Protein Synthesis using Frequencies

John White
Updated 05/12/2025

All living beings, including humans, have one fundamental thing in common: proteins. These vital substances act as the building blocks of life. They oversee nearly every function within our bodies, playing essential roles in everything from tissue construction and infection defence to communication between cells and food digestion.

They also control the progression of disease and healing. They are incredibly important.

Proteins are composed of chains of amino acids, just like pins in a padlock. Each pin represents a different amino acid.

Protein Simulation

The chain of amino acids is a pattern. We must match this pattern to copy the protein, just as a lock will only open when the correct key is inserted.

Each amino acid is linked to a specific frequency. Playing these frequencies in the corresponding order is like a song that tells cells how to copy or block the protein.

The pattern of proteins can also be likened to pieces of a jigsaw puzzle. Each protein has a unique pattern. Only matching pieces of a jigsaw can be joined together.

Simulation Example

Serrapeptase is an enzyme like no other. It is often considered the Miracle Enzyme due to its multiple health-giving benefits. It is especially good for people with joint pain, external or internal scars, or an autoimmune disease. This high-cost protein which can be simulated for free.

Treating Diseases

Treating diseases by targeting proteins through inhibition or stimulation is a cornerstone of modern pharmacotherapy. Proteins play crucial roles in virtually all biological processes, and their dysfunction can lead to various diseases. By modulating these proteins, either by inhibiting their harmful actions or by enhancing their beneficial effects, treatments can effectively manage or cure many conditions, including cancer.

Proteins are fundamental in preventing cancer growth through various mechanisms, including controlling cell growth and division, repairing DNA, promoting cell death of damaged cells, enhancing the immune system, and blocking the supply of nutrients to tumors.

Proteins are crucial for helping our bodies heal from injuries and fight off illnesses. They work in several ways to make sure we recover properly:

Building and Repairing

Proteins like collagen help repair damaged tissues. Think of collagen as a kind of glue that helps hold everything together. When you get a cut or a bruise, collagen helps to patch things up and make them strong again.

Fighting Infections

Proteins are essential in our immune system, which protects us from germs. Antibodies, a type of protein, help identify and destroy bacteria and viruses that can make us sick.

Helping Cells Communicate

Some proteins act as messengers and help cells communicate with each other. This is really important when your body is healing because it helps coordinate the repair process, like calling workers to fix a broken road.

Detoxing

There are also proteins that help clean up dead cells and other debris at the site of an injury. This is like the clean-up crew that comes in after a construction job, making sure everything is tidy so new structures can be built.

Controlling Responses

Proteins help control how our bodies respond to injuries and stress. For example, some proteins help reduce swelling and manage pain during the healing process.
In simple terms, proteins are like the workers in a well-organized team, each with a specific job that helps us heal and stay healthy. They are vital for fixing damaged parts, fighting off invaders, and making sure our bodies work smoothly during the healing process.

Designing Custom Peptides

In addition to copying or blocking existing proteins, science now allows us to design new, optimised peptides which don't necessary exist in nature.

A peptide is simply a shorter, simpler version of a protein; a mini-protein that can still perform powerful jobs in the body. Many modern medicines are peptides because they are natural, safe, targeted, and extremely effective.

Think of peptides as custom tools, each crafted to solve a specific problem:

- Some reduce inflammation.
- Some repair cartilage or tendons.
- Some improve immune balance.
- Some regenerate skin or internal tissue.
- Some stop cancer cells from dividing.

Because peptides are modular; like Lego blocks, we can design them using modern methods to achieve the best possible effect.

Here is a simple explanation for some of the scientific methods used:

Rational Fragment-Based Design

This method is like building a new key out of the best pieces of many old keys.
Scientists:

- break down natural proteins into small fragments
- test which fragments perform useful actions (healing, anti-inflammatory, immune-modulating, etc.)
- recombine the best pieces into a brand-new, stronger peptide

This produces peptides that are targeted, efficient, and highly specific.

Structure-Based Modelling (3D Protein Simulation)

Imagine designing a puzzle piece by studying the exact shape of the empty space it must fit into.
Using 3D modeling:

- researchers examine the shape of receptors on cells
- design peptides that fit perfectly into these structures
- ensure they activate or block the desired biological pathways

This produces peptides with excellent precision and minimal side effects.

QSAR / Machine-Learning Peptide Prediction

QSAR stands for *Quantitative Structure–Activity Relationship*.
It is like showing a computer thousands of tools and teaching it which shapes and materials perform best for each task.
ML models analyze:

- amino-acid properties
- charge, polarity, hydrophobicity
- folding patterns
- past peptide successes and failures

The model then predicts new peptide sequences with maximal therapeutic potential.

Deep-Learning Generative Peptide Engineering

This is like asking an AI composer to invent entirely new "melodies" (peptide sequences) no human has ever considered.
Deep-learning models:

- simulate peptide behaviour at the molecular level
- generate sequences optimised for stability, potency, safety, and biological targeting
- test them in virtual environments before they are ever made in real life

This unlocks completely novel peptides far beyond what classical biology could design.

Motif Optimisation Using Display Technologies (Phage, mRNA, Ribosome Display)

These techniques are like using trillions of tiny test subjects, each carrying a slightly different peptide, and letting biology itself reveal which one performs best.
Phage display, mRNA display, and ribosome display:

- create libraries of millions to billions of peptide variations
- expose them to a target (like a cancer marker, inflammatory protein, or receptor)
- let only the best-binding peptides survive
- repeatedly refine them through selection cycles

The result is a peptide precisely evolved for maximum effect, and can be modelled using powerful computers.

Why Custom-Designed Peptides Work So Well

Peptides can be:

- more targeted than drugs

- more natural than chemicals
- safer with fewer side effects
- designed for very specific tissues
- fast-acting
- easy for the body to understand and use

If proteins are the “workers,” peptides are specialised experts, like a locksmith, electrician, or surgeon.

Custom-made peptides ensure the exact expert your body needs can be called into action.

This makes peptide-based approaches one of the most promising frontiers in future medicine. Frequency-encoded sequences allows this to happen today.

Summary

- Proteins run almost everything in the body.
- Their sequences can be represented as patterns of frequencies.
- These patterns can simulate beneficial proteins or inhibit harmful ones.
- Modern science can also design entirely new peptides optimised for healing.
- These novel peptides can:
    - repair tissue
    - calm inflammation
    - balance immunity
    - fight cancer
    - prevent disease progression
    - promote longevity

Modern computational design methods allow us to tailor-make ideal, optimised peptides for any disease or health condition. By translating these sequences of these peptides into frequency patterns, we gain an extraordinary new toolkit for improving health and promote healing.

References et al:

Abraham MJ, 2015, GROMACS: high-performance molecular simulations, SoftwareX.
Adessi C, 2002, Peptide therapeutics and strategies to improve bioavailability, Current Medicinal Chemistry.
Al-Omari AM, 2024, Accelerating antimicrobial peptide design using deep learning, PLOS ONE.
AlKharboush DF, 2025, Fragment-based drug discovery: a graphical review, Computational and Structural Biotechnology Journal.
Anand N, 2018, Generative modeling for protein structures, Advances in Neural Information Processing Systems.
André AS, 2022, In vivo phage display selection strategies, Frontiers in Microbiology.
Andrews DM, 2019, The evolution of fragment-based drug discovery, RSC Medicinal Chemistry.
Baek M, 2021, Accurate prediction of protein structures and interactions using a three-track neural network (RoseTTAFold), Science.
Bakhshinejad B, 2025, Cell-selective peptide discovery via phage display, Frontiers in Molecular Biosciences.
Barash D, 2024, Machine learning methods for improving peptide drug-likeness, Drug Discovery Today.
Barrass S, 2012, Designing effective auditory graphs, Information Visualization.
Barrass S, 2012, The aesthetic turn in sonification towards a social and cultural context, AI & Society.
Barrass S, 2019, Practical Sonification Design, Proceedings of ICAD.
Barrass S, 2019, Sonification design patterns for science and engineering, Proceedings of ICAD.
Bashir H, 2022, Fragment-based inhibitor design for protein–protein interactions, Bioorganic Chemistry.
Baurin N, 2004, Design and characterization of libraries of structurally diverse fragments for use in NMR screening, Journal of Chemical Information and Computer Sciences.
Best RB, 2012, Optimization of the additive CHARMM all-atom protein force field, Journal of Chemical Theory and Computation.
Bhardwaj S, 2023, Comparative QSAR approaches for peptide potency prediction, SAR and QSAR in Environmental Research.
Binz HK, 2004, High-affinity binders by ribosome display of designed ankyrin repeat proteins, Nature Biotechnology.
Bon M, 2022, High-quality fragment libraries in fragment-based drug discovery, Drug Discovery Today.
Bonebright TL, 2012, Perceptual issues in auditory displays, The Sonification Handbook.
Bovermann T, 2011, Designing interactive sonification systems, The Sonification Handbook.
Boyken SE, 2016, De novo design of protein homo-oligomers, Science.
Brandes N, 2022, ProteinBERT: a universal deep-learning model for protein sequence and function, Bioinformatics.
Braun R, 2024, Listening to life: sonification for discovery in life sciences, Biotechnology and Bioengineering.
Bresin R, 2011, Expressive sonification for cross-modal mappings, The Sonification Handbook.
Brookes DH, 2019, Conditioning generative models of proteins on structural information, Journal of Chemical Information and Modeling.
Buehler MJ, 2022, Sonifying science: from an amino acid scale to spider silk symphony, Physics World.
Cao L, 2022, Designing protein–protein interaction inhibitors using language models, Journal of Chemical Information and Modeling.
Cardoso MH, 2021, Computer-aided design of antimicrobial peptides, Frontiers in Microbiology.
Chandler DL, 2019, Translating proteins into music and back, MIT News.
Cheng F, 2012, AdmetSAR: a comprehensive source for ADMET QSAR models, Journal of Chemical Information and Modeling.
Ciemny MP, 2018, A review of peptide docking, Current Topics in Medicinal Chemistry.
Cieslak A, 2018, Pro-apoptotic peptides as anticancer agents, Frontiers in Oncology.
Colas P, 1996, Genetic selection of peptide aptamers, Proceedings of the National Academy of Sciences.
Congreve M, 2008, A 'rule of three' for fragment-based lead discovery, Drug Discovery Today.
Cosic I, 1994, Macromolecular bioactivity: is it resonant interaction between macromolecules? IEEE Transactions on Biomedical Engineering.
Cosic I, 1995, The Resonant Recognition Model: prediction of protein-protein interactions, Journal of Molecular Structure (THEOCHEM).
Cosic I, 1997, The Resonant Recognition Model of macromolecular bioactivity: theory and applications, BMC Structural Biology.
Cosic I, 2006, Virtual spectroscopy: a new concept for analysis of biological systems, IEEE Transactions on Biomedical Engineering.
Cosic I, 2012, Protein electromagnetic resonance and its role in neural signalling, Neuroscience Letters.
Cosic I, 2015, The Resonant Recognition Model: theory and applications to bio-macromolecular interactions, Current Opinion in Biotechnology.
Craik DJ, 2013, The future of peptide-based drugs, Chemical Biology & Drug Design.
Cramer RD, 1988, Comparative molecular field analysis (CoMFA), Journal of the American Chemical Society.
Curtis EA, 2021, Ribosome display: a review of methods and applications, Methods.
Cvetkovic D, Cosic I, 2007, Alterations of the resting EEG caused by monophasic pulsed current stimulation, International Journal of Psychophysiology.
da Silva F, 2018, Docking-based virtual screening of peptide libraries, Journal of Molecular Modeling.
de Campo A, 2007, Toward a Sonification Design Space Map, Proceedings of ICAD.
Degiacomi MT, 2019, Generative models for small protein motifs, Journal of Chemical Theory and Computation.
Di L, 2015, Peptide absorption, distribution and stability, AAPS Journal.
Dijksteel GS, 2021, Application of AMPs in clinical settings, Antibiotics.
Doak BC, 2016, Oral druggable space beyond the rule of 5 from a fragment perspective, Drug Discovery Today.
Dong R, 2025, De novo designed bifunctional antimicrobial peptides, eLife.
Dror RO, 2012, Biomolecular simulation: a computational microscope for molecular biology, Annual Review of Biophysics.
Du QS, 2014, Two-level QSAR network for peptide inhibitor design, Journal of Computer-Aided Molecular Design.

Elnaggar A, 2021, ProtTrans: towards cracking the language of life's code through self-supervised deep learning, IEEE Transactions on Pattern Analysis and Machine Intelligence.
Erlanson DA, 2016, Twenty years on: the impact of fragments on drug discovery, Nature Reviews Drug Discovery.
Ertl P, 2003, QSAR and 3D-QSAR approaches for peptides and peptidomimetics, Mini-Reviews in Medicinal Chemistry.
Evans R, 2022, Protein complex prediction with AlphaFold-Multimer, bioRxiv preprint.
Ferruz N, 2022, ProtGPT2: generative transformer for protein design, Nature Communications.
Fiser A, 2003, Modeller: generation and refinement of homology-based protein structure models, Methods in Enzymology.
Fjell CD, 2012, Designing antimicrobial peptides: a review of techniques and approaches, Current Pharmaceutical Design.
Fosgerau K, 2015, Peptide therapeutics: current status and future directions, Drug Discovery Today.
Galluzzi L, 2019, Immunogenic cell death and peptide-based vaccines, Nature Reviews Immunology.
Gao J, 2022, Peptide–drug conjugates for targeted cancer therapy, Molecular Cancer Therapeutics.
Gao R, 2024, QSAR-aided design of anti-inflammatory peptides, Journal of Peptide Science.
García-Sosa AT, 2019, Peptides targeting oncogenic protein–protein interactions, Current Medicinal Chemistry.
Gautam A, 2014, In silico design of toxic/non-toxic therapeutic peptides, Scientific Reports.
Goles M, 2024, Peptide-based drug discovery through artificial intelligence, Briefings in Bioinformatics.
Gorelik B, 2019, Fragment-based discovery of ligands for peptide receptors, ACS Medicinal Chemistry Letters.
Greener JG, 2018, Deep generative models of protein structure and function, Cell Systems.
Grond F, 2010, Evaluation of parameter mapping strategies in sonification, Journal of New Music Research.
Grond F, 2011, Parameter mapping sonification, The Sonification Handbook, Logos Verlag.
Grosdidier A, 2011, SwissDock: a protein–ligand docking web service, Nucleic Acids Research.
Guo Z, 2021, Peptide–MHC docking and virtual screening, Briefings in Bioinformatics.
Hajduk PJ, 2005, Fragment-based approaches to drug discovery targeting protein–protein interactions, Drug Discovery Today.
Hampton JT, 2024, Diversification of phage-displayed libraries with noncanonical amino acids, Chemical Reviews.
Hancock REW, 2016, Host defense peptides and their potential as new therapeutics, Drugs.
Hanes J, 1997, In vitro selection and evolution of functional proteins by ribosome display, Proceedings of the National Academy of Sciences.
Hassan M, 2022, QSAR in therapeutic peptide research: a review, Current Topics in Medicinal Chemistry.
Hayashi K, 2008, Musical representation of protein sequences based on hydrophobicity scales, Bioacoustics Conference Proceedings.
He M, 2002, Ribosome display: an in vitro method for selection and evolution of antibodies, Trends in Biotechnology.
Hermann T, 2002, Sonification for exploratory data analysis, PhD Thesis, Bielefeld University.
Hermann T, 2011, Sonification: a definition, The Sonification Handbook.
Hess B, 2008, GROMACS 4: algorithms for highly efficient simulations, Journal of Chemical Theory and Computation.
Hesslow D, 2022, RITA: a study on scaling up protein language models, arXiv preprint.
Hie B, 2021, Learning the language of viral evolution and escape, Cell.
Hoet RM, 2005, Antibody library technologies: overview, Nature Biotechnology.
Hoogenboom HR, 2005, Overview of antibody and peptide phage display, Nature Reviews Immunology.
Huang P, 2024, Advances in peptide docking algorithms, Journal of Chemical Theory and Computation.
Huang PS, 2016, The coming of age of de novo protein design, Nature.
Huang S, 2023, PeptideBERT: transformer-based representation learning for therapeutic peptides, Molecular Informatics.
Ingraham J, 2019, Generative models for graph-based protein design, Advances in Neural Information Processing Systems.
Jacquemard C, 2019, Fragment-based drug discovery: from past to future, Expert Opinion on Drug Discovery.
Jahnke W, 2020, Fragment-to-lead medicinal chemistry trends, Journal of Medicinal Chemistry.
Jain N, 2020, QSAR and 3D-QSAR of peptide analogues targeting integrins, Medicinal Chemistry.
Jaroszewicz W, 2022, Phage display and peptide library technologies, FEMS Microbiology Reviews.
Jensen KJ, 2013, Peptidomimetics and constrained peptides in drug design, Chemical Reviews.
Jenssen H, 2006, Therapeutic potential of antimicrobial peptides, Nature Reviews Drug Discovery.
Jiang L, 2008, De novo computational design of retro-aldol enzymes, Science.
Jiang L, 2024, QSAR-driven optimization of therapeutic peptides, European Journal of Pharmaceutical Sciences.
Jiang T, 2019, Nanoparticle-based delivery of therapeutic peptides, Advanced Drug Delivery Reviews.
Josephson K, 2014, In vitro selection of peptides and proteins using mRNA display, Methods.
Jumper J, 2021, Highly accurate protein structure prediction with AlphaFold, Nature.
Kalman L, 2024, Sequence-to-function deep models in peptide design, BioSystems.
Kang HK, 2017, The therapeutic applications of antimicrobial peptides, Expert Review of Anti-infective Therapy.
Karplus M, 2002, Molecular dynamics simulations in chemistry, Current Opinion in Structural Biology.
Katare M, 2023, Peptide toxicity QSAR models, Regulatory Toxicology and Pharmacology.
Kaur H, 2020, Computational prediction of immunogenic and non-immunogenic peptides, Briefings in Bioinformatics.
Kawakami T, 2018, Ribozyme-based peptide display methods, Accounts of Chemical Research.
Keefe AD, 2001, Library-based selection technologies: overview, Nature Reviews Drug Discovery.
Khatib F, 2023, Using Rosetta for peptide–receptor modeling, Journal of Structural Biology.
Kim KH, 2022, Variational autoencoders for peptide generation targeting GPCRs, Journal of Molecular Graphics and Modelling.
Kirsch P, 2019, Concepts and core principles of fragment-based drug design, Molecules.
Knudsen LB, 2019, GLP-1 analogues and formulation strategies, Diabetes.
Kobayashi T, 2010, Chromatic sonification of DNA and protein motifs, BioSystems.

Kramer G, 1994, Auditory Display: Sonification, Audification and Auditory Interfaces, Addison-Wesley.
Krumpe LRH, 2007, Phage-displayed peptides for tumor targeting, Current Pharmaceutical Design.
Kubinyi H, 1997, 3D-QSAR in drug design: theory, methods and applications, Journal of Receptor and Signal Transduction.
Kundu S, 2021, QSAR modeling for peptide solubility and stability, Molecular Pharmaceutics.
Lambert S, 2017, Psychoacoustic mapping of protein folding energy landscapes, Journal of Sonic Studies.
Lau JL, 2018, Therapeutic peptides: historical perspectives and future trends, Bioorganic & Medicinal Chemistry.
Lee J, 2020, CHARMM-GUI input generator for biomolecular simulation, Journal of Chemical Physics.
Lei J, 2019, The antimicrobial peptide database (APD): updates and applications, Nucleic Acids Research.
Leman JK, 2020, Macromolecular modeling and design in Rosetta, Methods in Enzymology.
Li J, 2021, Peptide checkpoint inhibitors and immune modulation, Frontiers in Immunology.
Li Q, 2020, Fragment-based approaches to versatile drug targets, Frontiers in Molecular Biosciences.
Li S, 2022, Attention-based networks for predicting antimicrobial peptides, BMC Bioinformatics.
Lindorff-Larsen K, 2010, Improved side-chain torsion potentials for the Amber ff99SB protein force field, Proteins.
Lipovsek D, 2011, Evolution of novel binding proteins by ribosome display, Journal of Immunological Methods.
Liu Q, 2022, QSAR methodology for peptide affinity prediction, Journal of Chemical Information and Modeling.
Lodha SK, 1996, Ear: a sonification system for exploratory data analysis, Proceedings of Visualization.
MacKerell AD, 1998, All-atom empirical potential for molecular modeling: CHARMM, Journal of Physical Chemistry B.
Madani A, 2023, ProGen2: expanding deep generative models for protein design, Nature.
Mahlapuu M, 2020, Antimicrobial peptides as therapeutic agents, Frontiers in Cellular and Infection Microbiology.
Mahlapuu M, 2020, The future of antimicrobial peptides, Frontiers in Cellular and Infection Microbiology.
Mahmoodi-Reihani M, 2020, In silico rational design and virtual screening of bioactive peptides, ACS Omega.
Mao Y, 2023, Diffusion probabilistic models for de novo peptide design, Chemical Science.
Mardikoraem M, 2023, Generative models for protein sequence modeling, Briefings in Bioinformatics.
Martin EJ, 2021, Using sound to comprehend protein sequence data, BMC Bioinformatics.
Matsumoto S, 2020, Self-assembling peptide nanostructures for drug delivery, Advanced Materials.
McCafferty J, 1990, Phage antibodies: filamentous phage displaying antibody variable domains, Nature.
Meier J, 2021, Language models enable zero-shot prediction of the effects of mutations on protein function, Advances in Neural Information Processing Systems.
Miller BR, 2020, Structure-based peptide design: computational methods and tools, Computational Structural Biology.
Mitchell A, 2010, Cell-penetrating peptides: mechanisms and applications, Trends in Pharmacological Sciences.
Mitragotri S, 2014, Overcoming the challenges in administering biologics, Nature Reviews Drug Discovery.
Morris GM, 2009, AutoDock4 and AutoDockTools4: automated docking with selective receptor flexibility, Journal of Computational Chemistry.
Murray CW, 2012, Rational design of fragment-based screening libraries, Drug Discovery Today.
Mutasher SA, 2023, Overview of therapeutic peptides in oncology, Cancer Treatment Reviews.
Muttenthaler M, 2021, Trends in peptide drug discovery, Nature Reviews Drug Discovery.
Naimuddin M, 2011, Selection of cell-binding peptides via mRNA display, Journal of Molecular Recognition.
Newton MS, 2020, mRNA display for the selection of peptides and proteins, Current Opinion in Structural Biology.
Nguyen LT, 2011, Structural and molecular basis of antimicrobial peptides, Biochimica et Biophysica Acta.
Nielsen DS, 2022, Peptide stability and modification strategies, Advanced Drug Delivery Reviews.
Nielsen M, 2003, Prediction of peptide binding to MHC class I and II, Immunogenetics.
Nissan N, 2024, Harnessing the power of artificial intelligence for peptide drug discovery, Heliyon.
OECD, 2014, Guidance document on the validation of (Q)SAR models, OECD Series on Testing and Assessment.
Ortiz-González C, 2024, QSAR modeling for predicting peptide pharmacokinetics, SDF Meeting Abstracts.
Otvos L, 2017, Peptide therapeutics in clinical practice, Frontiers in Chemistry.
Pagadala NS, 2017, Software for molecular docking: a review, Biophysical Reviews.
Pan X, 2023, Computational design of peptide binders informed by AlphaFold, Nature Communications.
Pande J, 2010, Antibody phage display: concepts and applications, Journal of Biosciences.
Parker JL, 2014, Fragment-based discovery of peptide transporter ligands, Nature Chemical Biology.
Pellegrino F, 2024, Fragment merging strategies in peptidomimetic design, MedChemComm.
Pérez-Garrido A, 2013, 3D-QSAR modeling of ACE inhibitory peptides, Journal of Molecular Modeling.
Peters B, 2020, Peptide vaccine design using computational tools, Current Opinion in Immunology.
Piana S, 2014, Protein folding simulations at atomic resolution, Journal of the American Chemical Society.
Pires DEV, 2015, pkCSM: predicting small-molecule pharmacokinetic properties using graph-based signatures, Journal of Medicinal Chemistry.
Plückthun A, 2012, Ribosome display: development and applications, Molecules.
Porto WF, 2017, Computational approaches for antimicrobial peptide discovery, Frontiers in Microbiology.
Pripp AH, 2005, QSAR modelling of bioactive peptides, Journal of Theoretical Biology.
Renukuntla J, 2013, Approaches for enhancing oral bioavailability of peptides, International Journal of Pharmaceutics.
Rezaee K, 2025, Bridging machine learning and peptide design for cancer therapy, Artificial Intelligence Review.
Rives A, 2021, Biological structure and function emerge from scaling unsupervised learning to 250 million protein sequences, Proceedings of the National Academy of Sciences.

Roberts RW, 1997, mRNA–protein fusions for the in vitro selection of peptides and proteins, Proceedings of the National Academy of Sciences.
Rosinski M, 2023, Fragment hotspots in peptide ligand design, Future Medicinal Chemistry.
Roy K, 2012, On validation of QSAR models, Chemometrics and Intelligent Laboratory Systems.
Roy K, 2015, Advances in 3D-QSAR methodologies, SAR and QSAR in Environmental Research.
Sahu K, 2023, 3D-QSAR for peptide–enzyme interaction prediction, Molecular Diversity.
Sali A, 1993, Comparative protein modeling by satisfaction of spatial restraints, Proceedings of the National Academy of Sciences.
Santos J, 2018, CoMFA-based modelling of peptide GPCR ligands, European Journal of Medicinal Chemistry.
Santos-Filho OA, 2015, CoMSIA models of peptide inhibitors of metalloproteases, Chemical Biology and Drug Design.
Sarkar A, 2022, QSAR-guided optimization of peptide BBB permeability, European Journal of Medicinal Chemistry.
Scaletti C, 2018, Sonification and the sound of data, Acoustics Today.
Schellekens H, 2013, Immunogenicity of therapeutic proteins and peptides, Journal of Pharmaceutical Sciences.
Scott DE, 2016, Fragment-based approaches in drug discovery for protein–protein interactions, Chemical Society Reviews.
Scott JK, 1990, Phage display of peptide libraries, Science.
Shaw DE, 2010, Atomic-level characterization of the structural dynamics of proteins, Science.
Smith GP, 1985, Filamentous fusion phage: novel expression vectors that display cloned antigens on the virion surface, Science.
Song BPC, 2024, Review of phage display: a jack-of-all-trades and master of many, Colloids and Surfaces B: Biointerfaces.
Sternheimer J, 2001, Quantification des protéines par transposition musicale, Journal de Physique et Musique (INREES Editions).
Sternheimer J, 2001, Quantification des protéines par transposition musicale, Journal de Physique et Musique (INREES Editions).
Sternheimer J, 2007, Wave-based regulation of protein biosynthesis: theoretical foundations and experimental data, NeuroQuantology.
Sternheimer J, 2007, Wave-based regulation of protein biosynthesis: theoretical foundations and experimental data, NeuroQuantology.
Sternheimer J, 2008, Protéodies: a theoretical framework for protein melody interactions, Proceedings of the International Conference on Science and Consciousness.
Sternheimer J, 2008, Protéodies: a theoretical framework for protein melody interactions, Proceedings of the International Conference on Science and Consciousness.
Strokach A, 2021, Deep generative modeling for protein design, arXiv preprint.
Suga H, 2012, In vitro selection of functional peptides using genetic code reprogramming, Journal of Biochemistry.
Szymczak P, 2021, AI-driven antimicrobial peptide discovery, Accounts of Chemical Research.
Thundimadathil J, 2012, Cancer treatment using peptide-based approaches, Drug Discovery Today.
Torres J, 2024, Machine-learning QSAR for peptide transport efficiency, Journal of Molecular Graphics and Modelling.
Trott O, 2010, AutoDock Vina: improving the speed and accuracy of docking, Journal of Computational Chemistry.
Ueda T, 2010, Ribosome display and mRNA display of unnatural peptides, Current Opinion in Chemical Biology.
Vasilev B, 2025, Comprehensive review of QSAR in drug design, Applied Sciences.
Veltri D, 2018, Deep learning improves antimicrobial peptide recognition, Bioinformatics.
Vickers P, 2010, Auditory graphs in scientific data analysis, ACM Transactions on Applied Perception.
Vickers P, 2011, Sonification for scientific data representation, in The Sonification Handbook, Logos Verlag.
Walker BN, 2001, An ear for data: sonification of scientific information, Human Factors.
Walker BN, 2002, Mapping and metaphors in auditory displays, Proceedings of ICAD.
Walker BN, 2013, Sonification strategies for large multidimensional data sets, Information Visualization.
Wan F, 2022, Deep generative models for peptide design, Digital Discovery.
Wang G, 2016, Antimicrobial peptides: discovery, design and application, CABI.
Wang R, 2025, Discovery of cyclic peptides by mRNA display, Cell Chemical Biology.
Wang Y, 2021, Design, synthesis and structure–activity relationships of therapeutic peptides, Acta Pharmaceutica Sinica B.
Wibowo N, 2020, Peptide vaccines and delivery systems, Journal of Controlled Release.
Wilcken R, 2013, Targeting protein–protein interactions with small molecules, Angewandte Chemie International Edition.
Wimley WC, 2010, Describing the mechanism of antimicrobial peptides, Biochimica et Biophysica Acta.
Wu K, 2023, GAN-based de novo design of antimicrobial peptides, Computational Biology and Chemistry.
Wu X, 2024, Deep learning for advancing peptide drug development, European Journal of Medicinal Chemistry.
Wu Z, 2021, Protein sequence design with deep generative models, Current Opinion in Structural Biology.
Xiao W, 2025, Advances in peptide drug development, Signal Transduction and Targeted Therapy.
Xu J, 2024, SeqDiff: diffusion models for constrained peptide sequence generation, Journal of Chemical Physics.
Yamaguchi J, 2009, cDNA display selection of peptides and proteins, Nucleic Acids Research.
Yang H, 2019, AADMET models for peptide-based agents, Journal of Pharmacy and Pharmacology.
Yap CW, 2011, 3D-QSAR for peptide HIV protease inhibitors, Journal of Computer-Aided Molecular Design.
Yin Y, 2024, Recent advances in macrocyclic peptide selections using mRNA display, Israel Journal of Chemistry.
Yu CH, 2019, Normal-mode vibration mapping for sound synthesis of proteins, Supplemental Methods to ACS Nano.
Yu CH, 2019, Sonification of amino acid sequences using vibrational normal modes, ACS Nano.
Zhang H, 2023, Deep learning-based bioactive therapeutic peptide design, Journal of Chemical Information and Modeling.
Zhang L, 2023, Peptide waveform encoding using hydrophobicity and charge scales, Journal of Molecular Aesthetics.
Zhang X, 2021, Liposomal and polymeric delivery of peptide therapeutics, Biomaterials.
Zhang Y, 2020, Immune-modulatory peptides in autoimmunity and cancer, Pharmacology & Therapeutics.