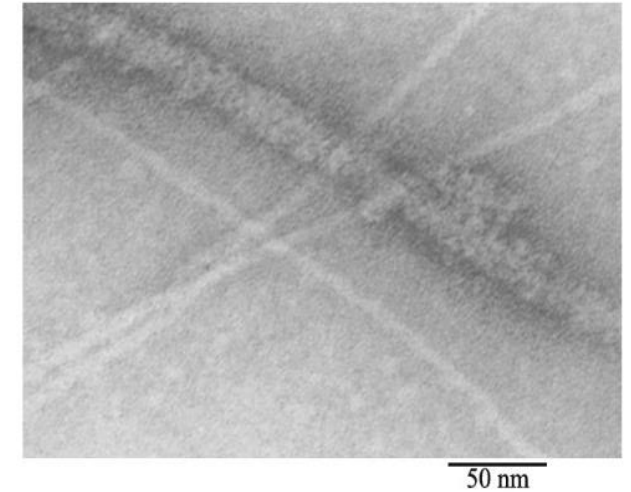
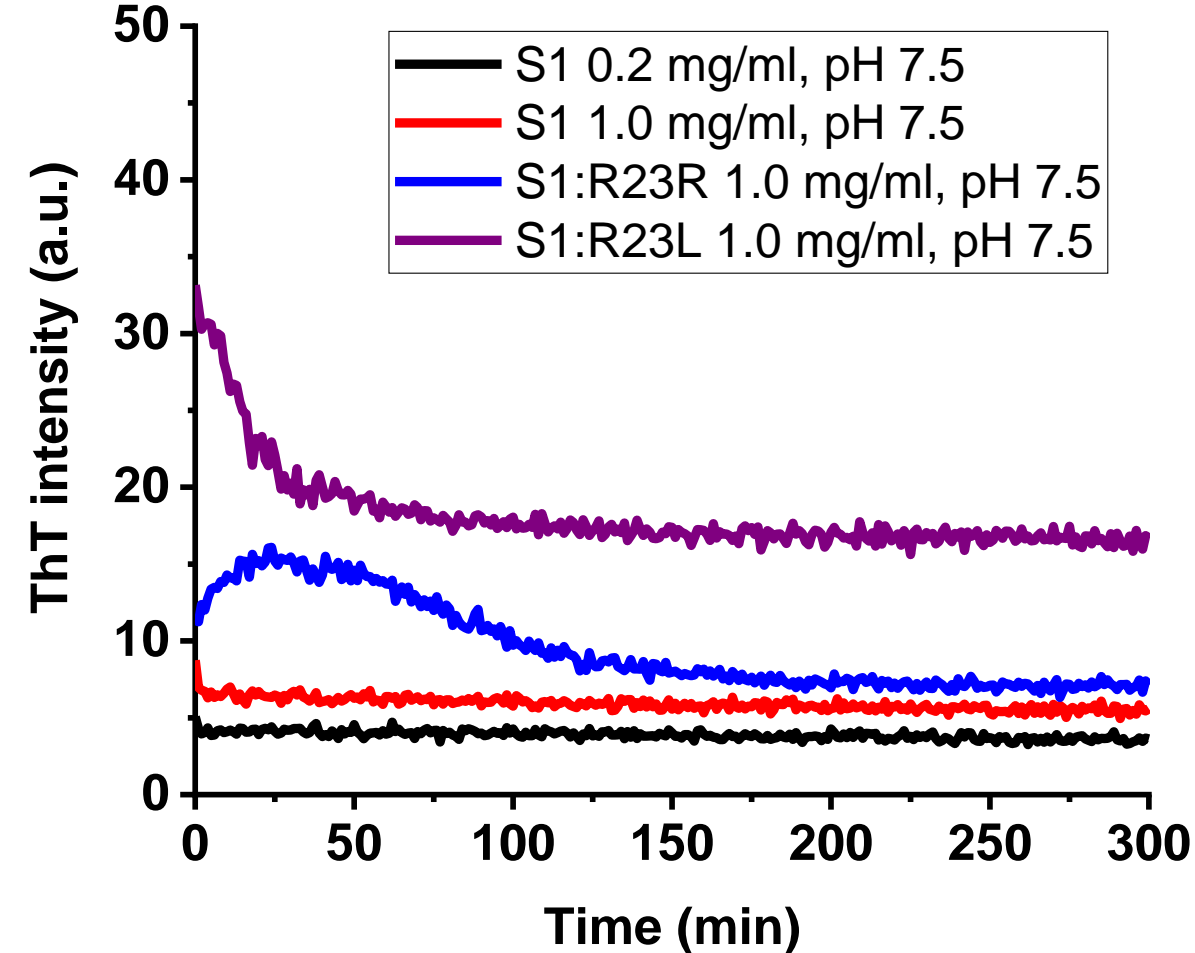
It was similarly verified that coaggregation of the V10T peptide and the S1 protein at 5:1 ratio led to the formation of fibrils.

# Kinetics of S1 coaggregation with peptides R23R and R23L

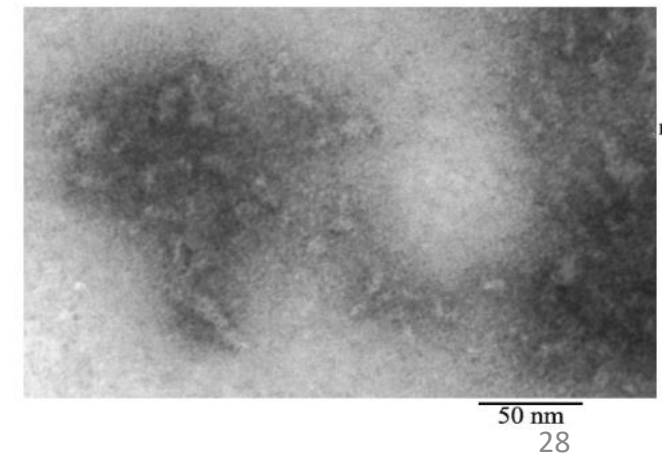
## Fluorescence results with ThT, incubation at 37 °C

ThT intensity for peptides and S1 *P.aeruginosa*

S1:R23R=1:5 (0.2 mg/ml and 1.0 mg/ml) from *P. aeruginosa*



S1:R23L=1:5 (0.2 mg/ml and 1.0 mg/ml) from *P. aeruginosa*



During co-aggregation of the S1 protein and R23R from *P. aeruginosa*, both aggregates of different sizes and fibrils of different diameters are observed. In addition, film-like polymers can sometimes be observed

# Antibacterial properties of peptides synthesized based on the predicted amyloidogenic sites of S1

$$E = 1 - \frac{A(\text{Experiment})}{A(\text{Control})} \quad (1)$$

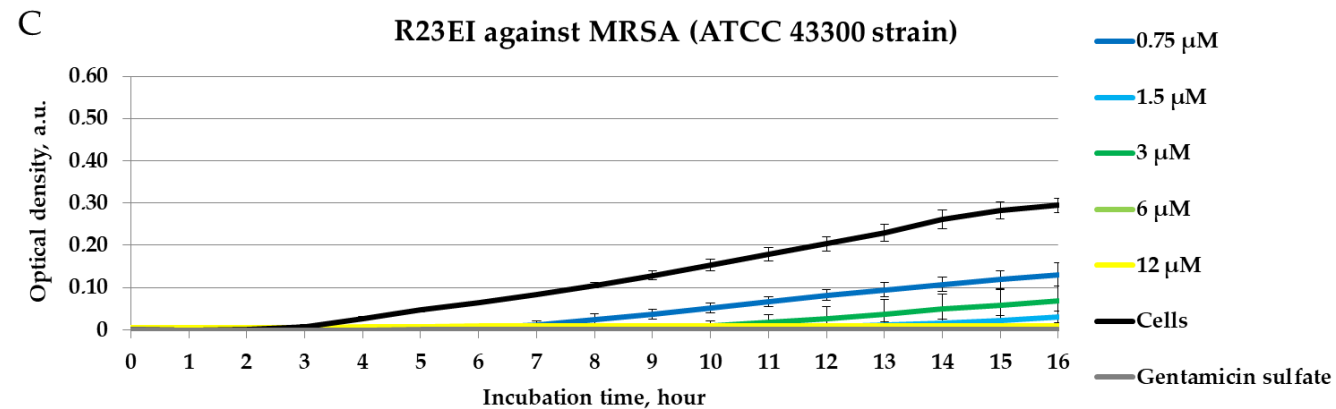
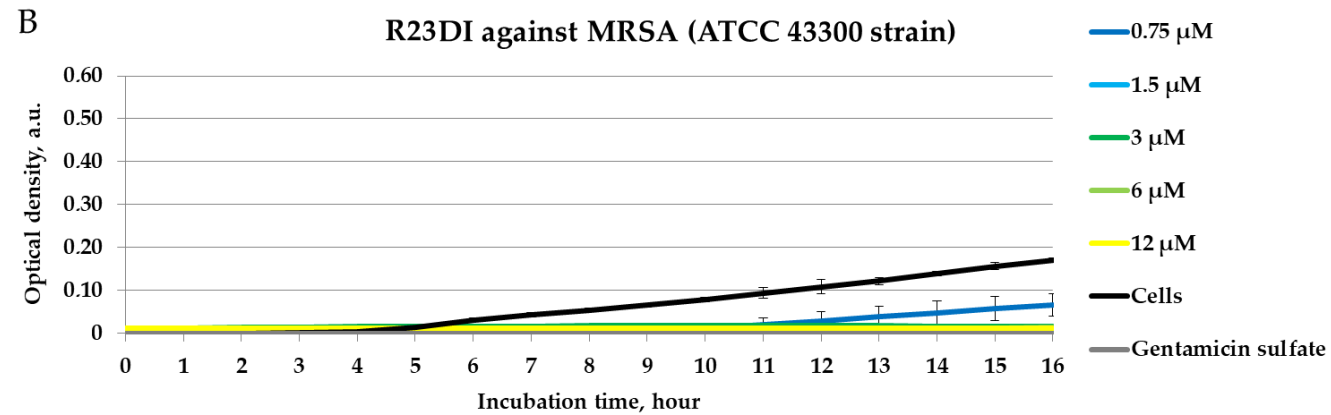
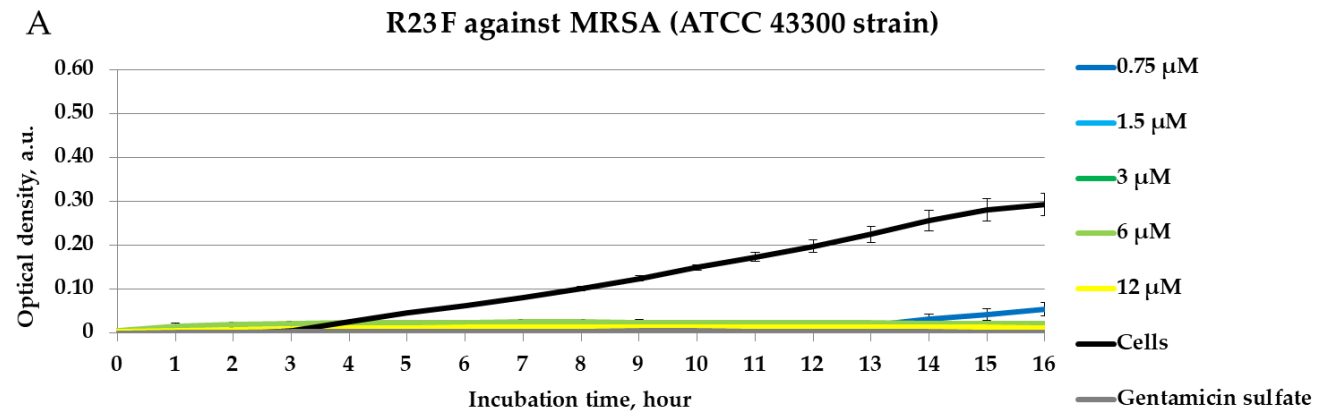
The evaluation of the antibacterial effect (E) was carried out according to formula (1), where A is the light absorption of the liquid culture of *T. thermophilus* after 24 hours of incubation.

An E value greater than 0.5 indicates an antibacterial effect.

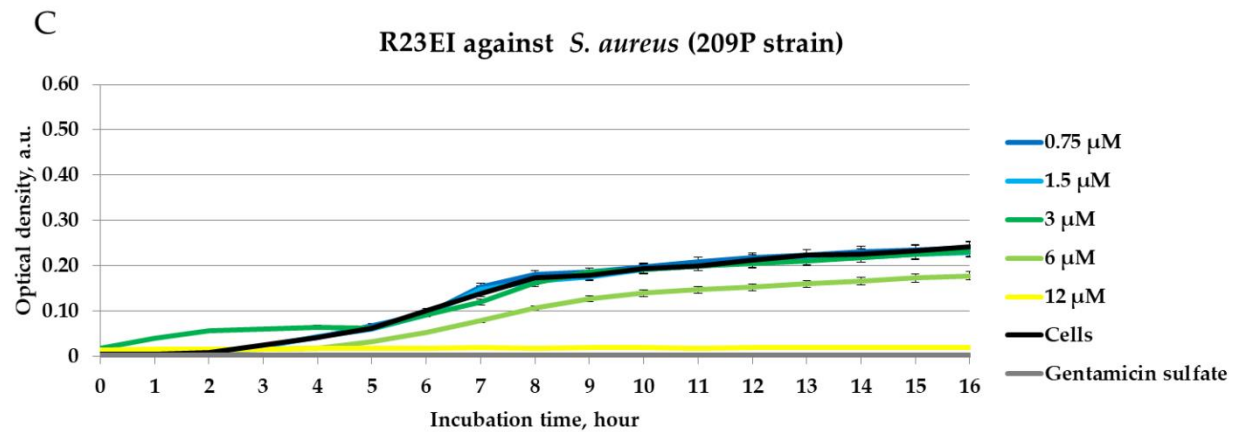
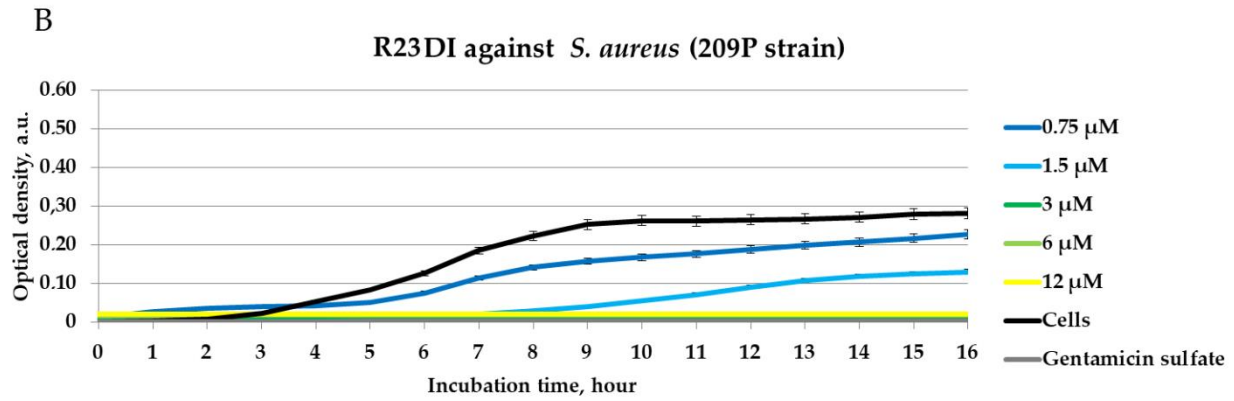
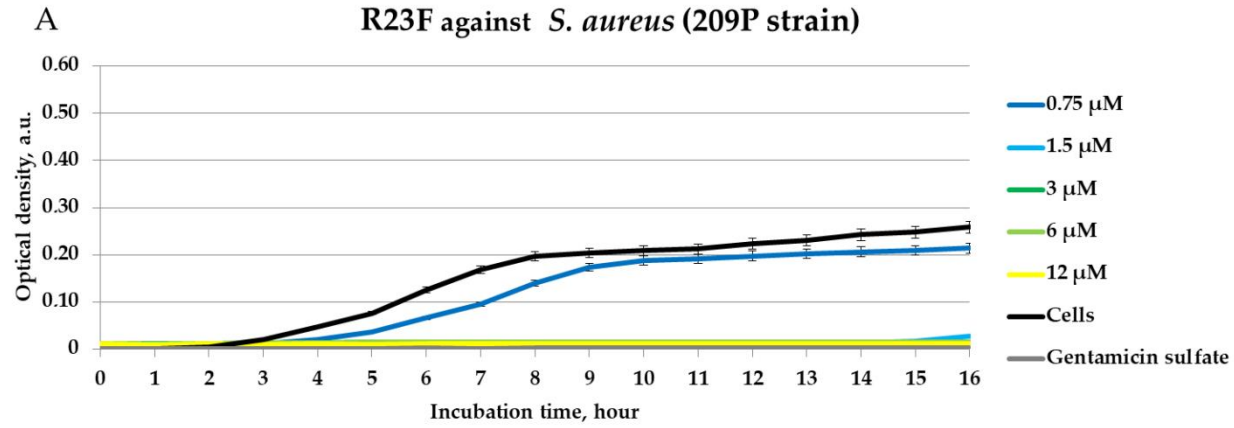
Sequence peptide	Peptide concentration and presence (+) or absence (-) antibacterial effect					
	1 μg/ml	10 μg/ml	50 μg/ml	100 μg/ml	500 μg/ml	1000 μg/ml
DFGVFVNLG	-	-	-	-	-	-
EMEVVVLNID	-	-	-	-	-	-
VTDFGVFVEI	-	-	-	-	-	+
VVEGTVVEVT	-	-	-	-	-	-
RKKRRQRRRGGSarG VTDFGVFVEI	-	-	+	+	+	-
RKKRRQRRRGGSarG VVEGTVVEVT	-	-	-	-	+	+

# Inhibitory activity of peptides

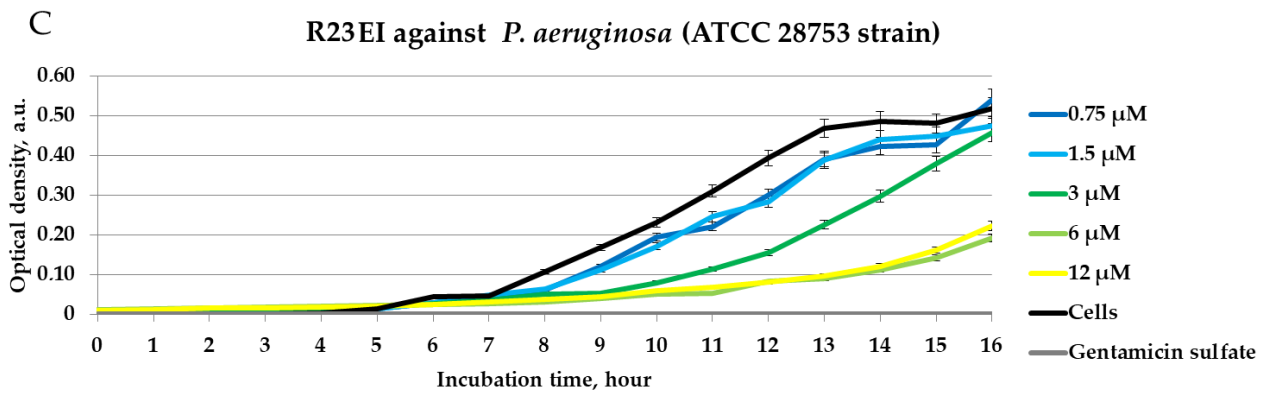
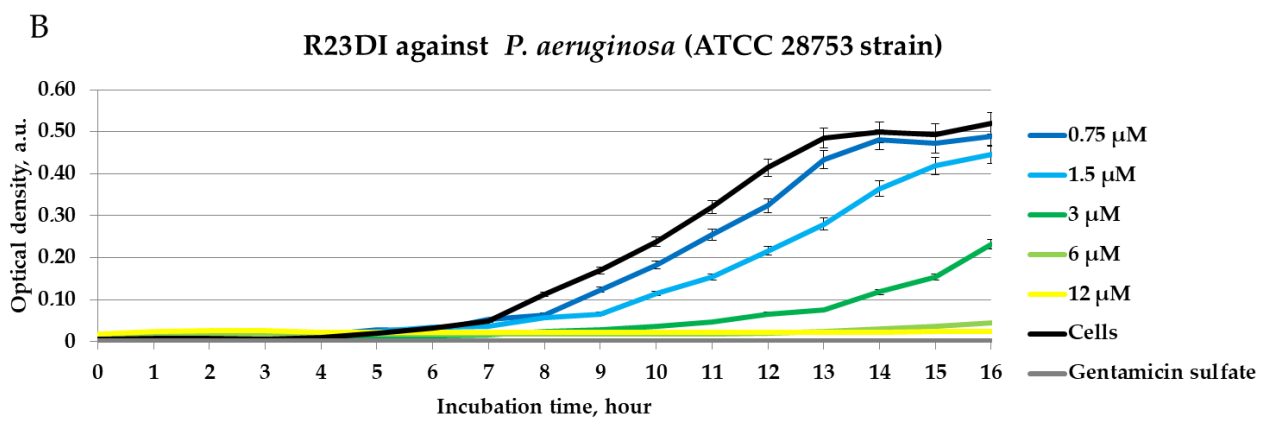
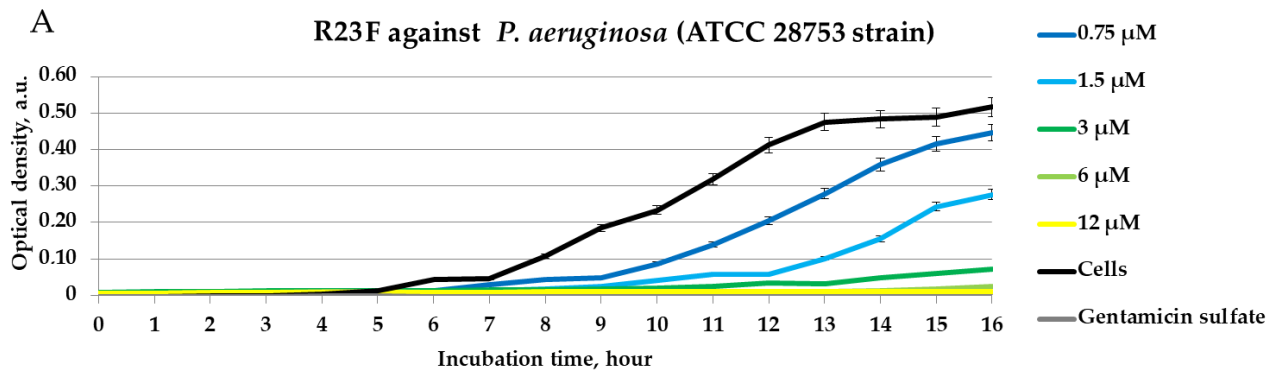
methicillin-resistant *S. aureus*



# Inhibitory activity of peptides






# Inhibitory activity of peptides








# Amyloidogenic AMP peptides based on S1 ribosomal protein *P. aeruginosa*

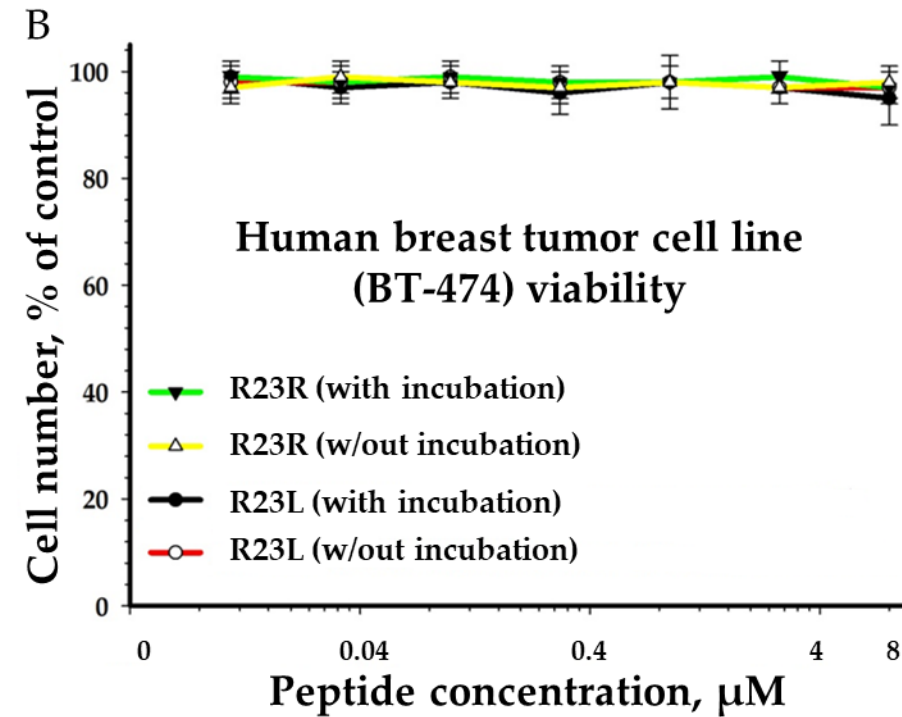
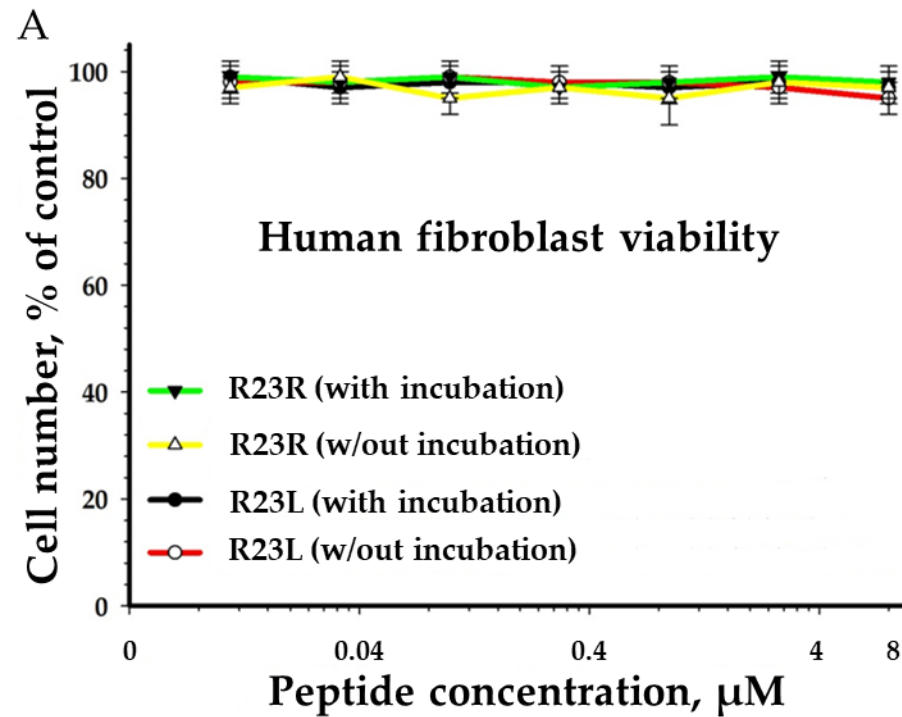
Sequence of hybrid peptides and folding patterns predicted by AlphaFold	Strain of the pathogenic microorganism	MIC for the tested hybrid peptide (μM)
<b>Based on the sequence S1 protein from <i>P. aeruginosa</i></b>		
<b>RKKRRQRRRGGGGITDFGIFGL</b> 	MRSA strain ATCC 43300 (resistant to ampicillin)	12
	<i>S. aureus</i> strain 209 (resistant to aztreonam)	>12
	<i>P. aeruginosa</i> (strain ATCC 28753) (resistant to sulfamethoxazole)	12
<b>RKKRRQRRRGGSarGLHITD-Nle-AWKR</b> 	<i>P. aeruginosa</i> (strain ATCC 28753) (resistant to sulfamethoxazole)	12
	<i>P. aeruginosa</i> (strain PA 103) (resistant to levomycetin)	>12
<b>RKKRRQRRRGGSarGITDFGIFGL</b> 	<i>P. aeruginosa</i> (strain ATCC 28753) (resistant to sulfamethoxazole)	12
	<i>P. aeruginosa</i> (strain PA 103) (resistant to levomycetin)	>12

Grishin SY, Domnin PA, Kravchenko SV, Azev VN, Mustaeva LG, Gorbunova EY, Kobayakova MI, Surin AK, Makarova MA, Kurpe SR, Fadeev RS, Vasilchenko AS, Firstova VV, Ermolaeva SA, Galzitskaya OV. Int J Mol Sci.;22(18):9776. **(2021)**

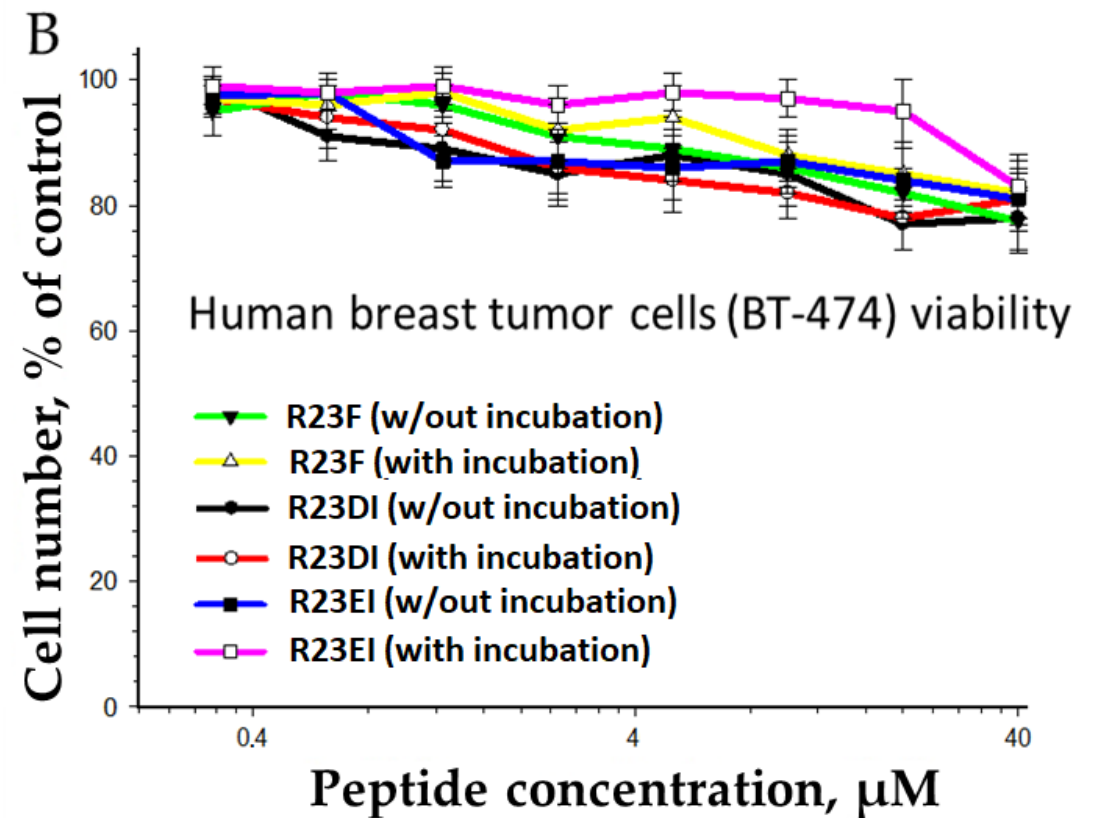
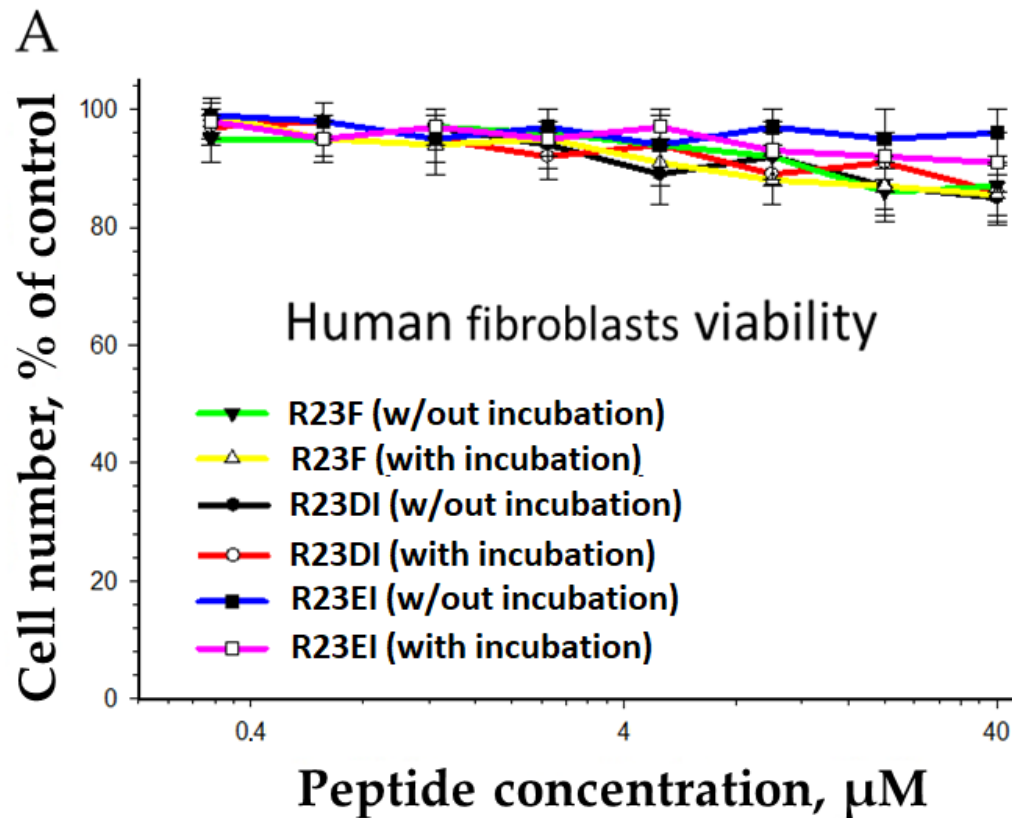
# Amyloidogenic AMP peptides based on S1 ribosomal protein *S. aureus*

Based on the sequence S1 protein from <i>S. aureus</i>		
<p><b>RKKRRQRRRGGSarGVVVHI-Asi-GGKF</b></p> 	<p>MRSA strain ATCC 43300 (resistant only to ampicillin)  <i>S. aureus</i> strain 209 (resistant to aztreonam)  <i>P. aeruginosa</i> strain ATCC 28753 (resistant to sulfamethoxazole)</p>	<p>3 3 12</p>
<p><b>RKKRRQRRRGGSarGLTQFGAFIDI</b></p> 	<p>MRSA strain ATCC 43300 (resistant only to ampicillin)  <i>S. aureus</i> strain 209 (resistant to aztreonam)  <i>P. aeruginosa</i> strain ATCC 28753 (resistant to sulfamethoxazole)</p>	<p>3 6 12</p>
<p><b>RKKRRQRRRGGSarGVQGLVHISEI</b></p> 	<p>MRSA strain ATCC 43300 (resistant only to ampicillin)  <i>S. aureus</i> strain 209 (resistant to aztreonam)  <i>P. aeruginosa</i> strain ATCC 28753 (resistant to sulfamethoxazole)</p>	<p>6 12 &gt;12</p>

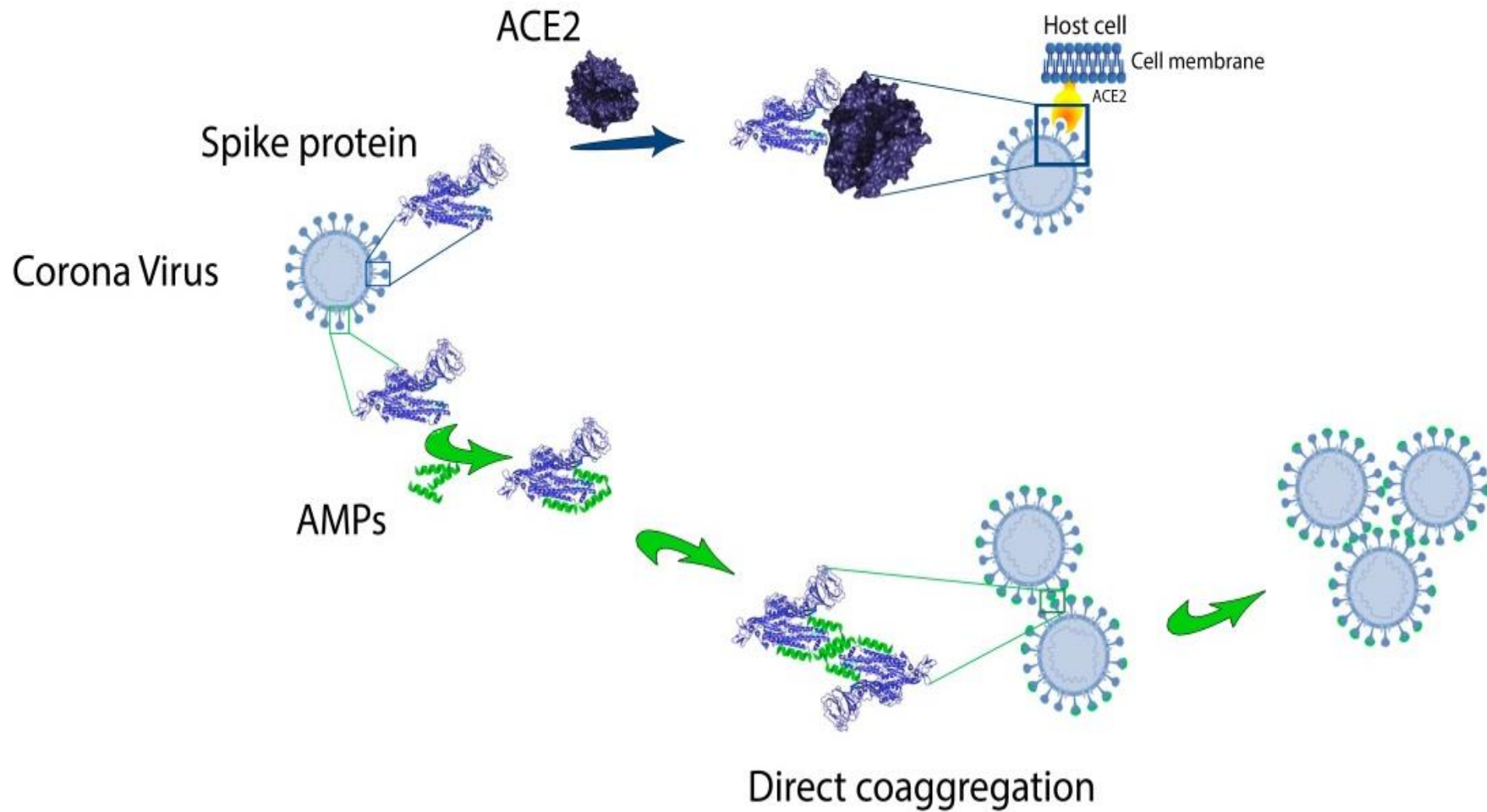
Effects of peptide treatment on survival the human fibroblasts (A) and breast tumor cell line BT-474 (B). Error bars show standard errors



Effect of peptide treatment on the survival of human fibroblasts (A) and the breast tumor cell line BT-474 (B) without preliminary incubation (18 h, 37 °C, in DMEM with 10% FBS) and after 72 h of co-incubation with peptide. Each of the experiments was carried out at least three times ( $n \geq 3$ )



# Hypothetical mechanism of targeted co-aggregation against CoV



Kurpe S.R., Grishin S.Yu., Surin A.K., Panfilov A.V., Slizen M.V., Chowdhury S.D., **Galzitskaya** O.V. Antimicrobial and Amyloidogenic Activity of Peptides. Can Antimicrobial Peptides Be Used Against SARS-CoV-2? INTERNATIONAL JOURNAL OF MOLECULAR SCIENCES 21, 9552. <https://doi.org/10.3390/ijms21249552> (2020)

# Conclusion

Theoretically predicted and experimentally confirmed the ability to manifest aggregation (amyloidogenic) and antibacterial properties of the studied peptides.

New antibacterial peptides have been created that effectively suppress the growth of *Pseudomonas aeruginosa* and *Staphylococcus aureus*, pathogenic bacteria that cause hospital infections.

## Acknowledgments

Grishin SY, Kravchenko SV, Domnin PA, Azev VN, Mustaeva LG, Gorbunova EY, Kurpe SR, Kobyakova MI, Surin AK, Suvorina MY, Makarova MA, Dzhus UF, Glukhov AS, Selivanova OM, Balobanov VA, Panfilov AV, Glyakina AV, Deruysheva EI, Machulin AV., Kochetov AP, Slizen MV, Fadeev RS, Vasilchenko AS, Firstova VV, Ermolaeva SA

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Thank you for your attention! Questions?