

# Amyloidogenic Regions in bPaS1

Subjects: [Biochemistry & Molecular Biology](#) | [Microbiology](#)

Contributor: Oxana Galzitskaya , Sergei Grishin

Bacterial S1 protein is a functionally important ribosomal protein. It is a part of the 30S ribosomal subunit and is also able to interact with mRNA and tmRNA. An important feature of the S1 protein family is a strong tendency towards aggregation.

ribosomal S1 proteins

amyloidogenic regions

toxicity

antibacterial peptides

amyloid

mass spectrometry

## 1. Introduction

The study of amyloids as ordered fibrillar protein aggregates is of great importance for elucidating their role in human pathologies, especially in neurodegenerative diseases [\[1\]\[2\]\[3\]](#). It is known that, under certain conditions, most proteins and peptides tend not only to aggregation, but also to form amyloid-like fibrils [\[4\]\[5\]\[6\]](#); in a particular case, the formation of amyloids of some proteins can be induced by other amyloidogenic proteins and peptides [\[7\]\[8\]](#). Currently, interest in the study of amyloids is also associated with the fact that they can be used in various nano- and bio-technological developments, including as antimicrobial agents against pathogenic microorganisms [\[9\]\[10\]\[11\]](#). In recent reviews of scientific articles, the prospects of using antimicrobial peptides in medicine are discussed [\[12\]\[13\]](#), including those acting by the mechanism of directed coaggregation with the target protein due to the interaction of amyloidogenic sites that constitute the spine of amyloid fibrils [\[14\]](#). Disruption of the native structure of the most important bacterial proteins, in particular ribosomal ones, caused by directed aggregation, can be accompanied by a loss of the functional activity of the protein, which, in turn, can lead to a change in normal cellular metabolism and the death of bacteria.

The ribosomal S1 protein is the largest bacterial protein of the 30S ribosomal subunit and can perform, in addition to structural, many other functions, interacting with both RNA and other proteins [\[15\]\[16\]\[17\]\[18\]](#). It was shown that amber mutation and knockout of the gene encoding the bS1 protein lead to the death of bacterial cells [\[19\]\[20\]](#). The bS1 protein, which is present only in bacterial cells, contains, depending on the taxonomic affiliation of the microorganism, from one to six domains of the S1 protein (D1–D6), separated by flexible regions [\[21\]\[22\]](#). It is important that the S1 domain is a structural variant of the oligosaccharide/oligonucleotide-binding fold (OB-fold) [\[23\]\[24\]](#) and can exhibit amyloidogenic properties, like another analog of the OB-fold, the cold shock domain [\[25\]](#). Previously, peptides with amyloidogenic properties and antimicrobial activity against *Thermus thermophilus* were synthesized and studied based on the sequences of the S1 domains of the ribosomal S1 protein of the model organism *T. thermophilus* [\[26\]](#).

*P. aeruginosa* is a pathogenic bacterium that can cause nosocomial infections [27][28], and for which cases of multiple antibiotic resistance are increasingly being reported [29][30]. Recently, antimicrobial peptides have been considered as an alternative to classical antibiotics for the treatment of diseases caused by multidrug-resistant strains of *P. aeruginosa* [31][32][33]. Information about the amyloidogenic regions in the structure of the ribosomal S1 protein from *P. aeruginosa* (bPaS1) will allow the development of new antimicrobial peptides that specifically interact with this target protein and cause its aggregation, which will ultimately lead to disruption of the functioning of the ribosomal S1 protein and suppress the vital activity of this pathogenic bacteria.

The main contribution to the formation of amyloids is made by amino acid residues, which contribute to a denser packing of the protein structure [34][35]. Consequently, protein regions included in the spine of amyloid fibrils are characterized by high resistance to protease treatment, which is used to determine amyloidogenic regions in products of limited proteolysis of aggregates [36][37].

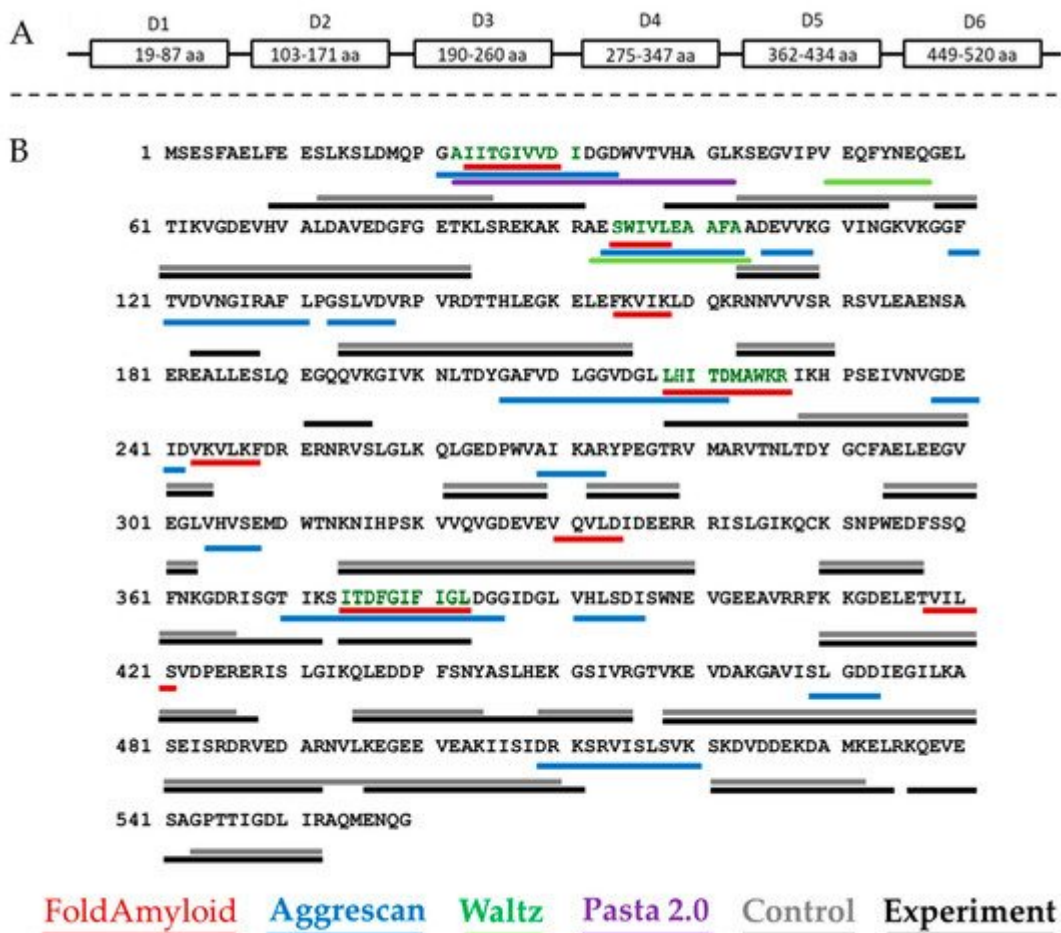
In the present work, amyloidogenic fragments were identified in the amino acid sequence of bPaS1, using the programs for searching and predicting amyloidogenic regions FoldAmyloid [38], Waltz [39], Pasta 2.0 [40] and AGGRESCAN [41], and experimentally by analyzing the products of limited proteolysis of bPaS1 aggregates using high performance liquid chromatography and mass spectrometry (LC-MS). The tendency to amyloid formation of peptides synthesized on the basis of amyloidogenic regions of bPaS1 was studied by electron microscopy (EM) and fluorescence spectroscopy (using thioflavin T (ThT)), which are widely used to detect amyloids [42][43][44].

## 2. Isolation and Purification of bPaS1

The *E. coli* strain was obtained, the genetic construct allows us to obtain the recombinant bPaS1 with additional inserts: an N-terminal sequence with 6 His, which allows the use of affinity chromatography purification; a specific TEV protease recognition site for cleaving intact bPaS1. Nucleic acids were precipitated with streptomycin sulfate and the precipitates were removed from protein samples. The degree of purification of bPaS1 preparations was assessed by electrophoresis of samples under denaturing conditions. The resulting final preparation had a purity of at least 90%.

## 3. Prediction and Experimental Determination of bPaS1 Regions Prone to Aggregation

The ability of a protein to aggregate and form amyloid-like fibrils is primarily determined by the presence of amyloidogenic regions in its structure, which can be predicted using special programs developed for this purpose. Prediction of amyloidogenic sites for bPaS1 was performed using four programs: FoldAmyloid, Waltz, AGGRESCAN, and Pasta 2.0 (Figure 1B).



**Figure 1.** Schematic representation of the domain organization of bPaS1 (A) and comparison of predicting amyloidogenic regions using programs with the results of peptide coverage after LC-MS analysis of hydrolysates of control and experimental (aggregate) protein preparations (B). The peptides identified in the control and experimental samples, respectively, are underlined in gray and black. The bPaS1 sequence is taken from the UniProt database (UniProt. Available online: <https://www.uniprot.org/uniprot/Q9HZ71> (accessed on 20 January 2021)). The regions of bPaS1, prototype peptide synthesis, are shown black–green color.

Each program predicts at least one region prone to amyloid formation in the bPaS1 sequence. However, the prediction results differ between different programs as they use different algorithms to find amyloidogenic regions. Subsequently, an experimental search for protein regions resistant to the action of proteases was carried out in the course of limited proteolysis and analysis of hydrolysates by LC-MS. In total, 146 significant peptides were found in the products of limited proteolysis of bPaS1 aggregates. At the same time, only 96 significant peptides were detected in the control sample without incubation for aggregation. Subsequently, significant peptides identified in the hydrolysates of control and experimental bPaS1 samples were ranked by length, the longest of them was compared with the bPaS1 sequence in order to determine the regions most protected from the action of proteases in aggregates and control preparations (Figure 1).

As shown in Figure 1B, the overall peptide coverage for protein aggregate hydrolysates and controls is similar. At the same time, additional amino acid sequences for aggregates have been identified that may play a role in the

formation of associates. LC-MS data were analyzed, and peptides with a length of at least five amino acid residues were selected (similar to the selection criterion in programs predicting amyloidogenic sequences of at least five amino acid residues), which are present only in hydrolysates of aggregates and are not observed in control samples (**Table 1**).

**Table 1.** Unique peptides identified as a result of comparing data from LC-MS analysis of hydrolysates of bPaS1 aggregates.

Peptide	Prediction of Amyloidogenicity	Percentage of Most Non-Polar a.a. [45] (V,I,F,C,L,A,M), %	Observed Mass, Da	Theoretical Mass, Da	Measurement Error, ppm *	Molecular Ion, <i>m/z</i>	Charge (z)	Value of the Function T **
FEESLK (9–14 a.a.)	No	0	751.376	751.3752	0.5	376.6951	+2	35.71
AITGIVVDI (22–31 a.a.)	AGGRESCAN, Pasta 2.0, partially FoldAmyloid (23–30 a.a.)	70	1012.618	1012.6168	0.9	507.3162	+2	41.51
VHAGLK (38–43 a.a.)	Pasta 2.0	50	623.374	623.3755	−1.8	312.6945	+2	17.19
DVNGIR (123–128 a.a.)	AGGRESCAN	33	672.356	672.3555	0.7	337.1852	+2	32
E (+27.99) GQQVK *** (191–196 a.a.)	No	17	715.35	715.35	−0.3	358.6822	+2	16.8
LHITDMAWKR (218–227 a.a.)	FoldAmyloid, partially AGGRESCAN (218–223 a.a.)	40	1269.666	1269.6652	0.4	635.8401	+2	114.36
ISGTIK (367–372 a.a.)	partially AGGRESCAN (370–372 a.a.)	33	617.375	617.3748	0.7	309.6949	+2	27.5
ITDFGIFIGL (374–383 a.a.)	AGGRESCAN, partially FoldAmyloid (375–382 a.a.)	60	1094.601	1094.6012	−0.1	548.3078	+2	76.43
ASLHEK (445–450 a.a.)	No	33	683.361	683.3602	1	342.6877	+2	30.93

\*—The accuracy of molecular weight measurement of 1 ppm (parts per million) corresponds to 0.001 Da for an ion with a molecular weight of 1000 Da. \*\*—For the PEAKS Studio 7.5 software we used (Bioinformatics Solution Inc., Waterloo, ON N2L 6J2, Canada) the value of the function  $T = -10 \lg P$ , where  $P$  is the probability that a false

Peptide	Prediction of Amyloidogenicity	Percentage of Most Non-Polar a.a. (V,I,F,C,L,A,M), % [45]	Observed Mass, Da	Theoretical Mass, Da	Measurement Error, ppm *	Molecular Ion, <i>m/z</i>	Charge (z)	Value of the T Function ** [46]. ***_	peptide
KQEVESA (536–542 a.a.)	No	29	789.388	789.3868	1.1	395.7011	+2	41.89	peptide

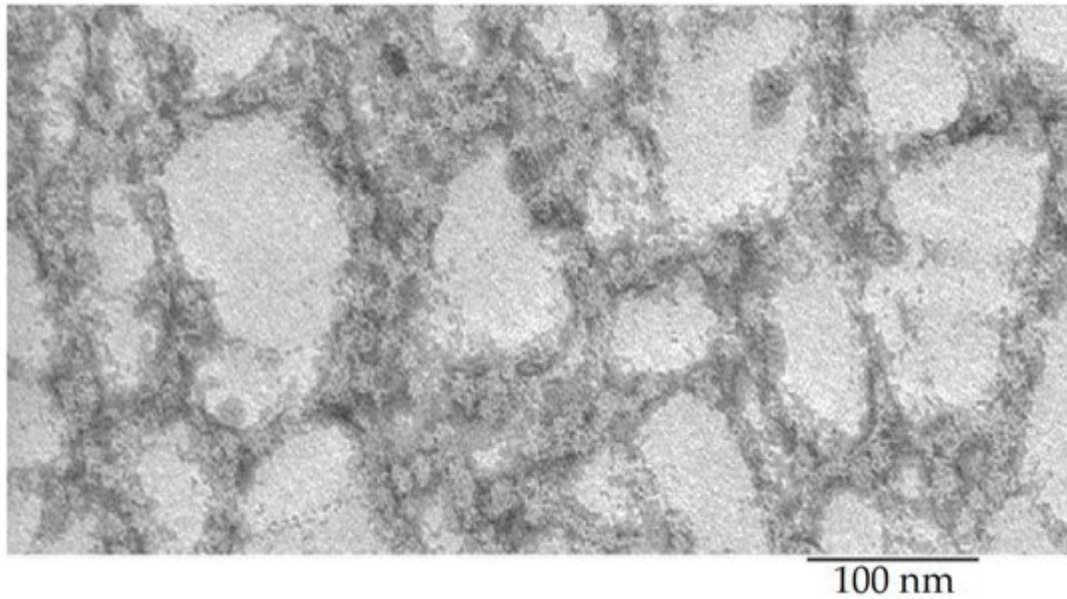
As follows from **Table 1**, the results of bioinformatic analysis and experimental determination of amyloidogenic regions in the bPaS1 sequence do not coincide for all protease-resistant peptides found in protein aggregates. At the same time, for the identified peptides FEESLK, AITGIVVDI, DVNGIR, LHITDMAWKR, ITDFGIFIGL, ASLHEK, KQEVESA, the accuracy of molecular weight measurement was no worse than 1.8 ppm, and the T function value was at least two times higher than the threshold value, which on the whole indicates a high reliability of the experimental determination. Thus, the bPaS1 regions that overlap with the results of predicting amyloidogenicity by at least two programs, or are identified only in the products of limited proteolysis of bPaS1 aggregates, were used as prototypes for the synthesis of peptides: AITGIVVDI, SWIVLEAAFA, ITDFGIFIGL and LHITDMAWKR (**Figure 1B**). Interestingly, the local distribution of non-polar amino acid residues, especially V, I, F, C, can be used to assess the propensity of a peptide to form amyloid structures [45]. The AITGIVVDI, SWIVLEAAFA, ITDFGIFIGL fragments are characterized by a high percentage of nonpolar amino acid residues (70%, 70%, and 60%, respectively), in contrast to the LHITDMAWKR peptide (40%).

The bPaS1 regions, which are theoretically predicted to be amyloidogenic and experimentally resistant to the action of proteases, are of interest for further study and discussion of the prospects for using antimicrobial peptides acting on the basis of directed coaggregation in the development of antimicrobial peptides.

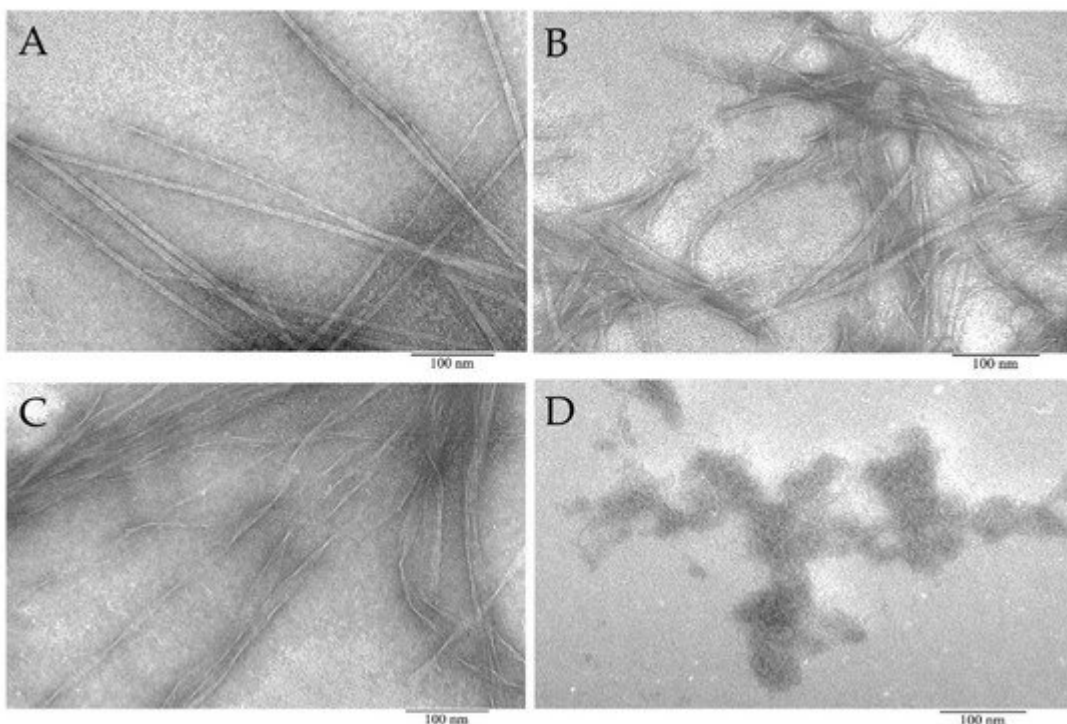
## 4. Electron Microscopic Images of Aggregates

Recombinant bPaS1 was isolated, purified and analyzed using the EM method. According to EM data (**Figure 2**), bPaS1 under conditions of 50 mM TrisHCl, pH 8.0; 100 mM NaCl; 10 mM MgCl<sub>2</sub>; 5 mM β-mercaptoethanol forms disordered aggregates. That is, as in the case of the recombinant protein bS1 from *T. thermophilus* [47], bPaS1 does not form fibrils. However, it should be noted that bPaS1, in contrast to the previously studied bS1 from *T. thermophilus*, is less prone to aggregation and forms small and less dense aggregates of various sizes [47]. The images of amyloids/aggregates of peptide synthesized based on the predicted amyloidogenic regions in the bPaS1 amino acid sequence are shown in **Figure 3**.





**Figure 2.** Electron microscopic image of the bPaS1 protein under conditions of 50 mM TrisHCl, pH 8.0; 100 mM NaCl; 10 mM MgCl<sub>2</sub>; 5 mM β-mercaptoethanol.



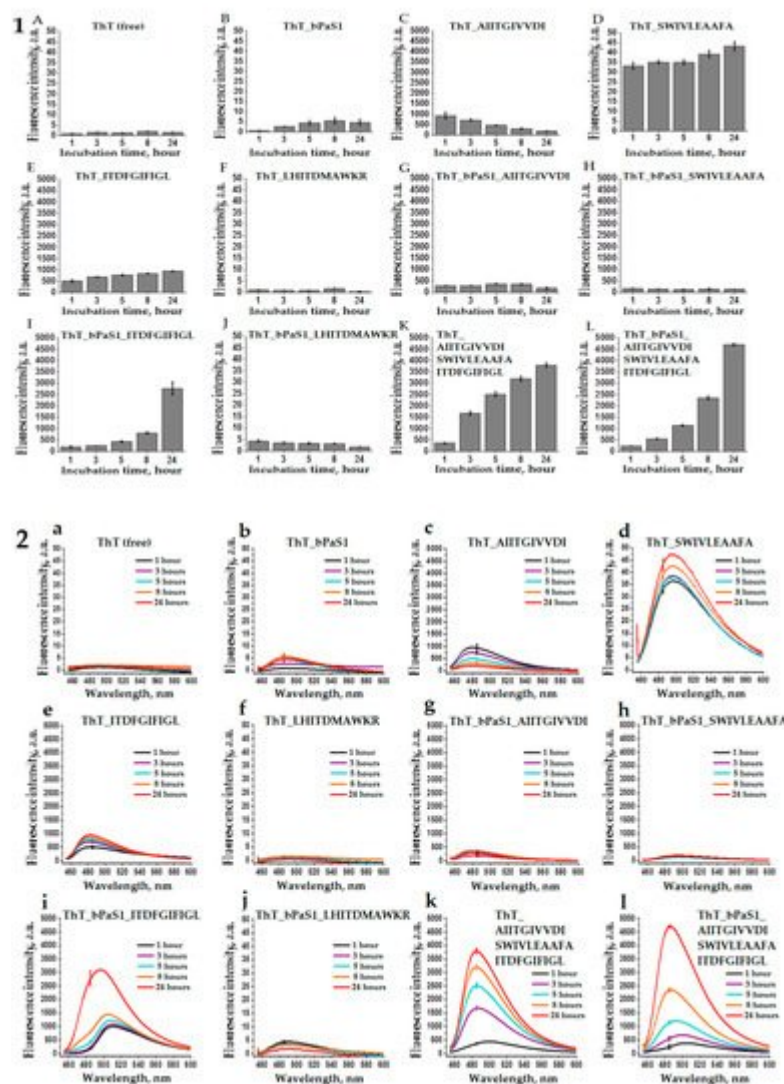
**Figure 3.** Electron microscopic images of aggregates formed from peptide preparations synthesized based on the bPaS1 sequence: AITGIVVDI (A), SWIVLEAAFA (B), ITDFGIFIGL (C), and disordered aggregates of the LHITDMAWKR peptide (D).

According to EM data, it was shown that the AITGIVVDI, SWIVLEAAFA, and ITDFGIFIGL peptides under conditions of 50 mM TrisHCl, pH 7.5; 150 mM NaCl, incubation for 5 h at 37 °C are able to form amyloid-like fibrils

of various morphologies. Under the same conditions, the LHITDMAWKR peptide did not form fibrils, but only disordered aggregates.

## 5. Thioflavin T Fluorescence Assay for Aggregation of bPaS1 and Peptides

The property of thioflavin T to bind to amyloid fibrils with a simultaneous multiple increase in fluorescence at a wavelength of  $\sim 485$  nm [48] was used by us to analyze the tendency towards the formation of amyloids in bPaS1 preparations and AITGVVDI, SWIVLEAFA, ITDFGIFGL, LHITDMAWKR peptides (Figure 4). In Figure 4 (Part 1), the ThT fluorescence intensity at a wavelength of  $\sim 485$  nm, exceeding the control values for free ThT by a factor of ten or more, was obtained for preparations of the AITGVVDI, SWIVLEAFA, ITDFGIFGL peptides (Figure 4C–E,K, Part 1), as well as in a mixture of these peptides with bPaS1 (Figure 4G–I,L, Part 1). At the same time, for bPaS1 preparations and the LHITDMAWKR peptide (Figure 4B,F, Part 1), as well as for their mixture in solution (Figure 4J, Part 1), a multiple increase in the ThT fluorescence intensity was not observed.



**Figure 4.** Histograms (1) and spectra (2) of fluorescence intensity of free thioflavin T (A,a) and in solution with bPaS1 (B,b), individual peptides AITGIVVDI (C,c), SWIVLEAAFA (D,d), ITDFGIFIGL (E,e), LHITDMAWKR (F,f), a mixture of peptides (K,k), as well as in mixtures of bPaS1 with peptides (G,g), (H,h), (I,i), (J,j), (L,l). Error bars with standard deviations for the mean values of the measured fluorescence intensity after 1, 3, 5, 8, and 24 h of incubation are shown.

Thus, the presence of the effect of a multiple increase in the ThT fluorescence intensity upon incubation with preparations of the AITGIVVDI, SWIVLEAAFA, ITDFGIFIGL peptides and the absence of such an effect for preparations with the LHITDMAWKR peptide is consistent with the data of electron microscopy that the AITGIVVDI, SWIVLEAAFA, ITDFGIFIGL peptides form amyloid fibrils, while only disordered aggregates of the peptide are found in the LHITDMAWKR preparations.

It should be noted that when testing the propensity for coaggregation of individual peptides with bPaS1, the greatest increase in the ThT fluorescence intensity was observed in a mixture of the ITDFGIFIGL peptide with bPaS1 after 24 h of incubation (Figure 4i, Part 2).

Thus, although bPaS1 preparations do not form amyloid-like fibrils, they affect the change in the relative intensity and wavelength of the maximum intensity of ThT fluorescence in mixtures with amyloidogenic peptides. No such effects were observed in mixtures of bPaS1 with the non-amyloidogenic LHITDMAWKR peptide.

---

## References

1. A. A. Nizhnikov; K. S. Antonets; S. G. Inge-Vechtomov; Amyloids: from pathogenesis to function. *Biochemistry (Moscow)* **2015**, *80*, 1127-1144, 10.1134/s0006297915090047.
2. Y. Y. Stroylova; G. G. Kiselev; E. V. Schmalhausen; V. I. Muronetz; Prions and chaperones: Friends or foes?. *Biochemistry (Moscow)* **2014**, *79*, 761-775, 10.1134/s0006297914080045.
3. Jacques Fantini; Henri Chahinian; Nouara Yahi; Progress toward Alzheimer's disease treatment: Leveraging the Achilles' heel of A $\beta$  oligomers?. *Protein Science* **2020**, *29*, 1748-1759, 10.1002/pro.3906.
4. A. B. Matiiv; N. P. Trubitsina; A. G. Matveenko; Y. A. Barbitoff; G. A. Zhouravleva; S. A. Bondarev; Amyloid and Amyloid-Like Aggregates: Diversity and the Term Crisis. *Biochemistry (Moscow)* **2020**, *85*, 1011-1034, 10.1134/s0006297920090035.
5. Mariya Yu. Suvorina; Olga M. Selivanova; Elizaveta I. Grigorashvili; Alexey D. Nikulin; Victor V. Marchenkov; Alexey K. Surin; Oxana V. Galzitskaya; Studies of Polymorphism of Amyloid- $\beta$  42 Peptide from Different Suppliers. *Journal of Alzheimer's Disease* **2015**, *47*, 583-593, 10.3233/jad-150147.



6. Yana A. Zabrodskaya; Dmitry V. Lebedev; Marja A. Egorova; Aram A. Shaldzhyan; Alexey Shvetsov; Alexander Kuklin; Daria S. Vinogradova; Nikolay V. Klopov; Oleg V. Matusевич; Taisiia Cheremnykh; et al. Rajeew Dattani Vladimir V. Egorov The amyloidogenicity of the influenza virus PB1-derived peptide sheds light on its antiviral activity. *Biophysical Chemistry* **2018**, *234*, 16-23, 10.1016/j.bpc.2018.01.001.
7. Rundong Hu; Baiping Ren; Mingzhen Zhang; Hong Chen; Yonglan Liu; Lingyun Liu; Xiong Gong; Binbo Jiang; Jie Ma; Jie Zheng; et al. Seed-Induced Heterogeneous Cross-Seeding Self-Assembly of Human and Rat Islet Polypeptides. *ACS Omega* **2017**, *2*, 784-792, 10.1021/acsomega.6b00559.
8. Ibrahim Javed; Zhenzhen Zhang; Jozef Adamcik; Nicholas Andrikopoulos; Yuhuan Li; Daniel E. Otzen; Sijie Lin; Raffaele Mezzenga; Thomas P. Davis; Feng Ding; et al. Pu Chun Ke Accelerated Amyloid Beta Pathogenesis by Bacterial Amyloid FapC. *Advanced Science* **2020**, *7*, 202001299, 10.1002/advs.202001299.
9. Pu Chun Ke; Ruhong Zhou; Louise C. Serpell; Roland Riek; Tuomas P. J. Knowles; Hilal A. Lashuel; Ehud Gazit; Ian W. Hamley; Thomas P. Davis; Marcus Fändrich; et al. Daniel Erik Otzen Matthew R. Chapman Christopher M. Dobson David S. Eisenberg Raffaele Mezzenga Half a century of amyloids: past, present and future. *Chemical Society Reviews* **2020**, *49*, 5473-5509, 10.1039/c9cs00199a.
10. Annalisa Pastore; Francesco Raimondi; Lawrence Rajendran; Piero Andrea Temussi; Why does the A $\beta$  peptide of Alzheimer share structural similarity with antimicrobial peptides?. *Communications Biology* **2020**, *3*, 1-7, 10.1038/s42003-020-0865-9.
11. Nir Salinas; Einav Tayeb-Fligelman; Massimo D. Sammito; Daniel Bloch; Raz Jelinek; Dror Noy; Isabel Usón; Meytal Landau; The amphibian antimicrobial peptide uperin 3.5 is a cross- $\alpha$ /cross- $\beta$  chameleon functional amyloid. *Proceedings of the National Academy of Sciences* **2021**, *118*, e2014442118, 10.1073/pnas.2014442118.
12. Giovanna Batoni; Giuseppantonio Maisetta; Semih Esin; Therapeutic Potential of Antimicrobial Peptides in Polymicrobial Biofilm-Associated Infections. *International Journal of Molecular Sciences* **2021**, *22*, 482, 10.3390/ijms22020482.
13. Mithoor Divyashree; Madhu K. Mani; Dhanasekhar Reddy; Ranjith Kumavath; Preetam Ghosh; Vasco Azevedo; Debmalya Barh; Clinical Applications of Antimicrobial Peptides (AMPs): Where do we Stand Now?. *Protein & Peptide Letters* **2020**, *27*, 120-134, 10.2174/0929866526666190925152957.
14. Stanislav R. Kurpe; Sergei Yu. Grishin; Alexey K. Surin; Alexander V. Panfilov; Mikhail V. Slizen; Saikat D. Chowdhury; Oxana V. Galzitskaya; Antimicrobial and Amyloidogenic Activity of Peptides. Can Antimicrobial Peptides Be Used Against SARS-CoV-2?. *International Journal of Molecular Sciences* **2020**, *21*, 9552, 10.3390/ijms21249552.

15. Nusrat Shahin Qureshi; Jasleen Kaur Bains; Sridhar Sreeramulu; Harald Schwalbe; Boris Fürtig; Conformational switch in the ribosomal protein S1 guides unfolding of structured RNAs for translation initiation. *Nucleic Acids Research* **2018**, *46*, 10917-10929, 10.1093/nar/gky746.
16. Paul E Lund; Surajit Chatterjee; May Daher; Nils G Walter; Protein unties the pseudoknot: S1-mediated unfolding of RNA higher order structure. *Nucleic Acids Research* **2019**, *48*, 2107-2125, 10.1093/nar/gkz1166.
17. Muhammad S. Azam; Carin K. Vanderpool; Translation inhibition from a distance: The small RNA SgrS silences a ribosomal protein S1-dependent enhancer. *Molecular Microbiology* **2020**, *114*, 391-408, 10.1111/mmi.14514.
18. Z. S. Kutlubaeva; H. V. Chetverina; A. B. Chetverin; The Contribution of Ribosomal Protein S1 to the Structure and Function of Q $\beta$  Replicase. *Acta Naturae* **1970**, *9*, 24-30.
19. Madoka Kitakawa; Katsumi Isono; An amber mutation in the gene rpsA for ribosomal protein S1 in *Escherichia coli*. *Molecular Genetics and Genomics* **1982**, *185*, 445-447, 10.1007/bf00334137.
20. Michael A. Sorensen; Jens Fricke; Steen Pedersen; Ribosomal protein S1 is required for translation of most, if not all, natural mRNAs in *Escherichia coli* in vivo. *Journal of Molecular Biology* **1998**, *280*, 561-569, 10.1006/jmbi.1998.1909.
21. Evgenia I. Deryusheva; Andrey V. Machulin; Maxim A. Matyunin; Oxana V. Galzitskaya; Investigation of the Relationship between the S1 Domain and Its Molecular Functions Derived from Studies of the Tertiary Structure.. *Molecules* **2019**, *24*, 3681, 10.3390/molecules24203681.
22. Andrey Machulin; Evgenia Deryusheva; Mikhail Lobanov; Oxana Galzitskaya; Repeats in S1 Proteins: Flexibility and Tendency for Intrinsic Disorder. *International Journal of Molecular Sciences* **2019**, *20*, 2377, 10.3390/ijms20102377.
23. Mohd. Amir; Vijay Kumar; Ravins Dohare; Asimul Islam; Faizan Ahmad; Imtaiyaz Hassan; Sequence, structure and evolutionary analysis of cold shock domain proteins, a member of OB fold family. *Journal of Evolutionary Biology* **2018**, *31*, 1903-1917, 10.1111/jeb.13382.
24. Evgenia Deryusheva; Andrey Machulin; Olga M. Selivanova; Oxana V. Galzitskaya; Taxonomic distribution, repeats, and functions of the S1 domain-containing proteins as members of the OB-fold family. *Proteins: Structure, Function, and Bioinformatics* **2017**, *85*, 602-613, 10.1002/prot.25237.
25. Sergey G. Guryanov; Olga M. Selivanova; Alexey D. Nikulin; Gennady A. Enin; Bogdan Melnik; Dmitry Kretov; Igor N. Serdyuk; Lev P. Ovchinnikov; Formation of Amyloid-Like Fibrils by Y-Box Binding Protein 1 (YB-1) Is Mediated by Its Cold Shock Domain and Modulated by Disordered Terminal Domains. *PLOS ONE* **2012**, *7*, e36969, 10.1371/journal.pone.0036969.
26. Stanislav R. Kurpe; Sergei Yu. Grishin; Alexey K. Surin; Olga M. Selivanova; Roman S. Fadeev; Ylyana F. Dzhus; Elena Yu. Gorbunova; Leila G. Mustaeva; Vyacheslav N. Azev; Oxana V.

- Galzitskaya; et al. Antimicrobial and Amyloidogenic Activity of Peptides Synthesized on the Basis of the Ribosomal S1 Protein from *Thermus Thermophilus*. *International Journal of Molecular Sciences* **2020**, *21*, 6382, 10.3390/ijms21176382.
27. Carlos Juan; Carmen Peña; Antonio Oliver; Host and Pathogen Biomarkers for Severe *Pseudomonas aeruginosa* Infections. *Journal of Infectious Diseases* **2017**, *215*, S44-S51, 10.1093/infdis/jiw299.
28. Yu-Xuan Ma; Chen-Yu Wang; Yuan-Yuan Li; Jing Li; Qian-Qian Wan; Ji-Hua Chen; Franklin R. Tay; Li-Na Niu; Considerations and Caveats in Combating ESKAPE Pathogens against Nosocomial Infections. *Advanced Science* **2019**, *7*, 1901872, 10.1002/advs.201901872.
29. Wontae Hwang; Sang Sun Yoon; Virulence Characteristics and an Action Mode of Antibiotic Resistance in Multidrug-Resistant *Pseudomonas aeruginosa*. *Scientific Reports* **2019**, *9*, 1-15, 10.1038/s41598-018-37422-9.
30. Mohd W. Azam; Asad U. Khan; Updates on the pathogenicity status of *Pseudomonas aeruginosa*. *Drug Discovery Today* **2019**, *24*, 350-359, 10.1016/j.drudis.2018.07.003.
31. Hyun Kim; Ju Hye Jang; Sun Chang Kim; Ju Hyun Cho; Development of a novel hybrid antimicrobial peptide for targeted killing of *Pseudomonas aeruginosa*. *European Journal of Medicinal Chemistry* **2020**, *185*, 111814, 10.1016/j.ejmech.2019.111814.
32. Muhammad Yasir; Debarun Dutta; Mark D. P. Willcox; Comparative mode of action of the antimicrobial peptide melimine and its derivative Mel4 against *Pseudomonas aeruginosa*. *Scientific Reports* **2019**, *9*, 1-12, 10.1038/s41598-019-42440-2.
33. Songhita Mukhopadhyay; A. S. Bharath Prasad; Chetan H. Mehta; Usha Y. Nayak; Antimicrobial peptide polymers: no escape to ESKAPE pathogens—a review. *World Journal of Microbiology and Biotechnology* **2020**, *36*, 1-14, 10.1007/s11274-020-02907-1.
34. Robert Dec; Wojciech Dzwolak; Extremely Amyloidogenic Single-Chain Analogues of Insulin's H-Fragment: Structural Adaptability of an Amyloid Stretch. *Langmuir* **2020**, *36*, 12150-12159, 10.1021/acs.langmuir.0c01747.
35. Hafida Bouziane; Abdallah Chouarfia; Sequence- and structure-based prediction of amyloidogenic regions in proteins. *Soft Computing* **2019**, *24*, 3285-3308, 10.1007/s00500-019-04087-z.
36. Vitaly V. Kushnirov; Alexander A. Dergalev; Alexander I. Alexandrov; Proteinase K resistant cores of prions and amyloids. *Prion* **2019**, *14*, 11-19, 10.1080/19336896.2019.1704612.
37. Alexey K. Surin; Sergei Yu. Grishin; Oxana V. Galzitskaya; Determination of amyloid core regions of insulin analogues fibrils. *Prion* **2020**, *14*, 149-162, 10.1080/19336896.2020.1776062.
38. Sergiy Garbuzynskiy; Michail Yu. Lobanov; Oxana V. Galzitskaya; FoldAmyloid: a method of prediction of amyloidogenic regions from protein sequence. *Bioinformatics* **2009**, *26*, 326-332, 10.

- 1093/bioinformatics/btp691.
39. Mikael Oliveberg; Waltz, an exciting new move in amyloid prediction. *Nature Methods* **2010**, *7*, 187-188, 10.1038/nmeth0310-187.
  40. Ian Walsh; Flavio Seno; Silvio C.E. Tosatto; Antonio Trovato; PASTA 2.0: an improved server for protein aggregation prediction. *Nucleic Acids Research* **2014**, *42*, W301-W307, 10.1093/nar/gku399.
  41. Oscar Conchillo-Solé; Natalia S. De Groot; Francesc X. Avilés; Josep Vendrell; Xavier Daura; Salvador Ventura; AGGRESKAN: a server for the prediction and evaluation of "hot spots" of aggregation in polypeptides. *BMC Bioinformatics* **2007**, *8*, 65-17, 10.1186/1471-2105-8-65.
  42. Olga M. Selivanova; Elizaveta I. Grigorashvili; Mariya Yu. Suvorina; Ulyana F. Dzhus; Alexey D. Nikulin; Victor V. Marchenkov; Alexey K. Surin; Oxana V. Galzitskaya; X-ray diffraction and electron microscopy data for amyloid formation of A $\beta$ 40 and A $\beta$ 42. *Data in Brief* **2016**, *8*, 108-113, 10.1016/j.dib.2016.05.020.
  43. Mantas Ziaunys; Vytautas Smirnovas; Additional Thioflavin-T Binding Mode in Insulin Fibril Inner Core Region. *The Journal of Physical Chemistry B* **2019**, *123*, 8727-8732, 10.1021/acs.jpccb.9b08652.
  44. Xue-Jiao Ma; Yin-Juan Zhang; Cheng-Ming Zeng; Inhibition of amyloid aggregation of bovine serum albumin by sodium dodecyl sulfate at submicellar concentrations. *Biochemistry (Moscow)* **2018**, *83*, 60-68, 10.1134/s000629791801008x.
  45. Jan Johansson; Charlotte Nerelius; Hanna Willander; Jenny Presto; Conformational preferences of non-polar amino acid residues: An additional factor in amyloid formation. *Biochemical and Biophysical Research Communications* **2010**, *402*, 515-518, 10.1016/j.bbrc.2010.10.062.
  46. Jing Zhang; Lei Xin; Baozhen Shan; Weiwu Chen; Mingjie Xie; Denis Yuen; Weiming Zhang; Zefeng Zhang; Gilles A. Lajoie; Bin Ma; et al. PEAKS DB: De Novo Sequencing Assisted Database Search for Sensitive and Accurate Peptide Identification. *Molecular & Cellular Proteomics* **2012**, *11*, M111.010587, 10.1074/mcp.m111.010587.
  47. Sergei Grishin; U. F. Dzhus; O. M. Selivanova; V. A. Balobanov; A. K. Surin; O. V. Galzitskaya; Comparative Analysis of Aggregation of *Thermus thermophilus* Ribosomal Protein bS1 and Its Stable Fragment. *Biochemistry (Moscow)* **2020**, *85*, 344-354, 10.1134/s0006297920030104.
  48. Matthew Biancalana; Shohei Koide; Molecular mechanism of Thioflavin-T binding to amyloid fibrils. *Biochimica et Biophysica Acta (BBA) - Proteins and Proteomics* **2010**, *1804*, 1405-1412, 10.1016/j.bbapap.2010.04.001.

---

Retrieved from <https://www.encyclopedia.pub/entry/history/show/28542>