Tropical Journal of Pharmaceutical Research September 2017; 16 (9): 2297-2302 ISSN: 1596-5996 (print); 1596-9827 (electronic) © Pharmacotherapy Group, Faculty of Pharmacy, University of Benin, Benin City, 300001 Nigeria. All rights reserved.

> Available online at http://www.tjpr.org http://dx.doi.org/10.4314/tjpr.v16i9.35

Review Article

Structure-based drug design approach to target toll-like receptor signaling pathways for disease treatment

Mohammed Alaidarous

Department of Medical Laboratory Sciences, College of Applied Medical Sciences, Majmaah University, Al-Majmaah 11952, PO Box 66, Saudi Arabia

*For correspondence: Email: m.alaidarous@mu.edu.sa; Tel: +966164042900

Sent for review: 27 April 2017

Revised accepted: 8 August 2017

Abstract

Toll-like receptor (TLR) signaling pathways are the first line of defence against many microbial organisms. The question of how TLRs recognize endogenous ligands remains controversial. Several studies have shown that TLRs are implicated in the pathogenesis of autoimmune diseases such as systemic lupus erythematosus and rheumatoid arthritis. Therefore, in structure-based drug design, TLRs are now viewed as potential therapeutic targets in the treatment of autoimmune diseases. This review shows how proteins, specifically TLRs, are used as therapeutic targets to design inhibitors (drugs) using the structure-based drug design approach for disease treatment.

Keywords: Structure-based drug design, Toll-like receptors, Autoimmune diseases, Endogenous ligands, X-ray crystallography, Homology modeling

Tropical Journal of Pharmaceutical Research is indexed by Science Citation Index (SciSearch), Scopus, International Pharmaceutical Abstract, Chemical Abstracts, Embase, Index Copernicus, EBSCO, African Index Medicus, JournalSeek, Journal Citation Reports/Science Edition, Directory of Open Access Journals (DOAJ), African Journal Online, Bioline International, Open-J-Gate and Pharmacy Abstracts

INTRODUCTION

Structure-based drug design has been a thriving field since the human genome project was completed. Advanced developments in proteomics. transcriptomics and structural genomics helped in improving the computational tools used for structure-based drug design. Potential drug targets can now be mined via the use of bioinformatics tools. The genes for these targets can then be cloned, and protein products can be synthesized and purified for use. The three-dimensional structures of proteins used to determine potential drug targets are derived through a number of techniques, and the efficiency of these techniques has improved in recent years [1]. Below, the principles behind choosing drug targets and determining the threedimensional structures of those targets will be reviewed. In addition, some receptor molecules

from the TLR signaling pathways that have been targeted by drugs will also be reviewed.

Choosing a drug target

The process of designing a drug involves a series of steps. The first step is the identification of a drug target. This step is typically based on the biochemical and biological characteristics of the target molecule. A target molecule should be uniquely associated with a certain human disease or a disease-causing pathogen. For example, in targeting a pathogen, the molecule chosen from the pathogen as a target should be unique in that no other molecules in the pathogen can perform its function [2]. The chosen molecule should be essential, and its absence should guarantee the death of the disease-causing organism [2]. When these conditions are met, targeting of these molecules by drugs of interest will succeed. Typically, drugs



Figure 1: Structure-based drug design pipeline modified from Grey and Thompson [3].

 Table 1: Examples of potential targets whose three-dimensional structures were determined using NMR, x-ray crystallography or homology modeling

Name of target	Technique	Reference
Human transforming growth factor alpha	NMR	[7]
HIV-1 reverse transcriptase	NMR	[8]
Vascular endothelial growth factor	NMR	[9]
Interleukin-13	NMR	[10]
Amyloidogenic beta 2-microglobulin	X-ray crystallography	[11]
Brucella methionyle-tRNA-synthetase	X-ray crystallography	[12]
Toll-interleukin 1 receptor (TIR) domain containing adaptor protein	X-ray crystallography	[13]
Human epidermal growth factor receptor 2	X-ray crystallography	[14]
Abl kinase	Homology modeling	[15]
Cyclin-dependent kinase 2	Homology modeling	[16]
Lymphocytic-specific kinase	Homology modeling	[17]
Tyrosine kinase	Homology modeling	[18]

of interest (or inhibitors) are made from protein molecules, but lately, RNA transcripts have been used as potential drug leads [2]. Examples of drugs and their target molecules will be discussed later in the review. Figure 1 shows a general pipeline for choosing a target for a structure-based drug design.

Obtaining the structure of the target molecule

The second step involves obtaining the structural details of the target molecule. These structural details can be obtained by using structural determination techniques such as nuclear magnetic resonance (NMR), X-ray crystallography or homology modeling. The first two methods require the expression and purification of the target molecule, after which sophisticated equipment and laboratory procedures are used to derive the threedimensional structure. For X-ray crystallography, the sample must be crystallized while NMR uses the liquid phase of the sample [4,5]. When homology modeling is used, the DNA sequence of the target molecule is used to identify homologous molecules with high levels of DNA sequence similarity and available threedimensional structures. Those three-dimensional structures are then used to determine the likely structure of the chosen target molecule [4,5]. For example, MODELLER is a famous computational software program used for homology-based protein structural modeling [6]. Table 1 shows examples of potential targets whose structures

were determined using NMR, X-ray crystallography or homology modeling.

The identification of the target molecule binding site is the next step in this process. This is a site at which a ligand can bind to a target molecule and thus alter its function. A huge number of chemical molecules obtained from available databases are then docked into the target molecule binding site using docking software. Chemical compounds with the higher scores are then optimized by the addition of small groups, such as carbonyl and benzene rings, to achieve the maximum interaction scores. Successful chemical compounds (drugs) may be synthesized and then characterized in a laboratory for use in in vivo studies before entering into clinical trials [19].

Protease inhibitors

A number of protease inhibitors have been designed using the structure-based drug design pipeline shown in Figure 1. Examples include Agenerase, which has the commercial names Amprenavir and Viracept and is also known as Nelfinavir [20]. Other agents produced via structure-based drug design include Relenza (Zanamivir), which was designed to inhibit the enzyme neuraminidase; Minitab mesylate (commercially known as Glivec), which was designed to inhibit Abelson tyrosine kinase, and Tomudex, which was designed to inhibit thymidylate synthase [21]. Other inhibitors have been developed against a number of enzymes,

Trop J Pharm Res, September 2017; 16(9): 2298

such as tyrosine phosphatase, β-lactamase, carbonic anhydrase and DNA gyrase. Furthermore, Iressa and Tarvesa are used to inhibit tyrosine kinase. Both drugs were used for lung cancer treatment, and Tarvesa is also used to treat pancreatic cancer [22]. In addition, Isoniazid is used in the treatment of Mycobacterium tuberculosis and was discovered via structure-based design methods. This drug inhibits the InhA's ability to facilitate the synthesis of mycolic acid, an important component of the Mycobacterium tuberculosis cell wall [23]. Carfilzomib and Bortezomib are proteasome inhibitors used to treat refractory multiple myeloma [24]. Lamivudine and Telbivudine inhibit the action of reverse transcriptase, a very important enzyme in hepatitis B virus (HBV) DNA replication [25]. Entecavir, an inhibitor of viral polymerase, is also used in HBV treatment [26].

Toll-like receptors (TLRs)

Toll-like receptors are a group of innate immunity receptors found in the cells of the immune system, such as the epithelial and endothelial cells of mucosal linings, macrophages, neutrophils, dendritic cells and Bcells [27]. These toll-like receptors recognize signature elements in pathogens, such as the bacterial lipopolysaccharide, single-stranded RNA, lipoproteins and unmethylated CpG DNA [27]. This immunity shields the body against pathogenic microorganisms by initiating inflammation to enable the body to elicit the correct immune response [28]. However, unregulated innate immune responses can lead to autoimmune disorders, in which the body attacks itself, causing organ damages [27]. In humans, various families of TLRs have been identified and due to their importance in defense against pathogens, they have been viewed as potential drug targets in the treatment of diseases such as autoimmune disorders [29].

TLR agonists

These are substances that work in synergy with TLRs to enhance their functioning. Imiquimod is a drug used for the treatment of diseases that target TLR signaling pathways [30]. Specifically, it targets the TLR7–MYD88-dependent pathway and causes the secretion of the proinflammatory cytokine IFN. In addition, Imiquimod is used against viral particles and tumor cells. Therefore, it is quite crucial in cancer therapy. It also induces the release of tumor necrosis factor (TNF) and interleukin-6 (IL-6). Imiquimod has been proven to cause the destruction of cancerous cells on the skin. Hence, it is used in the treatment of genital warts, melanomas and

hepatitis C [31]. Other imdazoquinolines are used in the treatment of chronic lymphocytic lymphoma [32]. Single-stranded RNA agonists are used to target TLR7 and TLR8. 7deazaguanosine is used to activate certain TLRs by replacing a guanosine residue in an RNA ligand and thus inducing responses mediated by T-cells that target tumors [33]. All these molecules activate TLR pathways to facilitate the activation of dendritic cells. These dendritic cells then reduce the suppressive abilities of the Tcells, resulting in an antitumor response [30-33].

There is a small agent known as "852A" that is used as an agonist of TLR7. It activates dendritic cells to trigger the release IFN α , a molecule with antitumor activity. In addition to cancer treatment, 852A is used in treating chronic lymphocytic leukemia. 852A causes cells displaying leukemic antigens to become more susceptible to cytokines [34].

Alternative anticancer drugs called CpG-based oligonucleotides are used to target the TLR9 pathway. These molecules are referred to as immune modulatory oligonucleotides. They are similar to bacterial DNA and hence act as ligands for TLR9 [35]. Agatolimod was developed to tackle hepatitis B infections, allergies, renal cancer and asthma [36]. CpG 7909 is used to treat patients with chronic lymphocytic leukemia. These oligonucleotides have shown elevated responses when used in combination with other drug agents that are already on the market [37].

Immunomodulation adjuvants MGN-1703 and MGN-1706, which contain noncoding DNA, were used as TLR9 agonists and thus function as anticancer agents. MGN-1703 is effective against colorectal and prostate cancer during the preclinical stages. IPH 3102 was developed for the treatment of breast cancer because it triggers NF- κ B and INF-1, leading to the destruction of breat cancer cells [38].

ISS1018 is a type of compound known as an immunostimulatory sequence. Such sequences stimulate the TLR9 pathway, eliciting responses on the part of T-cells and the production of memory cells due to the activation of type 1 T helper (Th1) cells. ISS1018 triggers the release of immunoglobulin and interferon (IFN α) by B-cells and also causes dendritic cells to release TNF α , interleukin-12 and interferon- β [39]. Immunoregulators, such as IRS-954, inhibit cascade activated by TLR7 and TLR9 to treat systemic lupus erythematosus [40].

TLR antagonists

TLR antagonists are used to suppress the signaling of TLR pathways in cases of overactive immune systems. These antagonists are used in the treatment of autoimmune disorders such as rheumatoid arthritis and systemic lupus erythematosus. Currently, these diseases are treated with antimalarial compounds such as hydroxychloroguine which acts as a TLR9 antagonist [41]. IRS-954 is a molecule that slows down the production of IFNa, thus combating systemic lupus erythematosus [40]. IMO3100 is used to treat multiple sclerosis psoriasis in addition to systemic lupus erythematosus and rheumatoid arthritis. It works by blocking TLR7 and TLR9 [42]. In addition, IMO2125 stimulates TLRs and is used in the treatment of hepatitis C infections, melanoma and other cancers. Azithromycin is used in the treatment of cystic fibrosis. This drug agent suppresses the activation of NF-kB, resulting in the release of inflammatory cytokines in the trachea, and it also significantly reduces the levels of TNF in the epithelial cells of the airways [39,43].

Ibudilast (Av411) has been found to suppress pain and treat the withdrawal symptoms associated with drug addiction. It slows down the production of TNFa and IL-6 [44]. IMO8400 is used in the treatment of dermatomyositis because it reduces the excessive stimulation of various TLRs [45]. Eritoran is another antagonist that is currently being investigated for use in the treatment of sepsis. It has been found to disable arise the responses that due to lipopolysaccharides' activation of TLRs [46]. Belimumab has been used to improve the conditions of those suffering from systemic lupus erythematosus. It is a human monoclonal antibody that prevents the activation of soluble Bcells, resulting in the programmed cell death of autoreactive B lymphocytes [47].

CONCLUSION

Structure-based drug design provides an excellent platform for the identification of novel inhibitors of target molecules to fight diseases. With the continuous advancement of X-ray crystallography, NMR and molecular homology modeling, new and important molecules will be targeted to fight diseases. Significant challenges involved in dealing with target molecules, such as membrane proteins, must be addressed in future studies. Current efforts in structure-based drug design will undoubtedly lead to the development of significant therapeutics to combat diseases.

DECLARATIONS

Acknowledgement

I would like to thank the College of Applied Medical Sciences at Majmaah University for the support in writing this manuscript. This work did not receive any specific grant from funding agencies in the public, commercial or not-forprofit sectors.

Conflict of Interest

No conflict of interest associated with this work.

Contribution of Authors

The author declares that this work was done by him and all liabilities pertaining to claims relating to the content of this article will be borne by him.

Open Access

This is an Open Access article that uses a funding model which does not charge readers or their institutions for access and distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/ 4.0) and the Budapest Open Access Initiative (http://www.budapestopenaccessinitiative.org/rea d), which permit unrestricted use, distribution, and reproduction in any medium, provided the original work is properly credited.

REFERENCES

- Lounnas V, Ritschel T, Kelder J, McGuire R, Bywater RP, Foloppe N. Current progress in Structure-Based Rational Drug Design marks a new mindset in drug discovery. Comput Struct Biotechnol J 2013; 5.
- 2. Anderson AC. The process of structure-based drug design. Chem Biol 2003; 10(9): 787-797.
- Grey JL, Thompson DH. Challenges and opportunities for new protein crystallization strategies in structure-based drug design. Expert Opin Drug Discov 2010; 5(11): 1039-1045.
- Wishart D. NMR spectroscopy and protein structure determination: applications to drug discovery and development. Curr Pharm Biotechnol 2005; 6(2): 105-120.
- Wieman H, Tøndel K, Anderssen E, Drabløs F. Homology-based modelling of targets for rational drug design. Mini Rev Med Chem 2004; 4(7): 793-804.
- 6. Webb B, Sali A. Comparative Protein Structure Modeling Using MODELLER. Curr Protoc Bioinformatics 2014; 47.
- 7. Kline TP, Brown FK, Brown SC, Jeffs PW, Kopple KD, Mueller L. Solution structures of human transforming

Trop J Pharm Res, September 2017; 16(9): 2300

growth factor alpha derived from 1H NMR data. Biochemistry 1990; 29: 7805-7813.

- Chong P, Sebahar P, Youngman M, Garrido D, Zhang H, Stewart EL, Nolte RT, Wang L, Ferris RG, Edelstein M, et al. Rational design of potent non-nucleoside inhibitors of HIV-1 reverse transcriptase. J Med Chem 2012; 55(23): 10601-10609.
- Pan B, Li B, Russell SJ, Tom JY, Cochran AG, Fairbrother WJ. Solution structure of a phage-derived peptide antagonist in complex with vascular endothelial growth factor. J Mol Biol 2002; 316(3): 769-787.
- Eisenmesser EZ, Horita DA, Altieri AS, Byrd RA. Solution structure of interleukin-13 and insights into receptor engagement. J Mol Biol 2001; 310(1): 231-241.
- Domanska K, Vanderhaegen S, Srinivasan V, Pardon E, Dupeux F, Marquez JA, Giorgetti S, Stoppini M, Wyns L, Bellotti V, et al. Atomic structure of a nanobody-trapped domain-swapped dimer of an amyloidogenic beta2microglobulin variant. Proc Natl Acad Sci U S A 2011; 108(4): 1314-1319.
- Ojo KK, Ranade RM, Zhang Z, Dranow DM, Myers JB, Choi R, Hewitt SN, Edwards TE, Davies DR, Lorimer D, et al. Brucella melitensis Methionyl-tRNA-Synthetase (MetRS), a Potential Drug Target for Brucellosis. PLoS One 2016; 11(8).
- 13. Valkov E, Stamp A, Dimaio F, Baker D, Verstak B, Roversi P, Kellie S, Sweet MJ, Mansell A, Gay NJ, et al. Crystal structure of Toll-like receptor adaptor MAL/TIRAP reveals the molecular basis for signal transduction and disease protection. Proc Natl Acad Sci U S A 2011; 108(36): 14879-14884.
- 14. Fu W, Wang Y, Zhang Y, Xiong L, Takeda H, Ding L, Xu Q, He L, Tan W, Bethune AN, et al. Insights into HER2 signaling from step-by-step optimization of anti-HER2 antibodies. MAbs 2014; 6(4): 978-990.
- Capdeville R, Buchdunger E, Zimmermann J, Matter A. Glivec (STI571, imatinib), a rationally developed, targeted anticancer drug. Nat Rev Drug Discov 2002; 1(7): 493-502.
- Davies TG, Tunnah P, Meijer L, Marko D, Eisenbrand G, Endicott JA, Noble ME. Inhibitor binding to active and inactive CDK2: the crystal structure of CDK2-cyclin A/indirubin-5-sulphonate. Structure 2001; 9(5): 389-397.
- 17. Zhu X, Kim JL, Newcomb JR, Rose PE, Stover DR, Toledo LM, Zhao H, Morgenstern KA. Structural analysis of the lymphocyte-specific kinase Lck in complex with non-selective and Src family selective kinase inhibitors. Structure 1999; 7(6): 651-661.
- Sawyer T, Boyce B, Dalgarno D, Iuliucci J. Src inhibitors: genomics to therapeutics. Expert Opin Investig Drugs 2001; 10(7): 1327-1344.
- Ferreira LG, Dos Santos RN, Oliva G, Andricopulo AD. Molecular docking and structure-based drug design strategies. Molecules 2015; 20(7): 13384-13421.
- Mahdi M, Szojka Z, Mótyán JA, Tőzsér J. Inhibition Profiling of Retroviral Protease Inhibitors Using an HIV-2 Modular System. Viruses 2015; 7(12): 6152-6162.

- Hada N, Netzer WJ, Belhassan F, Wennogle LP, Gizurarson S. Nose-to-brain transport of imatinib mesylate: A pharmacokinetic evaluation. Eur J Pharm Sci 2017; 102: 46-54.
- Noble ME, Endicott JA, Johnson LN. Protein kinase inhibitors: insights into drug design from structure. Science 2004; 303(5665): 1800-1805.
- Marrakchi H, Lanéelle G, Quémard A. InhA, a target of the antituberculous drug isoniazid, is involved in a mycobacterial fatty acid elongation system, FAS-II. Microbiology 2000; 146(2): 289-296.
- 24. Berenson A, Vardanyan S, David M, Wang J, Harutyunyan NM, Gottlieb J, Halleluyan R, Spektor TM, Udd KA, Eshaghian S, et al. Outcomes of multiple myeloma patients receiving bortezomib, lenalidomide, and carfilzomib. Ann Hematol 2017; 96(3): 449-459.
- 25. Yue-Meng W, Li YH, Wu HM, Yang J, Xu Y, Yang LH, Yang JH. Telbivudine versus lamivudine and entecavir for treatment-naive decompensated hepatitis B virusrelated cirrhosis. Clin Exp Med 2016; 17(2): 232-241.
- Shen H, Ding F, Wang Z, Sun F, Yu Y, Zhou J, Xu W, Ni J, Wang J, Yang Y. Comparison of Telbivudine and Entecavir Therapy on Nephritic Function and Drug Resistance in Patients with Hepatitis B Virus-Related Compensated Cirrhosis. Cell Physiol Biochem 2016; 40(1-2): 370-378.
- Pradhan VD, Das S, Surve P, Ghosh K. Toll-like receptors in autoimmunity with special reference to systemic lupus erythematosus. Indian J Hum Genet 2012; 18(2): 155-160.
- Maruyama K, Selmani Z, Ishii H, Yamaguchi K. Innate immunity and cancer therapy. Int Immunopharmacol 2011; 11(3): 350-357.
- 29. Achek A, Yesudhas D, Choi S. Toll-like receptors: promising therapeutic targets for inflammatory diseases. Arch Pharm Res 2016; 39(8): 1032-1049.
- Ueyama A, Yamamoto M, Tsujii K, Furue Y, Imura C, Shichijo M, Yasui K. Mechanism of pathogenesis of imiquimod-induced skin inflammation in the mouse: a role for interferon-alpha in dendritic cell activation by imiquimod. J Dermatol 2014; 41(2): 135-143.
- 31. Salazar LG, Lu H, Reichow JL, Childs JS, Coveler AL, Higgins DM, Waisman J, Allison KH, Dang Y, Disis ML. Topical Imiquimod Plus Nab-paclitaxel for Breast Cancer Cutaneous Metastases: A Phase 2 Clinical Trial. JAMA Oncol 2017.
- Hengge UR, Benninghoff B, Ruzicka T, Goos M. Topical immunomodulators--progress towards treating inflammation, infection, and cancer. Lancet Infect Dis 2001; 1(3): 189-198.
- Kore AR, Shanmugasundaram M, Barta TJ. Synthesis and substrate validation of cap analogs containing 7deazaguanosine moiety by RNA polymerase. Nucleosides Nucleotides Nucleic Acids 2010; 29(11): 821-830.
- Inglefield JR, Dumitru CD, Alkan SS, Gibson SJ, Lipson KE, Tomai MA, Larson CJ, Vasilakos JP. TLR7 agonist 852A inhibition of tumor cell proliferation is dependent

Trop J Pharm Res, September 2017; 16(9): 2301

on plasmacytoid dendritic cells and type I IFN. J Interferon Cytokine Res 2008; 28(4): 253-263.

- Gursel M, Gursel I. Development of CpG ODN Based Vaccine Adjuvant Formulations. Methods Mol Biol 2016; 1404: 289-298.
- Lu Z. Potential therapeutic interventions on toll like receptors for clinical applications. Research in pharmaceutical biotechnology 2010; 2(1): 7-13.
- 37. Zent CS, Smith BJ, Ballas ZK, Wooldridge JE, Link BK, Call TG, Shanafelt TD, Bowen DA, Kay NE, Witzig TE, et al. Phase I clinical trial of CpG oligonucleotide 7909 (PF-03512676) in patients with previously treated chronic lymphocytic leukemia. Leuk Lymphoma 2012; 53(2): 211-217.
- 38. Schmoll HJ, Wittig B, Arnold D, Riera-Knorrenschild J, Nitsche D, Kroening H, Mayer F, Andel J, Ziebermayr R, Scheithauer W. Maintenance treatment with the immunomodulator MGN1703, a Toll-like receptor 9 (TLR9) agonist, in patients with metastatic colorectal carcinoma and disease control after chemotherapy: a randomised, double-blind, placebo-controlled trial. J Cancer Res Clin Oncol 2014; 140(9): 1615-1624.
- Hennessy EJ, Parker AE, O'Neill LA. Targeting Toll-like receptors: emerging therapeutics? Nat Rev Drug Discov 2010; 9(4): 293-307.
- 40. Barrat FJ, Meeker T, Chan JH, Guiducci C, Coffman RL. Treatment of lupus-prone mice with a dual inhibitor of TLR7 and TLR9 leads to reduction of autoantibody production and amelioration of disease symptoms. Eur J Immunol 2007; 37(12): 3582-3586.

- 41. Rainsford KD, Parke AL, Clifford-Rashotte M, Kean WF. Therapy and pharmacological properties of hydroxychloroquine and chloroquine in treatment of systemic lupus erythematosus, rheumatoid arthritis and related diseases. Inflammopharmacology 2015; 23(5): 231-269.
- 42. Kandimalla ER, Bhagat L, Wang D, Yu D, Sullivan T, La Monica N, Agrawal S. Design, synthesis and biological evaluation of novel antagonist compounds of Toll-like receptors 7, 8 and 9. Nucleic Acids Res 2013; 41(6): 3947-3961.
- 43. Southern KW, Barker PM. Azithromycin for cyctic fibrosis. Eur Respir J 2004; 24(5): 834-838.
- 44. Ledeboer A, Hutchinson MR, Watkins LR, Johnson KW. Ibudilast (AV-411). A new class therapeutic candidate for neuropathic pain and opioid withdrawal syndromes. Expert Opin Investig Drugs 2007; 16(7): 935-950.
- 45. Benner L, Arbeit RD, Sullivan T. MO-8400, an Antagonist of Toll-like Receptors 7, 8, and 9, in Development for genetically Defined B-cell Lymphomas: safety and Activity in Phase 1 and Phase 2 Clinical Trials. Blood 2014; 124(21).
- 46. Opal SM, Laterre PF, Francois B, LaRosa SP, Angus DC, Mira JP, Wittebole X, Dugernier T, Perrotin D, Tidswell M, et al. Effect of eritoran, an antagonist of MD2-TLR4, on mortality in patients with severe sepsis: the ACCESS randomized trial. JAMA 2013; 309(11): 1154-1162.
- 47. Hui-Yuen, JS, Li XQ, Askanase AD. Belimumab in systemic lupus erythematosus: a perspective review. Ther Adv Musculoskelet Dis 2015; 7(4): 115-121.