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Molecular Docking for Computer-Aided Drug Design Secretory Proteins Nature-Inspired Intelligent Computing Techniques in Bioinformatics Natural Products as Enzyme Inhibitors Application Of Omics, Ai And Blockchain In Bioinformatics Research Applications of Evolutionary Computation Neural Information Processing Advanced Intelligent Systems for Sustainable Development (AI2SD'2020) Drug Repositioning: Current Advances and Future Perspectives Toxicity Mechanisms, Exposure, Toxicokinetic and Risk Assessment Aspects of Metals, Toxic for Animals and Humans, Volume II Inflammatory Immune Disease: Molecular Mechanisms, Translational Approaches and Therapeutics Hybrid Artificial Intelligent Systems Computational Collective Intelligence Interaction of Biomolecules and Bioactive Compounds with the SARS-CoV-2 Proteins: Molecular Simulations for the fight against Covid-19 Advanced Nanomaterials for Point of Care Diagnosis and Therapy Cannabinoids as potential treatment for neurological diseases Air Pollution Modelling 11th international meeting on visualizing biological data (VIZBI 2021) Computational and Structural Approaches to Drug Discovery Molecular Mechanisms of Neuropathic Pain and Novel Therapeutic Targets Marine Antioxidants Physico-Chemical and Computational Approaches to Drug Discovery Peptide, Protein and Enzyme Design Monoamine Oxidase Canadian Journal of Chemistry Role of Lipids in the Dynamics of Allergic

Airway Inflammation Homology Modeling and Molecular Docking of Antagonists to Class B G-Protein Coupled Receptor Pituitary Adenylate Cyclase Type 1 (PAC1R) Quick Guideline for Computational Drug Design Computational Systems-Biology and Bioinformatics Cellulose Science and Derivatives Phytochemicals as Lead Compounds for New Drug Discovery Computational Biology and Machine Learning for Metabolic Engineering and Synthetic Biology Advances in Artificial Life, Evolutionary Computation and Systems Chemistry Biophysics and Structure to Counter Threats and Challenges Encyclopedia of Bioinformatics and Computational Biology Innovative Computing Recent Advances in Recognition of Bioactive Phytonutrients for Specific Targets in Plant Foods Chemical and Biochemical Approaches for the Study of Anesthetic Function In Silico Chemistry and Biology Advances in the discovery of natural molecules and their analogues against microbial infection-related biofilms

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Molecular modeling and simulation play a central role in academic and industrial research focused on physico-chemical properties and processes. The efforts carried out in this field have crystallized in a variety of models, simulation methods, and computational techniques that are examining the relationship between the structure, dynamics and functional role of biomolecules and their interactions. In particular, there has been a huge advance in the understanding of the molecular determinants that

mediate the interaction between small compounds acting as ligands and their macromolecular targets. This book provides an updated description of the advances experienced in recent years in the field of molecular modeling and simulation of biomolecular recognition, with particular emphasis towards the development of efficient strategies in structure-based drug design. This book comprises select proceedings of the 5th International Conference on Innovative Computing (IC 2022) focusing on cutting-edge research carried out in the areas of information technology, science, and engineering. Some of the themes covered in this book are cloud communications and networking, high performance computing, architecture for secure and interactive IoT, satellite communication, wearable network and system, infrastructure management, etc. The essays are written by leading international experts, making it a valuable resource for researchers and practicing engineers alike. Molecular Docking for Computer-Aided Drug Design: Fundamentals, Techniques, Resources and Applications offers in-depth coverage on the use of molecular docking for drug design. The book is divided into three main sections that cover basic techniques, tools, web servers and applications. It is an essential reference for students and researchers involved in drug design and discovery. Covers the latest information and state-of-the-art trends in structure-based drug design methodologies Includes case studies that complement learning Consolidates fundamental concepts and current practice of molecular docking into one convenient resource This two-volume set (LNAI 9875 and LNAI 9876) constitutes the refereed proceedings of the 8th International Conference on

Collective Intelligence, ICCCI 2016, held in Halkidiki, Greece, in September 2016. The 108 full papers presented were carefully reviewed and selected from 277 submissions. The aim of this conference is to provide an internationally respected forum for scientific research in the computer-based methods of collective intelligence and their applications in (but not limited to) such fields as group decision making, consensus computing, knowledge integration, semantic web, social networks and multi-agent systems. This book provides an overview of the latest developments and future challenges in enzyme inhibitor research. It discusses the general enzyme inhibitory principles and mechanisms in enzyme activity regulation and application of enzyme inhibitors in different areas and sectors. The major areas of applications of enzyme inhibitors covered in this book are human health management, agriculture, food processing and research, which leads to drug discovery or enzyme activity mechanisms. The book also identifies the gaps in the existing knowledge and opens up new research ideas in this important area. Currently, most enzyme inhibitors are reported to inhibit various classes of enzymes. These enzyme inhibitors are the focus of the scientific community because they may answer an increasing array of questions in the research area of biological sciences, including biochemistry, medicine, physiology, pharmacy, agriculture, ecology etc. It also serves as a useful tool in the study of enzyme structures and reaction mechanisms and in the development of technologies in agriculture, food processing, and health management. Chapters in this book cover topics such as plant-derived inhibitors of serine proteases, pancreatic lipase (PL) inhibitors from

indigenous medicinal plants, amylase inhibitors and their applications in agriculture and food processing industries and advances in silico techniques used in the study of enzyme inhibitors. The book will serve as a valuable resource for students and researchers in Life Sciences, agriculture, medicine, food processing, and allied industries. This insightful book represents the experience and understanding of the global experts in the field and spotlights both the structural and medicinal chemistry aspects of drug design. The need to 'encode' the physiological factors of pharmacology, a key area, is explored. Cellulose and cellulose derivatives are a class of bio-based materials that have attracted scientific interest due to their unique structural features and properties such as biocompatibility, biodegradability, and renewability. They are promising candidates for applications in biomedicine, pharmaceuticals, electronics, barrier films, nanocomposites, membranes, and supercapacitors. New resources, extraction procedures, and treatments are currently under development to satisfy increasing demands for cost-effective and sustainable methods of manufacturing new types of cellulose nanoparticle-based materials on an industrial scale. This book, written by an international collection of contributors in the field, is a useful reference for graduate students and researchers in chemistry, materials science, nanoscience, and green nanotechnology. This book constitutes the revised selected papers of the 10th Italian Workshop on Advances in Artificial Life, Evolutionary Computation and Systems Chemistry, WIVACE 2015, held at Bari, Italy, in September 2015. The 18 papers presented have been

thoroughly reviewed and selected from 45 submissions. They cover the following topics: evolutionary computation, bioinspired algorithms, genetic algorithms, bioinformatics and computational biology, modeling and simulation of artificial and biological systems, complex systems, synthetic and systems biology, systems chemistry. With the increasing availability of omics data and mounting evidence of the usefulness of computational approaches to tackle multi-level data problems in bioinformatics and biomedical research in this post-genomics era, computational biology has been playing an increasingly important role in paving the way as basis for patient-centric healthcare.Two such areas are: (i) implementing AI algorithms supported by biomedical data would deliver significant benefits/improvements towards the goals of precision medicine (ii) blockchain technology will enable medical doctors to securely and privately build personal healthcare records, and identify the right therapeutic treatments and predict the progression of the diseases.A follow-up in the publication of our book Computation Methods with Applications in Bioinformatics Analysis (2017), topics in this volume include: clinical bioinformatics, omics-based data analysis, Artificial Intelligence (AI), blockchain, big data analytics, drug discovery, RNA-seq analysis, tensor decomposition and Boolean network. Marine Antioxidants: Preparations, Syntheses, and Applications provides the most updated and comprehensive knowledge on utilizing marine-derived substances for cosmeceutical, pharmaceutical and nutraceutical developments. The book delivers the isolation procedures and biological activity of marine-

derived antioxidant substances as discussed by international experts on antioxidant material from actinobacteria, crustaceans, diatoms, fish, microalgae, microbes, and mangrove-associated marine organisms and seagrasses. In addition, the book details marine-derived bioactive antioxidants substances in the form of proteins, peptides, polysaccharides and lipids. Finally, the book provides the latest information on the mechanistic pathways of antioxidant substances with various diseases and nutritional perspectives. This is an essential resource for marine biotechnologists and marine biologists who want to better understand isolation procedures and antioxidant applications. Researchers interested in pharmaceutical nutrients, polymer science, and cosmeceuticals industries scientists, as well as students and academics, will also benefit from this book. Explores under-utilized marine products for commercial applications Offers isolated information and biological applications of each identified marine antioxidant Discusses the latest approaches to treatments of diseases, such as diabetes, arthritis, and cancer using marine resources The air pollution problem inevitably accompanies our human activities. Severe air pollution situations have been reported, especially in emerging countries, and satisfying the air quality standards fully remains an underlying issue. Today, modeling research is one of the more valuable approaches to understanding the behavior of air pollutants, and is useful for regulation-, policy- and decision-making. Such modeling applications range, with regard to horizontal grid resolution, from a few km (local) to hundreds of km (regional), to thousands of km

(global). To foster our current scientific knowledge on modeling potentialities and limitations, scientific research related to multi-scale air pollution modeling is collected in this book. Secretory Proteins, Volume 133 in the Advances in Protein Chemistry and Structural Biology series highlights new advances in the field, including chapters on Proprotein Convertases regulate trafficking and maturation of key proteins within the secretory pathway, Secretory Proteins in Cancer Diagnosis, Senescent Cells and SASP in Cancer Microenvironment: new approaches in cancer therapy, Autophagy for secretory protein: Therapeutic targets in cancer, Secretory proteins and pathways of secretion of osteosarcoma, Monocyte secretory proteins as drug targets for arresting progression of atherosclerosis, The secretory phenotypes of envenomed cells: insights into venom cytotoxicity, Macromolecules for secretory pathway in SARS-CoV-2 infection, and much more. Other sections cover Exploring the role of secretory proteins in the human infectious diseases diagnosis and therapeutics, Secretory proteins in orchestration of microbial pathogenesis- the curious case of Staphylococcus aureus, Influence of pathological mutations in Aspartylglucosylamine Deaspartylase causing Aspartylglucosaminuria: an in silico approach, and Change in conformational dynamics of Lipase A secretory protein upon mutation causing Wolman disease. Provides the authority and expertise of leading contributors from an international board of authors Presents the latest release in the Advances in Protein Chemistry and Structural Biology series Updated release includes the latest information on the Secretory Proteins

Advanced Nanomaterials for Point of Care Diagnosis and Therapy provides an overview of technological and emerging novel trends in how point-of-care diagnostic devices are designed, miniaturized built, and delivered at different healthcare set ups. It describes the significant technological advances in fundamental diagnostic components and recent advances in fully integrated devices designed for specific clinical use. The book covers state-of-the-art fabrication of advances materials with broad spectrum therapeutic applications. It includes drug delivery, biosensing, bioimaging and targeting, and outlines the development of inexpensive, effective and portable in vitro diagnostics tools for any purpose that can be used onsite. Sections also discuss drug delivery, biosensing, bioimaging and targeting and various metal, metal oxide and non-metal-based nanomaterials that are developed, surface modified, and are being explored for diagnosis, targeting, drug delivery, drug release and imaging. The book concludes with current needs and future challenges in the field. Outlines the needs and challenges of point-of-care diagnostics Describes the fundamentals of application of nanomaterials as interesting building blocks for biosensing Overviews the different detection methods offered by using nanomaterials Explains the advantages and drawbacks of nanomaterial-based sensing strategies Describes the opportunities offered by technology as a cost-efficient biosensing platform Bioinformatics allows researchers to answer biological questions with advanced computational methods which involves the application of statistics and mathematical modeling. Structural bioinformatics enables the prediction and analysis of 3D structures of

macromolecules while Computer Aided Drug Designing (CADD) assists scientists to design effective active molecules against diseases. However, the concepts in structural bioinformatics and CADD can be complex to understand for students and educated laymen. This quick guideline is intended as a basic manual for beginner students and instructors involved in bioinformatics and computational chemistry courses. Readers will learn the basics of structural bioinformatics, primary and secondary analysis and prediction, structural visualization, structural analysis and molecular docking. Therefore, the book is a useful handbook for aspiring scholars who wish to learn the basic concepts in computational analysis of biomolecules. Phytochemicals as Lead Compounds for New Drug Discovery presents complete coverage of the recent advances in the discovery of phytochemicals from medicinal plants as models to the development of new drugs and chemical entities. Functional bioactive compounds of plant origin have been an invaluable source for many human therapeutic drugs and have played a major role in the treatment of diseases around the world. These compounds possess enormous structural and chemical diversity and have led to many important discoveries. This book presents fundament concepts and factors affecting the choice for plant-based products, as well as recent advances in computer-aided drug discovery and FDA drug candidacy acceptance criteria. It also details the various bioactive lead compounds and molecular targets for a range of life-threatening diseases including cancer, diabetes, and neurodegenerative diseases. Written by a global team of experts, Phytochemicals as

Lead Compounds for New Drug Discovery is an ideal resource for drug developers, phytochemists, plant biochemists, food and medicinal chemists, nutritionists and toxicologists, chemical ecologists, taxonomists, analytical chemists, and other researchers in those fields. It will also be very valuable to professors, students, and researchers in this domain. Presents fundamental concepts and factors affecting choice for plant-based products Details the FDA drug candidacy acceptance criteria, including bottlenecks and way forward Highlights recent advances in computational-based drug discovery Focuses on the discovery of new drugs and potential druggable targets for the treatment of chronic diseases of world importance This volume constitutes the refereed proceedings of the 12th International Conference on Hybrid Artificial Intelligent Systems, HAIS 2017, held in La Rioja, Spain, in June 2017. The 60 full papers published in this volume were carefully reviewed and selected from 130 submissions. They are organized in the following topical sections: data mining, knowledge discovery and big data; bioinspired models and evolutionary computing; learning algorithms; visual analysis and advanced data processing techniques; data mining applications; and hybrid intelligent applications. This book encapsulates and occupies recent advances and state-of-the-art applications of nature-inspired computing (NIC) techniques in the field of bioinformatics and computational biology, which would aid medical sciences in various clinical applications. This edited volume covers fundamental applications, scope, and future perspectives of NIC techniques in bioinformatics including genomic profiling, gene expression data classification, DNA

computation, systems and network biology, solving personalized therapy complications, antimicrobial resistance in bacterial pathogens, and computer-aided drug design, discovery, and therapeutics. It also covers the role of NIC techniques in various diseases and disorders, including cancer detection and diagnosis, breast cancer, lung disorder detection, disease biomarkers, and potential therapeutics identifications. This volume provides protocols for computational, statistical, and machine learning methods that are mainly applied to the study of metabolic engineering, synthetic biology, and disease applications. These techniques support the latest progress in cross-disciplinary research that integrates the different scales of biological complexity. The topics covered in this book are geared toward researchers with a background in engineering, computational analytical, and modeling experience and cover a broad range of topics in computational and machine learning approaches. Written in the highly successful Methods in Molecular Biology series format, chapters include introductions to their respective topics, lists of the necessary materials and reagents, step-by-step, readily reproducible laboratory protocols, and tips on troubleshooting and avoiding known pitfalls. Comprehensive and practical, Computational Biology and Machine Learning for Metabolic Engineering and Synthetic Biology is a valuable resource for any researcher or scientist who wants to learn more about the latest computational methods and how they are applied toward the understanding and prediction of complex biology. Chemical and Biochemical Approaches for the Study of Anesthetic Function, Part A, Volume 602

assembles new information on our understanding of anesthesia. This latest release in the series includes sections on how physical accuracy leads to biological relevance, best practices for simulating ligand-gated ion channels interacting with general anesthetics, computational approaches for studying voltage-gated ion channels modulation by general anesthetics, anesthetic parameterization, pharmacophore QSAR, QM, ONIOM, and kinetic modeling of electrophysiology data. We have selected the primary experts to write about each approach This provides one-stop shopping for all the means of addressing this complex question Anesthesia is enormously important as almost everybody receives it at some point This ASI brought together a diverse group of experts who span virology, biology, biophysics, chemistry, physics and engineering. Prominent lecturers representing world renowned scientists from nine (9) different countries, and students from around the world representing eighteen (18) countries, participated in the ASI organized by Professors Joseph Puglisi (Stanford University, USA) and Alexander Arseniev (Moscow, RU). The central hypothesis underlying this ASI was that interdisciplinary research, merging principles of physics, chemistry and biology, can drive new discovery in detecting and fighting chemical and bioterrorism agents, lead to cleaner environments and improved energy sources, and help propel development in NATO partner countries. At the end of the ASI students had an appreciation of how to apply each technique to their own particular research problem and to demonstrate that multifaceted approaches and new technologies are needed to solve the biological challenges of our time. The

course succeeded in training a new generation of biologists and chemists who will probe the molecular basis for life and disease. The five volume set LNCS 7663, LNCS 7664, LNCS 7665, LNCS 7666 and LNCS 7667 constitutes the proceedings of the 19th International Conference on Neural Information Processing, ICONIP 2012, held in Doha, Qatar, in November 2012. The 423 regular session papers presented were carefully reviewed and selected from numerous submissions. These papers cover all major topics of theoretical research, empirical study and applications of neural information processing research. The 5 volumes represent 5 topical sections containing articles on theoretical analysis, neural modeling, algorithms, applications, as well as simulation and synthesis. This book publishes the best papers accepted and presented at the 3rd edition of the International Conference on Advanced Intelligent Systems for Sustainable Development Applied to Agriculture, Energy, Health, Environment, Industry, Education, Economy, and Security (AI2SD'2020). This conference is one of the biggest amalgamations of eminent researchers, students, and delegates from both academia and industry where the collaborators have an interactive access to emerging technology and approaches globally. In this book, readers find the latest ideas addressing technological issues relevant to all areas of the social and human sciences for sustainable development. Due to the nature of the conference with its focus on innovative ideas and developments, the book provides the ideal scientific and brings together very high-quality chapters written by eminent researchers from different disciplines, to discover the most recent

developments in scientific research. Encyclopedia of Bioinformatics and Computational Biology: ABC of Bioinformatics combines elements of computer science, information technology, mathematics, statistics and biotechnology, providing the methodology and in silico solutions to mine biological data and processes. The book covers Theory, Topics and Applications, with a special focus on Integrative –omics and Systems Biology. The theoretical, methodological underpinnings of BCB, including phylogeny are covered, as are more current areas of focus, such as translational bioinformatics, cheminformatics, and environmental informatics. Finally, Applications provide guidance for commonly asked questions. This major reference work spans basic and cutting-edge methodologies authored by leaders in the field, providing an invaluable resource for students, scientists, professionals in research institutes, and a broad swath of researchers in biotechnology and the biomedical and pharmaceutical industries. Brings together information from computer science, information technology, mathematics, statistics and biotechnology Written and reviewed by leading experts in the field, providing a unique and authoritative resource Focuses on the main theoretical and methodological concepts before expanding on specific topics and applications Includes interactive images, multimedia tools and crosslinking to further resources and databases This eBook is a collection of articles from a Frontiers Research Topic. Frontiers Research Topics are very popular trademarks of the Frontiers Journals Series: they are collections of at least ten articles, all centered on a particular subject. With their unique mix of varied contributions from

Original Research to Review Articles, Frontiers Research Topics unify the most influential researchers, the latest key findings and historical advances in a hot research area! Find out more on how to host your own Frontiers Research Topic or contribute to one as an author by contacting the Frontiers Editorial Office: frontiersin.org/about/contact. De Novo Enzyme Design, the newest volume in the Methods in Enzymology series, continues the legacy of this premier serial with quality chapters authored by leaders in the field. This volume includes the design of metal binding maquettes, insertion of non-natural cofactors, Cu metallopeptides, non-covalent interactions in peptide assemblies, peptide binding and bundling, heteronuclear metalloenzymes, florinated peptides, De Novo imaging agents, and protein-protein interaction. Continues the legacy of this premier serial with quality chapters on de novo enzyme design Represents the newest volume in the Methods in Enzymology series, providing premier, quality chapters authored by leaders in the field Ideal reference for those interested in the study of enzyme design that looks at both structure and mechanism Drug repositioning is the process of identifying new indications for existing drugs. At present, the conventional de novo drug discovery process requires an average of about 14 years and US$2.5 billion to approve and launch a drug. Drug repositioning can reduce the time and cost of this process because it takes advantage of drugs already in clinical use for other indications or drugs that have cleared phase I safety trials but have failed to show efficacy in the intended diseases. Historically, drug repositioning has been realized through serendipitous clinical

observations or improved understanding of disease mechanisms. However, recent technological advances have enabled a more systematic approach to drug repositioning. This eBook collects 16 articles from 112 authors, providing readers with current advances and future perspectives of drug repositioning. Ussery. This detailed book examines the main methods to study mammalian monoamine oxidases (MAOs), ranging from cell biology to computational chemistry. Beginning with techniques on how to obtain pure samples of MAO A and MAO B, the volume continues by covering assays and techniques used to measure MAO enzymatic activity and perform inhibition studies, methods to address cellular localization and function of MAOs, either in cell lines or in animal models, as well as computational methods applied to rational drug design approaches that are used to develop new MAO inhibitors. Written for the highly successful Methods in Molecular Biology series format, chapters include introductions to their respective topics, lists of the necessary materials and reagents, step-by-step and readily reproducible laboratory protocols, and tips on troubleshooting and avoiding known pitfalls. Authoritative and practical, Monoamine Oxidase: Methods and Protocols serves as a vital resource for scientists who are interested in studying MAOs and other similar amine oxidase enzymes. This book constitutes the refereed proceedings of the 22nd International Conference on Applications of Evolutionary Computation, EvoApplications 2019, held in Leipzig, Germany, in April 2019, co-located with the Evo*2019 events EuroGP, EvoCOP and EvoMUSART. The 44 revised full papers presented were carefully reviewed and selected from 66

submissions. They were organized in topical sections named: Engineering and Real World Applications; Games; General; Image and Signal Processing; Life Sciences; Networks and Distributed Systems; Neuroevolution and Data Analytics; Numerical Optimization: Theory, Benchmarks, and Applications; Robotics. In Silico Chemistry and Biology: Current and Future Prospects provides a compact overview on recent advances in this highly dynamic branch of chemistry. Various methods of protein modelling and computer-assisted drug design are presented, including fragment- and ligand-based approaches. Many successful practical applications of these techniques are demonstrated. The authors also look to the future and describe the main challenges of the field. Recent studies have identified the Class B g-protein coupled receptor (GPCR) pituitary adenylate cyclase activating polypeptide type 1 (PAC1R) as a key component in physiological stress management. Over-activity of neurological stress response systems due to prolonged or extreme exposure to traumatic events has led researchers to investigate PAC1R inhibition as a possible treatment for anxiety disorders such as post-traumatic stress disorder (PTSD). In 2008, Beebe and coworkers identified two such small molecule hydrazide antagonists and a general pharmacaphore for PAC1R inhibition. However, a relative dearth of information about Class B GPCRs in general, and PAC1R in specific, has significantly hindered progress toward the development of small molecule antagonists of PAC1R. The recent crystallization of the homologically similar glucagon receptor (GCGR) by Siu and coworkers in 2013, also a Class B receptor, has provided an experimentally

resolved template from which to base computationally derived models of PAC1R. Initially, this research was focused towards synthesizing small molecule antagonists for PAC1R which were to be biologically screened via a qualitative western blot assay followed by a radioisotope binding assay for those hydrazides exhibiting down-stream signaling inhibitory capabilities. However, the resolution of the GCGR crystal structure shifted research objectives towards developing a homology model of PAC1R and evaluating that computationally created model with Beebe's known small molecule antagonists. Created using academic versions of on-line resources including UniProtKB, Swiss-Model and Maestro, a homology model for PAC1R is presented here. The model is validated and evaluated for the presence of conserved Class B GPCR residues and motifs, including expected disulfide bridges, a conserved tyrosine residue, a GWGxP motif, a conserved glutamic acid residue and the extension of the transmembrane helix 1 (TM1) into the extra-cellular domain. Having determined this virtual PAC1R an acceptable model, ligand docking studies of known antagonists to the receptor were undertaken using AutoDock Vina in conjunction with AutoDock Tools and PyMol. Computational docking results were evaluated via comparison of theoretical binding affinity results to Beebe's experimental data. Based on hydrogen bonding capabilities, several residues possibly key to the ligand-receptor binding complex are identified and include ASN 240, TYR 241 and HIST 365. Although the docking software does not identify non-bonding interactions other than hydrogen-bonding, the roles of additional proposed binding pocket residues are discussed in terms of

hydrophobic interactions, [pi]-[pi] interactions and halogen bonding. These residues include TYR 161, PHE 196, VAL 203, PHE 204, ILE 209, LEU 210, VAL 237, TRP 297, PHE 362 and LEU 386. Although theoretical in nature, this reported homology modeling and docking exercise details a proposed binding site that may potentially further the development of drugs designed for the treatment of PTSD.