

More than 50% of deaths worldwide are linked to chronic inflammatory disorders, including cancer, cardiovascular disease, dementia, stroke, and diabetes. This makes inflammation one of the most prevalent target processes and reactions in the human body [1,2]. A tissue injury triggers the body's inflammatory response, which leads to inflammatory diseases. Acute inflammation that is not regulated leads to chronic inflammation, which increases the risk of cancer, neurological disorders, and autoimmune diseases in the body [3,4]. The development of gastrointestinal illnesses is strongly influenced by the gut microbiota [5,6]. The link between the gut microbiota and health is becoming increasingly obvious. The diversity and quantity of microbiota is crucial and essential for human welfare. Age, stress, antibiotic use, poor nutrition, and other factors can cause dysbiosis, i.e., imbalance, which can lead to inflammation and the progression of chronic diseases. Chronic inflammatory bowel diseases, such as Crohn's disease and ulcerative colitis, are caused by gut dysbiosis [6,7].

Many signaling substances that are involved in the intricate pathophysiological process of inflammation are released by leucocytes, macrophages, and mast cells as they go through various biological responses. Examples of these include the production of inflammatory mediators like nitric oxide, prostaglandin (PG, PGE₂), and tumor necrosis factor (TNF-), as well as phagocytic uptake [8,9]. These elements contribute to the extravasation of fluids and proteins, and leucocyte accumulation at the inflammatory site, which causes edema to develop [10]. It is also generally acknowledged that cytokines, which are produced by the immune system or central nervous system cells, may directly sensitize the peripheral nociceptors [11].

Bradykinins, TNF, and interleukins (ILs), as well as PGs, all affect how well free nerve terminals can transduce signals, which results in hyperalgesia and pain. The pyrogens that an infection creates, such as ILs, TNF-, and interferon, are what drive the hypothalamus to produce PGE₂ and boost its internal temperature, which is what causes a fever. Inflammation is followed by a fever or pyrexia [12]. Increased prostaglandin synthesis has been associated with fever, discomfort, and inflammation [13]. As a result, analgesic and antipyretic characteristics are anticipated in the majority of anti-inflammatory medications [14,15]. Inflammation is also related to cancer; the growth and proliferation of tumors are significantly influenced by inflammation.

To relieve pain, fever, and inflammation, while also protecting the cardiovascular system, non-steroidal anti-inflammatory drugs are used. However, the side effects of currently available anti-inflammatory medications, which include gastric ulcers, renal damage, bronchospasms, and cardiac problems, have limited their usage [16,17]. Due to the adverse effects of non-steroidal anti-inflammatory drugs and opioids, there is a high demand for new drugs with fewer or no side effects. Finding novel drugs takes years of effort and funding, as well as a lot of hard work.

Over the past 100 years, pharmaceutical industry-discovered drugs have had a significant impact on many facets of our culture and the practice of medicine. For many years, the method of drug development relied on ethnobotanical expertise and was target- and mechanism-agnostic.

The process of finding new drugs usually includes identifying targets and creating effective pharmacological molecules to target them. Despite decades of experimental



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research in this field, around 96% of medication development projects fail. Likewise, the pharmaceutical business experiences a great deal of pressure due to the high attrition rate of drug candidates during the drug discovery process.

It has always been an important scientific topic to investigate the biological activities of newly synthesized compounds. This is connected to the never-ending interest in drug discovery or in finding a molecule with certain “useful” properties that can affect a function or process in the human body. Selecting the most promising targets from the huge pool of diverse potential candidates is one of the major difficulties of the post-genome era [18]. The choice of “the right” biological target may be the most crucial one made in pharmacological research and development [19]. This group includes biotherapeutics as well as small molecules.

Computational technologies and big data are becoming effective in predicting biological target drug ability and the drug-likeness of new therapeutic agents, as experimental research approaches become less common [20]. The multiple stages that must be completed between the decision to choose a target and the start of clinical trials to prove efficacy in humans typically follow a clear-cut pattern. After screening and hit identification, optimization rounds based on pharmacological and toxicological testing are conducted, and then pharmaceutical development and production take place.

There are a number of limitations to the systematic use of experiments in the drug discovery process. A few of these elements are the frequency of the newly synthesized compounds, the quantitative restrictions of tissue samples, and the need to restrict animal testing. In this situation, it is conceivable to presume that *in silico* computer models, which are both an excellent supplement and a practical replacement for biological investigations, may be used to replace biological investigations [21–23]. A drug candidate needs to reach its pharmacological target within the body, reach the right concentration at the site of action, and stay there long enough to be utilized as a medicine. Due to their poor pharmacokinetics and bioavailability, many promising biologically active compounds that are intended for use as medications fail. *In silico* research has made it possible to identify new drugs through target identification and validation, contributing to ongoing advancements in the drug discovery and development process. Several methods are employed to assess possible compounds with drug-like characteristics, including quantitative structure–activity and structure–property relationship models and *in silico* screening, which calculate anticipated biological effects, solubility, sufficient oral bioavailability, synthetic accessibility, intestinal absorption, and blood–brain barrier penetration [24–27].

Established through analyses of the physicochemical or structural characteristics of small-scale organic drugs or drug candidates, the concept of drug-likeness has been widely used to screen out compounds with undesirable properties, particularly those with poor ADMET (absorption, distribution, metabolism, excretion, and toxicity) profiles [23,28–33]. With varying goals, new computational algorithms and analytical techniques are being created as the volume of biological data continues to increase. This field covers a broad range of topics, including medication toxicity prediction and protein structure prediction. The majority of semi-empirical force-field- and quantum-mechanics-based molecular modeling methods demonstrate proven accuracy in analyzing small structural datasets, while statistics-based methods like machine learning, QSAR, and other specialized data analytics methods are robust for large-scale data analysis [34].

As a conclusion, modern drug discovery methodologies and technologies have had a significant impact on the increasing number of first-in-class pharmaceuticals approved in recent years, in line with the pharmaceutical industry’s drive to find breakthrough therapies [35,36].

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