Computers in Biology and Medicine 133 (2021) 104391

Contents lists available at ScienceDirect

Computers in Biology and Medicine

journal homepage: http://www.elsevier.com/locate/compbiomed

SAPdb: A database of short peptides and the corresponding nanostructures formed by self-assembly

Deepika Mathur [a,1], Harpreet Kaur [a,1], Anjali Dhall [b], Neelam Sharma [b], Gajendra P. S. Raghava [b,*]

[a] Bioinformatics Centre, CSIR-Institute of Microbial Technology, Chandigarh-160036, India
[b] Department of Computational Biology, Indraprastha Institute of Information Technology, New Delhi-110020, India

ARTICLE INFO

Keywords:
Nanostructure
Dipeptide
Tripeptide
Self-assembly
Database

ABSTRACT

Nanostructures generated by self-assembly of peptides yield nanomaterials that have many therapeutic applications, including drug delivery and biomedical engineering, due to their low cytotoxicity and higher uptake by targeted cells owing to their high affinity and specificity towards cell surface receptors. Despite the promising implications of this rapidly expanding field, there is no dedicated resource to study peptide nanostructures. This study endeavours to create a repository of short peptides, which may prove to be the best models to study ordered nanostructures formed by peptide self-assembly. SAPdb has a repertoire of 1049 entries of experimentally validated nanostructures formed by the self-assembly of small peptides. It consists of 328 tripeptides, 701 dipeptides, and 20 single amino acids with some conjugate partners. Each entry encompasses comprehensive information about the peptide, such as chemical modifications, the type of nanostructure formed, experimental conditions like pH, temperature, solvent required for the self-assembly, etc. Our analysis indicates that peptides containing aromatic amino acids favour the formation of self-assembling nanostructures. Additionally, we observed that these peptides form different nanostructures under different experimental conditions. SAPdb provides this comprehensive information in a hassle-free tabulated manner at a glance. User-friendly browsing, searching, and analysis modules have been integrated for easy data retrieval, data comparison, and examination of properties. We anticipate SAPdb to be a valuable repository for researchers engaged in the burgeoning arena of nanobiotechnology. It is freely available at https://webs.iiitd.edu.in/raghava/sapdb.

1. Introduction

Peptides have been reported as key players in diverse fields like immunotherapeutic [1–7], disease biomarkers [8–10], antibacterial [11–15], antiviral [16–20], anticancer [21–25], antiparasitic [26–30], and antihypertensive [31–33] drugs owing to their properties such as cell-penetration [34], stability [35–37] and low toxicity [38,39]. Besides these areas, peptides are rapidly gaining the attention of researchers in the field of nanobiotechnology [40–43] by virtue of their property to get self-assembly into well-defined nanostructures. Besides, biocompatibility, biodegradability, low cytotoxicity, and higher uptake of SAPs (self-assembling peptides) by targeted cells play a significant role in their therapeutic applications [44,45]. Owing to these attractive properties, bioactive peptides having the ability to undergo self-assembly are being explored to serve as building blocks of hydrogels and scaffolds. These building blocks can be used in various fields such as in cell culture [46], and tissue engineering [47,48], controlled drug delivery in response to changes in pH [49,50] for diagnostics and biosensors [51], as well as in the field of bioelectronics [52], and material sciences [52].

Self-assembly of peptides can lead to the formation of well-defined nanostructures like nanofibers, nanorods, nanoparticles, hydrogels, nanotubes, etc. [53–61], where the size of nanostructures/nanomaterials vary from 1 to 100 nm [62]. Nanofibers, nanorods, and nanotubes are one-dimensional nanomaterials mainly

* Corresponding author. Head and Professor Department of Computational Biology Indraprastha Institute of Information Technology, Okhla Industrial Estate, Phase III, (Near Govind Puri Metro Station), Office: A-302 (R&D Block) New Delhi, 110020, India.
E-mail addresses: matdeepika@gmail.com (D. Mathur), hks04180@gmail.com (H. Kaur), anjalid@iiitd.ac.in (A. Dhall), neelams@iiitd.ac.in (N. Sharma), raghava@iiitd.ac.in (G.P.S. Raghava).
URL: http://webs.iiitd.edu.in/raghava/ (G.P.S. Raghava).
[1] - Contributed Equally.

https://doi.org/10.1016/j.compbiomed.2021.104391
Received 19 January 2021; Received in revised form 7 April 2021; Accepted 7 April 2021
Available online 10 April 2021

used to generate polymer nanocomposites and elongated nanostructures [63]. On the other hand, hydrogels are 3D-nanomaterials that can hold a huge amount of water content and can be used in tissue engineering, wound healing bandages, biosensors, etc [64].

These nanostructures' assembly depends on weak non-covalent interactions like van der Waals force, hydrophobic interactions, hydrogen bonds, and π-π stacking [65–68]. The lack of a comprehensive understanding of the properties and mechanisms of the formation of self-assembling peptides nanostructures can affect their configuration and utility.

The major advantages of using self-assembled short peptides as a nanomaterial compared to other drug delivery vehicles include simple structure, fast and low-cost synthesis, better chemical and physical stability, biocompatibility, diversity in morphology, and ease of synthesis in large quantities [69–72]. Though peptide nanocarriers have several advantages, there are a few drawbacks too. It is challenging to store and handle nanocarriers since they can aggregate to form different nanostructures due to their small size [73]. Some studies have shown that these nanocarriers may cause harmful effects; they can cross the nuclear membrane of a cell and cause mutation, which may lead to genetic damages [74–76]. It is difficult to control these nanostructures' shape, size, and stability during synthesis for successful integration and translation into biosensors and controlled release devices for drug delivery.

Though various studies have been carried out to design peptide-based nanoparticles, to the best of our knowledge, there is no dedicated platform that maintains comprehensive information about nanoparticles formed by the self-assembly of peptides. A systematic collection and compilation of experimental data is needed to examine the mechanisms and interactions governing the self-assembly of peptides into nanostructures for facilitating the rational designing of morphologies and the size of peptide assemblies. The present report is the first attempt to develop a repository of short peptides that undergo self-assembly to form nanostructures. Dipeptides and tripeptides are the smallest known peptide self-assemblers, which show fascinating morphologies and functionalities besides being cost-efficient and fast to synthesize. "SAPdb", which is a novel database dedicated to such short peptides will be very beneficial to study how experimental conditions and chemical modifications in the amino acid sequence of peptides affect the bottom-up process of self-assembly to form well-defined ordered nanostructures. Literature had shown the numerous applications of these small self-assembling peptides in diverse areas, i.e., as drug delivery vehicles, as cell culture scaffolds in tissue engineering, as nanofabrication models [77–86]. The information regarding these self-assembling peptides is widely spread across the literature in the form of bulky texts, which hinders the user from exploring it. The "Search", "Browse", and "Analysis" modules of the SAPdb web portal make it convenient for the researchers to retrieve, study and analyse the comprehensive information gathered in the form of a tabular display under a single umbrella. Using different modules, one can examine how the substitution of D-amino acids or non-natural amino acids in the peptide sequence and the experimental conditions like solvent, concentration, pH, etc., can influence the self-assembling property of the peptides.

Moreover, to facilitate the users, we have integrated a chemical modification browsing tool to highlight the impact of different modifications based on the different types of nanostructure formed by the same peptide sequence. The users can quickly analyse their query peptide sequence similarity with other SAPs at a single platform using SAPdb. Eventually, we believe that our proposed database (SAPdb) will boost the research in the field of the small self-assembling peptides as nanocarriers/nanomaterial as it encompasses comprehensive information for them in the form of a user-friendly web portal.

2. Methods

2.1. Data collection

To collate the relevant information for the di- and tri-peptides that self-assemble to form discrete and ordered nanostructure, the queries were submitted to PubMed was queried to obtain the research articles. Keywords like "(tripeptide AND self-assembly)","(tripeptide AND nanostructure)", "(tripeptide AND nanotube)", "(tripeptide AND nanofiber)", "(tripeptide AND nanorod)", "(tripeptide AND hydrogel)", "(tripeptide AND nanosphere)" and "(tripeptide AND nanoparticle)" for self-assembling tripeptides. Whereas to collect the research articles relevant to self-assembling dipeptides keywords like "(dipeptide AND self-assembly)", "(dipeptide AND nanotube)", "(dipeptide AND nanostructure)", "(dipeptide AND nanorod)", "(dipeptide AND nanosphere)", "(dipeptide AND nanofiber)", "(dipeptide AND hydrogel)", and "(dipeptide AND nanoparticle)" were used and collected around ~1500 publications till July 2019. We screened the obtained articles and included only those for further data curation, where information about peptides forming self-assembled nanostructures was available. These self-assembling peptides form various nanostructures, i.e., nanosphere, nanotube, hydrogel, nanovesicle, nanofibers, etc., as represented in Fig. 1.

After the thorough screening, relevant information was extracted from the selected articles concerning the sequence of peptides. The peptide information incorporates N-terminal modification, C-terminal modification, method, type of self-assembly, size of the self-assembled structure, and the experimental conditions like solvent, concentration, temperature, pH, and incubation time.

Multiple entries of the same peptide were reported under different experimental conditions. This extensive information is systematically catalogued in a tabulated manner. Consequently, 1049 entries were collated in the SAPdb database from 301 research articles.

2.2. Architecture and web-interface of the database

SAPdb was designed using Apache HTTP Server (version 2.2.17) on the Linux system following the collection and compilation of significant information. It is based on MySQL at the backend that was implemented to maintain the information. HTML5, PHP, and JavaScript were used to develop the front end and to build a mobile, tablet, and desktop compatible web resource. Different modules were integrated into SAPdb for data compilation, retrieval, and exploration. The complete architecture depicting the information and tools embedded into SAPdb is represented in Fig. 2.

2.3. Organization of database

In SAPdb, the collected information was classified into two categories such as primary information and secondary information. Primary information includes field like (i) PubMed ID, (ii) peptide sequence, (iii) N-terminal modification, (iv) C-terminal modification, (v) non-terminal modification, (vi) technique, (vii) method, (viii) solvent, (ix) concentration of peptide, (x) pH, (xi) temperature, (xii) incubation time, (xiii) type of self-assembly, (xiv) size of self-assembled structure and (xv) stability of self-assembled structure. While in secondary information, (xvi) SMILES and (xvii) tertiary structure of peptides were included.

3. Results

3.1. Statistical analysis of data of SAPdb

SAPdb is a collection of 1049 entries of experimentally validated short peptides that undergo self-assembly to form ordered nanostructures. The information was manually curated and compiled from 301 research articles published in the recent past with the rise of interest

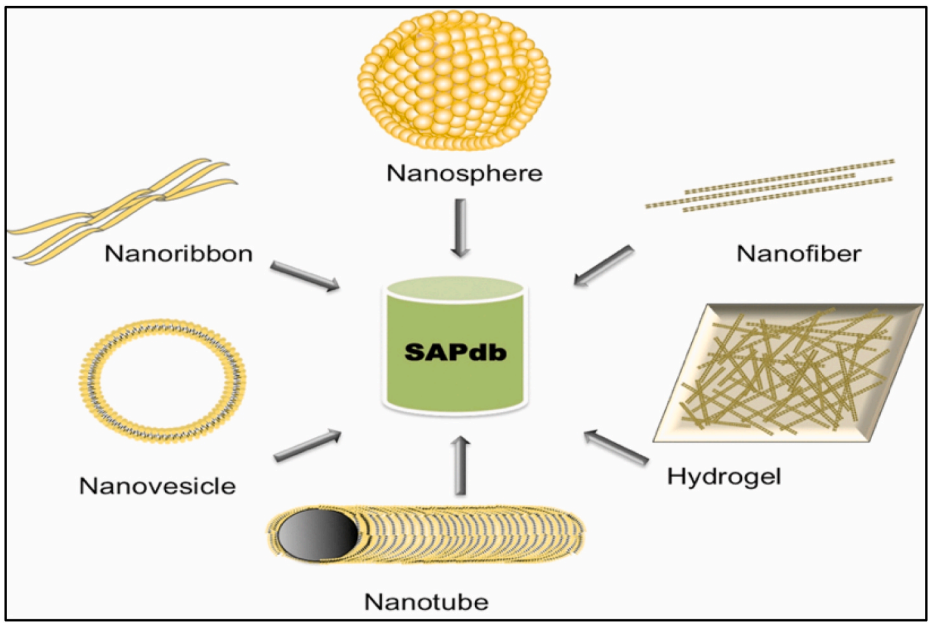


Fig. 1. Formation of different nanostructures from the self-assembly of small peptides.

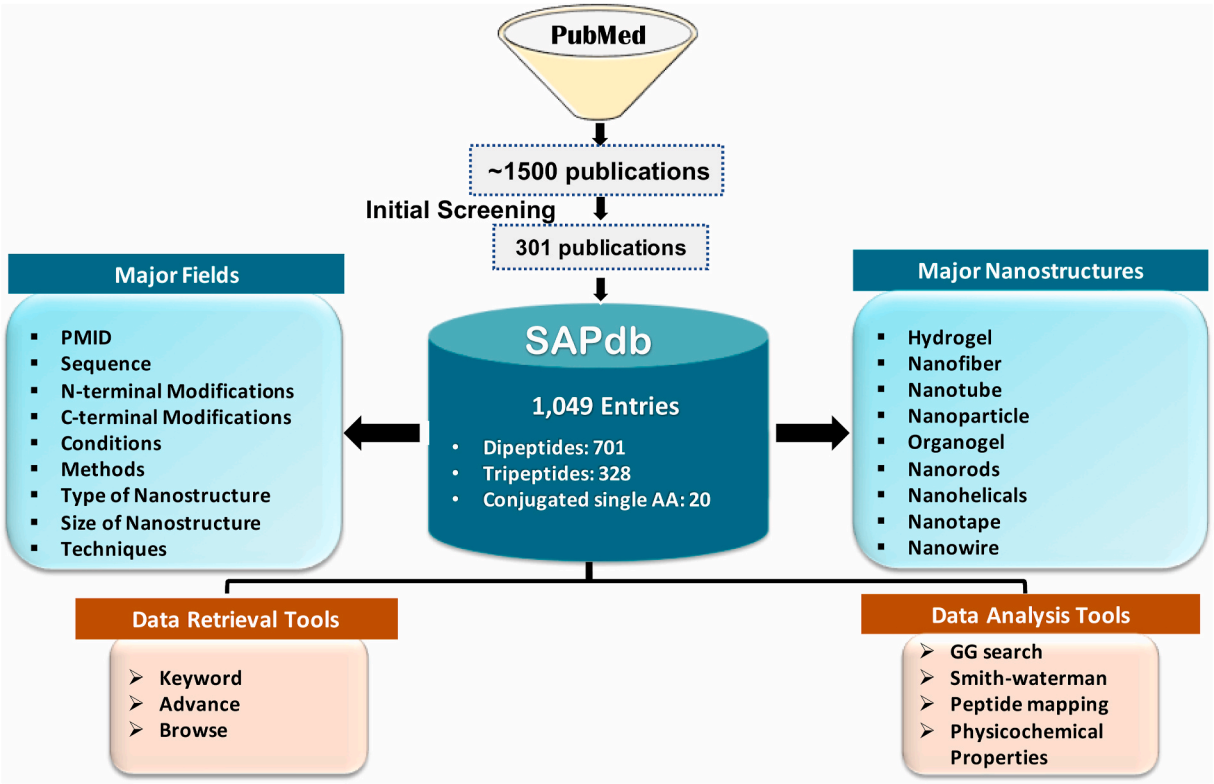


Fig. 2. Architecture depicting the information and tools integrated in SAPdb.

in nanobiotechnology (Fig. 3B). Out of these 1049 entries, 701 entries are of dipeptides, 328 entries are of tripeptides, and 20 entries are of single amino acids with their conjugate partners. Forty-eight of the peptides were cyclic, while the rest were linear (Fig. 3C). These model short peptides form 10 significant types of nanostructures, as shown in (Fig. 3A). Hydrogel (297 entries) is the most common type of structure, followed by nanofibers (127 entries), nanotubes (67 entries), nanospheres (50 entries), nanoparticles (47), and hundreds of entries of hybrid nanostructures. Different techniques have been described in the literature to study the phenomenon of self-assembly of peptides. The most common techniques like transmission electron microscopy, scanning electron microscopy, Fourier transforms infrared spectroscopy, and atomic force microscopy is also reported in database. To give different functionality, stability, and shape to nanostructure, some peptides have a cyclic structure. In contrast, various terminal modifications and non-natural amino acids have been incorporated with various other peptide sequences (Fig. 3D). There is a total of 382 entries in SAPdb that encompass modifications at the N-terminal. Most commonly reported N-

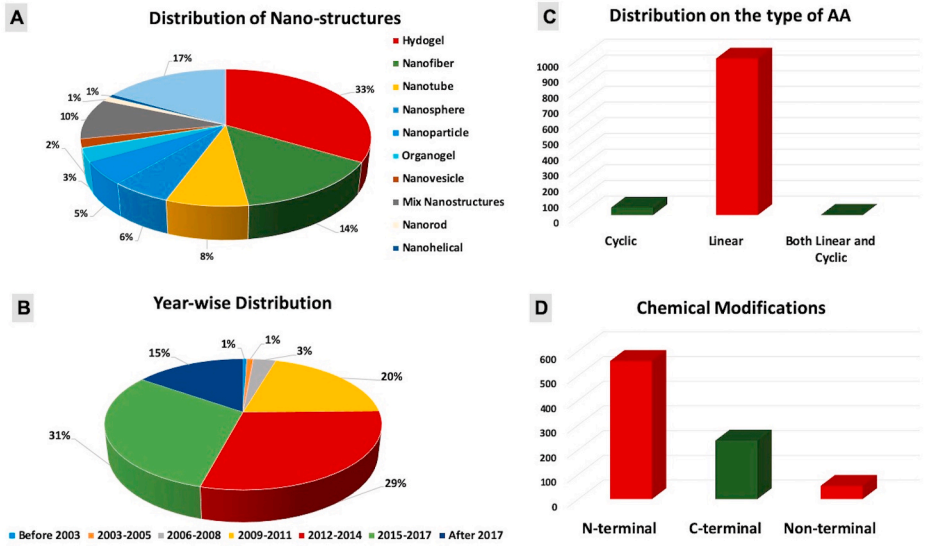


Fig. 3. Distribution of peptide entries in SAPdb according to (a) types of nanostructures, (b) modifications and conformation of peptides, (c) year of publication, and (d) chemical modifications.

terminal modifications include Fmoc (fluorenylmethoxycarbonyl; 160 entries), Boc (N-t-Butoxycarbonyl; 113 entries) and acetylation (46 entries); while, methoxylation (73), amidation (49 entries), benzylation (33 entries), were reported as primary modifications at C-terminal. Besides this, 54 reported entries had non-natural amino acids like dehydrophenylalanine (ΔPhe) (30 entries), beta-alanine (β-Ala) (16 entries), amino benzoic acid (ABA) (9 entries), amino isobutyric acid (Aib) (9 entries), etc. in their sequences.

3.2. Compositional analysis

In the current study, we have also computed the amino acid composition of SAPs and non-SAPs. The average composition analysis indicates that Aspartic acid (D), Phenylalanine (F), Lysine (K), and Serine (S) were higher in SAPs. On the other side, Alanine (A), Methionine (M), Proline (P), and Valine (V) are comparatively high in non-SAPs, as represented in Fig. 4.

3.3. Implementation of webtools

Various modules, i.e., search tools, browse tools, and analysis tools, were integrated into the database for users to explore SAPdb.

3.4. Search tools

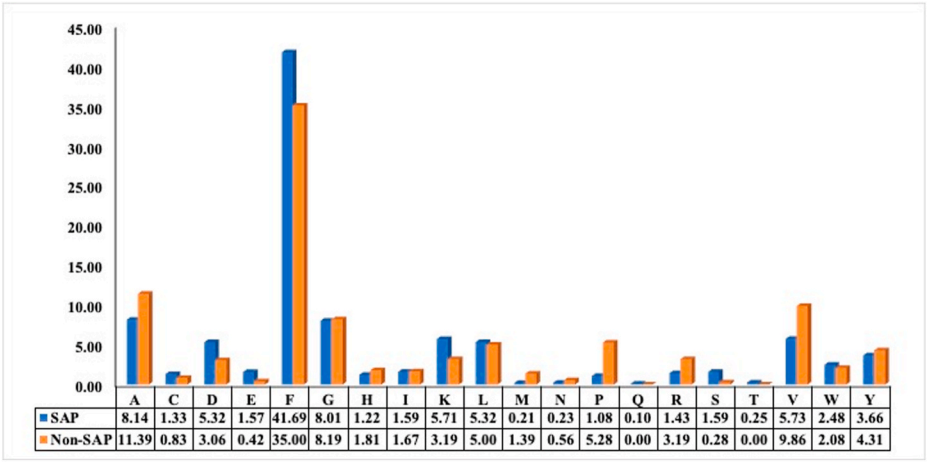
Two distinctive modules are implemented in SAPdb, i.e., Simple search, Advance search under search tool to assist the user in amiable data retrieval.

Simple search: This module offers the fundamental facility for data retrieval from the database. Here one can perform a keyword query search by selecting any required field of SAPdb, such as the type of self-assembly, technique, peptide sequence, etc. Besides, the simple search, this module also permits the users to select anticipated fields to be displayed in the result section.

Advance search: To retrieve relevant information from the SAPdb, the advanced search module presents the user's the facility to implement a multiple query system; for example, addition/removal of any desired query using the standard logical operators (=, >, <, and LIKE) and Boolean expressions like 'AND, OR, and NOT' in order to search the selected fields.

3.5. Browsing tools

The browsing facility has been integrated to facilitate data mining in a systematic mode from SAPdb. In this module, the data can be browsed



	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
SAP	8.14	1.33	5.32	1.57	41.69	8.01	1.22	1.59	5.71	5.32	0.21	0.23	1.08	0.10	1.43	1.59	0.25	5.73	2.48	3.66
Non-SAP	11.39	0.83	3.06	0.42	35.00	8.19	1.81	1.67	3.19	5.00	1.39	0.56	5.28	0.00	3.19	0.28	0.00	9.86	2.08	4.31

Fig. 4. Bar plot representing the amino acid compositional analysis of SAPs and non-SAPs.

by six different options (i) Chemical modification, (ii) Type of Nanostructure, (iii) Size of Nanostructure, (iv) Technique, (v) Publication year.

The chemical modification field assists the user to retrieve data of peptides that have different chemical modifications at the N or C termini. For instance, Fmoc (fluorenylmethoxycarbonyl; 160 entries), Boc (N-t-Butoxycarbonyl; 113 entries), and acetylation (47 entries) are major modification at N-terminal; while methoxy (73), amidation (49 entries), benzylation (33 entries) were reported as primary modifications at C-terminal. Type of nanostructure category allows the user to get details on peptides that form a particular nanostructure such as nanotube, nanosphere, nanofibers, hydrogel, etc. The size of the nanostructure category allows users to browse entries based on the size of the nanostructure reported. Further, the technique category enables the user to fetch the information related to peptides whose nanostructures were studied using a particular technique such as Transmission Electron Microscopy (TEM), Scanning Electron Microscopy (SEM), and Atomic Force Microscopy (AFM), and Fourier Transform Infrared (FTIR), etc. Additionally, users can also retrieve information of the peptides by the year of publication.

3.6. Analysis tools

This module enables the users to execute several examinations, such as sequence similarity, peptide mapping, and computation of physicochemical properties of peptides.

GGSearch: This tool is used to perform a similarly-based search against a short peptide in the SAPdb database. It is based on Needleman-Wunsch alignment [87].

Smith-Waterman Algorithm: It allows the user to submit multiple peptides as a query in the FASTA format to search for similar peptides in the database.

Peptide Mapping: This tool provides a facility to map the SAPdb peptides over the query protein sequence. It will be helpful for identifying motifs within protein sequences that tend to undergo self-assembly.

Physicochemical Properties: This module enables the user to examine the properties of the desired peptide sequences such as charge, polarity, volume, hydrophobicity, etc.

Graphical Peptide Representation: This module incorporates all the dipeptide and tripeptide information based on their amino acid components. The user can choose a desired peptide based on their amino acid composition in order to obtain the comprehensive details for each query.

3.7. Effect of experimental conditions

Previous studies have shown that the variation in experimental conditions like the type of solvent, change in concentration of the peptide, temperature, incubation time, pH, etc., can lead to the formation of different nanostructures by the same peptide [88]. Further, our analysis shows that the concentration of peptides is also an essential factor for controlling the shape and size of the nanostructure. For example, KFG tripeptide forms vesicles at a low concentration of 0.5 mg/ml, while at a higher concentration of 5 mg/ml, it forms nanotubes [88]. Furthermore, the role of solvent in directing the type of nanostructure formation is also revealed through this analysis. Most of the nanostructures are formed using water as a solvent, followed by phosphate buffer and organic solvents like methanol, ethanol, hexafluoropropanol, chloroform, and acetone. FF is reported to form nanovesicles in acetone, while in water, it forms nanotubes [89]. This analysis also shows that some specific experimental conditions that favour the formation of nanostructure as evidenced by the observation that the majority of the nanostructures are reported to be formed by self-assembly under room temperature or 25 °C (499 entries) and in the range of neutral pH of 7 to physiological pH of 7.4 (178 entries) followed by acidic pH of less than 6 (118). Besides, we have observed 258 entries (see Supplementary Table 1) where peptides form different nanostructures without any chemical modifications or conjugate partners. Out of 258 entries, 180 (70%) entries contain aromatics amino acids. This indicates the presence of aromatics amino acids favoured the self-assembly formation.

3.8. Case study

Our analysis has shown that the experimental condition changes the nature of self-assemblies. To understand the effect of conditions, we have considered an example of diphenylalanine (FF). FF forms hydrogels at different experimental conditions such as temperature = 55 °C, pH = ~3–4, 7.2 and 8, incubation time >24 h etc. On the other side, it forms nanostructures like nanosphere, nanotubes, and nanofibers at various conditions like pH, N-terminal modification, temperature, and incubation time, as represented in (Fig. 5).

In the absence of any user-friendly web platform, the user needs to go through widely spread literature in the bulky text publications. SAPdb allows easy access to this comprehensive information in tabulated form, which leads to a better understanding of the 3D shape of nanostructures formed by altering experimental conditions.

3.9. Working of SAPdb database

To understand how a user can retrieve data from the SAPdb database, we have demonstrated (Fig. 5) an example of a dipeptide, i.e., dipleneyalanine (FF). Fig. 6 represents the step-by-step information on how users can query SAPdb using a simple search module by a keyword like PMID, peptide sequence, peptide name, year of publication, etc. For instance, we queried the search module with peptide sequence, i.e., FF, in the given search space (Fig. 6A) of the database. Users can further select various display fields that are provided on a simple search page. After submitting the desired query (e.g., FF) using the “Submit” button, the next page will display all the entries related to the query; for instance, we retrieved 362 entries of FF shown in Fig. 6B. Each entry has a unique SAPdb ID, and the user can get the detailed information regarding peptides by further clicking on the SAPdb ID. The next page provides complete information about the selected SAPdb ID, as represented in Fig. 6C. It gives the peptide’s primary information (SAPdb ID, PMID, Year, Name, Sequence, N-terminal modification, C-terminal modification, non-terminal modification, peptide/conjugate/mixture, conjugate partner, technique, solvent, method, concentration, pH, temperature, etc. The secondary information provides physiochemical properties, structure, and SMILES of the given peptide. Users can further explore these properties, as shown in Fig. 6D. A help page has been incorporated in the SAPdb website to describe the usage of each module.

4. Discussion and conclusion

With the rising interest in nanobiotechnology, it is essential to understand the properties governing the self-assembly of peptides into nanostructures. Several previous databases like AmyLoad [90], CPAD [91], AMYPdb [92], have curated protein and peptide aggregation, properties [93], and stability [35,94]. Since there was no repository of experimentally validated and well-ordered self-assembling peptide nanostructures, we have developed SAPdb, a novel platform with comprehensive information about nanostructures formed by short peptides. Dipeptides and tripeptides are the shortest peptides that can assemble into higher-order structures. They are the model candidates to understand the process of self-assembly. SAPdb holds 167 unique dipeptides and 96 unique tripeptides that have been experimentally validated for undergoing ordered nanostructure formation by self-assembly.

Comprehensive analysis of SAPdb data has shown that different environmental conditions like temperature, pH, solvent, concentration, etc., and chemical modifications direct the size and shape or type of

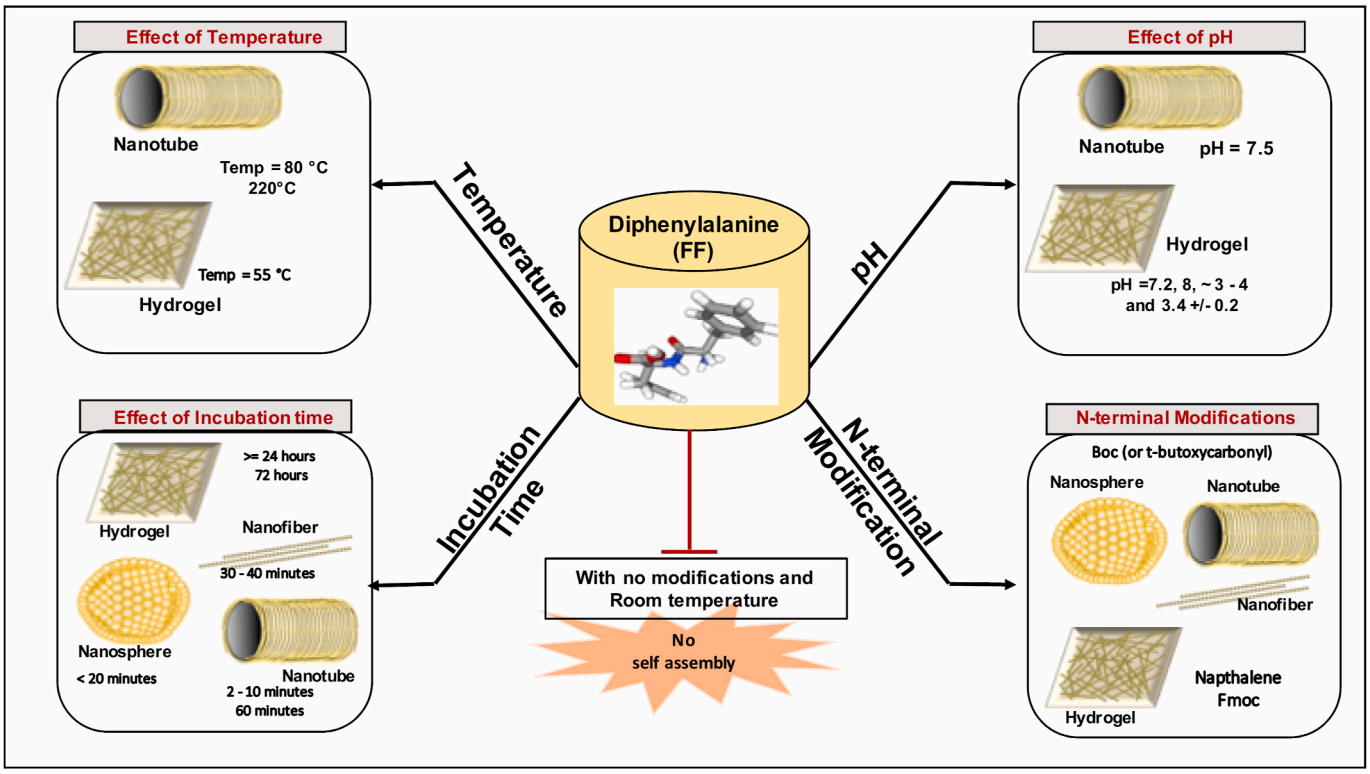


Fig. 5. The demonstration of the effect of experimental conditions (pH, temperature, incubation time and N-terminal modification) in the formation of different self-assembling peptides.

nanostructures formation. Further, the specific conditions, i.e., room temperature, acidic pH, favour the formation of nanostructure of self-assembling peptides. The amino acid composition analysis of peptides revealed that self-assembling peptides are rich in aspartic acid, phenylalanine, serine, and lysine. At the same time, they are depleted in alanine, methionine, proline, and valine compared to non-self-assembling peptides. Further, aromatic residues like phenylalanine and tyrosine are favoured at the second and third positions in tripeptides undergoing self-assembly. The chemical modifications of amino acids help the self-assembling property of peptides and improve their stability to enzymes [69].

A systematic attempt has been made to develop a well-curated database, in which we have provided detailed information of short peptides forming nanostructures on a single platform. Researchers working in the burgeoning field of nanobiotechnology can utilize these nanostructures and nanomaterials as functional materials for various applications ranging from tissue engineering to drug delivery vehicles [95]. Clinical researchers can check the toxicity, allergenicity, and immunogenicity of these small peptides and can use them as a drug delivery vehicle to treat several diseases. We anticipate that SAPdb will be a valuable resource for designing the next generation of size customized and stable bionanomaterials.

This study mainly focused on the dipeptides and tripeptides, which form several types of nanostructures like nanotubes, nanofibers, nanosphere, nanorod, and hydrogels. One of the major limitations of the current study is that while collecting the data, we have not considered the higher-order peptides and the micellar structures, which are very common nanostructures. As the scientific community is actively publishing articles pertaining to this emerging field, in the future, our first goal will be to update data available about short model peptides as well as to expand the database further to include higher-ordered peptides and micellar structures that form ordered nanostructures on self-assembly.

Funding

The authors are thankful to the funding agencies J. C. Bose National Fellowship (DST), Council of Scientific and Industrial Research (CSIR), Department of Science and Technology (DST-INSPIRE) for fellowships and financial support, and IIIT-Delhi for providing the infrastructure and facilities.

Availability of data and material

SAPdb is freely available at "https://webs.iiitd.edu.in/raghava/sapdb/".

Ethics approval

'Not applicable'.

Code availability

'Not applicable'.

Author's contribution

Conception and design: Deepika Mathur, Harpreet Kaur, and Gajendra P. S. Raghava.

Development of methodology: Deepika Mathur, Harpreet Kaur, and Gajendra P. S. Raghava.

Acquisition of data: Deepika Mathur, Harpreet Kaur, Anjali Dhall, Neelam Sharma.

Analysis and interpretation of data and results: Deepika Mathur, Harpreet Kaur, Anjali Dhall, Neelam Sharma, Gajendra P. S. Raghava.

Writing, reviewing, and revision of the manuscript: Deepika Mathur, Harpreet Kaur, Anjali Dhall, Neelam Sharma, Gajendra P. S. Raghava.

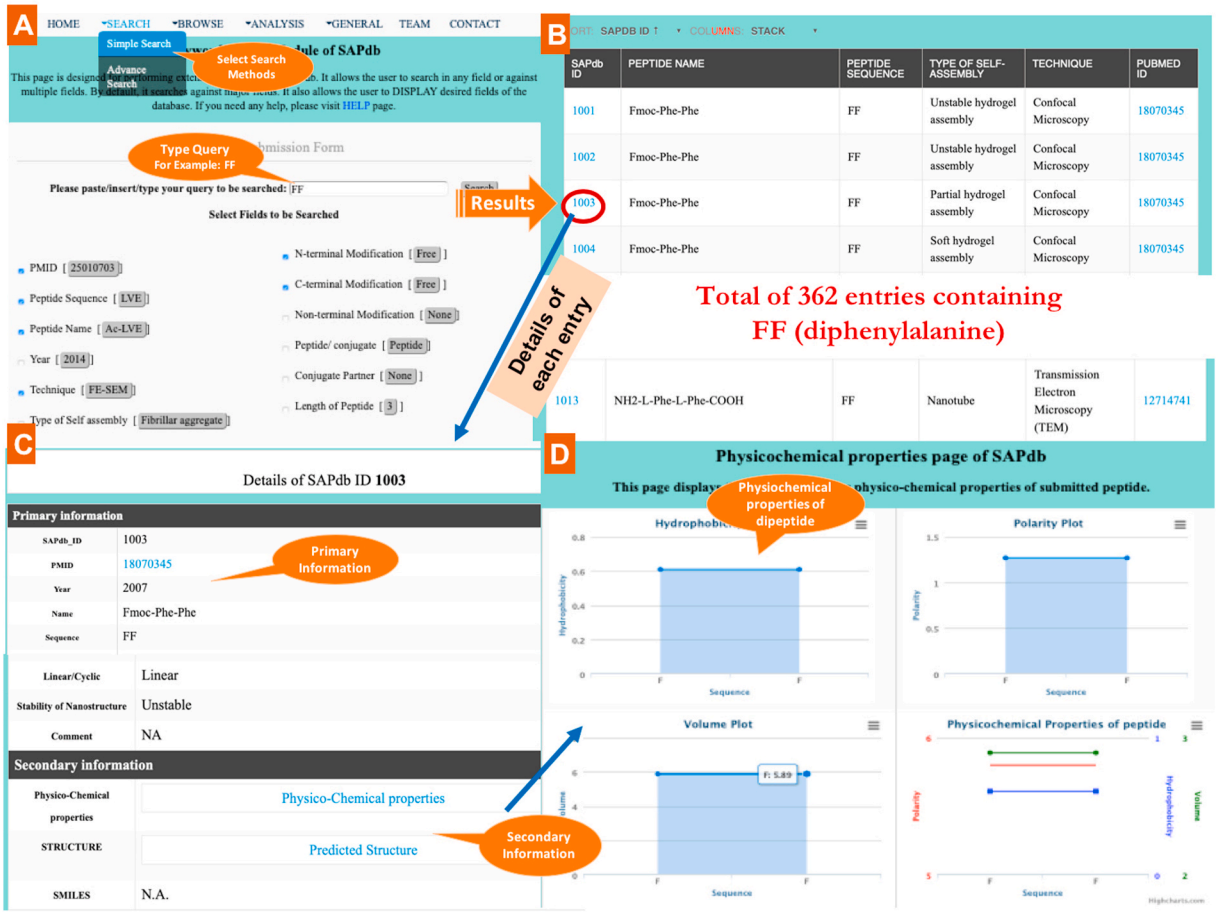


Fig. 6. Demonstration of querying and retrieval of information from SAPdb using the Simple Search module.

Biorxiv link

https://www.biorxiv.org/content/10.1101/685149v2
https://www.biorxiv.org/content/10.1101/685149v2.full.pdf.

Declaration of competing interest

The authors declare that they have no conflict of interest.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.compbiomed.2021.104391.

References

[1] G. Nagpal, S.S. Usmani, S.K. Dhanda, H. Kaur, S. Singh, M. Sharma, G.P. S. Raghava, Computer-aided designing of immunosuppressive peptides based on IL-10 inducing potential, Sci. Rep. 7 (2017) 42851, https://doi.org/10.1038/srep42851.
[2] S.K. Dhanda, S.S. Usmani, P. Agrawal, G. Nagpal, A. Gautam, G.P.S. Raghava, Novel in silico tools for designing peptide-based subunit vaccines and immunotherapeutics, Briefings Bioinf. 18 (2017) 467–478, https://doi.org/10.1093/bib/bbw025.
[3] M.J. Miller, K.C. Foy, P.T.P. Kaumaya, Cancer immunotherapy: present status, future perspective, and a new paradigm of peptide immunotherapeutics, Discov. Med. 15 (2013) 166–176.
[4] P. Reche, D.R. Flower, M. Fridkis-Hareli, Y. Hoshino, Peptide-based immunotherapeutics and vaccines 2015, J. Immunol. Res. (2015) 349049, https://doi.org/10.1155/2015/349049.
[5] S.K. Dhanda, S.S. Usmani, P. Agrawal, G. Nagpal, A. Gautam, G.P.S. Raghava, Novel *in silico* tools for designing peptide-based subunit vaccines and immunotherapeutics, Bioinform, Brief, 2016, p. bbw025, https://doi.org/10.1093/bib/bbw025.
[6] X. Zhan, C. Li, Y. Jiang, N. Li, Epitope-based vaccine for the treatment of der F 3 allergy, Nutr. Hosp. 32 (2015) 2763–2770, https://doi.org/10.3305/nh.2015.32.6.9878.
[7] H. Kobayashi, R. Kennedy, J. Lu, E. Davila, E. Celis, MHC-binding peptides as immunotherapeutics for cancer, Immunol. Invest. 29 (2000) 105–110, https://doi.org/10.3109/08820130009062291.
[8] S. Bhalla, R. Verma, H. Kaur, R. Kumar, S.S. Usmani, S. Sharma, G.P.S. Raghava, CancerPDF: a repository of cancer-associated peptidome found in human biofluids, Sci. Rep. 7 (2017) 1511, https://doi.org/10.1038/s41598-017-01633-3.
[9] A. Stalmach, H. Johnsson, I.B. McInnes, H. Husi, J. Klein, M. Dakna, W. Mullen, H. Mischak, D. Porter, Identification of urinary peptide biomarkers associated with rheumatoid arthritis, PloS One 9 (2014), e104625, https://doi.org/10.1371/journal.pone.0104625.
[10] D. Salamanca, J.L. Gómez-Chaparro, A. Hidalgo, F. Labella, Expresión diferencial del proteoma en humor acuoso de pacientes con y sin glaucoma, Arch. Soc. Esp. Oftalmol. 93 (2018) 160–168, https://doi.org/10.1016/j.oftal.2017.12.019.
[11] F.H. Waghu, L. Gopi, R.S. Barai, P. Ramteke, B. Nizami, S. Idicula-Thomas, CAMP: collection of sequences and structures of antimicrobial peptides, Nucleic Acids Res. 42 (2014) D1154–D1158, https://doi.org/10.1093/nar/gkt1157.
[12] S.P. Piotto, L. Sessa, S. Concilio, P. Iannelli, YADAMP: yet another database of antimicrobial peptides, Int. J. Antimicrob. Agents 39 (2012) 346–351, https://doi.org/10.1016/j.ijantimicag.2011.12.003.
[13] A.K. Marr, W.J. Gooderham, R.E. Hancock, Antibacterial peptides for therapeutic use: obstacles and realistic outlook, Curr. Opin. Pharmacol. 6 (2006) 468–472, https://doi.org/10.1016/j.coph.2006.04.006.
[14] H. Jenssen, P. Hamill, R.E.W. Hancock, Peptide antimicrobial agents, Clin. Microbiol. Rev. 19 (2006) 491–511, https://doi.org/10.1128/CMR.00056-05.
[15] D.A. Berges, W.E. DeWolf, G.L. Dunn, S.F. Grappel, D.J. Newman, J.J. Taggart, C. Gilvarg, Peptides of 2-aminopimelic acid: antibacterial agents that inhibit diaminopimelic acid biosynthesis, J. Med. Chem. 29 (1986) 89–95, https://doi.org/10.1021/jm00151a015.
[16] É.C.G. da Mata, C.B.F. Mourão, M. Rangel, E.F. Schwartz, Antiviral activity of animal venom peptides and related compounds, J. Venom. Anim. Toxins Incl. Trop. Dis. 23 (2017) 3, https://doi.org/10.1186/s40409-016-0089-0.
[17] H. Zhao, J. Zhou, K. Zhang, H. Chu, D. Liu, V.K.-M. Poon, C.C.-S. Chan, H.-C. Leung, N. Fai, Y.-P. Lin, A.J.-X. Zhang, D.-Y. Jin, K.-Y. Yuen, B.-J. Zheng, A novel peptide with potent and broad-spectrum antiviral activities against multiple respiratory viruses, Sci. Rep. 6 (2016) 22008, https://doi.org/10.1038/srep22008.

[18] A. Qureshi, N. Thakur, H. Tandon, M. Kumar, AVPdb: a database of experimentally validated antiviral peptides targeting medically important viruses, Nucleic Acids Res. 42 (2014) D1147–D1153, https://doi.org/10.1093/nar/gkt1191.
[19] K.V.K. Mohan, S.S. Rao, C.D. Atreya, Antiviral activity of selected antimicrobial peptides against vaccinia virus, Antivir. Res. 86 (2010) 306–311, https://doi.org/10.1016/j.antiviral.2010.03.012.
[20] M.C. Carriel-Gomes, J.M. Kratz, M.A. Barracco, E. Bachére, C.R.M. Barardi, C.M. O. Simões, In vitro antiviral activity of antimicrobial peptides against herpes simplex virus 1, adenovirus, and rotavirus, Mem. Inst. Oswaldo Cruz 102 (2007) 469–472, https://doi.org/10.1590/S0074-02762007005000028.
[21] M.R. Felício, O.N. Silva, S. Gonçalves, N.C. Santos, O.L. Franco, Peptides with dual antimicrobial and anticancer activities, Front. Chem. 5 (2017) 5, https://doi.org/10.3389/fchem.2017.00005.
[22] M. Akrami, S. Balalaie, S. Hosseinkhani, M. Alipour, F. Salehi, A. Bahador, I. Haririan, Tuning the anticancer activity of a novel pro-apoptotic peptide using gold nanoparticle platforms, Sci. Rep. 6 (2016) 31030, https://doi.org/10.1038/srep31030.
[23] H.-L. Chu, B.-S. Yip, K.-H. Chen, H.-Y. Yu, Y.-H. Chih, H.-T. Cheng, Y.-T. Chou, J.-W. Cheng, Novel antimicrobial peptides with high anticancer activity and selectivity, PloS One 10 (2015), e0126390, https://doi.org/10.1371/journal.pone.0126390.
[24] A. Tyagi, A. Tuknait, P. Anand, S. Gupta, M. Sharma, D. Mathur, A. Joshi, S. Singh, A. Gautam, G.P.S. Raghava, CancerPPD: a database of anticancer peptides and proteins, Nucleic Acids Res. 43 (2015) D837–D843, https://doi.org/10.1093/nar/gku892.
[25] F. Schweizer, Cationic amphiphilic peptides with cancer-selective toxicity, Eur. J. Pharmacol. 625 (2009) 190–194, https://doi.org/10.1016/j.ejphar.2009.08.043.
[26] A.F. Lacerda, P.B. Pelegrini, D.M. de Oliveira, É.A.R. Vasconcelos, M.F. Grossi-de-Sá, Anti-parasitic peptides from arthropods and their application in drug therapy, Front. Microbiol. 7 (2009) 91, https://doi.org/10.3389/fmicb.2016.00091.
[27] D. Mehta, P. Anand, V. Kumar, A. Joshi, D. Mathur, S. Singh, A. Tuknait, K. Chaudhary, S.K. Gautam, A. Gautam, G.C. Varshney, G.P.S. Raghava, ParaPep: a Web Resource for Experimentally Validated Antiparasitic Peptide Sequences and Their Structures, Database (Oxford), 2014, https://doi.org/10.1093/database/bau051 bau051–bau051.
[28] J. Pretzel, F. Mohring, S. Rahlfs, K. Becker, Antiparasitic peptides, Adv. Biochem. Eng. Biotechnol. 135 (2013) 157–192, https://doi.org/10.1007/10_2013_191.
[29] A. Mor, Multifunctional host defense peptides: antiparasitic activities, FEBS J. 276 (2009) 6474–6482, https://doi.org/10.1111/j.1742-4658.2009.07358.x.
[30] N. Boulanger, R.J.L. Munks, J.V. Hamilton, F. Vovelle, R. Brun, M.J. Lehane, P. Bulet, Epithelial innate immunity. A novel antimicrobial peptide with antiparasitic activity in the blood-sucking insect Stomoxys calcitrans, J. Biol. Chem. 277 (2002) 49921–49926, https://doi.org/10.1074/jbc.M206296200.
[31] R. Kumar, K. Chaudhary, M. Sharma, G. Nagpal, J.S. Chauhan, S. Singh, A. Gautam, G.P.S. Raghava, AHTPDB: a comprehensive platform for analysis and presentation of antihypertensive peptides, Nucleic Acids Res. 43 (2015) D956–D962, https://doi.org/10.1093/nar/gku1141.
[32] P. Puchalska, M.L. Marina Alegre, M.C. García López, Isolation and characterization of peptides with antihypertensive activity in foodstuffs, Crit. Rev. Food Sci. Nutr. 55 (2015) 521–551, https://doi.org/10.1080/10408398.2012.664829.
[33] A. Aleixandre, M. Miguel, B. Muguerza, Peptides with antihypertensive activity from milk and egg proteins, Nutr. Hosp. 23 (2008) 313–834. http://www.ncbi.nlm.nih.gov/pubmed/18604316.
[34] P. Agrawal, S. Bhalla, S.S. Usmani, S. Singh, K. Chaudhary, G.P.S. Raghava, A. Gautam, CPPsite 2.0: a repository of experimentally validated cell-penetrating peptides, Nucleic Acids Res. 44 (2016) D1098–D1103, https://doi.org/10.1093/nar/gkv1266.
[35] D. Mathur, S. Prakash, P. Anand, H. Kaur, P. Agrawal, A. Mehta, R. Kumar, S. Singh, G.P.S. Raghava, PEPlife: a repository of the half-life of peptides, Sci. Rep. 6 (2016) 36617, https://doi.org/10.1038/srep36617.
[36] S.C. Penchala, M.R. Miller, A. Pal, J. Dong, N.R. Madadi, J. Xie, H. Joo, J. Tsai, P. Batoon, V. Samoshin, A. Franz, T. Cox, J. Miles, W.K. Chan, M.S. Park, M. M. Alhamadsheh, A biomimetic approach for enhancing the in vivo half-life of peptides, Nat. Chem. Biol. 11 (2015) 793–798, https://doi.org/10.1038/nchembio.1907.
[37] M. Werle, A. Bernkop-Schnürch, Strategies to improve plasma half life time of peptide and protein drugs, Amino Acids 30 (2006) 351–367, https://doi.org/10.1007/s00726-005-0289-3.
[38] A. Gautam, K. Chaudhary, S. Singh, A. Joshi, P. Anand, A. Tuknait, D. Mathur, G. C. Varshney, G.P.S. Raghava, Hemolytik: a database of experimentally determined hemolytic and non-hemolytic peptides, Nucleic Acids Res. 42 (2014) D444–D449, https://doi.org/10.1093/nar/gkt1008.
[39] K. Chaudhary, R. Kumar, S. Singh, A. Tuknait, A. Gautam, D. Mathur, P. Anand, G. C. Varshney, G.P.S. Raghava, A web server and mobile app for computing hemolytic potency of peptides, Sci. Rep. 6 (2016) 22843, https://doi.org/10.1038/srep22843.
[40] C.-Y. Yu, W. Huang, Z.-P. Li, X.-Y. Lei, D.-X. He, L. Sun, Progress in self-assembling peptide-based nanomaterials for biomedical applications, Curr. Top. Med. Chem. 16 (2016) 281–290, https://doi.org/10.2174/1568026615666150701114527.
[41] Z. Luo, Y. Yue, Y. Zhang, X. Yuan, J. Gong, L. Wang, B. He, Z. Liu, Y. Sun, J. Liu, M. Hu, J. Zheng, Designer D-form self-assembling peptide nanofiber scaffolds for 3-dimensional cell cultures, Biomaterials 34 (2013) 4902, https://doi.org/10.1016/j.biomaterials.2013.03.081, 13.
[42] R. de la Rica, H. Matsui, Applications of peptide and protein-based materials in bionanotechnology, Chem. Soc. Rev. 39 (2010) 3499–3509, https://doi.org/10.1039/b917574c.
[43] X. Zhao, F. Pan, H. Xu, M. Yaseen, H. Shan, C.A.E. Hauser, S. Zhang, J.R. Lu, Molecular self-assembly and applications of designer peptide amphiphiles, Chem. Soc. Rev. 39 (2010) 3480, https://doi.org/10.1039/b915923c.
[44] N. Habibi, N. Kamaly, A. Memic, H. Shafiee, Self-assembled peptide-based nanostructures: smart nanomaterials toward targeted drug delivery, Nano Today 11 (2016) 41–60, https://doi.org/10.1016/j.nantod.2016.02.004.
[45] A.O. Elzoghby, M.M. Elgohary, N.M. Kamel, Implications of protein- and Peptide-based nanoparticles as potential vehicles for anticancer drugs, Adv. Protein Chem. Struct. Biol. 98 (2015) 169–221, https://doi.org/10.1016/bs.apcsb.2014.12.002.
[46] W. Liyanage, K. Vats, A. Rajbhandary, D.S.W. Benoit, B.L. Nilsson, Multicomponent dipeptide hydrogels as extracellular matrix-mimetic scaffolds for cell culture applications, Chem. Commun. 51 (2015) 11260–11263, https://doi.org/10.1039/C5CC03162A.
[47] S. Koutsopoulos, Self-assembling peptide nanofiber hydrogels in tissue engineering and regenerative medicine: progress, design guidelines, and applications, J. Biomed. Mater. Res. 104 (2016) 1002–1016, https://doi.org/10.1002/jbm.a.35638.
[48] J. Liu, H. Song, L. Zhang, H. Xu, X. Zhao, Self-assembly-peptide hydrogels as tissue-engineering scaffolds for three-dimensional culture of chondrocytes in vitro, Macromol. Biosci. 10 (2010) 1164–1170, https://doi.org/10.1002/mabi.200900450.
[49] B. Chen, X.-Y. He, X.-Q. Yi, R.-X. Zhuo, S.-X. Cheng, Dual-peptide-functionalized albumin-based nanoparticles with ph-dependent self-assembly behavior for drug delivery, ACS Appl. Mater. Interfaces 7 (2015) 15148–15153, https://doi.org/10.1021/acsami.5b03866.
[50] F.P. Seib, G.T. Jones, J. Rnjak-Kovacina, Y. Lin, D.L. Kaplan, pH-Dependent anticancer drug release from silk nanoparticles, Adv. Healthc. Mater. 2 (2013) 1606–1611, https://doi.org/10.1002/adhm.201300034.
[51] L. Sasso, I. Vedarethinam, J. Emnéus, W.E. Svendsen, J. Castillo-León, Self-assembled diphenylalanine nanowires for cellular studies and sensor applications, J. Nanosci. Nanotechnol. 12 (2012) 3077–3083, https://doi.org/10.1166/jnn.2012.4534.
[52] T. Scheibel, R. Parthasarathy, G. Sawicki, X.-M. Lin, H. Jaeger, S.L. Lindquist, Conducting nanowires built by controlled self-assembly of amyloid fibers and selective metal deposition, Proc. Natl. Acad. Sci. Unit. States Am. 100 (2003) 4527–4532, https://doi.org/10.1073/pnas.0431081100.
[53] S. Zhang, Emerging biological materials through molecular self-assembly, Biotechnol. Adv. 20 (5–6) (2002) 321–339, https://doi.org/10.1016/s0734-9750(02)00026-5.
[54] S. Zhang, Emerging biological materials through molecular self-assembly, Biotechnol. Adv. 20 (2002) 321–339, https://doi.org/10.1016/S0734-9750(02)00026-5.
[55] M. Hatip Koc, G. Cinar Ciftci, S. Baday, V. Castelletto, I.W. Hamley, M.O. Guler, Hierarchical self-assembly of histidine-functionalized peptide amphiphiles into supramolecular chiral nanostructures, Langmuir 33 (2017) 7947–7956, https://doi.org/10.1021/acs.langmuir.7b01266.
[56] N. Rodríguez-Vázquez, M. Amorín, J.R. Granja, Recent advances in controlling the internal and external properties of self-assembling cyclic peptide nanotubes and dimers, Org. Biomol. Chem. 15 (2017) 4490–4505, https://doi.org/10.1039/C7OB00351J.
[57] A. Fuertes, H.L. Ozores, M. Amorín, J.R. Granja, Self-assembling Venturi-like peptide nanotubes, Nanoscale 9 (2017) 748–753, https://doi.org/10.1039/C6NR08174F.
[58] P. Tamamis, E. Kasotakis, G. Archontis, A. Mitraki, Combination of theoretical and experimental approaches for the design and study of fibril-forming peptides, Methods Mol. Biol. 1216 (2014) 53–70, https://doi.org/10.1007/978-1-4939-1486-9_3.
[59] H.-K. Lee, S. Soukasene, H. Jiang, S. Zhang, W. Feng, S.I. Stupp, Light-induced self-assembly of nanofibers inside liposomes, Soft Matter 4 (2008) 962–964, https://doi.org/10.1039/b719486b.
[60] H. Cui, T. Muraoka, A.G. Cheetham, S.I. Stupp, Self-assembly of giant peptide nanobelts, Nano Lett. 9 (2009) 945–951, https://doi.org/10.1021/nl802813f.
[61] U. Khoe, Y. Yang, S. Zhang, Self-assembly of nanodonut structure from a cone-shaped designer lipid-like peptide surfactant, Langmuir 25 (2009) 4111–4114, https://doi.org/10.1021/la8025232.
[62] G. Guisbiers, S. Mejía-Rosales, F. Leonard Deepak, Nanomaterial properties: size and shape dependencies, J. Nanomater. 2012 (2012), https://doi.org/10.1155/2012/180976.
[63] N. Karak, Fundamentals of nanomaterials and polymer nanocomposites, in: Nanomater. Polym. Nanocomposites Raw Mater. To Appl., Elsevier, 2018, pp. 1–45, https://doi.org/10.1016/B978-0-12-814615-6.00001-1.
[64] E.M. Ahmed, Hydrogel: preparation, characterization, and applications: a review, J. Adv. Res. 6 (2015) 105–121, https://doi.org/10.1016/j.jare.2013.07.006.
[65] D. Mandal, A. Nasrolahi Shirazi, K. Parang, Self-assembly of peptides to nanostructures, Org. Biomol. Chem. 12 (2014) 3544–3561, https://doi.org/10.1039/c4ob00447g.
[66] I.W. Hamley, A. Dehsorkhi, V. Castelletto, Coassembly in binary mixtures of peptide amphiphiles containing oppositely charged residues, Langmuir 29 (2013) 5050–5059, https://doi.org/10.1021/la400163q.
[67] R.V. Ulijn, A.M. Smith, Designing peptide based nanomaterials, Chem. Soc. Rev. 37 (2008) 664–675, https://doi.org/10.1039/b609047h.

[68] G.M. Whitesides, J.P. Mathias, C.T. Seto, Molecular self-assembly and nanochemistry: a chemical strategy for the synthesis of nanostructures, Science 254 (1991) 1312–1319, https://doi.org/10.1126/science.1962191.
[69] N. Habibi, N. Kamaly, A. Memic, H. Shafiee, Self-assembled peptide-based nanostructures: smart nanomaterials toward targeted drug delivery, Nano Today 11 (2016) 41–60, https://doi.org/10.1016/j.nantod.2016.02.004.
[70] J. Castillo-Leon, Karsten B. Andersen, Winnie E. Svendsen, Self–assembled peptide nanostructures for biomedical applications: Advantages and challenges, Biomater. Sci. Eng. (2011), https://doi.org/10.5772/23322. InTech.
[71] S. Gupta, I. Singh, A.K. Sharma, P. Kumar, Ultrashort peptide self-assembly: front-runners to transport drug and gene cargos, Front. Bioeng. Biotechnol. 8 (2020) 504, https://doi.org/10.3389/fbioe.2020.00504.
[72] T. Fan, X. Yu, B. Shen, L. Sun, Peptide self-assembled nanostructures for drug delivery applications, J. Nanomater. 2017 (2017), https://doi.org/10.1155/2017/4562474.
[73] S. Gupta, P. Kumar, Drug delivery using nanocarriers: Indian perspective, Proc. Natl. Acad. Sci. India B Biol. Sci. 82 (2012) 167–206, https://doi.org/10.1007/s40011-012-0080-7.
[74] S. Lee, T.H.T. Trinh, M. Yoo, J. Shin, H. Lee, J. Kim, E. Hwang, Y.B. Lim, C. Ryou, Self-assembling peptides and their application in the treatment of diseases, Int. J. Mol. Sci. 20 (2019), https://doi.org/10.3390/ijms20235850.
[75] P.H.M. Hoet, I. Brüske-Hohlfeld, O.V. Salata, Nanoparticles - known and unknown health risks, J. Nanobiotechnol. 2 (2004) 1–15, https://doi.org/10.1186/1477-3155-2-12.
[76] B.E. Rabinow, Nanosuspensions in drug delivery, Nat. Rev. Drug Discov. 3 (2004) 785–796, https://doi.org/10.1038/nrd1494.
[77] J.J. Panda, A. Varshney, V.S. Chauhan, Self-assembled nanoparticles based on modified cationic dipeptides and DNA: novel systems for gene delivery, J. Nanobiotechnol. 11 (2013) 18, https://doi.org/10.1186/1477-3155-11-18.
[78] R. Ischakov, L. Adler-Abramovich, L. Buzhansky, T. Shekhter, E. Gazit, Peptide-based hydrogel nanoparticles as effective drug delivery agents, Bioorg. Med. Chem. 21 (2013) 3517–3522, https://doi.org/10.1016/j.bmc.2013.03.012.
[79] J.D. Hartgerink, E. Beniash, S.I. Stupp, Self-assembly and mineralization of peptide-amphiphile nanofibers, Science 84 294 (2001) 1684–1688, https://doi.org/10.1126/science.1063187.
[80] J.J. Panda, A. Kaul, S. Alam, A.K. Babbar, A.K. Mishra, V.S. Chauhan, Designed peptides as model self-assembling nanosystems: characterization and potential biomedical applications, Ther. Deliv. 2 (2011) 193–204. http://www.ncbi.nlm.nih.gov/pubmed/22833945.
[81] G. Liang, Z. Yang, R. Zhang, L. Li, Y. Fan, Y. Kuang, Y. Gao, T. Wang, W.W. Lu, B. Xu, Supramolecular hydrogel of a D-amino acid dipeptide for controlled drug release in vivo, Langmuir 25 (2009) 8419–8422. http://www.ncbi.nlm.nih.gov/pubmed/20050040.
[82] J.J. Panda, A. Mishra, A. Basu, V.S. Chauhan, Stimuli responsive self-assembled hydrogel of a low molecular weight free dipeptide with potential for tunable drug delivery, Biomacromolecules 9 (2008) 2244–2250, https://doi.org/10.1021/bm800404z.
[83] A. Mishra, J.J. Panda, A. Basu, V.S. Chauhan, Nanovesicles based on self-assembly of conformationally constrained aromatic residue containing amphiphilic dipeptides, Langmuir 24 (2008) 4571–4576, https://doi.org/10.1021/la7034533.
[84] S. Alam, J.J. Panda, V.S. Chauhan, Novel dipeptide nanoparticles for effective curcumin delivery, Int. J. Nanomed. 7 (2012) 4207–4222, https://doi.org/10.2147/IJN.S33015.
[85] V. Jayawarna, M. Ali, T.A. Jowitt, A.F. Miller, A. Saiani, J.E. Gough, R.V. Ulijn, Nanostructured hydrogels for three-dimensional cell culture through self-assembly of fluorenylmethoxycarbonyl–dipeptides, Adv. Mater. 18 (2006) 611–614, https://doi.org/10.1002/adma.200501522.
[86] J.J. Panda, R. Dua, A. Mishra, B. Mittra, V.S. Chauhan, 3D cell growth and proliferation on a RGD functionalized nanofibrillar hydrogel based on a conformationally restricted residue containing dipeptide, ACS Appl. Mater. Interfaces 2 (2010) 2839–2848, https://doi.org/10.1021/am1005173.
[87] S.B. Needleman, C.D. Wunsch, A general method applicable to the search for similarities in the amino acid sequence of two proteins, J. Mol. Biol. 48 (1970) 443–453, https://doi.org/10.1016/0022-2836(70)90057-4.
[88] A.D. Ozkan, A.B. Tekinay, M.O. Guler, E.D. Tekin, Effects of temperature, pH and counterions on the stability of peptide amphiphile nanofiber structures, RSC Adv. 6 (2016) 104201–104214, https://doi.org/10.1039/C6RA21261A.
[89] G. Demirel, N. Malvadkar, M.C. Demirel, Control of protein adsorption onto core-shell tubular and vesicular structures of diphenylalanine/parylene, Langmuir 26 (2010) 1460–1463, https://doi.org/10.1021/la903571y.
[90] P.P. Wozniak, M. Kotulska, AmyLoad: website dedicated to amyloidogenic protein fragments, Bioinformatics 31 (2015) 3395–3397, https://doi.org/10.1093/bioinformatics/btv375.
[91] A.M. Thangakani, R. Nagarajan, S. Kumar, R. Sakthivel, D. Velmurugan, M. M. Gromiha, CPAD, curated protein aggregation database: a repository of manually curated experimental data on protein and peptide aggregation, PloS One 11 (2016), e0152949, https://doi.org/10.1371/journal.pone.0152949.
[92] S. Pawlicki, A. Le Béchec, C. Delamarche, AMYPdb: a database dedicated to amyloid precursor proteins, BMC Bioinf. 9 (2008) 273, https://doi.org/10.1186/1471-2105-9-273.
[93] Sandeep Singh, Kumardeep Chaudhary, Sandeep Kumar Dhanda, Sherry Bhalla, , Salman Sadullah Usmani, Ankur Gautam, Abhishek Tuknait, Piyush Agrawal, Deepika Mathur, P.S. Gajendra, Raghava, SATPdb: a database of structurally annotated therapeutic peptides, Nucleic Acids Res. 44 (Issue D1) (2016) D1119–D1126, https://doi.org/10.1093/nar/gkv1114.
[94] D. Mathur, S. Singh, A. Mehta, P. Agrawal, G.P.S. Raghava, In silico approaches for predicting the half-life of natural and modified peptides in blood, PloS One 13 (6) (2018 Jun 1), e0196829. https://doi:10.1371/journal.pone.0196829.
[95] D. Silva, A. Natalello, B. Sanii, R. Vasita, G. Saracino, R.N. Zuckermann, S. M. Doglia, F. Gelain, Synthesis and characterization of designed BMHP1-derived self-assembling peptides for tissue engineering applications, Nanoscale 5 (2013) 704–718, https://doi.org/10.1039/c2nr32656f.